



T.R.

NİĞDE ÖMER HALİSDEMİR UNIVERSITY
GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
DEPARTMENT OF AGRICULTURAL GENETIC ENGINEERING

ASSOCIATION MAPPING OF QUALITY TRAITS IN POTATO
(*Solanum tuberosum* L.)

MUHAMMAD NAEEM

February 2021

T.R.
NİĞDE ÖMER HALİSDEMİR UNIVERSITY
GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
DEPARTMENT OF AGRICULTURAL GENETIC ENGINEERING

ASSOCIATION MAPPING OF QUALITY TRAITS IN POTATO (*Solanum
tuberosum* L.)

MUHAMMAD NAEEM

Doctor of Philosophy Thesis

Supervisor

Prof. Dr. Mehmet Emin ÇALIŞKAN

February 2021

The study entitled “**ASSOCIATION MAPPING OF QUALITY TRAITS IN POTATO (*Solanum tuberosum* L.)**” and presented by Muhammad Naeem under the supervision of Prof. Dr. Mehmet Emin Çaliskan has been accepted as Doctoral thesis by the jury at the Department of Agricultural Genetic Engineering of Niğde Ömer Halisdemir University, Graduate School of Natural and Applied Sciences.

Head: Prof. Dr. Mehmet Emin Çaliskan, Niğde Ömer Halisdemir University, Ayhan Şahenk Faculty of Agricultural Sciences and Technologies, Department of Agricultural Genetic Engineering.

Member: Prof. Dr. Mehmet ARSLAN Erciyes Üniversitesi Ziraat Fakültesi Tarımsal Biyoteknoloji Böl.

Member: Prof. Dr. Sedat SERÇE, Niğde Ömer Halisdemir University, Ayhan Şahenk Faculty of Agricultural Sciences and Technologies, Department of Agricultural Genetic Engineering.

Member: Doç. Dr. Muhammet ŞAKİROĞLU Adana Alparslan Türkeş Üniversitesi Mühendislik Fakültesi Biyomühendislik Böl.

Member: Doç. Dr. Ufuk DEMİREL Niğde Ömer Halisdemir Ü. Tarım Bil. ve Tek. Fak. Tarımsal Gen. Müh. Böl.

CONFIRMATION:

This thesis has been found appropriate on this date of/...../2021 by the jury member above who have been designated by the Board of Directors of Graduate School of Natural and Applied Sciences and has been confirmed with the resolution of Board of Directors on/...../2021 and has been accepted by the decision numbered

.....

...../...../2021

Prof. Dr. Murat BARUT
MÜDÜR

DECLARATION

I certify that the thesis has been written by me and that, to the best of my knowledge and belief. All information presented as part of this thesis is scientific and in accordance with the academic rules. Any help I have received in preparing the thesis, and all sources used, have been acknowledged in the thesis.



MUHAMMAD NAEEM

SUMMARY

ASSOCIATION MAPPING OF QUALITY TRAITS IN POTATO (*Solanum tuberosum* L.)

NAEEM, Muhammad

Niğde Ömer Halisdemir University

Graduate School of Natural and Applied Sciences

Department of Agricultural Genetic Engineering

Supervisor : Prof. Dr. Mehmet Emin ÇALIŞKAN

February 2021, 313 pages

In potato (*Solanum tuberosum* L.) breeding, improved tuber quality traits have long been a critical goal. The aim of current study was to perform an association mapping (AM) to identify the SNPs in tetraploid potato panel of 192 genotypes, associated with twelve important tuber quality traits, using 25K SolCAP array. Phenotyping was performed using high throughput platforms like HPLC, coupled with stability analysis to reveal the stable genotypes. Bayesian clustering approach identifies four sub-populations assessed through STRUCTURE algorithm. Robust 13606 polymorphic SNP markers were used for LD and AM. LD analysis revealed a LD decay at 2.31 Mbps, reflecting breeding history of potato. AM was performed using linear mixed model (Q+K) with 2 polyploid gene actions revealing 215 and 430 significant SNPs with additive and general models, respectively. The identified SNPs have multifarious gene functions related to transcriptional regulation of starch biosynthesis, asparagine metabolism, carotenoid biosynthesis (*bch*), signal transduction transporters and transcription factors (*MYB*, *bHLH*, *bZIP*) involved in polyphenolic biosynthetic pathways, stress responses and suberin biosynthesis. The findings of this study will provide resources for genomics enabled breeding such as development of selection markers for quality traits in potato.

Keywords: Association mapping, SolCAP array, phenotyping, SNP, quality, breeding

ÖZET

PATATESTE (*Solanum tuberosum* L.) KALİTE ÖZELLİKLERİNİN İLİŞKİLENDİRME HARİTALANDIRMASI

NAEEM, Muhammad

Niğde Ömer Halisdemir Üniversitesi

Fen Bilimleri Enstitüsü

Tarımsal Genetik Mühendisliği Anabilim Dalı

Danışman : Prof. Dr. Mehmet Emin ÇALIŞKAN

Şubat 2021, 313 sayfa

Patates (*Solanum tuberosum* L.) yetiştiriciliğinde, geliştirilmiş yumru kalitesi her zaman elde edilmek istenen özelliklerden biri olmuştur. Bu çalışmanın amacı, 192 adet tetraploid patates genotipinden oluşan panelde ilişkilendirme haritalaması yöntemiyle 25K SolCAP dizisini kullanarak on iki önemli yumru kalitesi özelliği ile ilişkili SNP'leri belirlemektir. Fenotipleme, HPLC gibi yeni nesil platformlar kullanılarak stabilite analizi ile kararlı genotipleri ortaya çıkarmak için gerçekleştirildi. Bayes kümeleme yaklaşımı, STRUCTURE algoritması aracılığıyla değerlendirilen dört alt popülasyonu tanımlar. LD ve ilişkilendirme haritalaması için 13606 polimorfik SNP markör kullanılmıştır. LD analizi, patatesin ıslah sürecini yansıtan 2.31 Mbs düzeyinde bir çözünme ortaya çıkarmıştır. İlişkilendirme Haritalaması, sırasıyla eklemeli ve genel modellerle 215 ve 430 önemli SNP ortaya çıkaran 2 poliploid gen aksiyonu ile doğrusal karışık model (Q + K) kullanılarak gerçekleştirildi. Tanımlanan SNP'ler, nişasta biyosentezinin, karotenoid biyosentezi (*bch*), stres tepkileri ve suberin biyosentezinde yer alan transkripsiyon faktörleri (*MYB*, *bHLH*, *bZIP*) ile ilgili çok çeşitli gen fonksiyonlarına sahiptir. Bu çalışmada elde edilen bulgular sonucunda patateste kalite özellikleriyle ilgili seleksiyon markörlerinin geliştirilmesiyle genomik destekli ıslaha kaynak sağlanacaktır.

Anahtar Sözcükler: İlişki haritalama, SolCAP dizisi, fenotipleme, SNP, kalite, yetiştirme

ACKNOWLEDGEMENTS

First and foremost, praises and thanks to **Almighty Allah** for His countless showers of blessings throughout my research work to complete the research successfully. I would like to express my sincere gratitude and heartiest commendation to my PhD supervisor **Prof. Dr. Mehmet Emin ÇALIŞKAN** for his continuous support in my PhD studies and research. I am highly thankful for his kind, prudent and efficient mentorship, patience, motivation, and immense knowledge which significantly helped me during my research and writing of this thesis. Furthermore, I am highly indebted and thankful to **Assoc. Prof. Dr. Ufuk DEMIREL** for his intellectual guidance in the subject of genome wide association mapping. It was a great privilege and honour to work, study and learn a lot of new methodologies with him. I would also like to thank the thesis jury members, **Prof. Dr. Mehmet ARSLAN, Prof. Dr. Sedat SERÇE and Assoc. Prof. Dr. Muhammet ŞAKİROĞLU** whose knowledge, worthy comments and scholarly advice were critical to this effort.

Special thanks to The Scientific and Technological Council of Turkey (**TÜBİTAK**) for the financial assistance throughout my research and PhD program. The research study was fully funded by TÜBİTAK under the project number 115O949. I am also thankful to International Office in Niğde Omer Halisdemir University for providing me the chance to avail an **ERASMUS** programme.

I also owe a gratitude to **Dr. Inga Smit** and her colleagues/team from Max Rubner Institute, Detmold Germany for their meticulous support and allowing me to learn analytical laboratory techniques, which helped me in phenotyping studies. Acknowledgments would not be complete without mentioning my research colleagues Muhammad Farhan, Caner Yavuz, Eric, Dr. Ayten, Ramazan, Hasan, Arslan Asim and Amir Maqbool who assisted and encouraged me in my field and lab research work. My deepest appreciation to all members of **Potato Group** at the Faculty of Agricultural Sciences and Technologies, Niğde Omer Halisdemir University for their gentle support. At last, I am humbled, appreciative and grateful for the prayers, encouragement and moral support of my **Parents** and **siblings** during all my endeavours.

TABLE OF CONTENTS

SUMMARY	iv
ÖZET.....	v
ACKNOWLEDGEMENTS.....	vi
LIST OF TABLES.....	xi
LIST OF FIGURES.....	xv
SYMBOLS AND ABBREVIATIONS.....	xxii
CHAPTER I INTRODUCTION.....	1
CHAPTER II LITERATURE REVIEW	7
2.1 Origin, Domestication and Breeding History of Potato.....	7
2.2 Potato Genetics and Ways of Enhancing Genetic Gains	9
2.3 Nutrition and Quality Characteristics of Potato.....	12
2.4 Genetic Studies of Complex Traits by Next Generation Breeding Tools.....	17
2.4.1 Infinium SolCAP SNP array	19
2.5 QTL Mapping	21
2.5.1 Review of QTL mapping studies for quality traits in potato	21
2.6 Genome Wide Association Mapping (GWAS)	26
2.6.1 Population structure and Kinship	28
2.6.2 Linkage Disequilibrium (LD)	29
2.6.3 Phenotyping.....	30
2.6.4 How GWAS works?.....	30
2.6.5 Software Packages for GWAS analysis	31
2.6.6 Review of genome-wide association studies (GWAS) related to quality traits in potato	33
2.7 Prospects	41
2.8 Rationale of Current Study	41
CHAPTER III MATERIALS AND METHODS	43
3.1 Plant Materials and Experimental Plan.....	43
3.2 Phenotyping of Tuber Quality Traits	50
3.2.1 Preparation of freeze-dried potato powder extract for quality analysis	50

3.2.1.1 Lyophilization of tuber samples	50
3.2.1.2 Milling of samples	51
3.2.2 Tuber dry matter content (TDM)	51
3.2.3 Tuber specific gravity (TSG)	53
3.2.4 Tuber skin colour (TSC)	53
3.2.5 Tuber flesh colour (TSC)	54
3.2.6 Reducing sugars and sucrose (RS and SUC)	54
..3.2.6.1 Sample preparation	54
..3.2.6.2 HPLC conditions	55
3.2.7 Free asparagine.....	57
..3.2.7.1 Extraction of free asparagine	57
..3.2.7.2 HPLC conditions	57
3.2.8 Tuber starch content.....	58
3.2.9 Beta carotene	59
3.2.10 Total antioxidant activity	60
3.2.11 Total phenolic contents	61
3.2.12 Tuber skin thickness.....	61
3.3 Statistical Analysis of phenotypic data.....	62
3.3.1 SAS 9.0 software.....	62
3.3.2 SPSS Software (v. 25).....	63
3.3.3 AMMISOFT and STABILITYSOFT	63
3.3.4 R Package (BLUPs estimation).....	64
3.4 Genotyping.....	64
3.4.1 Sample collection and genomic DNA extraction.....	64
3.4.2 SNP Genotyping of Potato Genotypes	66
..3.4.2.1 DNA drying (Centrivap Concentrator)	66
..3.4.2.2 SNP Genotyping by SolCAP 25K Potato Array.....	67
3.5 SNP Calling and HapMap File Preparation for STRUCTURE and GWASpoly R..	67
3.6 Inference of Population Structure and Kinship.....	68
3.7 Assessment of Linkage disequilibrium (LD).....	69
3.8 Association Mapping Through GWASpoly R.....	69
3.9 Gene Annotation	70
CHAPTER IV RESULTS AND DISCUSSION	71
4.1 Phenotypic Data Analysis.....	71

4.1.1 Dry matter content (DMC).....	71
4.1.2 Comparison of methods for dry matter content determination in Potato using multi-environments field data and stability statistics	72
..4.1.2.1 Analysis of variance	72
..4.1.2.2 Comparison of methods by correlation analysis and scatter matrix	74
..4.1.2.3 Comparison of methods by regression analysis.....	75
..4.1.2.4 Comparison of methods in multi-environments by stability statistics.	77
..4.1.2.5 Stability analysis.....	78
..4.1.2.6 Discussion.....	84
..4.1.2.7 Conclusion	86
4.1.3 Specific gravity (SG).....	87
4.1.4 Reducing sugars (RSS)	87
4.1.5 Sucrose (SUC).....	88
4.1.6 Free Asparagine (ASP)	89
4.1.7 Tuber starch content (ST).....	89
4.1.8 Beta-carotene (BCRT)	90
4.1.9 Total antioxidant activity (TAA)	90
4.1.10 Total phenolic contents (TPC)	91
4.1.11 Tuber Flesh colour “L* coordinate” (FCL)	91
4.1.12 Tuber flesh colour “b* coordinate” (FCb)	92
4.1.13 Tuber flesh colour “a* coordinate” (FCa).....	93
4.1.14 Tuber skin colour “L* coordinate” (SCL)	93
4.1.15 Tuber skin colour “b* coordinate” (SCb)	94
4.1.16 Tuber skin colour “a* coordinate” (SCa).....	94
4.1.17 Tuber skin (periderm) thickness (PT)	95
4.2 Correlation Analysis	99
4.3 Population Structure, Kinship and Clustering	102
4.4 Linkage disequilibrium (LD)	105
4.5 Association Mapping	107
4.5.1 Dry matter content (DMC).....	108
4.5.2 Tuber specific gravity (SG).....	114
4.5.3 Reducing sugars (RS).....	117
4.5.4 Sucrose (SUC).....	122
4.5.5 Free asparagine (ASP).....	127

4.5.6 Starch (ST)	131
4.5.7 Beta-carotene (BCRT)	136
4.5.8 Total antioxidant activity (TAA)	141
4.5.9 Total phenolic contents (TPC)	145
4.5.10 Tuber flesh colour_L* coordinate (FCL).....	149
4.5.11 Tuber flesh colour_b* coordinate (FCb).....	154
4.5.12 Skin colour_L* coordinate (SCL).....	159
4.5.13 Skin colour b* coordinate (SCb).....	165
4.5.14 Skin (periderm) thickness (PT)	172
CHAPTER V CONCLUSION.....	178
REFERENCES	185
APPENDIX.....	216
CURRICULUM VITAE.....	312
PUBLICATIONS PRODUCED DURING THESIS WORK.....	313

LIST OF TABLES

Table 2.1. Characteristics of some commonly used molecular markers in plant breeding.....	18
Table 2.2. Review of QTL mapping studies related to quality traits in potato.....	23
Table 2.3. Difference between QTL and Association mapping	27
Table 2.4. Genome-wide association mapping studies of quality traits in potato: A literature review.	34
Table 3.1. List of genotypes included in the study along with the information of clusters, origin and their progenies	44
Table 3.2. Description of temperature (°C) and relative humidity (RH%) during growing season.....	49
Table 3.3. List of genotypes with extracted genomic DNA concentration (ng/µl) and final dried amount i.e., 500 ng. Note: Final volume dried in above table is in µl	66
Table 4.1. Mean squares and their significance for set of treatments (environments-methods) of 189 genotypes for variable TDM% (tuber dry matter content in percent)	73
Table 4. 2. Descriptive statistics of variable tuber dry matter content	73
Table 4.3. Correlation (r) among the set of treatments (environments-methods) for variable tuber dry matter content.	75
Table 4.4. Analysis of variance for tuber dry matter content of 189 potato genotypes tested across three environments.	77
Table 4.5. Optimum means of tuber dry matter content with respective values of the stability parameters (b_i and $S^2_{d_i}$) for the 15 most stable genotypes along with 5 check cultivars tested across three environments with three methods	83
Table 4.6. Descriptive statistics for all tuber quality traits of tested 192 genotypes across four environmental conditions.	97
Table 4.7. AMMI ANOVA describing degree of freedom and mean squares of genotypes, environment and genotype by environment interactions, along with genotypic variance, phenotypic variance and broad sense heritability	

(H ²) for all tuber quality traits of tested 192 genotypes across four environmental conditions.....	98
Table 4.8. Pearson correlation (r) analysis regarding all traits; DMC (dry matter content), SG (specific gravity), Free_ASP (free asparagine), Red.Sug (reducing sugars), sucrose, BCRT (beta carotene), Starch, TPC (total phenolic content), TAA (total antioxidant activity), FC L*a*b (tuber flesh colour dimensions), SC L*a*b (tuber skin colour dimensions) and PST (periderm skin thickness).....	101
Table 4.9. Clustering of genotypes into admixed (Q < 0.40) and four clusters along with their relative distribution into several origins as common, DE_BL, DE_Var, TR_BL and TR_Var (Q ≥ 0.40)	105
Table 4.10. Linkage disequilibrium in the tetraploid potato (<i>Solanum tuberosum</i> L.).....	107
Table 4.11. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber dry matter content along with their respective scores* (threshold: -log ₁₀ (P) ≥ 3.23; P ≤ 0.001) and gene annotation.....	113
Table 4.12. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the specific gravity along with their respective scores* (threshold: -log ₁₀ (P) ≥ 3.23; P ≤ 0.001) and gene annotation	116
Table 4.13. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the reducing sugars along with their respective scores* (threshold: -log ₁₀ (P) ≥ 3.23; P ≤ 0.001) and gene annotation	121
Table 4.14. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the sucrose along with their respective scores* (threshold: -log ₁₀ (P) ≥ 3.23; P ≤ 0.001) and gene annotation.....	125
Table 4.15. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the free asparagine along with their respective scores* (threshold: -log ₁₀ (P) ≥ 3.23; P ≤ 0.001) and gene annotation	129

Table 4.16. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber starch content along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	132
Table 4.17. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the beta-carotene content along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	138
Table 4.18. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the total antioxidant activity along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	143
Table 4.19. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the total phenolic contents along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	147
Table 4.20. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber flesh colour L* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	150
Table 4.21. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber flesh colour b* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	156
Table 4.22. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber skin colour L* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	161
Table 4.23. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber skin colour b* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation	167
Table 4.24. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber skin (periderm)	

thickness along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation.....	173



LIST OF FIGURES

Figure 2.1. Complex interplay of starch, sucrose and reducing sugars in potato tuber	14
Figure 2.2. An illustration of genome wide association mapping (GWAS) model in potato breeding for the identification of QTL/diagnostic markers associated with a trait of interest.....	32
Figure 3.1. Lyophilizator (Left); Sliced tuber samples for lyophilization or Freeze drying (Right).....	50
Figure 3.2. Tuber samples after freeze drying and milled accordingly to make fine powder.....	51
Figure 3.3. Hydrometer (1), oven-dry (2), and quartz seasand methods (3) demonstration for the measurement of TDM%	52
Figure 3.4. Measurement of tuber skin colour with chroma-meter along with the numerical values of dimension “L” segregating with skin colour (dark brown and red to light yellow).....	53
Figure 3.5. Measurement of tuber flesh colour with chroma-meter along with the numerical values of dimension “L” segregating with flesh colour (dark yellow to white)	54
Figure 3.6. Calibration curve of reducing sugars (glucose + fructose) and sucrose with 8 standards along with regression line ($R^2=0.99$)	56
Figure 3.7. Peaks obtained for reducing sugars and sucrose through HPLC. Retention time for fructose, glucose and sucrose was 12.4, 14.8 and 23.7, respectively	56
Figure 3.8. Calibration curve of free asparagine with 6 standards along with regression line ($R^2=0.99$).....	58
Figure 3.9. Free asparagine peak at retention time (RT) of 3.56 in pure standard (above) and sample (below).....	58
Figure 3.10. Tuber skin (periderm) thickness observed under optical stereo microscope (Leica 165C) and image was taken from Leica application suite (LAS V4.12)	62

Figure 3.11. Sample collection for genomic DNA extraction and Gene JET Plant Genomic DNA Purification mini kit (Thermo scientific).....	65
Figure 3.12. Agarose gel electrophoresis of Genomic DNA samples; (Labelled from Left to Right).....	65
Figure 3.13. Centrivap Concentrator for drying DNA samples (a); Arrangement of Eppendorf tubes in a box containing 500ng of DNA in a dried form (b)....	67
Figure 4.1. Mean TDM% variation in check cultivars (Agria, Alegria, Hermes, Jelly, Rumba) in a set of treatments	74
Figure 4.2. Regression analysis of three different methods for the measurement of tuber dry matter content under three environmental conditions	76
Figure 4.3. AMMI biplot for TDM mean (%) of 189 potato genotypes (blue dots) and three environments (H018, KN18, KD18) plotted against IPC1 (Interactive principal component)	78
Figure 4.4 Generalized interpretation of graph plotted between regression coefficient (bi) and mean TDM (a); Relationship of genotype adaptation (regression coefficient 'bi') and mean TDM of 189 potato genotypes by various dry matter content determination methods in three diverse environments (b,c and d)	80
Figure 4.5 Relationship of genotype adaptation (mean square deviation ' S^2_{di} ') and mean TDM of 189 potato genotypes by various dry matter content determination methods in three diverse environments (zero indicates average stability) (a, b and c).....	81
Figure 4.6. Population structure of 192 potato genotypes based on SNP markers (a) Delta K values over 10 runs ($\Delta K=4$), (b) PCA scatter plot of the first two principal components (PC1 and PC2) depicting the clustering of genotypes into 4 clusters as indicated by delta K results from STRUCTURE.....	103
Figure 4.7. Bar plot displaying population sub-structure of 192 genotypes (K=4). Sub-population clusters 1, 2, 3 and 4 were represented by colours red, green, blue and yellow, respectively according to the Q values (estimated membership covariates). X axis represents serial no. of genotypes corresponding to each individual bar plot as mentioned in Table 3.1, whereas y axis symbolizes Q values obtained from structure software.....	104
Figure 4.8. Estimated LD (Linkage disequilibrium) decay plotted between r^2 and genetic distance (Mbps) with non-linear trend line. Mean estimated r^2	

value is 0.29 with LD decay at 2.31 Mbps calculated from each chromosome as mentioned in Table 4.10.	106
Figure 4.9. Histogram of LINEBLUPs for dry matter content. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	110
Figure 4.10. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing dry matter content (DMC) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	110
Figure 4.11. Histogram of LINEBLUPs for specific gravity. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	115
Figure 4.12. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing specific gravity (SG) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	116
Figure 4.13. Histogram of LINEBLUPs for reducing sugars without and with log transformation. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” = genotypes included in the study).....	118
Figure 4.14. Q-Q plots of observed vs expected p values of non-transformed and log10 transform BLUPs (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing reducing sugars (RSS) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	119
Figure 4.15. Histogram of LINEBLUPs for sucrose without and with log transformation. Scatter plot comparing estimated LINEBLUPs with mean	

of each genotype across all four environments (“LINE” = genotypes included in the study).....	123
Figure 4.16. Q-Q plots of observed vs expected p values of non-transformed and log10 transform BLUPs (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing sucrose (SUC) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	124
Figure 4.17. Histogram of LINEBLUPs for free asparagine. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	127
Figure 4.18. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing free asparagine (ASP) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	128
Figure 4.19. Histogram of LINEBLUPs for starch (percentage basis) and ST_DM (dry matter basis). Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	134
Figure 4.20. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing starch (ST_P “percentage basis”) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.	134
Figure 4.21. Histogram of LINEBLUPs for beta carotene. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	137
Figure 4.22. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP	

markers with additive and general models, showing beta-carotene associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	137
Figure 4.23. Histogram of LINEBLUPs for total antioxidant activity (TAA). Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	142
Figure 4.24. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing total antioxidant activity (TAA) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	142
Figure 4.25. Histogram of LINEBLUPs for TPC. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	146
Figure 4.26. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing total phenolics (TPC) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome	147
Figure 4.27. Histogram of LINEBLUPs for tuber flesh colour L* FCL. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	149
Figure 4.28. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing FCL associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.....	152
Figure 4.29. Histogram of LINEBLUPs for tuber flesh colour b* FCb. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all	

four environments (“LINE” here represents the genotypes included in the study).....	155
Figure 4.30. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing FCB associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.....	156
Figure 4.31. Histogram of LINEBLUPs for tuber skin colour L^* SCL. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	159
Figure 4.32. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing SCL associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.....	160
Figure 4.33. Histogram of LINEBLUPs for tuber skin colour b^* (SCb). Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	166
Figure 4.34. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing SCb associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.....	167
Figure 4.35. Histogram of LINEBLUPs for tuber skin (periderm) thickness. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study).....	172
Figure 4.36. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing periderm thickness (PT) associated SNPs from multi-environment BLUP estimates in the	

association mapping panel (b). Note: 0 refers to unmapped chromosome.....	173



SYMBOLS AND ABBREVIATIONS

Symbols

	Description
%	Percent sign
°C	Degree centigrade
Mbp	Mega base pair

Abbreviations

	Description
FAOSTAT	Food and Agriculture Organization Statistical Databases
AM	Association Mapping
QTL	Quantitative Trait Loci
LD	Linkage Disequilibrium
SolCAP	Solanaceae Coordinated Agricultural Project
MLM	Mixed Linear Model
TASSEL	Trait Analysis by aSSociation, Evolution and Linkage
SNP	Single Nucleotide Polymorphism
SSRs	Simple Sequence Repeats
cM	Centi Morgan
DNA	Deoxyribonucleic acid
BLUPs	Best Linear Unbiased Predictions
ANOVA	Analysis of Variance
Q-Q	Quantile-Quantile
HPLC	High Performance Liquid Chromatography
GWASpoly	Genome Wide Association Studies in Autopolyploids (R package)

CHAPTER I

INTRODUCTION

Potato (*Solanum tuberosum* L.) is substantially produced and consumed tuber crop around the globe with 1.3 billion people consuming it as a staple food (more than 50 kg/person/year) (Devaux et al., 2020). It is a crop of utmost significant value and ranked as the first non-cereal and third most produced food crop around the world, with an annual production of over 380 million tons (t) cultivated on a total area of 19.3 million hectares (ha) with an average yield of 22.2 t/ha in 2019, following rice and wheat (FAOSTAT, 2020). In Turkey, potato is cultivated on an area of 143,000 ha with a total production of 4.8 million tons with an average yield of 33.60 t/ha. Central Anatolian region for instance, Niğde, Konya, Kayseri, Nevsehir and Aksaray shared 16.1%, 13.4%, 7.3%, 5.9% and 4.4% of potato production in the country, respectively (TUIK, 2020). It is a noteworthy staple food crop in Turkey with a per capita consumption of 47.62 kg (FAOSTAT, 2020). In Pakistan, it is planted on an area of 193,992 ha with a total production of 4.59 million tons (FAOSTAT, 2020). *Solanum brevicaulis* is a wild species complex found in southern Peru (South America) assumed to be an ancestor of cultivated potato. Potato belongs to Solanaceae family comprising of 95 genera with an estimated 1500-2000 species within this genus. Approximately, 230 known wild species have been distributed widely from Southwest USA to Mexico and Central America. The germplasm diversity in wild species and cultivated landraces of potato is accredited due to their adaptation to vast range of niches and habitat (Hijmans and Spooner, 2001). Potato was introduced to the world through transportation, shipment and war expeditions. *S. stenotomum* was the first domesticated potato and considered as the descendant of diploid (2x) wild species. Modern cultivars evolved because of domestication, selection and breeding efforts from landraces and wild species found in the Andes (Spooner et al., 2005). *S. tuberosum* group *Chilotanum*, (2n = 4x = 48) is broadly considered as a progenitor of modern-day commercial cultivars (Ames and Spooner 2008). Today, more than 4,800 potato varieties from 125 countries have been widely distributed worldwide, particularly under tropical, subtropical and temperate regions (Hameed et al., 2018).

Potato is recommended as a food security crop due to its versatility in usage as food, feed and industrial raw material, in the problem-oriented scenario of population explosion,

food supply and nutrition (Devaux et al., 2014). Potatoes provide cheap source of energy (93 kcal/100g tuber) and can substitute other high-priced foods, thus sustaining a normal functioning of life (Burlingame et al., 2009). In both developed and developing countries, it is regarded as staple food due to its role in fighting against malnutrition, since potato tubers are known sources of carbohydrates, minerals, vitamins, proteins, antioxidant compounds such as carotenoids and phenolics (Çalışkan et al., 2010). Potato quality remained underestimated, breeding studies related to this aspect is still at its infancy compared with improvements in resistance/tolerance to abiotic or biotic stresses (Vos et al., 2015). A thorough knowledge of some significant quality traits of potato paved our path to enhance the selection strategy and genetic gains in potato breeding.

Potato is rich in carbohydrates especially starch is a major polysaccharide in tubers and provides an energy value of 17kJ/g (4kcal/g), which accounts for 40 to 75% energy intake (Ek et al., 2012). Starch and tuber dry matter content (TDM) are thought to be synonymous terms in potato, since about 60 to 80% of the TDM is starch. The sensory characteristics of potato such as taste, colour and aroma of tubers are altered during cooking, mainly due to the changes in tuber compositional traits. TDM is one of the major quality traits of potato alongside with starch, reducing sugars and proteins (Van Eck, 2007). There exists a complex interconversion and interesting interplay between starch, sucrose and reducing sugars mainly affected by stress (i.e., cold or during dormancy break). It influences the tuber quality and final yield of processed tuber products (dark coloured chips/crisps and French fries). The browning or dark colouration is caused by non-enzymatic Maillard reaction that occurs in carbohydrate rich foods involving free asparagine (most abundant amino acid in tuber) and reducing sugars (glucose and fructose) at high temperature (120°C) to yield acrylamide. Acrylamide is a potential carcinogen (Friedman et al., 1995) and mutagen (Segerback et al., 1995). The negative correlation of starch/DMC with reducing sugars put forward the worldwide breeding efforts towards development of potato cultivars with high TDM/starch (20-25%) combined with low levels of reducing sugars (<100 mg/100g FW) and free asparagine, acceptable to processing industry. Tuber skin and flesh colour may vary from white to yellow and red to purple. These peculiarities are thought to be linked with carotenoid and phenolics amounts and types (Burgos et al., 2009; Sulli et al., 2017). Beta carotene (precursor of vitamin A) is an important carotenoid and known to be present in yellow flesh tubers. The relative content of β -carotene in cv. Agria (yellow flesh) represented 2%

of total carotenoids (Lachman et al., 2016). Both carotenoids and phenolics have antioxidant properties having a characteristic mechanism of scavenging the free radicals and ultimately protecting bio-molecules/bio-membranes. The antioxidant properties of tuber skin are attributed to the direct uptake of mineral nutrients from soil by the periderm. Suberization and lignification of potato periderm provides protection against desiccation, excoriation, pathogen attack, heat and freezing injury. Significant losses to quality of tubers may occur due to defective and weak periderm. Consumer and industrial acceptance are reduced due to injured or discoloured potato skin (Singh et al., 2020). Since, consumer preference is one of the key objectives in plant breeding, improvement of quality traits for table and processing tuber quality is therefore indispensable.

Tuber quality is a complex and quantitative trait affected by multiple genetic (polygenes/minor genes) and environmental factors (Massa et al., 2018). Potato cultivars respond differently to fluctuating environments (location and year), generally described as genotype by environment interaction (G*E). The amount of G*E varies from trait to trait and has an implication on the selection process for a given trait. High G*E calls for a testing system with multiple locations at early stages, whereas low G*E allows for few locations in the whole selection process. Knowledge of the amount of G*E for quality traits will help to optimize the selection strategy by selecting stable genotypes with static and/or dynamic stability (Affleck et al., 2008).

Potato breeding faced challenges due to its complex genetics. Cultivated potato (*Solanum tuberosum* L.) is highly heterozygous and autotetraploid ($2n=4x=48$) crop. Inbreeding depression, tetrasomic inheritance and intraspecies incompatibilities are major limitations faced by potato breeders (Potato Genome Sequencing Consortium, 2011; Jansky et al., 2014; Hardigan et al., 2017). While the conventional or classical breeding methods are slow and strenuous, marker assisted methods involving the use of genome wide markers offered steadfast solutions to improve quality characteristics of potato efficiently. The world is rapidly adopting next generation breeding tools in the era of marker assisted selection (MAS), and recognized the potential of DNA markers in plant breeding. Among the DNA markers, SNPs (Single nucleotide polymorphisms) are codominant and highly abundant molecular markers in the genome (Nadeem et al., 2018). With an advent of NGS (next generation sequencing) technologies such as Illumina Infinium platform, SolCAP array has been developed for high density genetic mapping of potato using SNPs. Potato

has a genome size of 844 Mbp (Potato Genome Sequencing Consortium, 2011) and the utility of Infinium SolCAP 8K array provide an excellent coverage of potato genome (633-641 Mbp) with an estimated 4,400 mapped markers (Hamilton et al., 2011; Felcher et al., 2012). A high-density SNP map of tetraploid potato have been constructed based on Infinium SolCAP 8300 SNP array, which comprises of 1130 markers with an estimated coverage of 1087.5 cM (Hackett et al., 2013). The genome wide coverage of Infinium SolCAP potato array coupled with high-throughput nature of estimating population structure diversity, allele dosage and tetraploid calling of biallelic SNPs (nulliplex to quadriplex) makes it a valuable tool for genome wide association mapping studies (GWAS) in tetraploid potato (Stich et al., 2013; Vos et al., 2014). Linkage mapping can also be performed utilizing SolCAP platform in biparental populations. The probability of identified QTL in linkage/QTL mapping is reduced due to low mapping resolution and restricted meiotic events owing to biparental segregating population, thus the applicability of QTLs in MAS is doubtful (Hackett et al., 2014).

As opposed to QTL/linkage mapping, GWAS offers high resolution based on marker-trait association in already available germplasm, without any efforts of creating a mapping population. It explores allelic variation in diverse unrelated individuals from multiple meiotic and historical recombination events in collection of commercial cultivars and breeding clones. The effectiveness and robustness of GWAS is well documented for the dissection of complex quality traits in potato using genome wide markers (Vos et al., 2015; Sharma et al., 2018). GWAS is key approach for studying natural variation and mapping of quantitative traits. To avoid spurious marker-trait association and false positives in GWAS, it is important to consider several factors affecting its power. These includes phenotypic variation, number of individuals, population structure and kinship, allele frequency and linkage disequilibrium (LD). GWAS is based on linkage disequilibrium between casual polymorphism and markers. In potato, LD is important for GWAS, because most cultivated tetraploid genotypes have a narrow genetic base, consisting of small number of haplotypes, due to extensive LD. LD tells about co-inheritance of marker with associated trait or QTL (quantitative trait loci) to next generation. In order to enhance the power of marker-trait association, LD tests in conjunction with correction of population structure (Q) by taking into account accurate subpopulations (K) leads to reliable GWAS results (Simko et al., 2004). Stich et al., (2013) admonished that LD decay occurs with an intensity of 275 bp. Contrarily, Vos

et al. (2017) used LD1/2,90 estimator with LD values ranged between 0.7 to 0.9 Mb. 2 to 4 Mb distance is the general trend for LD decay values in potato crop. Linear mixed models (Q+K) along with dosage information of minor allele (0, 1, 2, 3, 4) is the most widely used single marker test in GWAS using polyploid gene action (Rosyara et al., 2016).

The capability to exploit the full potential of genomic and molecular breeding tools such as GWAS may be limited by ability to phenotype correctly (Araus and Cairns, 2014). Reliable and robust marker-trait associations to identify diagnostic SNP markers can be achieved efficiently by using high-throughput phenotyping techniques (HTPPs) (Zia et al., 2017). High performance liquid chromatography (HPLC), uv-vis spectrophotometry and polarimetry are the examples of some HTPPs using 2D, 3D and high-resolution imaging (refractive index detector, diode array detector) and novel handheld sensors (for instance, chroma-meter), for the profiling and quantification of important tuber quality traits. Comparison of automated and manual phenotyping methods of quality traits; for instance, TDM may reveal the reliability and robustness of HTTP technique and further avoiding spurious marker-trait associations in GWAS.

Keeping in view the advancements and use of genomics in plant breeding, it was hypothesized that phenotypic expression of tuber quality traits may be affected due to more complex interactions between genes and their allelic variants or higher levels of allelic dosage or by G*E interaction. The genetic gains in potato breeding for improved quality parameters can be obtained by understanding the allele-phenotype interactions leading to the development of selection markers facilitating MAS. There is a need of diagnostic SNP markers linked to tuber quality traits explaining a reasonable proportion of genetic variation. Until recently, markers have been identified in potato associated with starch, tuber skin colour, tuber flesh colour and proteins by using SolCAP 8K SNP array (Rosyara et al., 2016; Berdugo-Cely et al., 2017; Schönhals et al. 2017; Sharma et al., 2018), SolCAP 12K SNP array (Zia et al., 2020) and SolCAP 20K SNP array (Klassen et al., 2019). Infinium SolCAP 25K SNP array has not been used till now for GWAS analyses. Moreover, there exists a research gap in exploitation of high-throughput phenotyping platform in previous studies and marker-trait associations for some critical tuber quality variables such as reducing sugars, sucrose, free asparagine, total phenolics, total antioxidants, beta-carotene and tuber skin (periderm) thickness. The current study

aims to identify novel associations of diagnostic SNP markers with afore-mentioned tuber quality traits. It is also expected to develop new diagnostic SNP markers linked with tuber dry matter content, specific gravity, starch, tuber skin and flesh colour as well, since limited associations are reported for these traits. Moreover, practicability and reliability of three phenotyping methods for measurement of TDM have been evaluated under various environmental conditions along with stability statistics in order to identify the stable genotypes with an optimum TDM.



CHAPTER II

LITERATURE REVIEW

2.1 Origin, Domestication and Breeding History of Potato

It is predicted that the global population will increase to approximately 9.7 billion by the year 2050 and an approximate of 10.9 billion by 2100 (UN, 2019). Potato is a very versatile crop and provide assurance of feeding and supplying high nutrition along with low cost energy to people, irrespective of economic categories thus reducing malnutrition and hunger. It is used as a food, feed and industrial raw material, and has been recommended as a food security crop in the scenario of ever-increasing population and related problems with food supply and nutrition (Devaux et al., 2014). It is a crop of utmost significant value and ranked as the third most produced food and the first non-cereal crop in the world with an annual production of over 380 million tons (t) cultivated on a total area of 19.3 million hectares (ha) with an average yield of 22.2 t/ha in 2019, following rice and wheat (FAOSTAT, 2020).

According to botanical classification, the family of potato is nightshade or Solanaceae. The Solanaceae family is comprised of 95 genera. Potato belongs to the genus *Solanum* which accounts most economically important and largest genus (Bradeen et al., 2011). There are an estimated 1500-2000 species within the *Solanum* genus (PBI Solanum Project, 2014). There are more than 230 known species of wild potato in Central and South America (Hawkes, 1990). These inedible species are the original ancestors of today's cultivated potato. It is believed that the first potato cultivation started near Lake Titicaca, which sits at 3,800 m (12,500 ft) above sea level in the Andes mountain range of South America around 8,000 BC. Two diversity centers have been documented in America for wild potatoes; North & Central America (Mexican center), and South America (Andean center, spreading from Venezuela to Chile) (Hijmans and Spooner, 2001; Hijmans et al., 2007). A wild species, *S. brevicaulis* complex (single origin) found in southern Peru assumed to be an ancestor of common potato (*S. tuberosum* L.) by some scientists (Spooner et al., 2005). While, some scientists suggest multiple origins of cultivated potatoes (Hawkes, 1994; Huaman and Spooner, 2002). Juzepczuk and Bukasov (1929, cited in Huaman and Spooner, 2002) suggested that the Chiloe region (Chile) is

responsible for the introduction of potatoes in Europe. Contrastingly, Hawkes (1994) proposed that cultivated potatoes came from the wild species extensively cultivated in Andean region (Peru, Northern Argentina and Bolivia).

The domestication of cultivated potato (*Solanum tuberosum* L.) occurs some 8,000 to 10,000 years ago, from diploid wild species ($2n = 2x = 24$), and later it becomes the main pillar of food security around the globe (Pearsall, 2008). At first people assumed potato as suspicion relative of *S. nigrum* (a toxic member of nightshade family). Breeding and domestication efforts gradually introduced it to the rest of world as a human food source. *S. stenotomum* ($2x$) was the first domesticated potato and considered as the descendant of diploid ($2x$) wild species (Hawkes, 1990). The Andean cultivated tetraploids (*S. tuberosum* group *Andigena*; $2n = 4x = 48$) were produced as a result of autopolyploidization of early diploid landraces (*S. tuberosum* groups *Stenotomum* ($2x$) and *Phureja* ($2x$)). The domestication of potato from wild specie *S. brevicaulle* complex encompasses the selection for underground traits like large tubers with diverse shapes and colour, shorter stolon's, and reduced bitter taste due to tuber glycoalkaloids. Research on potato genome sequencing revealed a prodigious genetic variation and signatures of gene selection which controls domestication traits (Hardigan et al., 2017).

In the 16th century, after the Columbus voyages, two potato introductions were brought from South America to Europe encouraging the cultivation of potato and establishment of few cultivars till 18th century (Glendinning, 1983). By the end of the eighteenth century, Andean to Chilean migration yielded a long-day photoperiod potato (*S. tuberosum* group *Chilotanum*, $2n = 4x = 48$), which is a progenitor of modern-day commercial cultivars. Until mid-1800's, no serious breeding efforts were done for improvement of potato. Asexual propagation of clones was commonly practised by retaining few tubers at harvest for next year planting. The famous Irish potato famine caused by Late blight (caused by *Phytophthora infestans*), eliminated most of the potato cultivars and thus contributes in plummeting gene pool of potato in Europe. After the mid-19th century in the post famine era, serious efforts began by collecting sexually propagated wild potatoes from chile and cross-breeding them with the few surviving European cultivars. True potato seeds (TPS) were obtained from naturally occurring berries (largely through uncontrolled self-pollination) and selection strategy resulted in early tuberization cultivars and high-yielding clones (Kumari et al., 2018). It enhances

the variation and new cultivars were released such as “Garnet Chili or Rough Purple chili (open pollinated)”, later selection trials conducted by Albert Breese on “Garnet Chili” resulted in the release of “Early rose” in 1867. Luther Burbank focussed on an open pollinated population as a subject of potato improvement. His breeding efforts lead to the release of “Burbank Seedling” in 1876, later known as “Russet Burbank” in the mid-20th century. Hybridization through cross-breeding later got stern attention for potato germplasm improvements in the 20th century (Jansky and Spooner, 2018).

Brush et al. (1995) revealed that domestication reduces diversity in cultivars due to genetic bottleneck effect. An example to this scenario is the introduction of potato across continents (from America to Europe) that represents only part of variation found in domestication center. Today, more than 4,800 potato varieties from 125 countries have been widely distributed worldwide, particularly under temperate, subtropical and tropical regions (Pieterse and Judd, 2014; Seo et al., 2018; Hameed et al., 2018). Despite of the diversified cultivated gene pool, most of the modern-day cultivars possess a limited inbred gene pool owing to gene similarities with early 20th century cultivars (Ortiz, 2020). Most of the modern-day cultivars are separated from mid-20th century cultivars by only a few meiotic events. Genetic gains are slow in conventional/ classical breeding programmes due to lengthy breeding cycles, and selection in single hill environment is limited due to genotype by environment interactions (Jansky and Spooner, 2018). The development of new potato cultivars through careful selection of desired genotypes is a time-consuming and challenging breeding task. In order to understand the limited breeding gains in potato, knowledge of potato genetics is obligatory.

2.2 Potato Genetics and Ways of Enhancing Genetic Gains

Potato breeding is a cumbersome task due to its complex genetics. The basic chromosome number of the section *Petota* (tuber bearing *Solanum* species) is 12. There are four levels of ploidy in potato, ranging from diploid to pentaploid ($2n=2x=24$ (diploid); $2n=3x=36$ (triploid); $2n=4x=48$ (tetraploid); $2n=5x=60$ (pentaploid)). The wild relatives of potato may possess hexaploids ($2n=6x=72$) (Huaman and Spooner, 2002; Spooner et al., 2005). Cultivated potatoes *Solanum tuberosum* (ssp. *tuberosum*) have four alleles per locus hence termed as tetraploid ($2n=4x=48$). Moreover, the homologous chromosomes pair during the process of meiosis, so they are called as autotetraploid (Milbourne et al., 2007).

The ploidy levels variation forms the basis of huge germplasm diversity in cultivated potato and its wild relatives. All over the globe, there are 98,285 potato accessions, which includes 15% wild species, 20% landraces, 16% breeding lines, 14% advanced cultivars and 35% others (unknown or mixture of 2 or more types) (FAO, 2010; Machida-Hirano, 2015). Afonnikov et al. (2018) stated that there is high degree of genetic diversity in wild potato relatives, which can be utilized to hunt for superior alleles and to overcome domestication syndrome and genetic bottleneck. Potato has a greater genetic diversity than other major crops such as cotton, tomato, soybean and pigeon pea. Resequencing data of 67 accessions of cultivated and wild potatoes have identified 68.9 million SNPs (Hardigan et al., 2017).

Despite of huge genetic diversity in potato germplasm, improvements in the cultivated potato ($2n=4x=48$) is slow and hindered mainly due to its high heterozygosity, inbreeding depression, low sexual fertility, and complex polysomic tetraploid inheritance often referred to as tetrasomic inheritance and poor adaptation of wild germplasm (Potato Genome Sequencing Consortium, 2011; Jansky et al., 2014; Hardigan et al., 2017). The differences in EBN (endosperm balance number) and level of ploidy among the species also serve as a barrier for cross species compatibility. In order to overcome this barrier of hybridization and to obtain fertile interspecific hybrids, several techniques such as bridge cross, ploidy manipulations, embryo rescue, mentor pollinations, reciprocal crosses and somatic (protoplast) fusion have been reported (Bradshaw and Ramsay, 2005; Jansky, 2006; Hardigan et al., 2015). Ploidy manipulations can be done either by reducing EBN through haploid extraction and/or by increasing EBN by production of $2n$ gametes (Naess et al., 2000).

Due to heterozygous nature of tetraploid potato, alleles occur in five dosages (nulliplex (aaaa), simplex (Aaaa), duplex (AAaa), triplex (AAAa) and quadruplex (AAAA)) instead of only two (homozygous and heterozygous) in diploids. Upon repeated selfing, it is not possible to obtain pure lines due to severe inbreeding depression, since multiple allelism generates a multitude of genotypes. These genotypes are difficult to distinguish based on comparing expected with observed segregation ratios (Gebhardt, 2007). Furthermore, being a vegetatively propagated crop, severe inbreeding depression caused deleterious mutations in the pericentric chromosomal regions. Recombination offers limited purging of these mutations, moreover vegetative methods of propagation results in cultivars

highly related to each other, narrowing the genetic base (Zhang et al., 2019). The greater heterozygosity attributed to the presence of diverse alleles at each locus resulted in number of allelic and epistatic interactions (Carputo and Frusciante, 2011). Locus interactions, allelic combinations and genetic effects becomes even more complex when dealing with quantitative (polygenic) traits in the scenario of tetrasomic inheritance. Combining two or more recessive characters becomes much more complicated, for instance, the probability of getting aaaabbbb at the tetraploid level is 1/1296, while its 1/16 in case of aabb at the diploid level. Keeping in view the complex potato genetics as mentioned above, accumulation of desirable alleles in a breeding line or population is very difficult. It requires a screening of a progeny consisting of large sample size of thousands or even million seedlings for the identification of the desirable traits into single clonal line (Muthoni et al., 2015).

Potato breeding faces several global challenges now a days; such as delivering enough food combined with high quality to fulfil the dietary requirements of ever-increasing human population, continual supply of bio-sources to agricultural and processing industry and fitting newly bred cultivars into sustainable farming system in scenario of climate change (Andrison, 2017). Biotechnology and molecular genetics offered valuable solutions to the challenging endeavours of classical potato breeding, over the past 70 years to enhance the genetic gains over time. With an advent of linkage maps and molecular markers era, the breeding programs worldwide achieve genetic gains courtesy to marker assisted selection (MAS). In potato, SolCAP array establishment opens up new dimensions, we can perform genotyping of potato germplasm with 8K, 12K, 20K and now 69K SNPs at considerably less price facilitated by next generation sequencing (NGS) techniques. Potato SolCAP custom-made arrays offered the analysis of high-density SNPs per genotype (Hamilton et al., 2011, Vos et al., 2015). The genotyping of cultivars and breeding lines using NGS platform with highly polymorphic genome-wide marker set in elite germplasm substantially advance potato breeding. Characterization of loci, identification of alleles and candidate genes in potato and finding association between phenotype and genotype can be done using genome wide markers at a resolution never reached before. Genetically elite plants can be identified earlier in the plant growth by finding naturally occurring allelic variations at the molecular level and linking it with a phenotype of interest. The ability to discard non-elite plants and choosing elite plants with desired characteristics in the process of plant breeding saves both time and money without

observing the phenotype merely by the use of diagnostic molecular markers. This hypothesis suggests that marker assisted selection (MAS) for the trait of interest can be done efficiently by using next generation breeding approach. With the advent and advancements in NGS, next generation breeding is an area of greater interest by plant breeders and geneticists.

Several markers have been developed to be used in marker assisted breeding for important resistance genes in potato offering resilience to cyst nematodes, late blight, and viruses (Jacobs et al., 1996; Lopez-Pardo et al., 2013; Tiwari et al., 2013; Kuhl et al., 2016; Stefańczyk et al., 2020; Milczarek et al., 2020). Contrastingly, marker assisted breeding is still at infant stage for tuber yield and quality traits. The tuber quality traits are polygenic in nature and affected by minor alleles, so a deeper understanding of loci and deleterious alleles is essential (Vos et al., 2015). Having achieved the food sufficiency, currently there is a paradigm shift from quantity to quality improvement. At present, improvement in quality characteristics can be achieved through genetic approaches. With the availability of NGS, linkage mapping can be done to locate QTL (Quantitative trait loci) on corresponding genomes of biparental population to facilitate MAS. Alternatively, QTLs or genomic regions can be identified by extensive genotyping of germplasm panel of breeding populations or cultivars depicting biological variation/diversity in phenotypes across fluctuating environments, with an objective to reveal marker-trait associations. The former approach is termed as QTL mapping while latter is known as genome wide association mapping (GWAS). A subsequent marker assisted selection using KASP assay can be done to exploit genetic variation of interest for developing a selection marker. Before discussing in detail about the pros and cons, mechanism and details of exploiting these mapping techniques for quality enhancement in potato, it is necessary to elucidate various tuber quality traits.

2.3 Nutrition and Quality Characteristics of Potato

In both developed and developing countries, it is regarded as staple food due to its role in fighting against malnutrition, since potato tubers are known sources of carbohydrates, minerals, vitamins, proteins, antioxidant compounds such as carotenoids and phenolics (Çalışkan et al., 2010). Potatoes have less fat content and rich in several micronutrients, particularly vitamin C (84-145 mg/100g dry weight basis), when consumed with its skin.

A single medium size potato of 150 g fulfilled approximately half of the daily adult requirements (i.e., 100 mg). It promotes the absorption of iron in intestine due to a source of vitamin C. It is also rich in vitamins B1, B3, B6 and B9, and minerals such as phosphorus, magnesium, potassium, and contains riboflavin and pantothenic (Camire et al., 2009). Potatoes provide cheap source of energy (93 kcal/100g tuber) and can substitute other high-priced foods, thus sustaining a normal functioning of life (Burlingame et al., 2009).

The freshly harvested tubers comprise of about 80% water and 20% dry matter content (DMC). DMC is one of the major quality traits of potato alongside with starch, reducing sugars and proteins (Van Eck, 2007). It is an early determinant of tuber quality and influence the final yield of processed tuber products (chips/crisps and French fries). Studies revealed that high DM and low reducing sugars increases the crispy consistency of chips, decreases oil absorption while cooking, reduces bitter taste and dark colour of processed tuber products (Peiris et al., 1999; Asmamaw et al., 2010). Generally, the processing industry does not accept the tuber dry matter content (TDM) below 19.5% for French fries and 20% for chips. Upper limits do not apply, though penalties may be incurred for DM content more than 25% (McGregor, 2007). Selection of stable genotypes with optimum DM content is a major objective in potato breeding programmes aimed at improving processing tuber quality (Neele and Louwes, 1989). Genotypes and growing conditions may affect the DM content. Cultivars with high DM has better quality characteristics as compared to their lower counterpart (Asmamaw et al., 2010).

Starch and DMC are thought to be synonymous terms in potato, since about 60 to 80% of the DMC is starch. Starch is a polysaccharide and major source of carbohydrate in human diet. It provides an energy value of 17kJ/g (4kcal/g), which accounts for 40 to 75% energy intake (Ek et al., 2012). On tuber fresh weight basis, starch constitutes 11-45% (Jansen et al., 2001). The tuber starch content of table potatoes ranged between 10-17%, processing potatoes (French fries and chips) between 14 to 20% and upto 25% for industrial usage (Schönhals et al., 2016). The accumulation of starch and its breakdown are vital processes in tuber which decide the quality of processing potatoes (French fries and chips). The conversion of starch to sugars i.e., glucose, fructose (reducing sugars) and sucrose is a complex and interesting interplay (Fig. 2.1). It is being controlled by multiple environmental and genetic factors and inversely correlated to each other

(Schreiber et al., 2014). Sucrose formed as a result of photosynthesis and accumulated in tubers as starch under normal tuber growing conditions. Conversely, the break down of starch occurs under stress (cold or sprouting) to sucrose, this disaccharide ultimately disintegrates to form glucose and fructose. The concentration of sucrose, glucose, and fructose in raw tubers of tetraploid potatoes ranged from 3.25-255 mg/100 g fresh weight basis, 2.5-153.7 mg/100 g fresh weight basis, and 43 to 159.7 mg/100 g fresh weight basis, respectively (Rodríguez et al., 2010). Tubers are generally stored below 8°C, at around 4°C starch converted to reducing sugars which causes cold induced sweetening (CIS). Senescent sweetening also occurs in potatoes as they break dormancy and start sprouting. CIS is caused by vacuolar invertase (*VI_{inv}*) while the latter sweetening is due to phosphorylase L (*PhL*) and starch associated *R1* (Raffan and Halford, 2019).

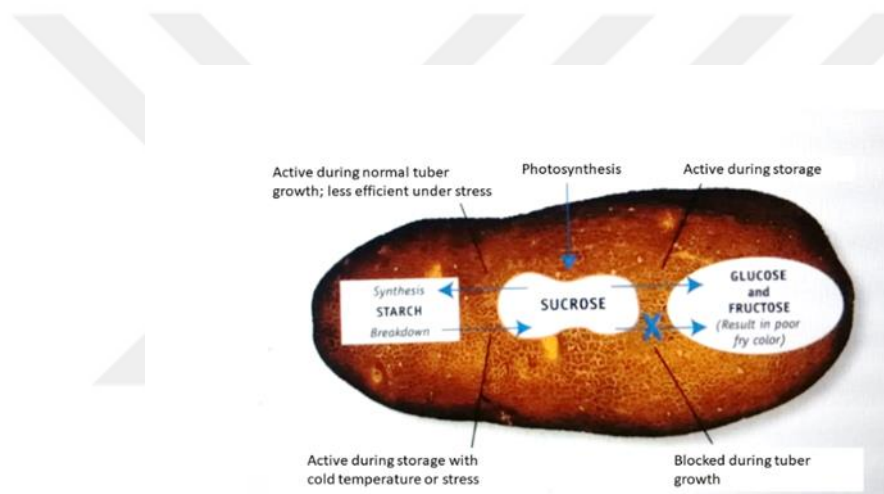


Figure 2.1. Complex interplay of starch, sucrose and reducing sugars in potato tuber

Potato is either consumed after boiling or as processed food such as French fries, potato chips, dehydrated and canned potatoes (Sinha and Naeem, 2018). Undesirable browning colour in frying process is still a matter of concern due to health aspects, especially its carcinogenicity. Indeed, acrylamide, a toxin formed during potato frying process, is known as a potential carcinogen (Friedman et al., 1995) and mutagen (Segerback et al., 1995). Consequently, the International Agency for Research on Cancer (IARC) had classified acrylamide in Class 2A as probable human carcinogen (International Agency for Research on cancer, 1994). The formation of acrylamide in carbohydrate rich foods generally occurs, when heated at high temperatures (in excess of 120°C) under limited humid conditions. It is mainly due to a Maillard reaction which involves reducing sugars (glucose and fructose) and an amino acid asparagine (most abundant amino-acid in

potato). It is important to note that sucrose can be hydrolyzed through acid, enzymatic or thermal treatment acting as a precursor for formation of reducing sugars (Stadler et al., 2002; De Vleeschouwer et al., 2009; Rady et. al., 2014). Reducing sugars are considered to be a limiting factor for acrylamide formation despite the presence of amino acid precursor free asparagine, during processing of potato products in excess of heat. In order to restrict the formation of acrylamide to low levels, the content of reducing sugars should not exceed 100 mg/100g FW (Kumar et al., 2004). Moreover, small size tuber (<50mm size) contains more acrylamide content (322ppb) because of high amount of reducing sugar as compared to the large size tubers (>50 mm size) which possess 148ppb (Sinha and Naeem, 2018).

Since the first reports about acrylamide in food in 2002 (Swedish National Food Administration, 2002), scientific community mobilized and started serious efforts to minimize this mutagen by involving food industry to develop mitigation strategies. One approach is to develop and use SNP-based molecular markers for the selection of potato varieties with low reducing sugar or sucrose and free asparagine levels on a large-scale potato breeding program (Fischer et al., 2013; Li et al., 2013; Schreiber et al., 2014). Molecular markers offer a valuable opportunity to accelerate selection for plant breeders in order to develop new potato cultivars with better processing quality (minimal reducing sugars and free asparagine, high dry matter content, high specific gravity and starch content). These traits are polygenic, so GWAS based on high density genome wide markers could be efficient for dissecting these complex traits in potato.

The protein content of potato ranged between 1-2.95 g/100g on fresh weight basis. Though it is low compared to maize and beans but it produced more protein per unit planting area in comparison to cereals. Moreover, potato protein is considered as high quality owing to the presence of methionine, lysine, tryptophan and threonine (Lutaladio and Castaldi, 2009).

Potatoes also contain secondary metabolites such as carotenoids (especially xanthophylls) and anthocyanins, which are known as dietary antioxidants and may play major roles in preventing human diseases related to ageing, cancer, obesity and heart attack, which benefits health. The carotenoids (varied from yellow to orange colours) and anthocyanins (red and purple colours) are the two most valuable colouring pigments in potato.

Carotenoid amounts and types in tubers exhibit a large variation and positively correlated with tuber peel and the flesh colour (Burgos et al., 2009; Sulli et al., 2017). The carotenoid contents of white flesh potatoes are generally low (<100 µg/100 g fresh weight), contrasting to higher amounts in the yellow fleshed varieties (about 560 µg/100 g FW) (Nesterenko and Sink, 2003). A diploid germplasm of *Solanum* showed carotenoid concentrations of more than 2000 µg/100 g FW with intense yellow to near orange flesh colour (Lu et al., 2001). The primary tuber carotenoids in potato are lutein, zeaxanthin and violanxanthin, although some studies (André et al., 2007; Bonierbale et al., 2009) have also reported the presence of beta-carotene (precursor of provitamin A activity). The relative content of β-carotene in cv. Agria (yellow flesh) represented 2% of total carotenoids (Lachman et al., 2016). White, yellow and orange tuber flesh colour is mainly due to the presence of carotenoids (xanthophylls and beta-carotene) (Eck et al., 2007). Moreover, antioxidant activity and various phenolic contents are also associated with tuber skin and flesh colour. It is a wrong perception that tuber flesh colour is associated with starch content. In fact, the change in flesh colour of tuber depends on concentration of carotenoids not on the starch content. Therefore, it is imperative to identify the SNP markers associated with tuber flesh/skin color, carotenoids and starch for genetic gains in potato keeping in view the consumer preferability (Ah-hen et al., 2012). Tuber also accumulates steroidal glycoalkaloids (α-chaconine and α-solanine together with their derivatives such as solasodine and solanidine) that are important for plant resistance to pathogens and pests, but toxic to humans (Friedman and McDonald, 1997; Friedman, 2015).

Phenolic compounds are another group of secondary metabolites and well-known antioxidants, which possess the ability of scavenging free radicals and therefore important in the reduction of diseases such as inflammatory disorders and cardiovascular diseases. Xu et al. (2009), Albishi et al. (2013) and Kim et al. (2019) reported that chlorogenic, p-coumaric, cryptochlorogenic, ferulic, caffeic, vanillic acids, and tryptophan were detected in the tuber flesh. About 90% of total phenolic content (TPC) of tubers is comprised of chlorogenic acid (Friedman, 1997). Hence, an accurate measurement of TPC provides an estimation of chlorogenic acid. It has been reported that potatoes constitute a third highest dietary intake of total phenolics after orange and apple, owing to their high daily consumption (Chun et al., 2005). Al-Weshahy and Rao (2009) were of the view that potato peels comprised of 50% of TPC while variable amounts are present in flesh and

decreases towards the centre of tuber. Carotenoids and phenolics compound are well known antioxidants. They prevent the formation of free radicals and protects membranes and biomolecules such as DNA and proteins.

Tuber periderm (cell wall) thickness is another important trait which protects potatoes from bruisability, excoriation and dehydration. The potato skins are soft and somewhat immature and can be easily bruised or wounded upon harvest. The deposition of suberin in tuber cell wall acts as barrier for pathogen attack and water loss. Association mapping of this critical trait will help identify novel SNP markers to select genotypes with better cell wall reinforcement against excoriation, pathogen attack and dehydration (Lobato et al., 2017; Singh et al., 2020).

In crop genetics, phenotypic evaluation of complex traits (i.e., tuber quality traits) can be done in conjunction with next generation breeding and genomic tools along with generation of marker dense genetic linkage maps to find selection markers. These markers will serve the tendency to improve genetic gains in potato by abridging the breeding cycle.

2.4 Genetic Studies of Complex Traits by Next Generation Breeding Tools

Quality traits of tuber are categorized as complex traits affected by minor/poly-genes. Moreover, environment has a considerable impact on the quality and processing traits of potato. The world is rapidly adopting next generation breeding tools in the era of marker assisted selection, and recognized the potential of DNA markers in plant breeding. The genotypically different individuals can be screened phenotypically following forward genetics. Phenotypic variation and genetic polymorphism and their interrelationship are of great interest. Revealing the genetic factors underlying polygenic/complex traits such as tuber quality, needs a thorough and detailed understanding of allelic variation at specific locus controlling the phenotype and genetic architecture of a trait of interest. The biological phenotypic variation can be directly associated to the underlying causative loci through mapping approaches. Gene mapping is a major area of research now a days, working on the principle of chromosomal recombination during meiosis that resulted in gene segregation. The chromosomal regions or loci carrying the alleles/genes accountable for the genetic variation of polygenic traits (also termed as quantitative traits) is called

QTL (Quantitative Trait Loci). In order to achieve the goal of genetic mapping, bi-parental mapping populations (F1, RILs, NILs, backcross, and double haploid) are used for QTL (linkage) mapping, while unrelated individuals having natural variation are chosen for GWAS. Both of these mapping approaches has an objective to identify molecular markers associated with a QTL (Alqudah et al., 2020). Numerous DNA markers; for instance, RAPD (Random Amplified Polymorphic DNA), AFLP (Amplified Fragment Length Polymorphism), RFLP (Restriction Fragment Length Polymorphism), SSR (Simple Sequence Repeats), DArT (Diversity Array Technology) and SNP (Single Nucleotide Polymorphism) are used for linkage mapping and GWAS, the major characteristics of these markers are listed in **Table 2.1**.

Linkage maps have been constructed in potato through the use of markers like RFLPs, SSRs, AFLPs and SNPs (Bonierbale et al., 1988, Milbourne et al., 1998, Van Os et al., 2006, Anithakumari et al., 2010). High quality and dense SNP arrays are the product of next generation

Table 2.1. Characteristics of some commonly used molecular markers in plant breeding

Characteristics	RFLP	AFLP	RAPD	SSR	SNP	DArT
Codominant/Dominant	Co-dominant	Dominant	Dominant	Co-dominant	Co-dominant	Dominant
Polymorphism level	Medium	High	Very high	High	High	High
Reproducibility	High	Intermediate	Poor	High	High	High
DNA quantity required	High	Low	Medium	Low	Low	Low
DNA quality required	High	High	High	Low	High	High
Genome abundance	High	High	High	Medium	Very high	Very high
Marker index	Low	Medium	Medium	Medium	High	High
Sequencing	Yes	No	No	Yes	Yes	Yes
Cost	High	High	Less	High	Variable	Cheapest
PCR requirement	No	Yes	Yes	Yes	Yes	No
Visualization	Radioactive	Agarose gel	Agarose gel	Agarose gel	Infinium SolCAP/ SNP-VISTA	Microarray
Required DNA (ng)	10000	500–1000	20	50	50	50–100
Status	Past	Past	Past	Present	Present	Present

sequencing (NGS). This technique produced hundreds to millions and even billion of DNA bases per run (Shendure, 2008). Many organizations worldwide are now engaged in NGS and provide low cost-efficient services to the customers such as Illumina HiSeq and MiSeq 2500, Titanium, Ion Torrent PGM and Roche 454 FLX (Bentley et al., 2008; Thudi et al., 2012). NGS has advantages like low cost, high-throughput, whole genome sequencing, linkage/haplotype maps construction and genome-wide association studies.

Illumina platform is being used for the genotyping of diverse set of species, particularly SolCAP SNP array has been developed in potato and discussed in next section.

2.4.1 Infinium SolCAP SNP array

Expressed sequence tags (EST) projects based on Sanger sequencing provide a starting platform for the SolCAP projects based on NGS incorporating SNPs. Sanger sequencing found 237, 583 sequences with low coverage polymorphisms for only three potato cultivars Bintje (1905), Kennebec (1948) and Shepody (1980). High throughput NGS platforms enable us to characterize sequence diversity by the generation of large datasets of SNPs, their physical positions on chromosomes, and high-quality markers with gene annotation. The sequence of three North American potato cultivars (Premier Russet, Snowden and Atlantic) along with already available database of “Kennebec”, “Shepody”, and European cultivar “Bintje in National Center for Biotechnology Information (NCBI) was used for the development of SolCAP SNP array for potato. Transcriptome sequencing was performed extensively for each cultivar and results in generation of 2 Gb sequence with transcriptome of approximately 28-29 Mb in each cultivar. *de novo* assembly of reads were performed to get quality filtered reads of 575,340 SNPs among three North American cultivars. The existing sanger sequencing database identified 2,358 SNPs for additional three cultivars. Together with this information and high-density stringent filtering approach, in conjunction with potato reference genome, 69, 011 high confidence SNPs were identified (Potato Genome Sequencing Consortium, 2011; Hamilton et al., 2011). These SNPs were used with Infinium genotyping platform to develop subset of Infinium SolCAP 8303 SNP array (Solanaceous Coordinated Agricultural Project; http://solcap.msu.edu/potato_snp_table.shtml; Felcher et al., 2012). Hamilton et al., (2011) validated 85% of these SNPs in population of 244 potato clones. Two linkage maps were developed for validation of Infinium SolCAP 8303 potato array by Felcher et al., (2012) by genotyping of two diploid populations (DRH and D84). Potato had a genome size of 844 Mbp and the utility of Infinium SolCAP 8K array provide an excellent coverage of potato genome (633-641 Mbp) with an estimated 4,400 mapped markers (Hamilton et al., 2011, Felcher et al., 2012).

A biparental tetraploid mapping population can be genotyped efficiently with SolCAP potato array (Hackett et al., 2013). SolCAP 8K array was used for the genotyping (using

Illumina platform) of 36 different tetraploid cultivars and eight diploid clones. This was the first pilot study that use SolCAP 8K array in order to test population structure (Q) and Linkage disequilibrium (LD). Allele dosage (nulliplex to quadriplex) along with tetraploid calling of SNPs was performed efficiently using this array (Stich et al., 2013). Identification of introgression segments, founder and selection signatures were helpful in understanding the breeding history and recombination patterns in a population of 569 potato genotypes (537 tetraploid and 32 diploid) by using Infinium 20k SNP array (Vos et al., 2014). A SolCAP 12K SNP array was successfully employed by Ellis et al. (2018) for the diversity analysis and fingerprinting of 250 CIP (International Potato Center) accessions.

The genome wide coverage of Infinium SolCAP potato array coupled with high-throughput nature of estimating population structure diversity makes it a valuable tool for QTL mapping studies, map-based gene cloning and particularly GWAS. With the establishment of Infinium SolCAP Array, potato germplasm can now be genotyped with 8K, 12K, 20K, 25K and 69K SNPs at considerably less price using these high-density genotyping techniques. Potato SolCAP custom-made arrays offered the analysis of high-density SNPs per genotype with availability of allele dosage for autotetraploids (Hamilton et al., 2011).

Contrastingly, a GBS (Genotype by sequencing) method revealed 129,156 SNPs originated from Uitdewilligen et al. (2013). Since, only a small subset of SNPs can be used, stringent filtering is essential and redundant SNPs should be eliminated. This process narrows down the potential SNP number and results in selection of 15,123 SNPs, based on SNP dosage. The SNPs originated from Uitdewilligen et al. (2013) are referred to as “PotVar SNPs”, while the SNPs derived from Hamilton et al. (2011) are designated as “Solcap SNPs”.

Several studies used Infinium SolCAP 8k, 12k, 20k potato array for GWAS in potato to detect genomic regions associated with tuber quality traits (Berdugo-Cely et al., 2017, Schönhals et al., 2017, Sharma et al., 2018, Klaassen et al., 2019; Zia et al., 2020). QTL mapping was performed using SolCAP 8K SNP array by Massa et al. (2018). Majority of these studies focus on finding QTLs linked to starch, processing quality traits like fry and chip colour, and flesh colour. Review of literature suggests the research gap for the

implementation of 25K Infinium SolCAP SNP array along with high throughput phenotyping protocols and detecting genomic regions associated with tuber quality traits.

2.5 QTL Mapping

QTL mapping is a method involving molecular markers to locate the genomic regions/loci that affects the trait of interest. The steps involved in QTL mapping includes the selection of two diverse parents (bi-parental cross) with allelic variation affecting the trait of interest. Mapping population consists of F2 populations, DHs, Near-isogenic lines (NILs), recombinant inbred lines (RILs) and backcrosses (BCs). The construction of mapping populations through bi-parental crosses depends on genetic recombination and segregation since it affects the allele richness and genetic mapping resolution. Mapping population is subjected to phenotyping followed by acquirement of genetic data through molecular markers. The linkage or genetic map is then constructed along with the aid of some statistical platforms for the identification of loci cosegregating with trait of interest (Nadeem et al., 2019; Alqudah et al., 2020). The individuals in a mapping population may range from 25 to 250 with restricted recombinations but for higher resolution and fine mapping large populations is desired (Dhingani et al., 2015).

Environment directly affects the detection of QTL; therefore, complex traits are examined across multiple environments (location and year) to take into consideration genotype by environment interaction (GEI). This is particularly important to identify stable QTLs. A major limitation in QTL mapping is that it relies on the reduced number of recombination's/ meiotic events, and the diversity of segregated alleles occurs only in bi-parental populations. Furthermore, the development of homozygous lines (pure lines) for mapping populations is time consuming and results in low mapping resolution. Large number of markers are thus required for linkage mapping (Hackett et al., 2014). QTL mapping studies in potato is discussed in next section.

2.5.1 Review of QTL mapping studies for quality traits in potato

Detection of QTLs in potato associated with quality traits have been done in the past using QTL mapping approach. Studies found major QTLs on chromosomes 1, 2, 5, 7, 9, 10 and 11 within the positions of 10.46 to 114 cM associated with tuber starch content (Schäfer-

Pregl and Ritter, 1998; Chen et al., 2001; Li et al., 2005; Gebhardt et al., 2005; Werij et al., 2012; Śliwka et al., 2016; Li et al., 2019). Dry matter content (DMC) is synonymous to tuber starch content. QTLs linked to DMC was located on chromosomes 2, 3, 5, 8, 9 and 11 (Bradshaw et al., 2008; McCord et al., 2011; Manrique-Carpintero et al., 2015). QTL for chip colour was found on short arms of chromosomes 2 (8 and 21 cM) and 9 (18 cM). Candidate gene, "apoplastic invertase (*Invap-b*)" was found on chr 9 (Rak et al., 2017). The genes involved in carbohydrate metabolism and transport such as ADP-glucose pyrophosphorylase (*AGPase*), invertases, sucrose synthase, sucrose phosphate synthase and starch phosphorylases co-localized with QTLs linked with tuber starch and sugar contents. *AGPase* in particular found on chr 1 and 8 were found to be associated with tuber starch and chip quality (Gebhardt et al., 2005; Li et al., 2008). QTLs linked to candidate genes which functioned as sucrose transporter and sucrose sensor were located on chromosomes 11 and 5, respectively (Barker et al., 2000). Studies depict that genetic variation in chip colour is caused by variation in amount of reducing sugars and the allelic variants of these variables are located on almost all chromosomes with genes encoding function in carbohydrate metabolic pathways (Menendez et al., 2002).

Table 2.2. Review of QTL mapping studies related to quality traits in potato

Phenotypic Trait	Markers	Parents/Population	Major Findings	References
Tuber starch content (TSC)	DArT	Diploid potato clones (seed parent DG 00-683, pollinator DG 08-28/13) and F1 progeny	Most important QTL spanned a wide region of chr 1 (42.0–104.6 cM) with peaks at 63 and 84 cM, explaining 17.6 and 19.2 % of phenotypic variation.	Śliwka et al. (2016)
Tuber starch content	RFLP	K31 lines from crossing dihaploid <i>S. tuberosum</i> , LH: <i>S. tuberosum</i> (m) and <i>S. chacoense</i> (f) /K31 and LH	Detection of 18 QTLs on all 12 chromosomes. Some highly significant QTLs for starch content are present on chr 4, 5, 7 and 9 in K31 population. In LH population QTLs were found on chr 1 and 5.	Schäfer-Pregl and Ritter (1998)
Tuber starch content	RFLP	Parents and 90–150 F1 hybrids of the diploid mapping population K3149 F1 hybrids of the diploid mapping population LH/ K31 and LH	QTLs detected on all chromosomes except chr 5.	Chen et al. (2001)
Tuber starch and chip quality	AFLP	188 breeding clones from 3 cross combination populations; NZ1–NZ63, population BNA and NR1–NR70, population NORIKA and SR1–SR55, population SARA	Alleles, invGF-4d and invGF-6f, were significantly associated with chip quality on chr 9. Allele invGF-b associated with lower tuber starch content.	Li et al. (2005)
Tuber starch	AFLP and SSR	Diploid C (USW5337.3) × E (77.2102.37), C is the recurrent parent / Backcross	QTLs found on chr 5, 8, 9, 10, 12 for TSC, and all QTLs involved in TSC are consistent between years, high phenotypic correlation between years.	Werij et al. (2012)
Tuber Starch	RFLP, AFLP	8 diploid mapping populations; BC916, F1840, P49*P40, K31, LH, Erwinia, H94A, H94C	QTLs detected on all chromosomes associated with starch in tuber. Important candidate genes enclosing these QTLs were identified functional in apoplastic invertases and ADP-glucose pyrophosphorylase.	Gebhardt et al. 2005

Table 2.2. (Continue)

Phenotypic Trait	Markers	Parents/Population	Major Findings	References
Tuber starch content	AFLP and SSR	Longshu 8 (L8) (f) × Zaodabai (ZDB) (m)/ tetraploid F1 progeny	11 QTLs associated with starch on chr 1, 2, 4, 5, 7, 8 and 11 (10.46 cM to 114 cM). High heritabilities with 54–92% in clones over 3 years period.	Li et al. (2019)
DMC	AFLP and SSR	Atlantic (chip processing cultivar) × B1829-5 (advanced breeding line) / B2721 mapping population (F1)	QTLs were detected on chr 2, 3, 5 and 7 while QTL on chr 8 was associated with reduced DMC.	McCord et al. (2011)
DMC	582 SNPs	Pseudo-testcross; <i>S. tuberosum</i> Group Phureja DM 1-3 516 R44 and a heterozygous outcrossing <i>S. tuberosum</i> Group Tuberosum clone RH89-039-16	QTLs were detected for DMC on Chr. 2, 5, 8, 9, and 11 QTL on chr 9 co-localized with QTL and candidate genes for specific gravity, starch content, sugar (fructose and sucrose) content, and chip quality.	Manrique-Carpintero et al. (2015)
Specific gravity (SG)	RFLPs and RAPDs	<i>S. tuberosum</i> (Zr) × <i>S. chaeoense</i> Bitter/ F1 diploid	Identification of 10 QTLs across 3 environments on chr 1, 2, 3, 5, 7 and 11.	Freyre and Douches (1994)
SG	AFLP and SSR	Atlantic (chip processing cultivar) × B1829-5 (advanced breeding line) / B2721 mapping population (F1)	QTL on chr 2 was detected in both parents, QTL on chr 5 have additive and complex effects ; chr 8 have QTL with decreased SG whereas QTL on chr 9 linked with increased SG.	McCord et al. (2011)
Chip quality	AFLP And SSR	Diploid C (USW5337.3) × E (77.2102.37), C is the recurrent parent / Backcross	5 chromosomal regions (3, 5, 8, 9 and 10) influenced chipping colour.	Werij et al. (2012)
Chip colour	2095 SNPs	Chipping cultivar Liberator × Wisconsin breeding clone W4013-1 /110 biparental tetraploid	Chip color QTL localized to the short arms of chr 2 (8 and 21 cM) and 9 (18 cM). Candidate gene "apoplastic invertase (<i>Invap-b</i>)" found on chr 9.	Rak et al. (2017)

Table 2.2. (Continue)

Phenotypic Trait	Markers	Parents/Population	Major Findings	References
Cold induced Sweetening	AFLP And SSR	Diploid C (USW5337.3) × E (77.2102.37)	2 QTLs on chr 5 and 1 on chr 8.	Werij et al. (2012)
Amylose content	AFLP And SSR	Diploid C (USW5337.3) × E (77.2102.37)	5 QTLs at chr 2, 3, 5, 7 and 10 are associated with amylose content.	Werij et al. (2012)
Sugars	RFLP, AFLP	8 diploid mapping populations; BC916, F1840, P49*P40, K31, LH, Erwinia, H94A, H94C	QTLs detected on all chromosomes associated with sugars in tuber. Important candidate genes enclosing QTLs were identified functional in sucrose transportes, putative sucrose sensors and apoplastic invertases.	Gebhardt et al. (2005)
Sugars	RFLP, AFLP and Candidate genes	Two diploid F1 populations; H94A and H94C	QTLs found on all chromosomes, QTLs of glucose and fructose mapped on same chromosomes, Candidate genes identified functional in putative sucrose transporter, sensor, sucrose synthase 3 and invertases.	Menéndez et al. (2002)
Glucose and fry colour	SolCAP 8K SNP array	Rio Grande Russet' (female parent)× 'Premier Russet' (male parent) / 162 F1 progeny	Significant QTLs were detected on chr 4, 5, 6, 10 and 11. Chr 5 associated with both fry colour and glucose. QTL in candidate gene was located on chr 5 with fry colour and function as "apoplastic invertases".	Massa et al. (2018)
Skin texture	AFLP and SSR	Atlantic (chip processing cultivar) × B1829-5 (advanced breeding line) / B2721 mapping population (F1)	QTL on chr 2, 6 and 12 of Atlantic explained 2.7 to 13.6% of the variation. Chr 6 and 12 linked with smooth skin	McCord et al. (2011)
Tuber flesh colour	493 AFLP, 8 CAPS, and 13 SSR markers	10618-01 (purple-diploid)×320-02 (white flesh) /F1 mapping population of 228 clones	QTLs on chr 5, 8 and 9 mediating tuber flesh pigmentation, bHLH transcriptional regulator of anthocyanin biosynthesis colocalize on chr 9.	Zhang et al. (2009)
Tuber carotenoids	AFLP, SSR and DArT	01H15 × 03TR2 / F1 diploid	QTLs identified on chr 3 and 9; chr 3 QTL is due to dominant allele <i>chy2</i> and associated to beta-carotene, flesh colour, Zeaxanthin, lutein and total carotenoids. Chr 9 unlinked to any carotenoid biosynthetic genes.	Campbell et al. (2014)

Genotyping of biparental F1 mapping population having biological variation in tuber skin and flesh colour with help of AFLP, CAPS and SSR markers revealed QTLs on chr 5, 8 and 9 mediating tuber flesh pigmentation. The identified QTLs code for important candidate genes such as those involved in anthocyanin biosynthesis pathways (chalcone isomerase (*chi*) and chalcone synthase (*chs*), *bHLH* transcriptional regulator of anthocyanin synthesis pathway colocalize on chr 9 (Zhang et al., 2009). Since consumers preferred red and purple flesh tubers owing to high levels of antioxidants, genetic studies showed that *R* locus co-segregating with dihydroflavonol 4-reductase is needed for the production of red anthocyanins (De Jong et al., 2003), while purple flesh pigmentation is encoded by *P* locus with candidate genes functioning as flavonoid 3',5'-hydroxylase (Jung et al., 2005). Some studies mapped flesh colour pigmentation QTLs to chr 10 encoded by *Pf* locus (Van Eck et al., 1994). Yellow flesh colour of potato is due to *Y* locus (presence of dominant allele), and the likely candidate gene involved for this yellow pigmentation is β -carotene hydroxylase 2 (*Chy2*). QTL of this gene has been detected on chr 3 (Bonierbale et al., 1988; Campbell et al., 2014). Beta carotene is the most important carotenoid responsible for yellow colour pigmentation in potato and is thought to be present on chr 3. Wolters et al., (2010) admonished that among eleven *Chy 2* alleles, only one is dominant converting white tuber flesh to yellow, while the presence of orange flesh tubers is caused by accumulation of zeaxanthin primarily due to recessive *Zep* (zeaxanthin epoxidase) allele. A detailed review of QTL mapping studies in potato has been outlined in Table 2.2. QTL mapping studies related to phenolics, crucial amino acids (asparagine and glutamine), tuber skin thickness, total antioxidants, and tuber skin colour are limited. The detected QTLs for starch, sugars, and tuber flesh colour have shortcomings in potato breeding since they only represent a small haplotype blocks with restricted meiotic events and diversity due to bi-parental populations. Therefore, it is inevitable to enhance mapping resolution for the detection of stable and reliable QTLs especially for complex quality traits.

2.6 Genome Wide Association Mapping (GWAS)

GWAS explores allelic variation in diverse unrelated individuals from multiple meiotic and recombination events in breeding programme in contrast to genetic studies in bi-parental populations. It has high mapping resolution in contrast to traditional linkage mapping to identify the candidate alleles/genes (Baldwin et al., 2011). GWAS is a

powerful tool for association of phenotype with a genotype and identification of a causative gene/loci with higher resolution. It is considered as a valuable alternative to biparental crosses to identify QTL. A diverse association panel consisting of commercial cultivars and breeding lines/clones improve the detection of superior alleles within a gene pool of breeder. It efficiently manages the diversity of tetraploid gene pool (Björn et al., 2014). Mapping population is not required for GWAS, moreover historical recombination's accumulated over generations is considered for GWAS that enhanced the resolution of mapping. GWAS can be hypothesized as 'one (or more) of the genetic loci being considered is either causal for the trait or in linkage disequilibrium with the causal locus' (Rafalski, 2010). In linkage mapping for diploid population, the segregating alleles at a locus are 4 compared to 8 in tetraploid mapping using GWAS. The difference between association mapping and QTL mapping is envisioned in Table 2.3. The effectiveness and robustness of GWAS is well documented for the dissection of complex quality traits in potato using genome wide markers (Vos et al., 2015; Sharma et al., 2018). GWAS is key approach for studying natural variation and mapping of quantitative traits. To avoid spurious marker-trait association and false positives in GWAS, it is important to consider several factors affecting its power.

Table 2.3. Difference between QTL and Association mapping

QTL Mapping		Association mapping	
Benefits	Limitations	Benefits	Limitations
Crossing between two parents (biparental population)	Requirement of crossable and contrasting parents and multiple generations in order to develop pedigrees	No mapping population or crossing parents required	Population structure and kinship effect with false relatedness
Requirement of fewer number of markers	A limited number of genotypes based on the success of crossing Allele richness is low	Unlimited number of contrasting accessions Allele richness is high with high density markers such as SNPs	High number of individuals are required Allele frequency (minor allele frequency)
Expecting the segregating trait(s)	Low recombination and hence lower mapping resolution	High phenotypic variation	Natural variation may be misleading
More robust in heterogeneity	Genetic base is narrow	Highly density linkage maps	Heritability value may be low
Less prone to false positives	Sparse markers owing to the restricted recombination's	Tests at marker positions with higher mapping resolution	Markers requirement may be high for higher resolution and genome coverage.
Tests between markers			Errors of type I or II i.e., false positive associations.

These includes phenotypic variation, number of individuals, population structure and kinship, allele frequency and linkage disequilibrium (LD).

2.6.1 Population structure and Kinship

During the analysis and interpretation of GWAS, the relatedness correlation among the individuals in a selected population due to historical structure and admixture is determined by a statistical approach. The population structure is carefully generated for selected panel of individuals used in association analysis. The structure gives a hint of genetic diversity based on geographic origin or growth habit of individuals in a population. Ignoring the correction for population structure will lead to spurious marker-trait associations, since all individuals are not equally distantly related to each other.

The most common statistical software used for the analysis of population structure is STRUCTURE program. It estimates the clusters proportion or unknown number of subpopulations within the population referred to as Q matrix (Pritchard et al., 2000). The software used multi-locus data of diverse genotypes in a population and produced highly accurate clustering in order to explain the population structure. “Q” referred to a genotype membership coefficient matrix which is used as a covariate in GWAS.

Kinship matrix (K) explains the pairwise relatedness and genetic covariance among the random and multiple individuals in a population by using genotypic information. High genetic similarity means that the individuals are highly connected and related sharing same geographical origin, thus they can be clustered in the same group. A mixed-model approach by accounting Q+K model can control spurious marker-trait associations (Yu et al. 2006). The population structure in STRUCTURE software is determined using Structure Harvester (<http://taylor0.biology.ucla.edu/structureHarvester/>) which takes into consideration delta K values (Evanno et al., 2005; Earl et al., 2012). The proposed subpopulations (K) is plotted against delta K values to obtain the number of subpopulations or clusters. For instance, delta K=4 indicates the presence of four subpopulations or clusters, while delta K=2 showed no population structure or genetic similarity among the individuals in a population. Higher delta K is an indication of genetic diversity or unrelatedness of individuals in an association panel. Variable number “clusters/sub-populations” or “Kinship groups” were identified in literature for GWAS,

such as K = 6 (Rosyara et al., 2016), K= 3 (Vos et al., 2017), K=10 (Sharma et al., 2018), K =3 (Klassen et al., 2019) and K = 4 (Zia et al., 2020)

2.6.2 Linkage Disequilibrium (LD)

In population genetics, the co-occurrence of alleles at various loci in a population can be explained by two terminologies; Linkage Equilibrium (LE) and Linkage Disequilibrium (LD). These two terminologies depend on haplotype (combination of alleles) frequency in a population. LE is random association of alleles at different loci with same haplotype frequency in a population. LD referred to increase or decrease in haplotype frequency in a population, with non-random association of alleles at different loci. Though LD is present between tightly linked genes/alleles but LD is not the same as linkage. LD could be present in more distant allelic sites or between genetic factors on different chromosomes. Association mapping works on the principle of LD. This term is used for the position of a specific allele that is adjoining to one another on the same chromosome or the different chromosomes. LD indicates the distance between loci and is critical to decide the number of markers required to cover the whole genome. It is important to avoid false associations, high LD means that less markers are required for whole genome scan and vice versa. LD is measured by the two most common statistical terms showing the pairwise calculation of disequilibrium matrix among loci, which includes r^2 and D' . These coefficients showed that, how likely two loci are associated and sharing the history of recombination and mutation (Flint-Garcia et al., 2003). LD is therefore affected by recombination frequency of genome and population structure history of association panel. LD decay is an important parameter in GWAS, since it explains the extent of LD for particular gene or chromosome and also tells the size of LD block with minimum to no recombination. LD decay plot is made by plotting r^2 or D' against the genetic distance (cM or Mbp). In potato, LD is important for GWAS, because most cultivated tetraploid genotypes have a narrow genetic base, consisting of small number of haplotypes, due to extensive LD. In order to enhance the power of marker-trait association, LD tests in conjunction with correction of population structure by taking into account accurate subpopulations leads to reliable GWAS results (Simko et al., 2004). Zhu et al. (2003) was of the view that 2.0-2.5 cM distance is roughly equivalent to 1.0-1.5 Mbp. 5cM is the range for genome-wide LD stated by Björn et al. (2010). Zhao et al. (2011) showed that half of the initial LD is decayed at a distance of 600 Kb in potato. This LD decay is longer

than the values obtained in rice (100-300 Kb) and *Arabidopsis thaliana* (3-4 Kb) (Zhao et al., 2011; Kim et al., 2007). Stich et al. (2013) admonished that LD decay occurs with an intensity of 275 bp. Contrarily, Vos et al. (2017) used LD1/2,90 estimator with LD values ranged between 0.7 to 0.9 Mb. 2 to 4 Mb distance is the general trend for LD decay values in potato crop. Rapid LD decay indicates the tendency of markers co-inherited because LD is linked to marker density and population composition (Tamisier et al., 2020). Zia et al. (2020) used SolCAP 12K SNP array to find marker-trait association of morphological and tuber yield traits and admonished that LD decays with almost 1.22 Mbps to an r^2 value of 0.20.

2.6.3 Phenotyping

The capability to exploit the full potential of genomic and molecular breeding tools such as GWAS may be limited by ability to phenotype correctly (Araus and Cairns, 2014). Reliable and robust marker-trait associations to identify diagnostic SNP markers can be achieved efficiently by using high-throughput phenotyping techniques (HTPPs) (Zia et al., 2017). High performance liquid chromatography (HPLC), uv-vis spectrophotometry and polarimetry are the examples of some HTPPs using 2D, 3D and high-resolution imaging (refractive index detector, diode array detector) and novel handheld sensors (for instance, chroma-meter), for the profiling and quantification of important tuber quality traits. Comparison of automated (Martin Lishman potato hydrometer) and manual (oven-dry) phenotyping methods of quality traits; for instance, TDM revealed the reliability and robustness of HTTP technique and further avoiding spurious marker-trait associations in GWAS.

2.6.4 How GWAS works?

The association mapping studies consist of five main steps. The first step of association mapping in tetraploid potato is the formation of an association panel (association mapping population) including random collection cultivars and/or breeding lines. Then this potato panel is phenotyped for many traits of interest under field or controlled environmental conditions according to the feature of the trait. Most of agricultural important traits are evaluated at different environmental conditions (locations and years) to reduce environmental effects on the trait. The same potato panel is genotyped using a large

number of molecular markers. Recently, SNP markers are most commonly used in potato due to their abundance in the genome, and availability of genome sequence information. SolCAP array has been developed in potato and discussed in detail in **section**. As a next step, population structure and kinship of the association panel are estimated by analysing genotyping data using STRUCTURE software. The last step includes performing association analysis using phenotypic data and genotyping data. To minimize false marker-trait association, population structure and kinship data are used in association mapping analysis. Finally, SNP markers associated with traits are identified and then, those markers can be converted to KASP markers for MAS (Marker assisted selection) in breeding programs. By association mapping studies, several markers were associated with quality traits in potato. The flowchart depicting the process of GWAS is presented in Figure 2.2.

2.6.5 Software Packages for GWAS analysis

The utilization of statistical methods for GWAS have been evolved considerably for the past 20 years. Earlier tests include transmission disequilibrium test (TDT) which works on the relationship of parent-offspring for the identification of significant associations (Allison, 1997). Furthermore, the marker data of genotypes were used to estimate subpopulations or clusters to be used as a covariate in analysis. For this purpose STRUCTURE and EIGENSTRAT software's were used. We can obtain Q and P matrices, respectively from these software's ((Pritchard et al., 2000; Price et al., 2006). Kinship (K) matrix was estimated by Yu et al. (2006), which takes into consideration the random polygenic effect in the model.

Population member estimates or covariates (Q) can be assessed as GLM (Generalized Linear Model for association analysis in TASSEL (Trait Analysis by association, Evolution and Linkage). TASSEL can also calculate kinship matrix based on marker data. Q+K model is widely used model for the analysis of GWAS in autotetraploids particularly potato. MLM (Mixed Linear Model) can be implemented in TASSEL using Q+K model also termed as linear

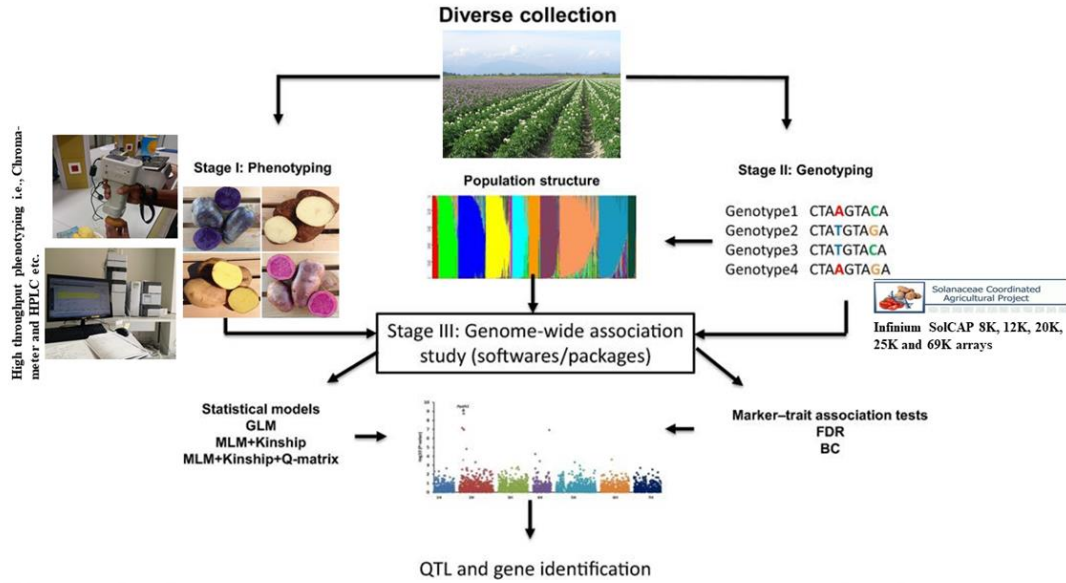


Figure 2.2. An illustration of genome wide association mapping (GWAS) model in potato breeding for the identification of QTL/diagnostic markers associated with a trait of interest.

mixed model (Bradbury et al., 2007). The equation 2.1 is as follows;

$$Y = X\beta + Zu + e \quad (2.1)$$

Where, Y= observation vector;

b = vector of fixed effects with population structure (Q) and genetic marker.

u = Random additive genetic effects from multiple QTL for individuals or lines.

X and Z = design matrices of known vector

e = residuals.

Marker-trait associations in TASSEL can be performed on marker data having diploid allele dosage. It is a major limitation of TASSEL as heterozygotes could not be differentiated in a co-dominant marker system. Association analysis of potato being autotetraploid with five allele dosage (nulliplex, simplex, duplex, triplex and quadriplex) becomes difficult and misleading in TASSEL. Therefore, another software package in R software have been developed by Rosyara et al. (2016). GWASpoly R package can be used in R software. This package is specially developed GWAS of complex traits in autotetraploids and makes use of BLUP (Best Linear Unbiased Prediction). It takes into consideration the tetraploid allele dosage and polyploid gene action comprising of

general, additive, simplex dominant (recessive and dominant) and duplex dominant (recessive and dominant). This package was successfully utilized in potato to find SNP markers and QTLs associated with chip colour, tuber eye depth, tuber shape, tuber length and total yield (Rosyara et al., 2016). The statistical power of this package is high as it considers multiple gene action, therefore avoids false positive associations.

2.6.6 Review of genome-wide association studies (GWAS) related to quality traits in potato

Potato has long been a subject of molecular studies owing to its nutritional value and significance for processing industry. Successful studies have been performed in potato for the detection of diagnostic SNP markers using GWAS approach related to tuber quality traits. Some of these studies have been highlighted in Table 2.4.

Tuber flesh colour is a trait of vital value as the biological variation (white to yellow/dark yellow) in this variable indirectly relates to the carotenoids in tuber tissue. GWAS studies identified the genomic region between 8 cM to 38.5 cM associated with this trait on chr 1, 3, 5, 6, 9, and 12 (Bjorn et al., 2014). The Y-locus has been mapped on chr 3 (Bonierbale et al. 1988) responsible for the yellow flesh colour in potato encoding candidate gene *beta-carotene hydroxylase* (often referred to as *Chy2* or *Bch*). A nice illustration has been presented by Wolters et al. (2010) in tetraploid potato that *Chy2* allele 3 is in fact the key determining factor for flesh colour. Contrastingly, chromosome 12 was associated with tuber flesh colour in a study by Sliwka et al. (2008). Some other QTLs associated with flesh colour were detected on chromosomes 1, 2, 3 (31.5 cM), 4, 6 and 7 (Björn et al. 2008). The fitted models used by Björn et al. (2008) were similar to Björn et al. (2014) for the detection of associations with quality traits. These GWAS studies proposed that the gene responsible for yellow colour in potato is present on chr 3 at a position of 31.5 cM. Tuber skin colour is an important trait considered by the consumers while purchasing potatoes. It also possesses several carotenoids and anthocyanin pigments that contributes to human nutrition. Mapping of genomic regions associated with this trait will help to select desirable skin colour of tubers in a breeding programme efficiently, without rigorous selection in the field. A diverse panel of 237 genotypes were genotyped with Infinium SolCAP 12K array to find out the marker-trait associations. GWAS detected 16 SNPs associated with tuber skin colour. These SNPs are present in the candidate genes

Table 2.4. Genome-wide association mapping studies of quality traits in potato: A literature review.

Phenotypic Trait	Markers	Population	Number of associated loci	Chromosome (Position)	References
Fry Colour	SNPs (GBS)	219 tetraploid genotypes	2; 29	4 (67 and 68 Mbp); 10 (49 to 59 Mbp)	Byrne et al. (2020)
	AFLP + SSR	205 cultivars and 299. breeding clones.	19	1 (43.8 cM); 4 (19.7 cM); 6 (6.6, 35, 51.8 cM); 7 (53.9 cM); 9 (15.8, 16.6 cM); 10 (57.6); 12 (43.6)	Björn et al. (2014)
	AFLP	221 tetraploid cultivars.	3	1 (4.6 cM); 2 (3.7cM); 7 (63 cM)	Björn et al. (2008)
Chipping colour	AFLP	221 tetraploid cultivars.	6	1; 2 (3.7 cM); 4 (27.5 cM); 7; 10 (49.3 cM)	Björn et al. (2008)
Underwater weight/	AFLP + SSR	205 cultivars and 299 breeding clones.	1	2 (62.8 cM)	Björn et al. (2014)
Dry matter content	AFLP	221 tetraploid cultivars	6	1 (8.4, 9.2 & 24.9 cM); 4 (21.3 cM); 5 (16.2 cM); 9(46 cM)	Björn et al. (2008)
Starch	183 SSR+ 221 SNPs	282 genotypes	8	1 (86.09 Mbp); 3 (39.25 Mbp); 4 (64.78 Mbp); 9 (60.56 Mbp); 10 (50.94, 50.85 Mbp); 11(08.21 Mbp); 12 (02.34 Mbp)	Schönhals et al. (2016)
	SNPs (SolCAP 8.3K)	264 varieties and breeding clones	127	All chromosomes; 0.3 Mbp to 86.3 Mbp with a width of 0.5 - 4 Mbp	Schönhals et al. (2017)
	SNP	40 cultivars	1	12	Fischer et al. (2013)
	SNP	243 tetraploid cultivars	2	1 (9 cM); 3	Li et al. (2013)
	SolCAP 20 K SNP array	277 genotypes	4	3 (61.49, 61.55, 61.55 and 61.89 Mbp)	Klaassen et al. (2019)
	SNPs (GBS)	762 clones (MASPOT population)	372	10 (45 and 60Mbp)	Sverrisdottie et al. (2017)
Specific gravity	33 candidate genes + 29 SSR loci	205 tetraploids	6	2; 3; 5 and 8	Urbany et al. (2011)

Table 2.4. (Continue)

Phenotypic Traits	Markers	Population	Number of associated loci	Chromosomes (Positions)	References
Tuber bruising	33 candidate genes + 29 SSR loci	205 tetraploids	9	2; 3; and 8	Urbany et al. (2011)
Protein	SolCAP 20 K SNP array	277 genotypes	12	3 (60.84 Mbp); 5 (4.40 - 5.69 Mbp); 7 (50.15 Mbp)	Klaassen et al. (2019)
Anthocyanin	7520 SNPs (GBS)	109 diploid landraces (Group <i>Phureja</i>)	7	1 (50.7 Mbp); 10 (52-57 Mbp); 11 (40 Mbp); 12 (24.2 Mbp)	Parra-Galindo et al. (2019)
Tuber skin colour	SolCAP 12K SNPs	237 tetraploids	16	1, 4, 5, 7, 8, 10, 11 and 12	Zia et al. (2020)
Tuber skin colour	SolCAP 8303 SNPs	809 accessions of Central Colombian Collection	3	2 (25.05 Mbp), 7 (53.65 Mbp), 10 (58.43 Mbp)	Berdugo-Cely et al. (2017)
Tuber Flesh colour	SolCAP 8303 SNPs	809 accessions of Central Colombian Collection	4	2 (45.69 and 47.32 Mbp), 4 (57.89 Mbp), 7 (53.07 Mbp)	Berdugo-Cely et al. (2017)
	GBS	83 tetraploid cultivars	27	3 (near <i>Chy</i> 2; beta-carotene hydroxylase), 4 and 12	Uitdewilligen et al. (2013)
	SolCAP 8K SNP array	351 tetraploid genotypes	2	3 (49.4 Mbp and 45.6 Mbp)	Sharma et al. (2018)
	AFLP + SSR	205 cultivars and 299 breeding clones	8	1 (8.8 cM); 3 (31.5 cM); 5(8.5 cM); 6 (13.7, 38.5 cM); 9 (16.6 cM); 12 (8.8 cM)	Björn et al. (2014)
	AFLP	221 tetraploid cultivars	6	1; 2; 3 (31.5 cM); 4; 6; 7	Björn et al. (2008)

functional in carotenoid pathways such as Lycopene epsilon-cyclase. The genomic regions associated with skin colour were present on chromosomes 1, 4, 5, 7, 8, 10, 11 and 12 (Zia et al., 2020). Berdugo-Cely et al. (2017) reported that chromosomes 2 (25.05 Mbp), 7 (53.65 Mbp) and 10 (58.43 Mbp) were associated with tuber skin colour. Infinium SolCAP 8k array was used for genotyping of 803 accessions of Central Colombian Collections for the detection of marker-trait associations. The same study dictated that 4 SNPs were associated with tuber flesh colour located on chromosomes 2, 4 and 7 with loci positions as 45.69 and 47.32 Mbp, 57.89 Mbp, and 53.07 Mbp, respectively. The SolCAP 8K array genotyped 803 accessions and provide informative data about 72% polymorphic loci (Berdugo-Cely et al., 2017) as opposed to 63.60% in case of Infinium SolCAP 12K array implemented for genotyping of 237 genotypes (Zia et al., 2020).

Fry colour is an important processing quality trait of potato indicating the discoloration of potato chips or French fries due to Maillard reaction. A major QTLs on chromosome (chr) 10 for fry colour in potato was reported by Byrne et al. (2020) using SNP database of 46,406 SNPs developed through genotyping by sequencing protocol. SNP clustering was observed towards the telomeres, a region notorious in potato for a much higher gene density. Although significant QTL associated with fry colour was also detected on chr 4 at 67 Mbp and 68 Mbp, but a large agglomerative group was found on chr 10 between 49 Mbp to 59 Mbp. This region enclosed several genes linked with sucrose synthesis, cleavage, metabolism and starch storage. It includes three invertase inhibitors, a cell-wall invertase, a sucrose-phosphatase, a fructose-1,6-biphosphatase, and two patatin genes (Potato Genome Sequencing Consortium, 2011; Byrne et al., 2020). Sverrisdottie et al. (2017) also showed the clustering of 372 SNPs on chr 10 (50 and 60Mbp) associated with fry colour by employing genotyping by sequencing approach on 762 offspring of 18 biparental cross and 74 breeding clones. Basically, the study was designed for genomic prediction models, however due to unclear population structure, a different SNP dataset was proposed to identify the genomic variants underpinning the observed biological differences.

Another study on the processing tuber quality traits using an “academic panel” of 205 tetraploid cultivars along with “industrial panel” of 299 cultivars from Dutch potato breeding companies detected marker-trait association related to fry colour at 57.6 Mbp

on chromosome 10. The analysis of the aforementioned panel was done with ultra-dense 720 mapped AFLPs and 53 SSR marker sets to find out association with 19 tuber quality characteristics (Björn et al., 2014). The marker-trait associations showed disparity with baseline (i.e., Marker + error) and advanced/correction for population structure (i.e., Marker + Genotype + Error) models, depicting 161 associations with the former models followed by reduction to 43 marker-trait associations in the latter. These differences originate due to different genotype sets, moreover phenotyping of tubers was subjected to genotype by environment interactions and also due to various storage treatments. Interestingly, several QTLs were shared by one or more traits like after baking darkening, after cooking darkening, fry colour and tuber flesh colour. A plausible reason for this shared marker-trait association could be polygenically control traits, pleiotropic effects of the candidate genes involved and are found to be in high LD with associated markers or maybe it showed the detection of true QTL or an inability to phenotype correctly. Accurate phenotyping is thus key to avoid false positives in GWAS for improving the signal-noise ratio (Björn et al., 2014). It necessitates a need to replace manual methods (breeders' eye) of phenotyping with automatic and systematised high throughput phenotyping platforms. A similar study utilized 551 AFLP markers and found marker-trait associations for frying colour on chr 1 (4.6 cM); 2 (3.7cM); 7 (63 cM), whereas chipping colour was associated on chr 1; 2 (3.7 cM); 4 (27.5 cM); 7 (63 cM); 10 (49.3 cM). Both these traits are indicators of cold induced sweetening in potato and found to be correlated ($r=0.49$). The detected loci (2 (3.7 cM) and 7 (63 cM)) linked to both traits seemed pleiotropic since they are related to same AFLP markers (Björn et al., 2008).

Dry matter content (DMC) is often referred to as underwater weight because it is measured through this principle and is a main determinant of processed tuber quality. About 60-80% of tuber dry matter content is starch. Starch and sugars are interconnected and part of the same metabolic network as described in section 2.3. Several GWAS studies have been reported in literature for the detection of markers/loci associated with tuber starch content, underwater weight (DMC), and sugars. GWAS was performed using QUEST population comprised of 264 varieties and PIN184 population consisting of 184 tetraploid breeding clones using RADseq (restriction-site associated DNA sequencing) and 8303k SolCAP SNP genotyping array. 127 SolCAP SNPs were identified using mixed linear model approach in 117 genes associated with tuber starch content. The identified genes were unequally distributed on all chromosomes and clusters between 0.5

to 4 Mbp width, with a putative regulatory and signalling functions (Schönhals et al., 2017). Underwater weight is an indicative of tuber starch content. GWAS studies conducted by Björn et al. in 2008 and 2014 detected loci at chr 1 (8.4, 9.2 & 24.9 cM); 2 (62.8 cM); 4 (21.3 cM); 5 (16.2 cM); 9(46 cM) associated with underwater weight. They also concluded that higher underwater weight is negatively correlated with early maturity in tubers. Association mapping study involving genotype by environment interaction (GEI) based on differences in soil type and rainfall patterns detected QTLs in association panel of 205 tetraploid cultivars. 21 QTLs were obtained hereinafter called as GEI QTLs associated with underwater weight, flesh colour, after cooking types, tuber maturity, size and shape. The GEI QTLs associated with frying colour; flesh colour and underwater weight were detected on chromosomes (positions) 9 (16.6 cM), 10 (14.1 cM); 6 (15.2 cM) and 7 (56.5 cM), 12 (46.6 cM), respectively (Björn et al., 2014).

Infinium SolCAP 20K array was used for genotyping of 277 tetraploid potato genotypes to be used for association mapping of proteins and starch (underwater weight of tuber). GWAS was performed using mixed model, naïve model and conditional mixed model. Naïve model was analysed by associating BLUEs (Best Linear Unbiased Estimates) with SNP dosage. Mixed model takes into account Kinship and population structure while conditional mixed model was performed using a maturity allele (*StCDF1.1*) as a cofactor along with corrected kinship. Naïve model gave false positive associations and did not identify QTLs in the subpopulation of “Starch”. Mixed model detected 12 significant QTLs using Li and Ji threshold ($-\log_{10}(P) = 3.9$). The QTLs for protein content were detected on chr 3 (60.84 Mbp); chr 5 (4.40 - 5.69 Mbp) and chr 7 (50.15 Mbp), while 4 marker-trait associations were significant for starch positioned at chr 3 (61.49, 61.55, 61.55 and 61.89 Mbp). Starch and protein content were positively correlated because photosynthesis derived carbon and nitrogen assimilation pathways are interconnected. Moreover, molecular studies showed that intracellular glucose is used by plants to synthesize both starch and protein. Hence, concluded that the genes that affect starch content may also regulate protein content in potato (Klaassen et al., 2019).

A candidate gene approach was also used for association studies, meaning that genotyping was performed for known genes selected in a functional context. A study was conducted to find out new candidate genes and confirm the reproducibility of few already known candidate genes by the introduction of novel association mapping population of

282 potato genotypes (i.e., 73 tetraploid breeding clones, 191 tetraploid cultivars and 18 landraces) The population was genotyped with 183 microsatellites + 221 SNPs including 14 candidate genes and 8 known diagnostic markers for starch content and yield. Marker-trait associations were detected on chr 1 (86.09 Mbp); 3 (39.25 Mbp); 4 (64.78 Mbp); 9 (60.56 Mbp); 10 (50.94, 50.85 Mbp); 11(08.21 Mbp); 12 (02.34 Mbp) by using mixed linear model with kinship and population structure (MM-PK). The loci/markers identified are present in the candidate genes *AGPase S* (ADP-glucose pyrophosphorylase S), *StCDF1* (transcription factor), *Pain - 1*, *SSIV* (starch synthase), *InvCD141* (invertases), *LapN* (leucine aminopeptidase) associated with tuber starch content and tuber yield (Schönhals et al., 2016). Association mapping analysis was performed by generation of locus specific amplicons using the genomic DNA of CHIPS-ALL population (i.e., 209 tetraploid cultivars and 34 standard varieties from Germany) (Fischer et al., 2013). First identification reports of the SNP₂₇₄₆ in the candidate gene *StLapN* (leucine aminopeptidase) was illustrated by Fischer et al. (2013). This gene was associated with tuber starch content and its yield, quality of chips under cold storage, colocalized on chromosome 12. It plays a vital role in sugar metabolism converting starch into sugars and responsible for cold induced sweetening (CIS). CIS is caused by enhanced levels of reducing sugars. Association mapping of historical phenotypic data originated from a breeding programme was used to identify alleles of candidate genes associated with sugars and CIS. SSR, SCAR and CAPS markers were developed for eight candidate genes; citrate synthase (*Cis*), apoplastic invertase inhibitor (*Stinhap*), acid invertase (*Pain 1*), sucrose synthase (*sus 4*), UGPase (UDP-glucose pyrophosphorylase), vacuolar invertase inhibitor (*StInh*), Apoplastic invertase (*Stm1051*), β -amylase (*Bmy*). UGPase and apoplastic invertase genes were significantly linked with CIS and glucose sugar. Interaction was observed for apoplastic invertase inhibitor and apoplastic invertase genes. SSR was identified as highly polymorphic marker (Baldwin et al., 2011).

Furthermore, a candidate gene association mapping approach detected SNPs in eight candidate genes *AGPaseS* (ADP-glucose pyrophosphorylase S, chr 1), *PGM1-3* (plastidial phosphoglucomutase, chr 3), *SssI* (soluble starch synthase I, chr 3), *PHO1b* (L-type starch phosphorylase b, chr 5), *INV-8/2* (invertase, chr 8), *BMV-8/2* (beta-amylase, chr 8), *PWD* (phosphoglucan water dikinase, chr 9), *InvCD141* (apoplastic invertase, chr 10), associated with tuber starch and chipping quality. *INV-8/2* has a crucial role in plastidial starch biosynthesis and degradation. These eight genes function in

starch-sugar interconversion, these two traits are inversely correlated. An increased tuber starch content was found to be associated with *PHO1b* (Schreiber et al., 2014). Tuber starch content, starch yield and chip quality were associated with polymorphisms in the candidate genes *AGPaseS-a* locus located on chr 1 and in *Pain-1* promoter region found on chr 3. *Pain-1* candidate gene encodes soluble acid invertases (converts sucrose to reducing sugars) on chr 3, important for chipping quality (Li et al., 2013). Tuber starch content and starch yield have shown epistatic interactions between candidate gene and alleles (Li et al., 2010).

Association genetics using a candidate gene approach identified allelic variants in genes functioning in enzymatic browning and tuber bruising. 205 tetraploid potato varieties and breeding clones were used as an association population panel. This panel was evaluated in 6 different environments for specific gravity, plant maturity, shape, yield, and tuber bruising susceptibility. 33 candidate genes and 29 SSR loci derived from 362 polymorphic DNA fragments, were tested for association with the already mentioned traits using a mixed model approach (taking into account population structure and kinship). 21 robust and highly significant ($p < 0.001$) marker-trait associations were identified. The identified genes for bruising and specific gravity were derived from Starch phosphorylase L-type (*PHO1A* and *PHO1B*), Lipase class III (*LIPIII-27-1h*), PPO isoform potpoloxA, 4-coumarate CoA Ligase genes (Urbany et al., 2011).

A diploid population from *S. tuberosum* Group *Phureja* consisting of 109 landraces was genotyped with 7520 SNPs using genotyping by sequencing. SNPs associated to 5 anthocyanidins (cyanidin, delphinidin, pelargonidin, petunidin, and peonidin) were analysed through GWAS. Seven QTLs associated to these five anthocyanins were detected on chr 1 (50.7 Mbp); 10 (52-57 Mbp); 11 (40 Mbp) and 12 (24.2 Mbp). The most stable QTLs were found on chromosomes 1 and 10. The SNPs in the candidate genes have functional roles related to the production of purple delphinidin-based pigments found on locus P (flavonoid 3',5'-hydroxylase-f3'5'h). Furthermore, the identified SNPs are a part of PAL enzyme, critical for anthocyanin biosynthetic pathway converting phenylalanine to coumarate-CoA (Parra-Galindo et al., 2019).

There is a huge research gap in association mapping studies of amino acids in potato. Asparagine (ASN) and glutamine (GLU) are thought to be crucial for transport and

storage of nitrogen in tubers, with ASN alone constituting about 25% of total free amino acid pool in potato. Asparagine synthase (*Ast*) gene is responsible for the synthesis of ASN and the genetic and molecular studies indicate that it is being altered by environment and is polygenic in nature. Furthermore, *Ast* genes are poorly characterized in potato (Chawla et al., 2012). Transgenic studies have been done to silenced this gene but molecular breeding approach following GWAS will prove to be more fruitful in development of selection markers for this trait.

2.7 Prospects

Reproducibility of the detected marker-trait associations in another population of same species is a big challenge. The main rationale for failure of marker-trait association reproducibility are different allele frequencies and recombination history, genotype by environment interactions, different phenotyping standards and sampling strategies. The accuracy and resolution of marker/loci identification controlling polygenic tuber traits can be improved by enhancing density of markers either through SNP genotyping arrays (SolCAP platform) or by GBS (Genotyping by sequencing). Robust analysis of multi-allelic haplotype along with distinction of three heterozygous states of potato (simplex, duplex and triplex) increase the power of marker-trait associations. The use of efficient high-throughput phenotyping protocols with rigorous field testing of genotypes in diverse environments, using advanced mixed models with correction of kinship, population structure and pedigree relationships, along with comparison of different marker types would enhance the genetic gains from GWAS.

2.8 Rationale of Current Study

Development of new varieties of potato with better quality traits (low reducing sugars and free asparagine, high dry matter content and starch, antioxidant properties) is always one of the major targets of potato breeding programs worldwide. Potato breeders are always interested in development of rapid and reliable screening tools for desired traits. Genetic gains in potato breeding can be achieved through marker assisted selection. The literature cited in above sections suggests that AFLPs, SSR and SolCAP 8K array has been used for GWAS, while linkage mapping was performed using RFLP, AFLP, SSR, DArT, CAPS and to lesser extent with SNPs. The identification of QTL using linkage

mapping is reduced due to low mapping resolution and restricted meiotic events owing to biparental segregating population, thus the applicability of QTLs in MAS is doubtful. Dominant markers are not readily linked to potato genome such as AFLP and DArT, while codominant nature of SNPs coupled with NGS Illumina platform (Infinium SolCAP SNP array) enhanced the genome wide high density genotyping in potato. GWAS provide reliable platform for the development of diagnostic SNP markers using Infinium SolCAP SNP array. Until recently, markers have been identified associated with starch, tuber skin colour, tuber flesh colour and proteins by using SolCAP 8K SNP array (Rosyara et al., 2016; Berdugo-Cely et al., 2017; Schönhals et al., 2017; Sharma et al., 2018), SolCAP 12K SNP array (Zia et al., 2020) and SolCAP 20K SNP array (Klassen et al., 2019). No GWAS study until now has used Infinium SolCAP 25K SNP array. Rosyara et al. (2016) conclusively stated that marker-trait association can be strengthen by inclusion of high marker density. Moreover, there is a scarcity of diagnostic SNP markers associated with phenotypic tuber quality traits like sugars (reducing sugars and sucrose), amino acids (for instance free asparagine), phenolics, antioxidants, beta-carotene and tuber skin thickness. Tuber quality traits (for instance; starch) are quantitative traits affected by minor/polygenes, therefore it needs careful assessment at multiple environments (locations and years) for optimization of selection strategy and MAS using diagnostic SNP markers. The current study aims to identify novel associations of diagnostic SNP markers with some tuber quality traits (dry matter content, specific gravity, reducing sugars, sucrose, free asparagine, total phenolics, total antioxidants, beta-carotene and tuber skin thickness). It is also expected to develop new diagnostic SNP markers linked with starch, tuber skin and flesh colour as well.

CHAPTER III

MATERIALS AND METHODS

3.1 Plant Materials and Experimental Plan

The research was conducted with diverse set of 192 tetraploid potato genotypes. All the genotypes used in this study belongs to *Solanum tuberosum* L. 91 (47.3%) genotypes were taken from the German (Norika) breeding company, 86 (44.7%) genotypes from the Turkish (Doğa) breeding company, and 15 (7.81%) genotypes commonly grown in both countries were also included to the genotype set. A defined explanation of the pedigree information of all genotypes is also elucidated (Table 3.1). The field experiments were carried out in Hatay province and Konya province between 2018 and 2019 representing four different environments, i.e., Hatay standard water application-2018 (HS-18), Konya standard water application-2018 (KS-18), Konya drought condition-2018 (KD-18) and Hatay standard water application-2019 (HS-19). KD-18 environment was subjected to deficit irrigation (35% of full irrigation) starting four weeks after emergence until harvest, while full or standard water/irrigation (100% of evapotranspiration) applied throughout growing season in other environments. The province of Hatay (36.26° N, 36.56° E, 183 m elevation) constitutes a Mediterranean climate and represents an early potato production area. The area has a characteristic clay silt loam soil with pH of 7.6 (slightly alkaline). Contrarily, the province of Konya (37.87° N, 32.49° E, 1016 m elevation) is the main crop area for potato production with continental type of climate. This experimental site has sandy clay loam soil with a pH of 8.1. Temperature (°C) and relative humidity (RH%) during growing season are shown in Table 3.2. The field experiments were set up in all four environments with same set of potato genotypes in Augmented block design (Petersen, 1985) using five check cultivars (Agria, Alegria, Jelly, Hermes, Rumba). Each plot consists of two rows 75 cm apart, having 25 plants per row at each site, with plant-to-plant distance of 30 cm. Standard potato production practices were followed during the growing period at each environment. After harvesting, the tubers of each genotype were collected and stored at +8 °C with relative humidity of 95%. All of the 192 genotypes from each environment were subjected to phenotypic evaluation for tuber quality traits as well as genotyping was carried out with an objective to find out diagnostic SNP markers associated with the tuber quality through GWAS approach.

Table 3.1. List of the genotypes included in the study along with the information of clusters, origin and their pedigrees

Serial No.	Genotypic Codes	Genotypes	^d Clusters	Origin	Parents (Female x Male)
1	2	JELLY	Cluster2	Common genotypes in both DE and TR	MARABEL x L 173/92/921
2	3	RUMBA	Cluster1	Common genotypes in both DE and TR	BOLESTA x MIRA
3	4	HERMES	Cluster1	Common genotypes in both DE and TR	DDR 5158 x SW 163 55
4	5	ALEGRIA	Cluster3	^a DE variety	Divina x 3.169 010-86
5	6	ROYAL	Cluster1	Common genotypes in both DE and TR	Midas x 92-BUY-1
6	7	ELECTRA	Cluster1	DE variety	C1992/42 x Picasso
7	9	^c DT14003.01	Cluster1	^b TR breeding line	Agria x CIP 397039.51
8	10	DT14038.01	Cluster3	TR breeding line	Fasan x Alegria
9	11	DT14010.18	Cluster1	TR breeding line	Bettina x CIP 397039.51
10	12	DT14004.17	Cluster1	TR breeding line	Alegria x CIP 397039.51
11	13	DT14010.14	Cluster1	TR breeding line	Banba x CIP 397039.51
12	14	DT14085.03	Cluster2	TR breeding line	Soraya x Lindita
13	16	DT14013.15	Cluster2	TR breeding line	Bettina x Jelly
14	18	DT14018.32	Cluster1	TR breeding line	Borwina x CIP 397039.51
15	19	DT14042.27	Cluster2	TR breeding line	Fasan x Jelly
16	20	DT14005.09	Cluster3	TR breeding line	Alegria x CIP 397039.51
17	21	DT14030.11	Cluster1	TR breeding line	CIP 397006.18 x Lindita
18	22	DT14057.37	Cluster2	TR breeding line	K2 x Jelly
19	23	DT14065.01	Cluster3	TR breeding line	Lady Rosetta x Alegria
20	24	DT14016.01	Cluster2	TR breeding line	Bettina x CIP 397039.51
21	25	DT14016.34	Cluster1	TR breeding line	Bettina x CIP 397039.51
22	26	DT14078.03	Cluster1	TR breeding line	Pomqueen x Jelly
23	27	DT14028.03	Cluster2	TR breeding line	CIP 397006.18 x Jelly
24	28	DT14054.11	Cluster1	TR breeding line	Jaerla x CIP 397039.51
25	29	DT14037.18	Cluster2	TR breeding line	Demon x Jelly
26	30	DT14091.04	^e Admixed	TR breeding line	(Tucan x Alegria) x Borwina
27	31	DT14083.28	Admixed	TR breeding line	Soraya x Hermes
28	32	DT14015.22	Cluster2	TR breeding line	Bettina x Unknown
29	33	DT14051.15	Cluster1	TR breeding line	Isla of Jura x Lindita

30	34	DT14047.38	Cluster1	TR breeding line	(Fasan x Tucan) x Borwina
31	35	DT14026.04	Cluster2	TR breeding line	CIP 396286.6 x Jelly
32	36	DT14068.07	Cluster2	TR breeding line	Maris Bard x Bettina Lady Olympia x CIP 397039.51
33	37	DT14063.12	Cluster1	TR breeding line	CIP 397077.16 x Lindita
34	38	DT14036.01	Cluster1	TR breeding line	Jelly x Lindita
35	39	DT14055.25	Cluster2	TR breeding line	Agria x KW 78-34- 470
36	41	LadyOlympia	Cluster1	Common genotypes in both DE and TR	Slaney x Estima
37	42	BANBA	Cluster1	DE variety	ZPC 69 C 239 x Gloria
38	43	VanGOGH	Admixed	Common genotypes in both DE and TR	Innavator x Alegria
39	44	DT14049.10	Cluster1	TR breeding line	Lady Olympia x Lindita
40	45	DT14061.23	Cluster1	TR breeding line	Atlantic x Soleia
41	46	DT14006.07	Cluster1	TR breeding line	(Fasan x Hermes) x Jelly
42	47	DT14046.19	Cluster2	TR breeding line	Bettina x Lindita
43	48	DT14014.27	Cluster1	TR breeding line	Banba x Lindita
44	49	DT14011.18	Cluster1	TR breeding line	Madeleine x CIP 397039.51
45	50	DT14069.13	Cluster1	TR breeding line	CIP 396286.6 x Jelly
46	52	DT14026.21	Cluster2	TR breeding line	Fasan x Jelly
47	53	DT14042.24	Cluster3	TR breeding line	(Tucan x Challenger)
48	54	DT14090.11	Cluster3	TR breeding line	x Alegria
49	55	DT14071.19	Cluster1	TR breeding line	Marabel x CIP 397039.51
50	56	DT14027.08	Cluster1	TR breeding line	CIP 396286.6 x Lindita
51	57	DT14034.03	Cluster2	TR breeding line	CIP 397065.28 x Jelly
52	58	DT14057.36	Cluster2	TR breeding line	K2 x Jelly
53	59	DT14062.08	Cluster1	TR breeding line	Lady Olympia x Jelly
54	60	DT14079.02	Cluster1	TR breeding line	Pomqueen x Lindita
55	61	DT14053.03	Cluster2	TR breeding line	Jearla x Jelly
56	63	DT13088.03	Cluster3	TR breeding line	Maris Bard x Alegria
57	64	DT14051.66	Cluster1	TR breeding line	Isla of Jura x Tucan
58	65	DT13100.02	Cluster1	TR breeding line	Agria x Alegria
59	66	DT13162.15	Cluster3	TR breeding line	Van Gogh x Alegria
60	67	DT13162.12	Cluster3	TR breeding line	Van Gogh x Alegria
61	68	DT11107.01	Cluster3	TR breeding line	Tucan x Alegria
62	69	ZIRVE	Cluster3	TR variety	Saturna x Lady Olympia
63	70	DT12012.02	Cluster3	TR breeding line	Alegria x Tucan
64	71	DT13136.22	Cluster1	TR breeding line	Shepody x Alegria
65	72	DT13045.74	Cluster4	TR breeding line	Isla of Jura x Challanger
66	73	DT13124.21	Cluster3	TR breeding line	Saturna x Alegria

67	74	BORWINA	Admixed	DE variety	Berber x 2.6 720-86
68	75	BROOKE	Cluster1	DE variety	FL1867 x Hermes
69	76	TESSA	Cluster4	Common genotypes in both DE and TR	Carmona x Diplomat
70	77	DT13143.49	Cluster3	TR breeding line	Soraya x Alegria
71	78	DT13130.48	Admixed	TR breeding line	Saturna x Nandu
72	79	DT13143.54	Cluster3	TR breeding line	Soraya x Alegria
73	80	DT13007.03	Cluster2	TR breeding line	Alegria x Hermes
74	81	KUTUP	Cluster1	TR variety	Pomqueen x Tucan
75	82	DT13028.01	Cluster4	TR breeding line	Fasan x Romanze
76	83	DT13093.92	Cluster4	TR breeding line	Melody x Romanze
77	84	DT13051.10	Cluster1	TR breeding line	Isla of Jura x Tucan
78	85	DT13143.58	Cluster3	TR breeding line	Soraya x Alegria
79	86	DT13026.10	Cluster1	TR breeding line	Fasan x Maris Bard Isla of Jura x Maris Bard
80	87	DT13049.50	Cluster1	TR breeding line	Lady Olympia x Romanze
81	88	DT13072.19	Cluster1	TR breeding line	Marabel x Melody
82	89	DT13083.01	Cluster1	TR breeding line	Cardinal x SVP
83	90	LadyRosetta	Cluster1	Common genotypes in both DE and TR	VTn2 62 33 3
84	91	DT11007.01	Cluster3	TR breeding line	Alegria x Challenger
85	92	DT11108.02	Cluster1	TR breeding line	Tucan x Banba
86	93	DORUK	Cluster3	TR variety	Fasan x Alegria
87	94	DT13085.01	Cluster1	TR breeding line	Marfona x Felsina
88	95	DT12068.21	Cluster3	TR breeding line	Marabel x Alegria
89	96	DT11088.01	Cluster3	TR breeding line	Saturna x Alegria Isla of Jura x Challenger
90	97	DT13045.42	Cluster2	TR breeding line	Spunta x Alegria
91	98	DT13147.17	Cluster3	TR breeding line	Isla of Jura x Jelly
92	99	DT13048.10	Cluster2	TR breeding line	Innara x Alegria
93	100	DT13052.23	Cluster3	TR breeding line	Horizon x Alegria
94	101	DT13037.31	Cluster1	TR breeding line	Isla of Jura x Challenger
95	102	DT13045.103	Cluster1	TR breeding line	Horizon x Alegria
96	103	DT13037.35	Cluster3	TR breeding line	Isla of Jura x Gala
97	104	DT13047.08	Cluster1	TR breeding line	Van Gogh x Alegria
98	105	DT13162.16	Cluster3	TR breeding line	Lady Claire x Challenger
99	106	DT13067.03	Cluster2	TR breeding line	Marabel x 1.307 120-93
100	107	SORAYA	Cluster2	Common genotypes in both DE and TR	
101	108	LAURA	Cluster2	Common genotypes in both DE and TR	Rosella x L 6140/2
102	109	SHEPODY	Cluster1	Common genotypes in both DE and TR	Bake King x F 58050
103	110	43-111-11	Cluster4	DE breeding line	581 115-03 x Tessa Adretta x 3-69.121/55
104	111	KARLENA	Cluster4	DE variety	668 106-03 x Kiwi
105	112	139-101-11	Cluster4	DE breeding line	Margit x 821 208-04
106	113	84-105-11	Admixed	DE breeding line	

107	114	NANDU	Cluster4	DE variety	1. 45 210-92 x Tristan
108	115	882-202-10	Admixed	DE breeding line	320 206-02 x W 1348 rus
109	116	TALENT	Cluster2	DE variety	3.716 143-85 x Marabel
110	117	57-104-11	Cluster4	DE breeding line	591 107-03 x Delikat 320 206-02 x
111	118	878-202-10	Cluster1	DE breeding line	Innovator 668 106-03 x 617
112	120	146-103-11	Cluster4	DE breeding line	107-03 1.230 101-93 x
113	121	SALUTE	Cluster4	DE variety	Baltica
114	122	68-105-11	Cluster4	DE breeding line	599 103-03 x Delikat
115	123	63-113-11	Admixed	DE breeding line	599 103-03 x Tessa AR 00-0799 x
116	124	106-105-11	Cluster2	DE breeding line	Delikat
117	125	939-201-10	Cluster1	DE breeding line	Kiebitz x W 2133-1 852 105-99 x 916
118	126	NIXE	Admixed	DE variety	218-00
119	127	51-109-11	Cluster4	DE breeding line	Dukata x Tessa
120	128	ETIKETSIZNORIK	Cluster4	DE variety	-
121	130	40-103-11	Cluster4	DE breeding line	581 115-03 x Delikat
122	131	99-115-11	Cluster1	DE breeding line	Naviga x Nautilus 668 106-03 x 630
123	132	141-104-11	Cluster4	DE breeding line	104-03
124	133	89-105-11	Cluster4	DE breeding line	Margit x Delikat Innovator x 107 204-
125	134	NAUTILUS	Cluster1	DE variety	96
126	136	157-103-11	Cluster4	DE breeding line	Baltic Cream x 735 103-99
127	137	133-112-11	Cluster4	DE breeding line	332 201-02 x 668 106-03
128	138	944-208-10	Cluster4	DE breeding line	332 201-02 x 1.87 204-92
129	139	PRIVELIGE	Cluster4	DE variety	Carmona x 107 204-
130	140	966-203-10	Cluster4	DE breeding line	96
131	141	904-212-10	Cluster2	DE breeding line	Jumbo x 1133 203-00 581 115-03 x 600
132	142	BETTINA	Cluster2	DE variety	111-03
133	143	125-104-11	Cluster4	DE breeding line	Franzi x 795 / 883
134	144	SWING	Cluster2	DE variety	Kea x Omega
135	145	758-109-09	Cluster4	DE breeding line	Talent x Topas
136	146	735-102-09	Cluster4	DE breeding line	Opal x 999 211-00
137	147	99-102-11	Cluster1	DE breeding line	Kiwi x Clarina
138	148	TERRANA	Cluster4	DE variety	Naviga x Nautilus 1.195 311-70 x
139	149	104-103-11	Cluster1	DE breeding line	51.4212 158-83 AR 00-0799 x
140	150	SFHIT	Cluster4	DE variety	Fontane Diana x PomQueen

141	151	KIWI	Cluster4	DE variety	1. 33 201-91 x Tristan
142	152	KIEBITZ	Cluster4	DE variety	1.599 004-90 x 1. 87 204-92
143	153	BONUS	Cluster4	DE variety	3.608 001-85 x Panda AR 98-0452 x 947 204-00
144	154	509-104-09	Cluster4	DE breeding line	581 115-03 x Tessa
145	155	43-118-11	Cluster4	DE breeding line	Pirol x Kiwi
146	156	BEO	Cluster4	DE variety	Diana x Jupiter
147	157	BALTICCREAM	Cluster4	DE variety	Carmona x 581 115- 03
148	158	868-201-10	Cluster3	DE breeding line	Jelly x Topas
149	159	860-201-10	Cluster2	DE breeding line	1.833 103-95 x Talent
150	160	DUKATA	Cluster4	DE variety	Margit x 821 208-04
151	161	84-107-11	Admixed	DE breeding line	Kea x 668 106-03
152	162	128-105-11	Cluster4	DE breeding line	668 106-03 x Pelikan
153	163	140-107-11	Cluster4	DE breeding line	1. 97 201-92 x 1. 87 204-92
154	164	PELIKAN	Cluster2	DE variety	61.107 018-80 x 1.328 001-73
155	165	KOLIBRI	Cluster4	DE variety	1077 201-00 x 320 206-02
156	167	82-119-11	Cluster4	DE breeding line	1.742 102-95 x Gala
157	168	WENDY	Admixed	DE variety	3. 14 104-90 x Rasant
158	169	ROMANZE	Cluster4	DE variety	Sjamero x Panda
159	170	PRESTIGE	Cluster1	DE variety	Sibu x W2899/9b
160	171	MAXI	Cluster4	DE variety	6.915 2023-77 x 1.299 103-77
161	172	FASAN	Cluster4	Common genotypes in both DE and TR	Leyla x KO 85-1002
162	173	Madaleine	Admixed	Common genotypes in both DE and TR	Agria x Disco
163	174	POMQUEEN	Cluster1	Common genotypes in both DE and TR	Bonza x W2899/9b
164	175	MUNGO	Cluster4	DE variety	1.293 112-77 x 1.3014 102-81
165	176	ALBATROS	Cluster4	DE variety	1.742 102-95 x Filea
166	177	FIDELIA	Admixed	Common genotypes in both DE and TR	Marabel x Borwina
167	178	TACOMA	Cluster2	DE variety	Petra x Maxilla
168	179	BONZA	Cluster4	DE variety	LU. 59.884/3 x Axilia
169	180	ADRETTA	Cluster4	DE variety	Indira x Bonanza
170	181	POWER	Cluster4	DE variety	Andante x Agila
171	182	GOLDMARIE	Admixed	DE variety	W978/334 x W7224/308
172	183	RITA	Admixed	DE variety	Indira x Eleisa
173	184	SUMMERGOLD	Cluster4	DE variety	Marabel x Melina
174	185	DIPLOMAT	Cluster4	DE variety	Solara x Gala
175	186	CASCADA	Cluster3	DE variety	Karlana x Karatop
176	187	SOLIST	Cluster2	DE variety	Exquisa x Ditta
177	188	LOLITA	Admixed	DE variety	

178	189	KARATOP	Admixed	DE variety	2-73.4312 x Karat Marabel x 1.236 103-93
179	190	INARA	Cluster1	DE variety	33. 36 020-79 x Karlana
180	191	ACAPELLA	Cluster4	DE variety	Apart x Borwina
181	192	ALLORA	Cluster4	DE variety	Axilia x (Saskia x Schwalbe)
182	193	ARKULA	Cluster1	DE variety	Inara x Amanda
183	194	TOKIO	Admixed	DE variety	Marabel x 1.572 101-90
184	195	BIRTE	Cluster2	DE variety	581 115-03 x Innovator
185	196	900-205-10	Admixed	DE breeding line	MA. 62.34/21 x LU. 62.356/11
186	197	MAXILLA	Cluster4	DE variety	Albatros x Pazifik
187	198	TUCAN	Cluster4	DE variety	332 201-02 x Troja
188	199	946-202-10	Cluster4	DE breeding line	3.608 001-85 x 51.4212 158-83
189	200	KORMORAN	Cluster4	DE variety	Assia x W2754/8b
190	202	JUMBO	Cluster4	DE variety	Ekra x (Panda x W610/33)
191	203	LOGO	Cluster4	DE variety	AR 01-0978 x 596 120-03
192	204	102-102-11	Admixed	DE breeding line	

^aDE= *Deutschland (Germany)*

^bTR= *Turkish (Turkey)*

^cDT= *Doğa Tohumculuk*

^dClusters= *Corresponds to clustering in Fig 4.6 and 4.7. Clusters in Fig. 4.7 followed the sequence of serial no. of genotypes.*

^eAdmixed= *Clusters having Q values (i.e., population structure covariates) less than 0.40*

Table 3.2. Description of temperature (°C) and relative humidity (RH%) during growing season

Hatay 2018 (early)				Konya 2018 (seasonal)				Hatay 2019 (early)			
Months	High/low (°C)	Temp ^b (°C)	RH ^a (%)	Months	High/low (°C)	Temp (°C)	RH (%)	Months	High/low (°C)	Temp (°C)	RH ^a (%)
January	18/-2	6	73	April	26/1	14	48	January	14/-5	5	80
February	17/-2	8	77	May	27/6	18	59	February	14/-2	6	81
March	24/3	12	67	June	33/11	21	51	March	20/-1	9	72
April	28/1	16	52	July	35/14	25	41	April	24/2	12	74
May	32/9	20	59	August	34/14	25	36	May	37/7	21	48
				September	33/9	20	43				

RH^a(%) = Average relative humidity; Temp^b (°C) = Average temperature

3.2 Phenotyping of Tuber Quality Traits

The research was conducted pertaining to twelve different potato tuber quality traits; i.e., tuber dry matter content (TDM), tuber specific gravity (TSG), tuber skin colour (TSC), tuber flesh colour (TFC), reducing sugars (RS), sucrose (SUC), free asparagine (ASN), tuber skin thickness (TST), total antioxidant activity (TAC), total phenolic content (TP), beta-carotene (β -C) and tuber starch content (TSA).

3.2.1 Preparation of freeze-dried potato powder extract for quality analysis

Tuber quality traits such as TDM, TSG, TSC and TFC were determined instantly after harvest. Analysis of remaining tuber quality characteristics were carried out on tuber samples kept in cold storage (+8 °C with 95% RH) for about 15 days prior to lyophilization or freeze drying.

3.2.1.1 Lyophilization of tuber samples

Eight to ten fresh raw tubers of each genotype were peeled and cut into small cubes/slices, later mixed together to obtain 300 g to 400 g of working sample. Samples were refrigerated at -20°C immediately to avoid colour change due to oxidation. Later, the samples were put to lyophilization for freeze drying. On an average, 12 samples were lyophilized or freeze dried in 4 days. Freeze drying was carried out with stringent conditions of -80 °C temperature with vacuum pressure of 0.110 mBar (Fig. 3.1).



Figure 3.1. Lyophilizer (Left); Sliced tuber samples for lyophilization or Freeze drying (Right)

.2.1.2 Milling of samples

After lyophilization, the samples were milled with help of coffee grinder to make a fine freeze-dried powder (Fig. 3.2). It was used further for the analysis of tuber quality traits such as reducing sugars, sucrose, free asparagine, total antioxidant activity, total phenolic contents, tuber starch contents and beta-carotene.

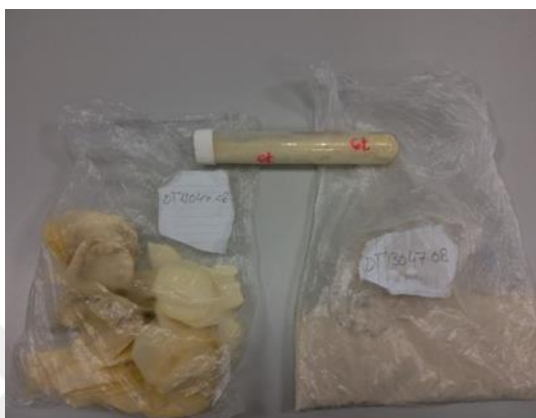


Figure 3.2. Tuber samples after freeze drying and milled accordingly to make fine powder

3.2.2 Tuber dry matter content (TDM)

Tuber dry matter content of 192 genotypes were measured by three methods; 1) Martin Lishman's digital potato hydrometer (based on under water weight measurement principle), 2) oven-dry method and 3) moisture-air oven method (AACC, 1993a; 1993b; Haase, 2003) also referred to as seasand method. The first two methods were employed in all four environmental conditions for each genotype included in the study, while seasand method was implemented for further in-depth analysis of TDM in Konya "standard water application" and Konya "drought conditions" for the same number of genotypes. The determination of TDM through hydrometer was carried out with a subsample of around 2500 g clean unpeeled raw tubers from each genotype replicated three times. It is a non-destructive method of TDM measurement in contrast to two other destructive methods discussed below (Fig. 3.3).

In oven-dry method, 5 to 8 raw tubers (randomly selected) were peeled, chopped and put in three aluminium boxes. Fresh weight of tuber samples was taken by using electronic

balance. Later, samples were oven dried at 90 °C for 16 h. Dried tuber samples were weighed again. Each genotype was replicated thrice. TDM% was calculated by formula:

$$TDM\% \text{ for oven-dried method} = \text{Oven dry weight} / \text{initial fresh weight} \times 100$$

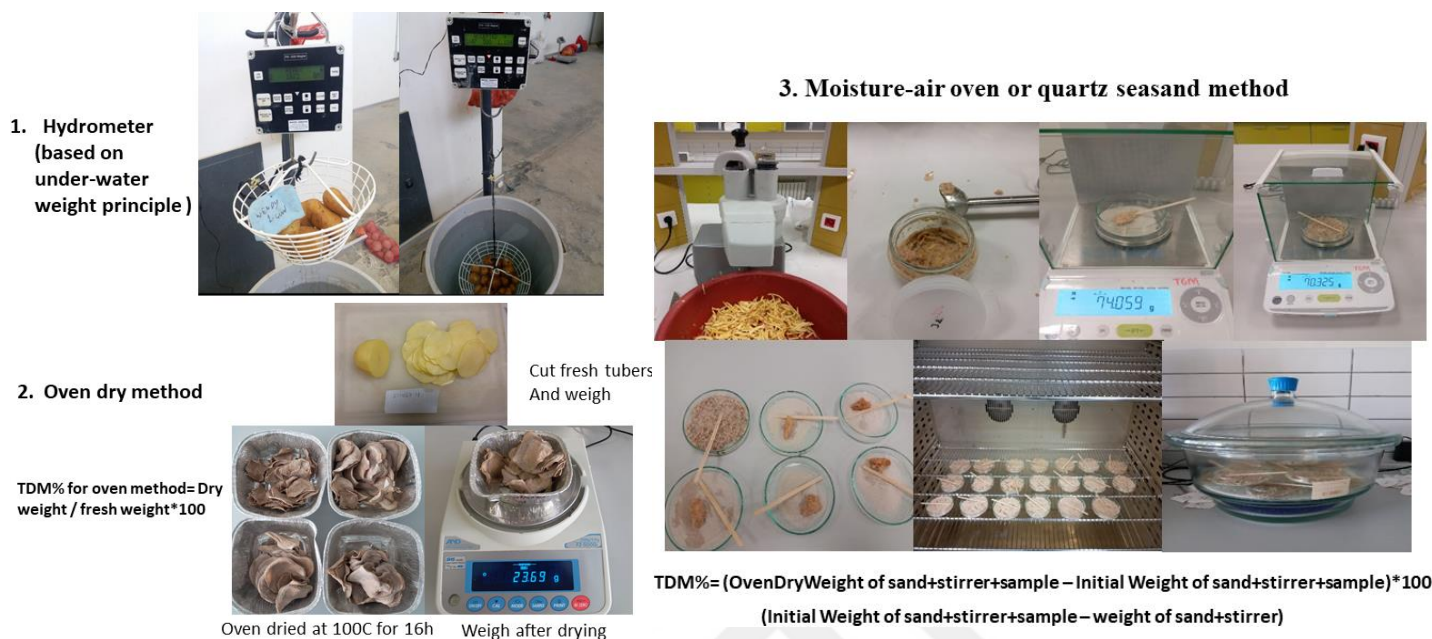


Figure 3.3. Hydrometer (1), oven-dry (2) and quartz seasand methods (3) demonstration for the measurement of TDM%

In moisture-air oven or quartz seasand method, 5 to 8 raw tubers were selected at random from each genotype. Tubers were cleaned under tap water and outer skin was dried prior to analysis. Tubers were sliced and later an aliquot of around 350 g was homogenized (mash) with a kitchen mixer. Dry quartz seasand was taken in petri dishes along with stirrer and weighed. 2.5 g to 5.0 g of homogenized tuber mash was placed in a petri dish and weighed along with stirrer. Sample was dried in an oven at 105 °C for 15 h, subsequently cooled down in a desiccator and weighed again on sensitive electronic balance (Fig. 3.3). All measurements were replicated three times. The TDM% was calculated by formula:

$$TDM\% = \frac{(\text{Oven dry weight of seasand} + \text{stirrer} + \text{sample} (g) - \text{weight of seasand} + \text{stirrer} (g)) \times 100}{(\text{weight of seasand} + \text{stirrer} + \text{sample} (g) - \text{weight of seasand} + \text{stirrer} (g))}$$

3.2.3 Tuber specific gravity (TSG)

Specific gravity of the genotypes was measured by using Martin Lishman's Digital Potato Hydrometer. The determination of specific gravity through hydrometer was carried out with a subsample of around 2500 g clean unpeeled raw tubers from each genotype replicated three times.

3.2.4 Tuber skin colour (TSC)

The skin colour of the tubers was measured with the help of chroma meter CIELab colour scale (CR-400 Konica Minolta Sensing, Inc., Osaka, Japan) (Fig. 3.4). An aperture size of 8 mm was used and the colour was designated in three dimensions L^* a^* b^* . The L^* values state the position on the white/black axis, the a^* values state the position on the red/green axis, and the b^* values state the position on the yellow/blue axis. Five replications were used for analysis of tuber skin colour for each genotype.

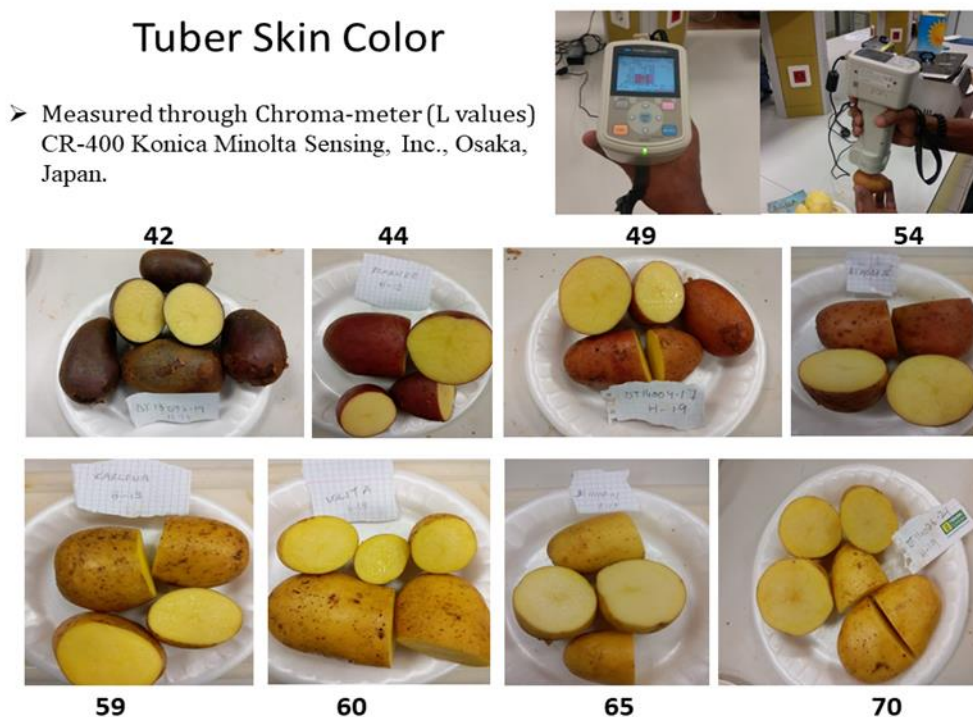


Figure 3.4. Measurement of tuber skin colour with chroma-meter along with the numerical values of dimension “L” segregating with skin colour (dark brown and red to light yellow)

3.2.5 Tuber flesh colour (TSC)

The flesh colour of the tubers was measured with the help of chroma meter CIELab colour scale (CR-400 Konica Minolta Sensing, Inc., Osaka, Japan) (Fig. 3.5). An aperture size of 8 mm was used and the colour was designated in three dimensions L^* a^* b^* . The L^* values state the position on the white/black axis or lightness, the a^* values state the position on the red/green axis, and the b^* values state the position on the yellow/blue axis. Five replications were used for analysis of tuber flesh colour for each genotype.

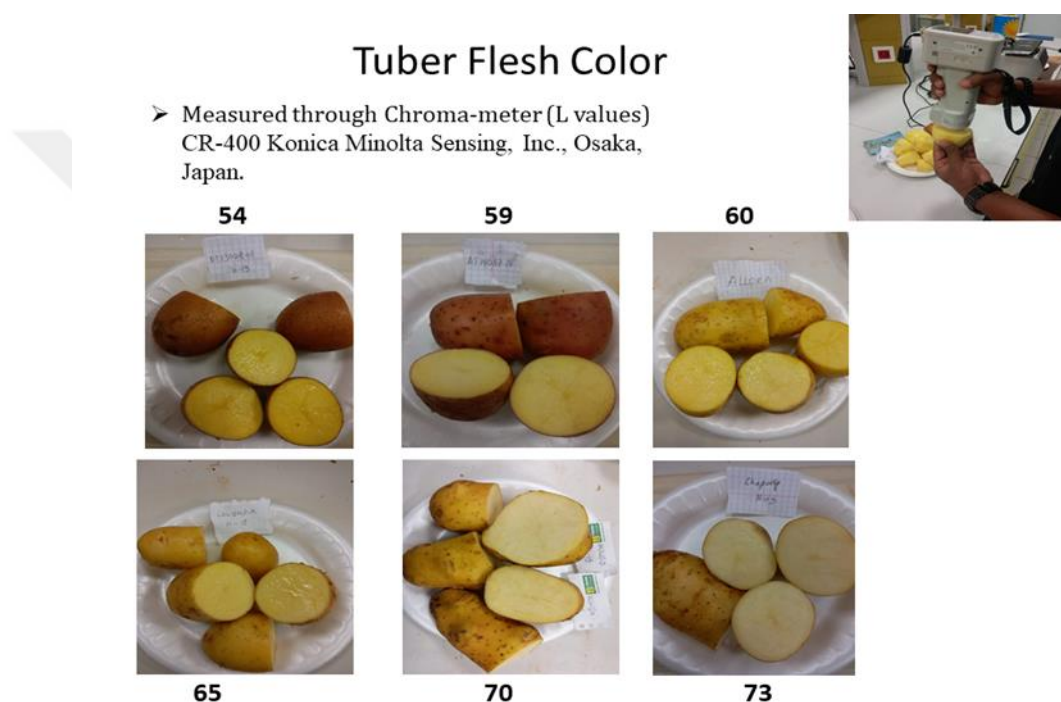


Figure 3.5. Measurement of tuber flesh colour with chroma-meter along with the numerical values of dimension “L” segregating with flesh colour (dark yellow to white)

3.2.6 Reducing sugars and sucrose (RS and SUC)

3.2.6.1 Sample preparation

The reducing sugars in potato tubers was measured through HPLC (high performance liquid chromatography) according to method described by Plata-Guerrero et al. (2009) with few modifications. Approximately, 3 g to 5 g lyophilized freeze-dried potato powder was weighed in a 50 ml falcon tube. Add 25 ml of bidistilled/ultrapure water and mix the solution by vortex mixer for a period of 5 min. Now, 2 mL of each Carrez 1 solution (250

mM Zinc sulphate) and Carrez 2 solution (85 mM Potassium hexacyanoferrate (II) trihydrate) was added to the falcon tube and mixed for 30 seconds each. Fill the solution up to 50 ml with bidistilled water. The solution was vortexed for 5 min again and centrifuged at 14000g for 10 min. The supernatant was filtered with Whatman filter paper No. 42. The filtrate was again filtered with 0.45 μ m nylon membrane filter before HPLC measurement. The filtered suspension was then transferred to 1.5 ml vial for HPLC (Shimadzu Prominence Series) measurement.

The standards ($\geq 99.9\%$ pure) fructose, glucose and sucrose were purchased from Merck and Sigma Aldrich. 0.25 g of each fructose, glucose and sucrose were weighed accurately on a sensitive electronic balance and mixed in 50 ml ultra-pure water to prepare a stock solution of 5000 ppm (5 mg/ml). The dilutions were done with ultra-pure water to prepare concentrations of 2500 ppm, 1250 ppm, 1000 ppm, 500 ppm, 250 ppm, 100 ppm and 50 ppm as follows:

1.5 ml from stock solution = 5000 ppm
750 μ l stock + 750 μ l ddH₂O = 2500 ppm
375 μ l stock + 1125 μ l ddH₂O = 1250 ppm
300 μ l stock + 1200 μ l ddH₂O = 1000 ppm
150 μ l stock + 1350 μ l ddH₂O = 500 ppm
75 μ l stock + 1425 μ l ddH₂O = 250 ppm
30 μ l stock + 1470 μ l ddH₂O = 100 ppm
15 μ l stock + 1485 μ l ddH₂O = 50 ppm

These 8 standard solutions of reducing sugars and sucrose with a final volume of 1.5 ml was used to calculate the standard calibration curve in HPLC (Fig. 3.6). Area under the detected peaks of samples (reducing sugars and sucrose) at their respective retention times was determined according to the calibration curve (Fig. 3.7)

3.2.6.2 HPLC conditions

Acetonitrile and ddH₂O was used as a mobile phase/eluent in 80%:20% (w/w) precisely 628.8 g:199.6 g. The flow rate was 0.9 ml/min with isocratic flow. 20 μ l sample was injected in NH₂ inertsil column (GL Sciences). The temperature of the column was

maintained at 40 °C. The analytes were detected with the help of refractive index (RI) detector.

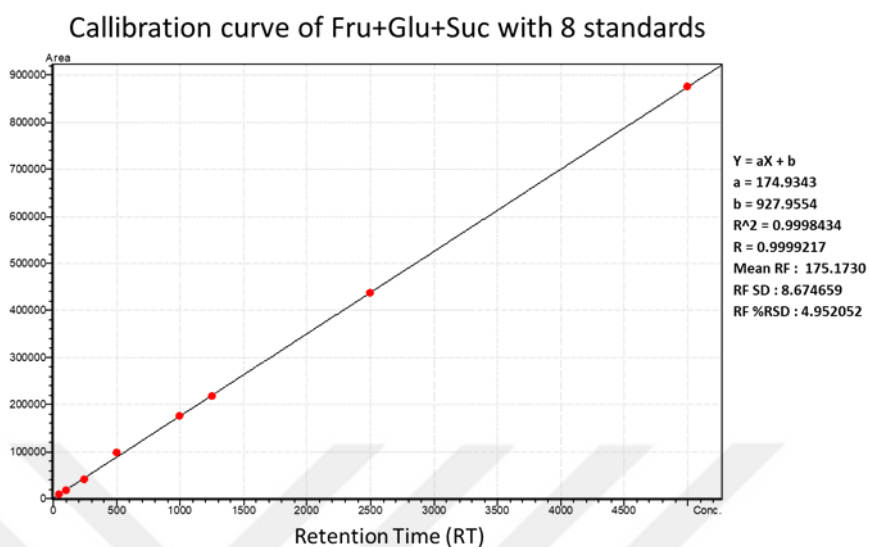


Figure 3.6. Calibration curve of reducing sugars (glucose + fructose) and sucrose with 8 standards along with regression line ($R^2=0.99$)

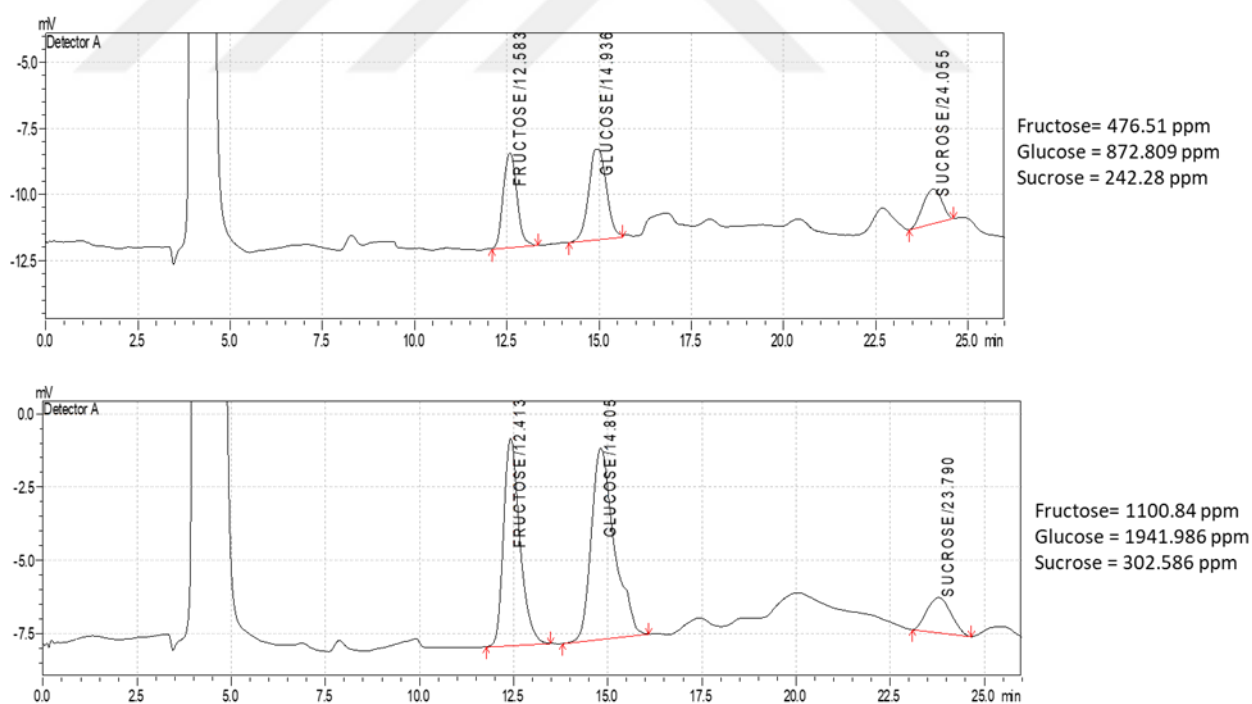


Figure 3.7. Peaks obtained for reducing sugars and sucrose through HPLC. Retention time for fructose, glucose and sucrose was 12.4, 14.8 and 23.7, respectively

3.2.7 Free asparagine

3.2.7.1 Extraction of free asparagine

5% (w/v) trichloroacetic acid (TCA) was prepared. 1 g freeze dried lyophilized potato sample was taken in 50 ml falcon tube and extracted with 25 ml of 5% TCA. Sample was shaken and vortexed for 10 min. Later, it was centrifuged at 6000 rpm for 15 min at 4°C. The supernatant was filtered with Whatman filter paper no. 42. The filtered supernatant was again filtered with 0.45 µm nylon filter and analysed through HPLC in a 1.5 ml vial. The calibration curve was prepared by using 6 standard solutions of pure L Asparagine (Fig. 3.8). Pure L Asparagine (99%) was purchased from Thermo Fischer Scientific (Alfa Aesar). 0.25 g of pure asparagine was dissolved in 50 ml of bidistilled water to prepare 5000 ppm stock solution. Further standard concentrations of 2500 ppm, 1250 ppm, 1000 ppm, 500 ppm and 250 ppm were prepared similar to reducing sugars and sucrose standards by series dilution with bidistilled water.

3.2.7.2 HPLC conditions

30 mM potassium phosphate buffer (pH 3.2) and methanol were used as a mobile phase in 80:20 ratio (v/v). 30 mM potassium phosphate buffer (pH 3.2) was prepared by mixing K_2HPO_4 and KH_2PO_4 . 0.305 g K_2HPO_4 (MW: 174.18 g/mol) was taken with a molarity of 0.0018 M along with 3.844 g of KH_2PO_4 (mw: 136.086 g/mol) with a molarity of 0.0282 M to prepare 0.03 M potassium phosphate buffer. Orthophosphoric acid was added to adjust pH precisely to 3.2.

C18 reverse phase column (CAPCELL PAK, JM Science Inc.) was used with a flow rate of 0.8 ml/min. DAD (Diode array detector) was used for the detection of free asparagine. It has a diverse range of detection from 190 nm to 800 nm. Free asparagine was detected at 190 nm with a retention time of 3.56 (Fig. 3.9). 20 µl sample was injected in the column maintained at constant temperature of 40 °C.

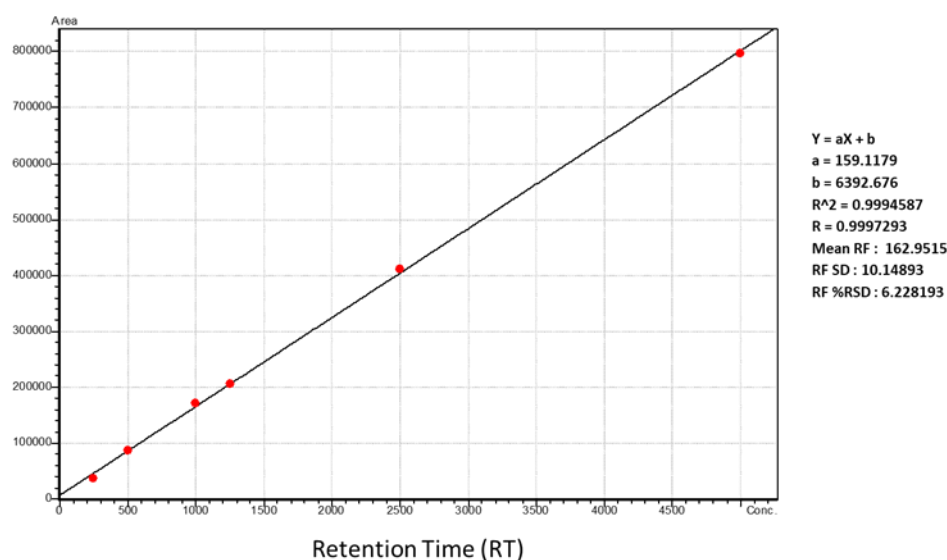


Figure 3.8. Calibration curve of free asparagine with 6 standards along with regression line ($R^2=0.99$)

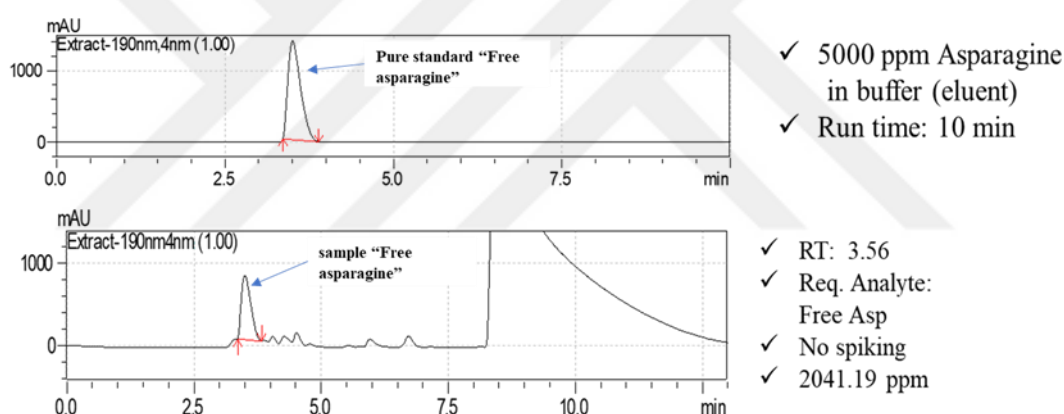


Figure 3.9. Free asparagine peak at retention time (RT) of 3.56 in pure standard (above) and sample (below)

3.2.8 Tuber starch content

Tuber starch content was measured by Ewer's Polarimetric method (Mitchell, 1990). An aliquot of 1.25 g of a lyophilized freeze-dried tuber sample was weighed accurately in a 50 mL volumetric flask and 25 mL of 1.128 N HCl solution was added for the purpose of hydrolysis. The suspension was heated on a boiling water bath for 15 min (mixed constantly after 3 min to avoid coagulation) followed by fast cooling on ice bath. Once the hydrolysis is finished, add 10 ml of 1.128 N HCl again to improve the starch hydrolysis. 1 ml of each Carrez I (30% ZnSO₄ solution) and Carrez II (15% K₄[Fe (CN)₆]

solution) solutions were added to the flask and agitated. Finally, the volumetric flask was filled up by distilled water. Transfer the mixture to 50 ml falcon tubes and centrifuged at 6000 rpm for 10 min at temperature of 4°C. The supernatant was filtered with Whatman paper No. 42 and the obtained filtrate was then transferred to a polarisation tube (1 dm) and measured using a polarimeter.

The amount of starch (X) in the sample was calculated using following equation as percentage dry basis.

$$X (\%) = 10^4 \times \alpha / [\alpha]_{\lambda}^t \times \ell \times m \quad 3.1$$

where α is calculated value of optical rotation, $[\alpha]_{\lambda}^t$ is the optical activity (specific rotation) depending on the discharge lamp and wavelength of light used and variety of starch, ℓ is the path length (1 dm), and m is the sample weight (1.25 g).

$$[\alpha]_{\lambda}^t = \alpha \times 100 / \ell \times c \quad 3.2$$

For a sodium discharge lamp and a wavelength (λ) of 589.3 nm, the $[\alpha]_{\lambda}^t$ value is 244.8 for pure potato starch as calculated by formula shown above. All analysis were done in triplicate.

3.2.9 Beta carotene

β -carotene was measured with the help of UV-Vis spectrophotometer as illustrated by Biswas et al. (2011). β -carotene standard (97% purity, UV) was purchased from Teknik Kimya. Standard stock solution with concentration of 1 mg/ml was prepared by dissolving β -carotene standard in acetone. Working standard solutions of 0.25, 0.5, 1, 2, 4 and 8 ug/ml were prepared from stock solution. A calibration curve of β -carotene was made by plotting Optical Density (O.D) values (absorbance at 449 nm) to the respective analyte concentrations. Linear regression curve was generated by using Microsoft excel and further used to quantify the content of β -carotene in the analysed samples. The equation for the standard calibration curve is as follows:

$$y = 4.1374x + 0.2989 \quad (R^2 = 0.9956) \quad (\text{where, } y = \text{conc. in ug/ml; } x = \text{O. D. value}) \quad 3.3$$

A representative freeze-dried tuber sample (1 g) was weighed precisely in 15 ml falcon tubes. Later, 5 ml of chilled acetone was added to falcon tube and shaken for 15 min with automatic shaker at $4\pm1^{\circ}\text{C}$. The suspension was vortexed for 10 min at high speed followed by centrifugation at 1370g for 10 min. A supernatant was filtered with Whatman filter paper No. 42. The extract absorbance was measured at 449 nm with the aid of UV-Vis spectrophotometer. All solutions were protected against light by covering them with aluminium foil and maintained at 4°C . All analysis was done in duplicate.

3.2.10 Total antioxidant activity

The total antioxidant activity was measured through 2,2-diphenyl-1-picryl-hydrazyl (DPPH) free radical scavenging assay as described by Huang et al. (2006) and Lachman et al. (2008) with some modifications. Ascorbic acid (40 mg ml^{-1}) was used as standard and working standard solutions were prepared with various concentrations of (4, 8, 12, 16, 20, 40 mg ml^{-1}) ascorbic acid in methanol. 0.1 mM methanolic DPPH was freshly prepared and 3 ml of 0.1mM DPPH was subsequently added to each concentration solution. The methanolic DPPH solution containing sample extract (ascorbic acid) was allowed to stand in dark place for 30 min at 25°C . The absorbance of the sample was measured against the blank at 517 nm with the aid of UV-vis spectrophotometer.

The sample extract (40 mg ml^{-1}) was prepared by adding 10 ml methanol (99%) to 0.4 g (400 mg) of lyophilized potato tuber sample. The solution was allowed to stand on shaking water bath for 150 min at room temperature, followed by centrifugation at 6000 rpm for 15 min and filtration with Whatman filter paper No. 42. Take one ml of sample extract and add 3 ml of 0.1mM DPPH solution. The methanolic DPPH solution containing sample extract was allowed to stand in dark place for 30 min at 25°C . The absorbance of the sample extract was measured against the blank at 517 nm with the aid of UV-vis spectrophotometer. All analysis were done in duplicate. A lower absorbance is an indication of higher scavenging activity. The radical scavenging activity was calculated as follows:

$$\text{Percent inhibition activity} = [1 - (\text{absorbance of sample} / \text{absorbance of blank})] \times 100 \quad 3.4$$

Standard calibration curve of ascorbic acid was plotted between percent inhibition and various ascorbic acid concentrations in DPPH. Quantification of total antioxidant activity of samples was done using standard equation in mg ascorbic acid equivalent (AAE)/100 g dry weight. The standard equation used is as follows:

$$y = 10.244x \quad (R^2 = 0.997) \quad 3.5$$

where; y = % inhibition activity; x = concentration mg AAE ml⁻¹

3.2.11 Total phenolic contents

Folin-Ciocalteu photo-colorimetric method was used to determine the total phenolic contents of potato tuber according to the method illustrated by Ah-Hen et al. (2012). 1 g of freeze-dried tuber sample was carefully weighed on an analytical balance and mixed with 10 ml of aqueous solvent of 80% methanol acidified with 1% HCl to extract the phenolic compounds. The mixture was protected from sunlight and shaken (200 rpm) for 2h at room temperature with automatic shaker. Later centrifuged for 15 min at 7000 rpm, and finally supernatant was filtered through Whatman filter paper. 100 µL of an aliquot was taken from filtrate and mixed with 750 µL of Folin-Ciocalteu reagent. It was allowed to stand for 5 min followed by the addition of 750 µL of aqueous sodium bicarbonate (60 g/L). This mixture was kept in dark for 90 min at room temperature. The absorbance was measured at 725 nm with a UV-visible spectrophotometer. The total phenolics were calculated based on ferulic acid (mg L⁻¹) equivalents from standard curve of ferulic acid (0, 50, 100, 150, 200, and 250 mg L⁻¹). All samples were assayed in duplicate. The standard equation is given as follows:

$$y = 0.0011x + 0.0265 \quad (R^2 = 0.991) \quad 3.6$$

y = Absorbance at 725 nm; x = ferulic acid concentration (mg L⁻¹).

3.2.12 Tuber skin thickness

The outer layer of tuber skin is called periderm, which is composed of phellem, phellogen and phelloderm. Its thickness was measured with the help of optical stereo microscope

(Leica 165C) and image was taken from Leica application suite (LAS V4.12). Tissue blocks containing periderm were cut from the middle section of three randomly selected tubers of each genotype and hand sectioned with razor blade. Three independent sections were further obtained from each individual selected tuber. The sections were directly visualized under stereo microscope. Relative quantification of skin (periderm) thickness was done with Image J software (Fig. 3.10).

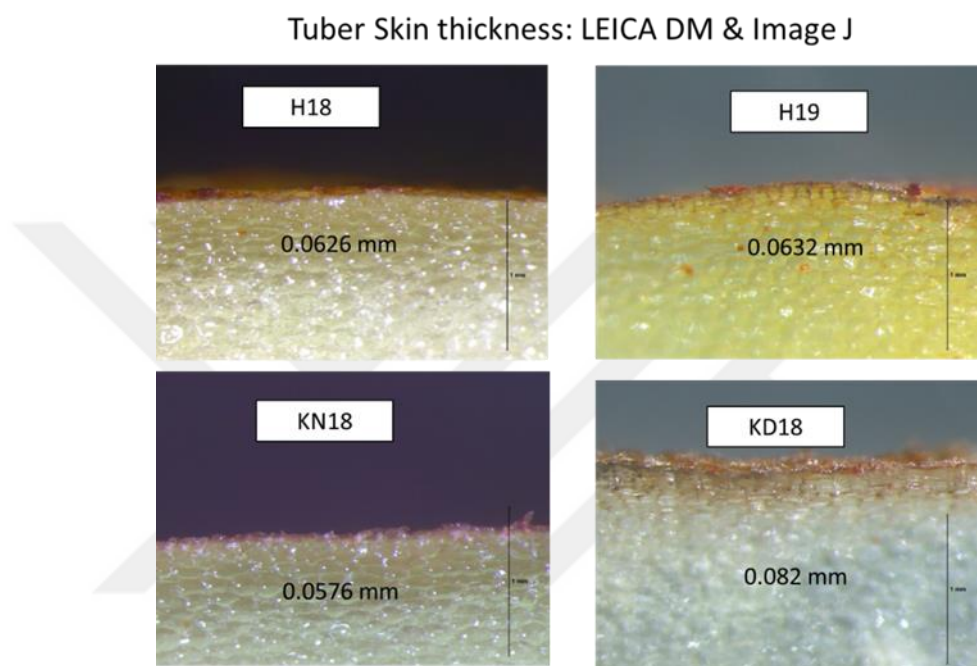


Figure 3.10. Tuber skin (periderm) thickness observed under optical stereo microscope (Leica 165C) and image was taken from Leica application suite (LAS V4.12)

3.3 Statistical Analysis of phenotypic data

3.3.1 SAS 9.0 software

SAS 9.0 software was used to calculate the estimated values of all genotypes for the measured phenotypic variables following an augmented design in each environment. The statistical model for augmented design can be written as (Wolfinger et al., 1997):

$$Y_{ij} = \mu + \beta_i + c_j + \tau_{k(i)} + \varepsilon_{ij} \quad 3.6$$

where, μ = mean ; β_i = blocks ; c_j = checks ; $\tau_{k(i)}$ = new entries ; ε_{ij} = error

ANOVA was performed following the SAS codes elaborated as follows;

```
PROC MIXED;  
TITLE 'Augmented Design using PROC MIXED – entries fixed';  
CLASS block entry;  
MODEL variable=entry;  
RANDOM block;  
/*compare all means using Tukey's test*/  
LSMEANS entry/pdiff adjust=tukey;  
RUN;
```

```
PROC GLM;  
TITLE 'Augmented Design using GLM – entries random';  
CLASS block entry entryc;  
MODEL variable = block entryc entry*new/solution;  
RANDOM block/test;  
RUN;
```

3.3.2 SPSS Software (v. 25)

Pearson correlations (r) were performed using estimated BLUPs among the traits under study, using SPSS software.

3.3.3 AMMISOFT and STABILITYSOFT

The mean estimated values of each environment were utilized in AMMISOFT to investigate genotype by environment interactions (GEI) for all phenotypic variables. AMMI combines ANOVA into a single model with additive and multiplicative parameters (Gauch and Moran, 2019). The broad-sense heritability (H^2) for each trait was estimated by an equation; $H^2 = V_G/V_P$, using genotypic (V_G) and phenotypic (V_P) variance components (Toker 2004; Ogunniyan and Olakojo 2014). Parametric stability statistics such as regression coefficient (bi) was calculated through STABILITYSOFT (Finlay and Wilkinson, 1963).

3.3.4 R Package (BLUPs estimation)

BLUPs (Best Linear Unbiased Predictions) were estimated by using mixed-effects model in R software using *lme4* package (Bates et al., 2015). The global mixed effect model was used to account for different variances of genotypes among the various environmental conditions. In order to generate the phenotypic BLUP values for association mapping analysis, random effects of genotypes and environments were considered with an assumption that individual-specific effects are uncorrelated (Piepho et al., 2008).

$$P_{ijk} = \mu + G_i + E_j + B_{k/j} + \epsilon_{ijk}, \quad 3.7$$

Where; P_{ijk} refers to variable measured for the i genotype, k replicate and j environment. G_i = random effect of genotype; E_j = random effect of environment; $B_{k/j}$ = random effect of replicate and ϵ_{ijk} = random residual “error effect”. The estimated BLUPs (Best Linear Unbiased Predictions) calculated for each genotype among four environments encompassing all tuber quality traits were used further to calculate significant marker-trait associations using the *GWASpoly* R package. Histograms of estimated BLUPs for each variable and scatter plot of mean vs BLUPs was also measured within R package.

3.4 Genotyping

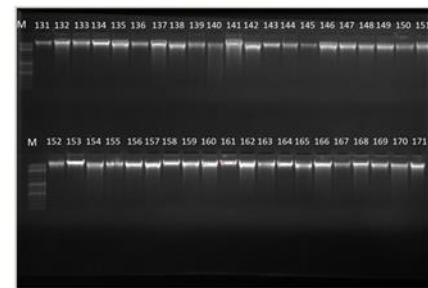
3.4.1 Sample collection and genomic DNA extraction

Young leaf samples were collected (as shown in image below) from 192 genotypes included in the study. Samples were collected in minitubes with beads and immediately preserved on ice to avoid deterioration.

Genomic DNA was extracted from all genotypes using the Gene JET Plant Genomic DNA Purification mini kit (Thermo scientific) according to the supplier’s instructions. DNA concentration and quality were determined using the BioSpec-nano (Shimadzu) spectrophotometry and standard electrophoresis on 1.2% agarose gel was performed (Fig. 3.11 and 3.12).

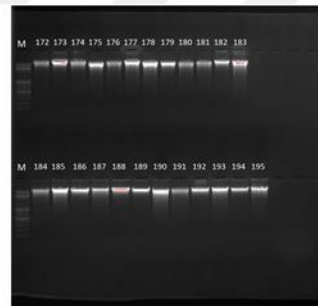


Figure 3.11. Sample collection for genomic DNA extraction and Gene JET Plant Genomic DNA Purification mini kit (Thermo scientific).



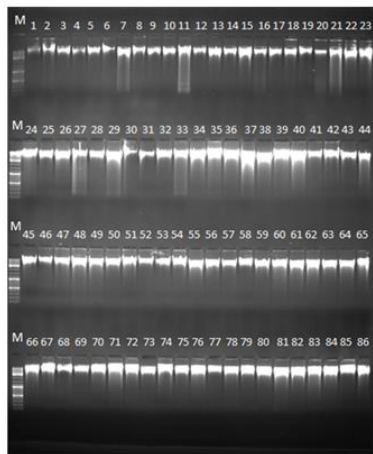
M: Gene Ruler Mix Marker;

131. TOKYO; 132. DT1108.02; 133. GOLD MARIE; 134. ARKULA; 135. 106-105-11; 136. ACAPPELLA; 137. DT1301.10; 138. DT1402.08; 139. DT1304.08; 140. DT1307.31; 141. DT1405.11; 142. DT1304.05; 143. 944-208-10; 144. DT1401.18; 145. DT1312.21; 146. ETIKETTSZ NORIKI; 147. ROMANZE; 148. POMQUEEN 149. DT1107.01; 150. DT1107.01; 151. WENDY; 152. DT1407.37; 153. DT1310.48; 154. ZIRVE; 155. DT1407.36; 156. SORAYA; 157. DT1301.11; 158. DT1108.01; 159. DT1310.54; 160. 99-115-11; 161. TALENT; 162. DORUK; 163. DT1302.01; 164. 860-204-10; 165. DT1403.03; 166. DT1406.03; 167. 878-202-10; 168. MELODY; 169. 900-205-10; 170. 89-105-11; 171. ALLORA



M: Gene Ruler Mix Marker;

172. DT1307.35; 173. 506-104-09; 174. DT1409.11; 175. BIRTE; 176. BETTINA; 177. BANBA; 178. PELIKAN; 179. BALTIC CREAM; 180. DT1408.28; 181. DT1408.03; 182. MUNDO; 183. DT1401.14; 184. DT1403.01; 185. DT1403.01; 186. 140-107-11; 187. DT1407.18; 188. NIXE; 189. SINKER GOLD; 190. DT1408.03; 191. BONZE; 192. DT1401.22; 193. DT1406.12; 194. MAXI; 195. 735-102-09



1. JUMBO; 2. SALUTE; 3. KALIBRI; 4. DT1302.23; 5. DUKATA; 6. BONZA; 7. DT1201.2.8; 8. LOKITA; 9. DT1314.49; 10. TACOMA; 11. KIEBITZ; 12. DT1314.17; 13. DT1309.92; 14. CASCADE; 15. 102-102-11; 16. BEO; 17. 939-201-10; 18. ROYAL; 19. 868-201-10; 20. TESSA; 21. KORMORAN; 22. 82-119-11; 23. PIRIVELEG; 24. DT1402.03; 25. DT1401.18; 26. DT1308.01; 27. DT1316.15; 28. DT1404.24; 29. DT1310.02; 30. 84-107-11; 31. SWING; 32. DIPLOMAT; 33. BORWINA; 34. DT1404.17; 35. DT1402.21; 36. DT1307.03; 37. DT1406.13; 38. DT1407.03; 39. KUTUP; 40. DT1304.42; 41. DT1405.25; 42. AGRIA; 43. RINBA; 44. HERDES; 45. JELLY; 46. NAUTILUS; 47. LAURA; 48. ALEGRIA; 49. TERRANA; 50. 104-103-11; 51. DT1404.38; 52. DT1313.36; 53. FIDELIA; 54. 946-202-10; 55. RBB; 56. MADELAINE; 57. DT1406.07; 58. V. GOGH; 59. SFHIT; 60. KARATOP; 61. ADRETTA; 62. DT1405.09; 63. BROOKE; 64. 68-105-11; 65. 40-103-11; 66. 904-212-10; 67. MAXILLA; 68. 157-103-11; 69. LOGO; 70. DT1406.01; 71. L. OLYMPIA; 72. SHEPODY; 73. DT1304.74; 74. 128-105-11; 75. KINW; 76. 43-118-11; 77. 43-111-11; 78. TUCAN; 79. 51-109-11; 80. ALBATROS; 81. KARLENA; 82. 57-104-11; 83. 882-202-10; 84. DT1402.04; 85. 125-104-11; 86. DT1407.02



M: Gene Ruler Mix Marker;

87. PRESTIGE; 88. SOLIST; 89. DT1404.27; 90. 735-102-09; 91. 758-109-09; 92. DT1307.19; 93. NANDO; 94. 133-112-11; 95. 63-113-11; 96. DT1406.13; 97. DT1308.01; 98. DT1401.15; 99. DT1304.10; 100. 141-104-11; 101. 99-102-11; 102. DT1316.12; 103. DT1405.15; 104. L. ROSETTA; 105. 146-103-11; 106. DT1316.16; 107. POWER; 108. 84-105-11; 109. DT1407.19; 110. DT1401.01; 111. DT1403.03; 112. DT1304.10; 113. DT1404.27; 114. DT1406.01; 115. DT1409.14; 116. 1401.32; 117. DT1403.11; 118. RITA; 119. DT1314.58; 120. DT1206.21; 121. 966-203-10; 122. DT1406.19; 123. DT1406.08; 124. DT1401.64; 125. DT1302.10; 126. DT1401.06; 127. DT1406.13; 128. 14006.07; 129. ELECTRA; 130. INNARA

Figure 3.12. Agarose gel electrophoresis of Genomic DNA samples; (Labelled from Left to Right)

3.4.2 SNP Genotyping of Potato Genotypes

3.4.2.1 DNA drying (Centrivap Concentrator)

The extracted genomic DNA (gDNA) was dried using Centrivap Benchtop Vacuum concentrator (Fig. 3.12). A total of 500 ng of good quality DNA was dried prior to sending it for SNP genotyping. A list of genotypes with extracted gDNA concentration (ng/μl) and final volume (μl) dried having 500 ng of gDNA is shown in Table 3.3.

Table 3.3. List of genotypes with extracted genomic DNA concentration (ng/μl) and final dried amount i.e., 500 ng. Note: Final volume dried in above table is in μl

Genotype	DNA Conc (ng/μl)	final vol dried	Genotype	DNA Conc (ng/μl)	final vol dried	Genotype	DNA Conc (ng/μl)	final vol dried	Genotype	DNA Conc (ng/μl)	final vol dried	Genotype	DNA Conc (ng/μl)	final vol dried
JUMBO	97.68	5.12	NAUTILUS	46.10	10.85	DT14051.15	48.48	10.31	DT14011.18	102.43	4.88	MUNGO	174.44	2.87
SAUTE	141.25	3.54	LAURA	67.86	7.37	LROSETTA	58.24	8.59	DT13124.21	340.74	1.47	DT14010.14	169.44	2.95
KOLIBRI	149.12	3.35	TERRANA	120.36	4.15	146-103-11	88.58	5.64	ETIKETSIZ NORIKA	560.08	0.89	DT14038.01	100.09	5.00
DT13052.23	123.82	4.04	104-103-11	189.71	2.64	DT13162.16	68.28	7.32	ROMANZE	191.91	2.61	DT14003.01	217.39	2.30
DUKATA	52.84	9.46	DT14047.38	207.39	2.41	POWER	125.53	3.98	POMQUEEN	131.79	3.79	140-107-11	160.95	3.11
BONZA	136.89	3.65	DT13136.22	126.12	3.96	84-105-11	140.56	3.56	DT11007.01	154.04	3.25	DT14037.18	100.43	4.98
DT12012.2	92.48	5.41	FIDELIA	136.58	3.66	DT14071.19	114.76	4.36	DT11107.01	515.75	0.97	NIXE	193.80	2.58
LOUTA	69.98	7.14	946-202-10	109.13	4.58	DT14016.01	48.99	10.21	WENDY	255.79	1.95	SUMMER GOLD	126.34	3.96
DT13143.49	112.66	4.44	RBB	123.05	4.06	DT14053.03	208.08	2.40	DT14057.37	615.38	0.81	DT14085.03	180.43	2.77
TACOMA	131.75	3.80	MADELAINE	189.79	2.63	DT13045.103	49.36	10.13	DT13130.48	210.06	2.38	BONUS	91.02	5.49
KIEBITZ	75.45	6.63	DT14068.07	64.14	7.80	DT14042.27	104.41	4.79	ZIRVE	130.02	3.85	DT14015.22	216.89	2.31
DT13147.17	127.68	3.92	V.GOGH	167.33	2.99	DT14065.01	100.19	4.99	DT14057.36	211.22	2.37	DT14063.12	127.99	3.91
DT13093.92	132.00	3.79	SHIT	134.24	3.72	DT14091.04	145.33	3.44	SORAYA	380.96	1.31	MAXI	226.77	2.20
CASCADA	64.72	7.73	KARATOP	57.18	8.74	DT14018.32	109.28	4.58	139-101-11	286.01	1.75	735-102-09	261.68	1.91
102-102-11	117.21	4.27	ADRETTA	121.71	4.11	DT14030.11	199.44	2.51	DT11088.01	157.48	3.18	FASAN	145.32	3.44
BEO	51.46	9.72	DT14005.09	167.13	2.99	RITA	340.99	1.47	DT13143.54	595.75	0.84	758-109-09	120.01	4.17
939-201-10	125.05	4.00	BROOKE	161.33	3.10	DT13143.58	167.55	2.98	99-115-11	154.06	3.25	DT13072.19	132.18	3.78
ROYAL	41.37	12.09	68-105-11	133.28	3.75	DT12068.21	321.38	1.56	TALENT	130.24	3.84	NANDO	192.14	2.60
868-201-10	118.03	4.24	40-103-11	289.46	1.73	966-203-10	35.46	14.10	DORUK	243.76	2.05	133-112-11	116.21	4.30
TESSA	21.78	22.96	904-212-10	36.39	13.74	DT14046.19	116.36	4.30	DT13028.01	352.07	1.42	63-113-11	160.57	3.11
KORMORAN	75.94	6.58	MAXILLA	115.59	4.93	DT14062.08	41.18	12.14	860-204-10	175.70	2.85	DT14061.23	178.27	2.80
82-119-11	47.62	10.50	157-103-11	68.73	7.27	DT14016.34	123.41	4.05	DT14034.03	219.49	2.28	DT13083.01	347.65	1.44
PIRVELEG	122.68	4.08	LOGO	120.05	4.16	DT14051.06	216.31	2.31	DT13067.03	199.06	2.51	DT14013.15	150.70	3.32
DT14028.03	122.28	4.09	DT14006.01	153.92	3.25	DT13026.10	54.99	9.09	878-202-10	46.97	10.65	DT13048.10	163.34	3.06
DT14010.18	143.71	3.48	L.OLYMPIA	125.88	3.97	DT14061.23	267.71	1.87	MELODY	130.78	3.82	141-104-11	166.95	2.99
DT13085.01	63.69	7.85	SHEPODY	84.47	5.92	DT14006.07	196.38	2.55	900-205-10	211.61	2.36	99-102-11	213.42	2.34
DT13162.15	127.76	3.91	DT13045.74	148.07	3.38	ELECTRA	203.00	2.46	89-105-11	147.32	3.39	DT13162.12	84.88	5.89
DT14042.24	155.30	3.22	128-105-11	137.30	3.64	INNARA	88.18	5.67	ALLORA	250.16	2.00			
DT13100.02	58.17	8.60	KIWI	159.06	3.14	TOKIO	51.33	9.74	DT13037.35	95.35	5.24			
84-107-11	145.80	3.43	49-118-11	144.73	3.45	DT11108.02	125.84	3.97	509-104-09	154.32	3.24			
SWING	163.07	3.07	49-111-11	90.36	5.53	GOLD MARIE	95.45	5.24	DT14090.11	162.53	3.08			
DIFLOMAT	143.28	3.49	TUCAN	142.52	3.51	ARKULA	135.03	3.70	BRTE	148.87	3.36			
BORWINA	60.31	8.29	51-109-11	181.44	2.76	106-105-11	283.12	1.77	BETTINA	82.05	6.09			
DT14004.17	100.03	5.00	ALBATROS	100.91	4.95	ACAPELLA	100.74	4.96	BANBA	175.43	2.85			
DT14026.21	178.66	2.80	KARLENA	80.62	6.20	DT13051.10	168.12	2.97	PELIKAN	268.97	1.86			
DT13007.03	114.18	4.38	DT14049.10	25.74	19.43	DT14027.08	144.33	3.46	BALTIC CREAM	126.66	3.95			
DT14069.13	124.26	4.02	57-104-11	171.93	2.91	DT13047.08	93.06	5.37	PERSTIGE	96.14	5.20			
DT14078.03	59.23	8.44	882-202-10	110.98	4.51	DT13037.31	77.20	6.48	SOLIST	55.45	9.02			
KUTUP	124.14	4.03	DT14026.04	188.78	2.65	DT14054.11	271.66	1.84	DT14014.27	38.36	13.04			
DT13045.42	122.86	4.07	125-104-11	97.39	5.13	DT13049.50	164.37	3.04	DT14083.28	150.99	3.31			
DT14055.25	120.11	4.16	DT14079.02	66.97	7.47	944-208-10	104.85	4.77	DT14088.03	188.21	2.66			
AGRIA	177.11	2.82												
RUMBA	179.93	2.78												
HERMES	125.92	3.97												
JELLY	130.58	3.83												
ALEGRIA	87.52	5.71												



Figure 3.13. Centrivap Concentrator for drying DNA samples (a); Arrangement of Eppendorf tubes in a box containing 500ng of DNA in a dried form (b)

3.4.2.2 SNP Genotyping by SolCAP 25K Potato Array

SNP genotyping was done for 192 genotypes by using SolCAP 25K potato array, which includes tetraploid SNPs and utilizes ILMN'S (Illumina) new Genome Studio tetraploid calling. SNP genotyping was done by NEOGEN GeneSeek Laboratory, Lincoln Nebraska (NE), USA. Illumina HiScan SQ system was used to read the array. The Genome Studio software was used for an assignment of genotypes to each locus. Tetraploid allelic combinations from nulliplex to quadriplex, with a total of diverse 21226 markers were obtained after SolCAP 25K array.

3.5 SNP Calling and HapMap File Preparation for STRUCTURE and GWASpoly R

The SNP genotyping revealed information about tetraploid allele dosage (nulliplex to quadriplex) of biallelic SNP markers/loci (for e.g., [A/T], [A/G], [T/C] etc) for 21,226 SNPs called for each genotype. The numeric file was made for population structure analysis according to the following format. Based on the count of alternative allele/alleles of biallelic SNP for a particular SNP marker in a tetraploid genotypic population, the nulliplex (AAAA) was coded as 0, simplex (AAAB) as 1, duplex (AABB) as 2, triplex (ABBB) as 3 and quadriplex (BBBB) as 4. For example; biallelic SNP [T/C] was coded as TTTT=AAAA=0; TTTC=AAAB=1; TTCC=AABB=2; TCCC=ABBB=3; CCCC=BBBB=4. After the tetraploid allele calling for each genotype in a numeric format, SNPs were subjected to filtration process in order to select and keep information for only polymorphic marker loci excluding monomorphic markers. The filtration was performed using standard set of parameters such as calculation of P and Q allele

frequency, minor allele frequency (MAF) and missing percentage (%) of SNPs. During the hunt for polymorphic SNPs, the SNPs were screened based on $MAF > 0.05$, whereas only SNPs with missing percentage of less than and equal to ($\leq$) 10% (sample call rate = 0.9) were selected. After filtering, 13,606 (64.10%) polymorphic SNPs or variants were obtained. 35.90% SNP markers were removed as being monomorphic in nature. The selected polymorphic markers were supposed to explain the population structure “Q” and kinship “K” of our population.

STRUCTURE software reads, analyze and process SNP markers in a properly organized numeric data set. Each allele of a SNP marker must be represented by a unique integer. The coding was done as 1, 2, 3, 4 and -9 representing A, C, G, T and missing alleles, respectively. SNP marker information was placed in rows while the genotypes were organized in columns. Owing to the presence of four alleles per locus, each SNP marker for each genotype were called accordingly for instance, TTTC (4442).

HapMap genotypic file for GWASpoly R software required allele data coded in either “ACGT”/nucleotide format or numeric (0, 1, 2, 3 and 4) format. The first column constitutes the SNP marker names, the second and third columns contain the genetic (chromosome information) or physical map (position ‘Mbp’), and subsequent columns contain the allele data of particular biallelic SNP marker for each genotype. Missing marker data are imputed with the population mode (most frequent genotype).

3.6 Inference of Population Structure and Kinship

Population structure is a main pillar for association mapping, and it was analysed through STRUCTURE software which worked on the methodology of Bayesian clustering (Pritchard et al., 2000). The admixture-based clustering model was applied with STRUCTURE v.2.3.4. Set the simulation like 100000 burn-in and 100000 iterations. For each K value, ten independent runs were performed, ranging from 1 to 10 with 5 replications each. The sub-population (K) was chosen based on Evanno et al. (2005) using STRUCTURE HARVESTER (Earl 2012). To visualize the population structure, a bar plot was used based on Q sorting with an optimum ΔK value. *Prcomp* package in R v. 3.6.3 was used for principal component analysis (PCA) to visualize the genotype

clustering based on sub-population. The function *ggplot2* in R v. 3.6.3 was used to plot the first two principal components (PCs).

3.7 Assessment of Linkage disequilibrium (LD)

TASSEL was used to determine the LD between marker pairs based on D' and r^2 (Hill 1968; Achenbach et al., 2009). A permutation test was applied to check the LD significance level among the various loci. Since, TASSEL analysed data in diploid form, we have to transform tetraploid allelic data into diploid form as follows for measurement of LD.

AAAA----- AA
 AAAB, AABB, ABBB----- AB
 BBBB----- BB

3.8 Association Mapping Through GWASpoly R

Association mapping was performed by using GWASpoly R package, using the “**Q + K**” linear mixed model approach for auto-polyploids (Rosyara et al., 2016). R is the most significant programming language with open source, flexible and effective data handling and statistical computation properties. In the world of statistics and data science, R provides several packages and libraries (CRAN) for performing a variety of tasks (R Core Team 2013). Five allele dosages of biallelic SNPs found in autotetraploids (i.e., potato) can be effectively evaluated in R package GWASpoly for their association with phenotype of interest. GWASpoly has its unique features; i.e., it can analyze the diverse panel of tetraploids and work based on a different type of polyploid gene actions, including general, additive, simplex, and duplex dominant (Ref/Alt). Additive gene action was considered in the current study, since it distinguishes among all the five different allele dosages (0, 1, 2, 3, 4) of tetraploid potato. Additive model hypothesized that SNP effect is proportional to the minor allele dosage. GWASpoly needs rrBLUP for its proper and accurate functioning. (Quantile-Quantile) Q-Q plots were drawn through this package. Q-Q plots tell us whether phenotypic data is logical or in other words, shows a normal distribution around the mean. A threshold of $-\log_{10}(P)=5.4$ was calculated following Bonferroni correction method (α/m ; where “ α ” refers to P

value=0.05 and “m” corresponds to number of markers equals to 13606). However, this threshold value is very strict and may lead to false negative marker-trait associations (possibility of avoiding/missing some important associations present). Instead, an arbitrary corrected significant threshold of $-\log_{10}(P)$ was set at 3.00, similar to the approach used in previous association mapping studies (Riaz et al., 2018; Phan et al., 2018; Ferrão et al., 2018). Manhattan plots were envisioned utilizing the GWASpoly R package.

Q + K linear mixed model for GWASpoly can be written as:

$$y = X\beta + ZS_T + ZQv + Zu + e \quad 3.8$$

y = vector of observed phenotypes

e = residuals vector

X = matrix of covariates effect or environmental effects

β = matrix vector of fixed effects

Z = genotypes effect

S = matrix for population structure

T = matrix for SNP effect

Q = matrix for population of *n* size

v = subpopulations effect

u = polygenic effects (covariance proportional to Kinship *K* matrix)

3.9 Gene Annotation

The putative gene function of detected associated SNPs was analysed through NCBI BLAST database of *Solanum tuberosum*. The BLAST search results revealed the gene annotation of SolCAP SNPs (Hamilton et al., 2011). Another SNP array study was performed by Uitdewilligen et al. (2013) and resulted in discovery of PotVar SNPs included in present study. This study was used for finding the gene annotation of PotVar SNPs.

CHAPTER IV

RESULTS AND DISCUSSION

4.1 Phenotypic Data Analysis

The results of phenotypic data analysis for association mapping panel of 192 genotypes measured for twelve important tuber quality traits are outlined in this section.

4.1.1 Dry matter content (DMC)

A detailed data of tuber dry matter content % (DMC) for 192 genotypes measured across four environmental conditions is given in Appendix-A. The data depicted the estimated values obtained after augmented design analysis (Appendix Q1) along with total and individual means of each genotype in four environments. Moreover, a descriptive statistic of DMC is mentioned in Table 4.6. The range of DMC was found to be 17.52% to 30%. Drought conditions recorded high DMC of 24.29% as compared to the other three environments. It might be due to restricted water supply which ultimately decrease the tuber water contents. Genotypic variance and phenotypic variance were calculated to be 4.38 and 4.84, respectively. Broad sense heritability was found to be 0.91, which means that 91% variability in a trait was caused by genetic differences among genotypes. The trait was less influenced by the environment and allows the selection of genotypes with high dry matter content (Shumbusha et al., 2014). AMMI analysis was performed for DMC and demonstrated that there were significant differences ($P < 0.01$) among genotypes, environments and genotype by environment interaction (GEI) (Table 4.7). Konya standard water conditions-2018 (21.98%) and Hatay-2019 (22.19%) were the best stable environments for determination of DMC (Fig. S1). Regression coefficient (bi) was calculated based on Finlay and Wilkinson (1963) stability model to identify the adaptability of genotypes across environments. $bi=1$ showed average stability, $bi < 1$ depict less sensitivity to environmental change (more adaptable to unfavourable environments due to higher average stability), whereas $bi > 1$ showed below average stability (more sensitive) and thus adapted for favourable environments. Plant breeders are mainly interested in genotypes with optimum DMC and average stability. In our study, 15 genotypes having average stability with optimum DMC includes Hermes,

Rumba, DT11107.01, 63-113-11, Lady Olympia, 43-111-11, Wendy, DT14038.01, DT13085.01, 944-208-10, Borwina, Pelikan, Innara, 102-102-11 and DT14027.08. *bi* values of all genotypes are listed in Appendix A. Check cultivar Jelly showed *bi* value of 0.48, meaning that it is less sensitive to environmental change, contrarily, Alegria was designated as more sensitive (*bi*=1.88), and thus can be grown under favourable environments

4.1.2 Comparison of methods for dry matter content determination in Potato using multi-environments field data and stability statistics

A study was designed to measure tuber dry matter content (TDM) with three different methods as illustrated in chapter 3, in order to investigate rapid, practicable and reliable methods for the measurement of tuber dry matter content. 189 genotypes were considered for the measurement of dry matter content across three environments (Hatay standard water conditions-2018, Konya standard water conditions-2018 and Konya drought conditions-2018). The results of this experiment have been published in the Journal of field crops (DOI: 10.17557/tjfc.742244).

4.1.2.1 Analysis of variance

The analysis of variance (ANOVA) for 189 genotypes depicting the mean squares, MSE (mean squared error) and CV% (coefficient of variation) for the set of treatments encompassing environmental conditions and methods, to measure the TDM is delineated in Table 4.1. ANOVA revealed highly significant differences ($p<0.01$) for all treatments (environments-methods) among tests, checks (control) and tests vs check genotypes. Since, checks were standard cultivars, their effects were fixed. While blocks, new entries (test genotypes) and error were considered as random effects. The significance among tests and check genotypes disclosed the presence of variability, which allows the selection of genotypes with optimum, and stable TDM across tested environments. Statistical description of TDM in set of treatments is given in Table 4.2. Wide variation of TDM showed diversity in genotypes as indicated by minimum and maximum values.

Table 4.1. Mean squares and their significance for set of treatments (environments-methods) of 189 genotypes for variable TDM% (tuber dry matter content in percent)

Environments- Methods	Block (7)	MEAN SQUARES			Error	CV%
		Among checks (4)	Among Test genotypes (183)	Checks vs Test genotypes (188)		
HS-H	0.86	12.79**	6.42**	7.32**	1.107	11.59
HS-O	4.12	19.84**	8.66**	9.77**	1.632	13.06
KS-H	0.66	6.55**	6.03**	6.48**	0.818	11.18
KS-SS	0.50	11.30**	7.94**	8.50**	0.550	12.98
KS-O	0.13	17.30**	8.37**	9.23**	0.767	12.51
KD-H	1.89	11.35**	6.78**	7.20**	0.977	10.80
KD-SS	0.57	9.43**	7.25**	7.88**	0.989	11.21
KD-O	0.31	8.87**	10.81**	11.40**	0.498	13.10

Table 4. 2. Descriptive statistics of variable tuber dry matter content

Environments- Methods	Number of genotypes	Mean (%) $\pm$ SEM	Minimum	Maximum
HS-H	189	21.708 $\pm$ 0.194	15.810	29.430
HS-O	189	22.445 $\pm$ 0.219	13.579	29.832
KS-H	189	20.929 $\pm$ 0.182	15.447	29.987
KS-SS	189	20.585 $\pm$ 0.209	16.797	31.882
KS-O	189	20.885 $\pm$ 0.216	15.990	30.291
KD-H	189	24.246 $\pm$ 0.195	17.986	33.468
KD-SS	189	24.344 $\pm$ 0.201	16.923	34.501
KD-O	189	24.735 $\pm$ 0.242	15.198	34.21

In an augmented analysis, the variation in test genotypes can be assessed by the variation among the check cultivars. The mean estimated values of each check cultivar (Agria, Alegria, Hermes, Jelly, Rumba) showed significant difference in each set of treatments (Fig. 4.1). Cultivars,

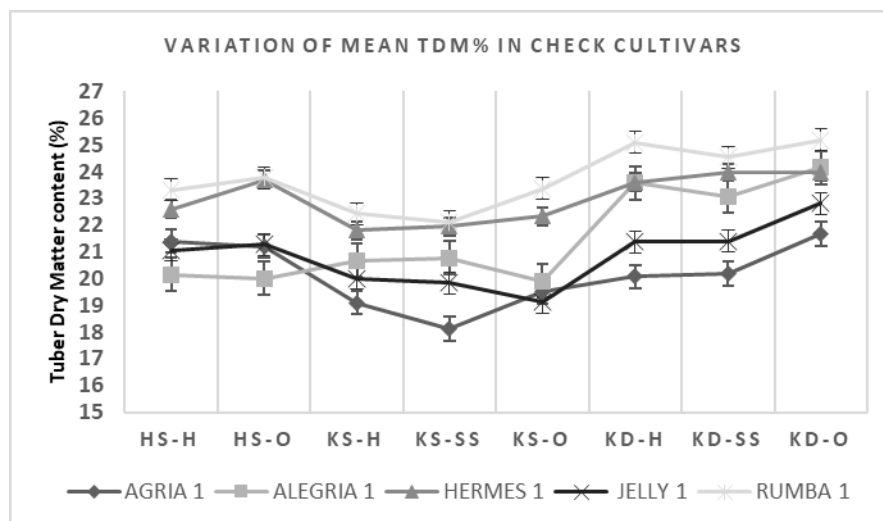


Figure 4.1. Mean TDM% variation in check cultivars (Agria, Alegria, Hermes, Jelly, Rumba) in a set of treatments

Acronyms: HS-H (Hatay Standard water application-Hydrometer method); HS-O (Hatay Standard water application-Oven method); KS-H (Konya Standard water application-Hydrometer method); KS-SS (Konya Standard water application-Seasand method); KS-O (Konya Standard water application-Oven method); KD-H (Konya Drought-Hydrometer method); KD-SS (Konya Drought-Seasand method); KD-O (Konya Drought-Oven method).

Rumba and Hermes showed high dry matter content compared to other three check cultivars except Alegria, which was statistically at par with Hermes under Konya drought conditions. Alegria and Agria recorded same TDM under Hatay standard water conditions. Alegria also showed statistically same TDM in Hatay and Konya standard water conditions and may be regarded as stable genotype. Drought conditions depicted high dry matter content in all check cultivars, when compared to standard water conditions in Konya. The graph disclosed that environmental conditions significantly affect the TDM. Discrepancy was observed among the TDM determination methods within the environments. Same trend was observed in test genotypes (Table 3 and Figure 1). Further, statistical tools such as correlation, and regression were performed to dissect the methods within each environment.

4.1.2.2 Comparison of methods by correlation analysis and scatter matrix

The results of Pearson correlation coefficient (r) among the set of treatments (environments-methods) for the variable tuber dry matter content (TDM) are summarized in Table 4.3. It was observed that all correlations (r) were highly significant ($p < 0.01$). It means that null hypothesis was rejected and thus concluded that population correlation

coefficient (ρ) was not equal to zero. Results showed significant strong correlation of $r=0.892$ and $r=0.882$ between seasand and hydrometer methods in Konya standard water application and Konya drought conditions, respectively. Though, a correlation of $r=0.849$ was recorded between oven-dry and hydrometer methods in Hatay standard water application, but comparatively weaker “ r ” values of 0.656 and 0.606 were observed with same methods, in Konya standard water and drought conditions, respectively. Interestingly, oven-dry method showed $r=0.739$ and $r=0.749$ with hydrometer and seasand methods, respectively under Konya drought conditions. Weak to moderate correlations were present among the different environmental conditions. It could possibly explain the variation of TDM in different environmental conditions, while all three methods were comparable to each other. Pearson correlation coefficient also showed similar findings by exhibiting strong correlation between hydrometer and seasand methods.

Table 4.3. Correlation (r) among the set of treatments (environments-methods) for variable tuber dry matter content.

Pearson correlation coefficients, N = 189 Prob > $ r $ under $H_0: \rho = 0$								
	HS-H	HS-O	KS-H	KS-SS	KS-O	KD-H	KD-SS	KD-O
HS-H	1	0.849**	0.667**	0.651**	0.535**	0.622**	0.580**	0.394**
HS-O		1	0.656**	0.617**	0.451**	0.607**	0.568**	0.421**
KS-H			1	0.892**	0.710**	0.768**	0.741**	0.580**
KS-SS				1	0.752**	0.775**	0.731**	0.577**
KS-O					1	0.675**	0.598**	0.480**
KD-H						1	0.882**	0.739**
KD-SS							1	0.749**
KD-O								1

Prob=Probability; H_0 = Null hypothesis; ρ = correlation; **significant at $p<0.01$; CV% = Coefficient of variation in percent. Acronyms: HS-H (Hatay Standard water application-Hydrometer method); HS-O (Hatay Standard water application-Oven method); KS-H (Konya Standard water application-Hydrometer method); KS-SS (Konya Standard water application-Seasand method); KS-O (Konya Standard water application-Oven method); KD-H (Konya Drought-Hydrometer method); KD-SS (Konya Drought- Seasand method); KD-O (Konya Drought-Oven method).

4.1.2.3 Comparison of methods by regression analysis

Regression analysis were performed to unveil the strength of variable methods under different environmental conditions (Fig 4.2). The Figure 4.2 showed fitted linear regression model along with coefficient of determination (R^2). The graphs revealed that

the maximum values of $R^2=0.796$ and $R^2=0.776$, were recorded with hydrometer and seasand methods, under Konya standard water and drought conditions.

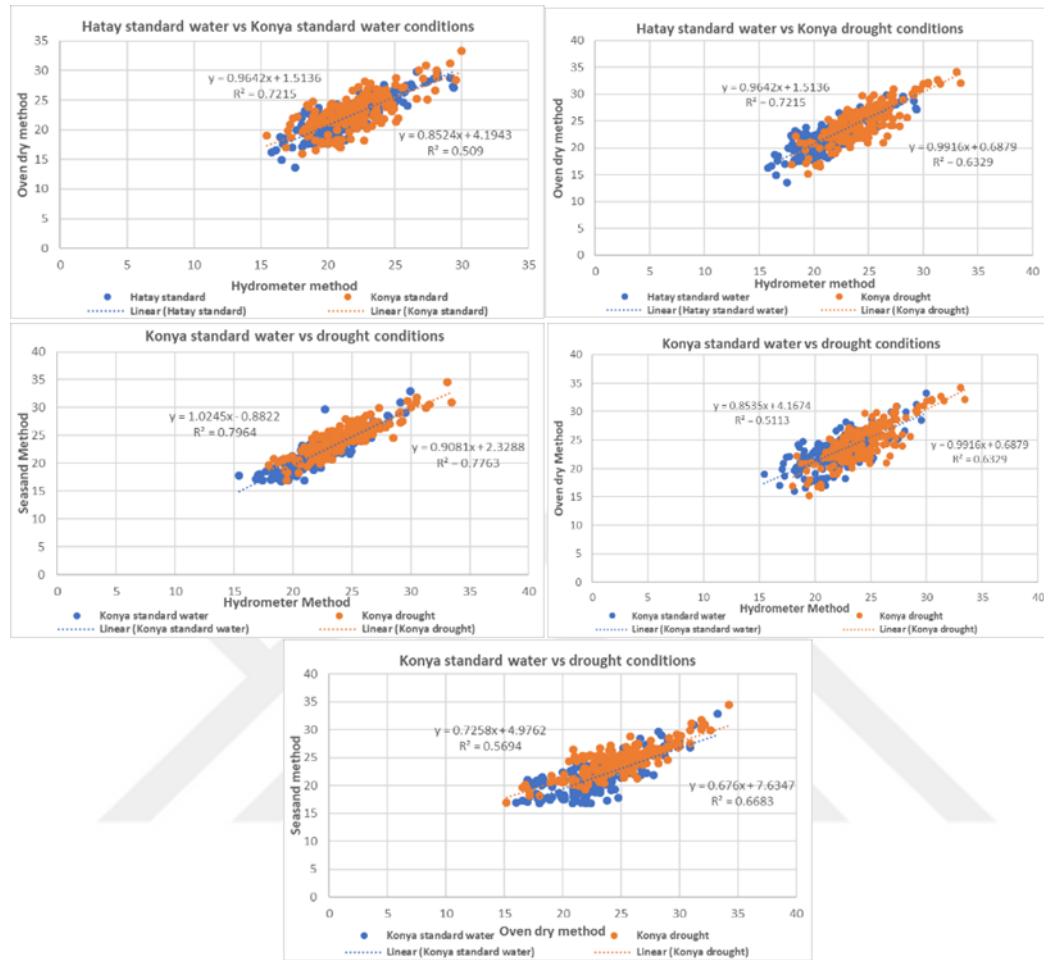


Figure 4.2. Regression analysis of three different methods for the measurement of tuber dry matter content under three environmental conditions

According to fitted model, it implies that 79.64% and 77.63% of variance in the hydrometer method can be explained by seasand method. Relatively lower R^2 values were obtained when oven method was compared to seasand and hydrometer methods. The comparison of oven dry method with hydrometer revealed 72.15% variance as indicated by the model (Fig. 4.2) under Hatay standard water conditions, but the same methods showed relatively low goodness of fit ($R^2=50.90\%$ and $R^2=63.29\%$) under Konya standard water and Konya drought conditions, respectively. So, an efficacy of oven dry method was affected by the shift in environment. A total of 56.94% and 66.83% variance was justified by oven method in comparison to seasand method under Konya standard water and drought conditions.

4.1.2.4 Comparison of methods in multi-environments by stability statistics

AMMI (Additive Main effects and Multiplicative Interaction) analysis

Analysis of variance for GEI (genotype by environment interaction) for the variable TDM tested across three environments is depicted in Table 4.4. The large mean square value of environment showed that the environments were diverse, with large differences among environmental means causing most of the variation in TDM. The significant GEI is an indication that substantial differences were present in genotypic response across the environments. Since, treatments were significant, methods showed differential response within the tested environments. Mean values of TDM vary remarkably from 15.19% to 34.50% in three tested environments and methods, with CV ranging from 10.80% to 13.10% (Table 4.1 and 4.2).

Table 4.4. Analysis of variance for tuber dry matter content of 189 potato genotypes tested across three environments.

Source	df	SS	MS
Total	1511	15703.78	10.39
TRT	566	13755.76	24.30**
GEN	188	9111.79	48.47**
ENV	2	1882.79	941.40**
GxE	376	2761.18	7.34**
IPC1	189	1878.21	9.94**
Residual	187	882.97	4.72**
Error	945	1948.02	2.06

*significant at $p < 0.01$

AMMI biplot showed visual interpretation of interrelationship among genotypes and environments. Mean TDM is plotted against IPC1 (Interactive principal component) as shown in Figure 4.3. The displacement along abscissa describes the additive (main) effects, while interactive effects can be explained by displacements along the ordinate. If a genotype or an environment has IPC1 score of nearly zero, it has small interaction effects and considered as stable. All three environments were diverse. Interestingly, Konya standard water conditions (KN18) would be considered as most stable environment. It had positive IPC1 score close to zero, indicating small interaction effects and hence most suitable environment for all genotypes. Abscissa (IPC1) and ordinate (mean TDM) lines bisect each other at the point of intersection. Genotypes which clusters

near IPC1 score of zero at the point of intersection, indicates that they were less influenced by the environment. Moreover, they also exhibit an optimum stable TDM content desired by the breeders as well as by the processing industry.

4.1.2.5 Stability analysis

The adaptation response of large number of genotypes to changing environments can be explained by plotting stability parametric models against mean TDM. Finlay and Wilkinson

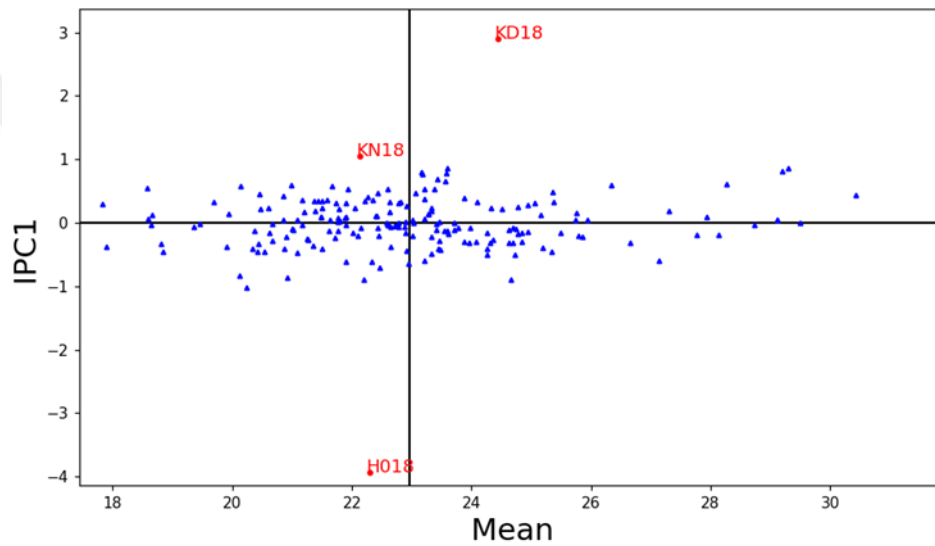


Figure 4. 3. AMMI biplot for TDM mean (%) of 189 potato genotypes (blue dots) and three environments (H018, KN18, KD18) plotted against IPC1 (Interactive principal component)
H018=Hatay-2018; KN18=Konya standard water conditions-2018; KD18=Konya drought conditions-2018

(1963) and Eberhart and Russell's (1966) proposed stability models such as regression coefficient (bi) and deviations from regression (S^2_{di}). TDM determination methods can be compared in terms of stability response of genotypes under various environments to dissect the efficacy of each method. Figures (4.4 and 4.5) illustrates two-dimensional scatter plot of each method, by plotting stability indices (bi and S^2_{di}) against mean TDM for 189 potato genotypes tested across three environments. Figure (4.4a) represents a generalized interpretation version of adaptability which can be applied to Figures (4.4b, c, and d). Each point on scatter diagram represents a single genotype and position of the point indicates its adaptability status. Genotypes characterized by bi values approximating 1.0 (not significantly different from unity at $p<0.05$) coupled with S^2_{di} of

zero indicates an average stability. An association of bi with high mean TDM showed general adaptability to all environments (represented by circle in Figure 4.4a) as compared to poor adaptability with low mean TDM values. However, mean TDM values greater than 25% were considered as inadmissible limits (Figure 4.4a). Genotypes characterized by $bi > 1$ showed higher sensitivity to environmental change (i.e., small environmental variation produce large changes), thus specifically adapted to favourable environments.



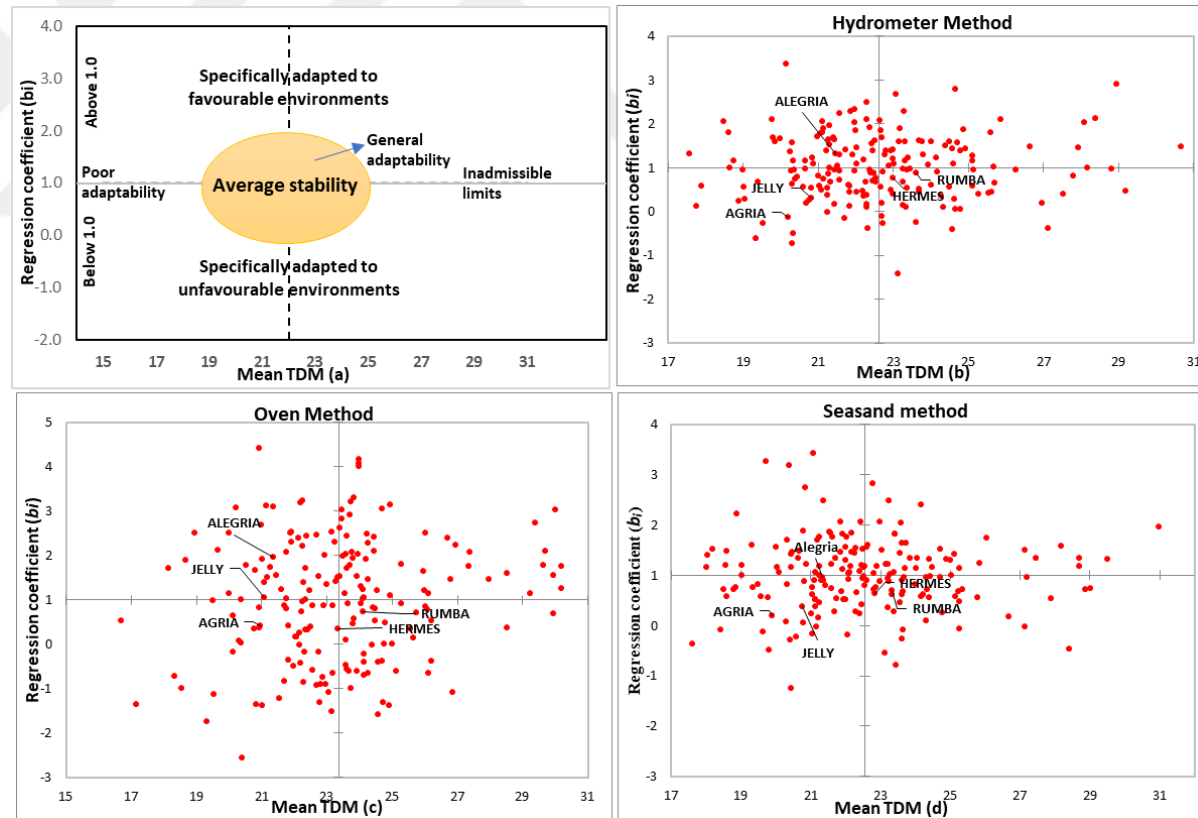


Figure 4.4 Generalized interpretation of graph plotted between regression coefficient (b_i) and mean TDM (a); Relationship of genotype adaptation (regression coefficient ' b_i ') and mean TDM of 189 potato genotypes by various dry matter content determination methods in three diverse environments (b,c and d)

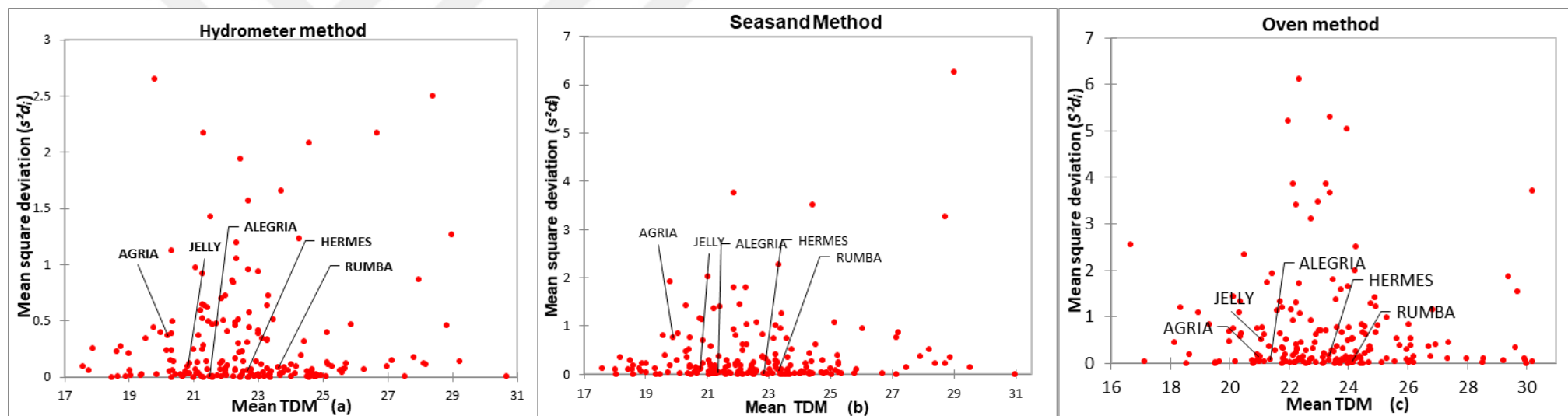


Figure 4.5 Relationship of genotype adaptation (mean square deviation ' s^2_{di} ') and mean TDM of 189 potato genotypes by various dry matter content determination methods in three diverse environments (zero indicates average stability) (a, b and c)

Contrarily, $bi < 1$ refers to a measure of greater resistance to environmental change, thereby specifically adapted to unfavourable environments.

The quality of processed tuber products (French fries and crisp) is mainly dependent upon ideal range of TDM i.e., between 20% to 25% (McGregor, 2007). Based on this information, Table 4.5 revealed an optimum mean TDM with respective values of the stability parameters (bi and $S^2_{d_i}$) for the 15 most stable genotypes along with 5 check cultivars tested across three environments with three methods. A genotype was considered as stable, when $S^2_{d_i}$ values were lower than the mean, with zero as measure of average stability. The mean values of $S^2_{d_i}$ for hydrometer, seasand and oven methods were 0.30, 0.39 and 0.68, respectively. An average stability was observed with three methods, in all check cultivars except Agria, when $S^2_{d_i}$ was considered as stability parameter. Oven method showed Agria as stable cultivar ($S^2_{d_i}=0.14$) while remaining two methods render it unstable. Deviation from regression was observed to be 0.37 and 0.75 (higher than mean) in hydrometer and seasand methods (Table 4.5 & Figure 4.5).

Table 4.5. Optimum means of tuber dry matter content with respective values of the stability parameters (bi and $S^2_{d_i}$) for the 15 most stable genotypes along with 5 check cultivars tested across three environments with three methods

Genotypes	Hydrometer method			Seasand method			Oven method		
	mean	bi^a	$S^2_{d_i}^b$	mean	bi	$S^2_{d_i}$	mean	bi	$S^2_{d_i}$
Agria	20.19	-0.13	0.37	19.90	0.20	0.75	20.96	0.41	0.14
Alegria	21.47	1.29	0.00	21.33	0.96	0.04	21.36	1.96	0.07
Hermes	22.67	0.78	0.06	22.84	0.77	0.02	23.34	0.35	0.17
Jelly	20.81	0.31	0.09	20.77	0.37	0.10	21.07	1.06	0.51
Rumba	23.61	0.89	0.09	23.33	0.79	0.09	24.11	0.73	0.04
Russet burbank	21.58	0.93	0.00	21.94	0.71	0.17	22.23	0.73	0.40
Van Gogh	22.76	1.29	0.07	22.39	1.07	0.04	23.57	2.02	0.06
Inara	21.58	0.72	0.00	21.37	0.89	0.05	22.36	1.01	0.11
Pomqueen	23.02	1.08	0.00	22.17	1.84	0.39	23.18	-0.65	0.02
Baltic cream	24.60	1.08	0.02	24.31	0.96	0.03	24.13	1.06	0.00
Bonus	23.40	1.24	0.05	22.49	0.94	0.01	24.12	1.24	0.52
43-118-11	21.56	1.29	0.00	21.14	1.06	0.01	21.91	2.53	0.52
Lady Olympia	22.40	0.87	0.22	22.51	0.98	0.23	22.18	3.19	0.01
DT11007.01	23.93	1.07	0.06	23.28	1.02	0.25	23.25	2.30	3.85
DT12068.21	20.65	0.97	0.00	21.26	0.99	0.09	21.27	1.74	1.73
DT13026.10	22.37	0.96	0.30	22.09	0.92	0.18	22.57	0.86	0.00
DT14030.11	23.30	1.16	0.01	22.55	0.81	0.01	24.25	2.27	0.26
DT14088.03	20.66	1.15	0.00	21.53	1.86	0.06	21.90	2.30	0.04
102-102-11	20.37	0.74	0.13	20.10	1.05	0.01	21.77	1.03	0.00
133-112-11	22.88	1.04	0.00	23.24	0.88	0.13	22.07	0.16	1.16

^aprinted values in bold are not significantly different from unity at $p < 0.05$; genotypes with values in bold are considered stable; ^bprinted values in bold are lower than the mean and considered stable. Bold integers have general adaptability to all environments

Oven method recorded higher $S^2_{d_i}$ values in lines DT12068.21, DT13026.10 and 133-112-11 declaring them unstable, while same lines were tagged as most stable lines by hydrometer and seasand methods. The latter two methods were found to provide similar results while discrepancy had been observed with former method. Regression coefficient (bi) values of check cultivars (Alegria and Hermes) were not significantly different from unity (1.0), in hydrometer and seasand methods, which depicts their general adaptability to all environments. Oven method, however, showed Alegria as precisely adapted to favourable environments ($bi=1.96$, significantly different from unity), while Hermes to unfavourable environments ($bi=0.35$). Same method provides contradictory report in case of cultivar Jelly, as $bi=1.06$ was not significantly different from unity, in contrast to unity significance obtained in hydrometer ($bi=0.31$) and seasand ($bi=0.37$) methods. In terms of adaptability/stability, latter two methods describe Jelly as being specifically adapted to unfavourable environment, while the former (oven method) interprets its general

adaptability to all environments. Rumba exhibits general adaptability in all three methods. Interestingly, Agria was designated as precisely adapted to unfavourable environments by all three methods. Genotypes and lines such as Van Gogh, Lady Olympia, Pomqueen, 43-118-11, DT11007.01, DT12068.21, DT14030.11, DT14088.03 and 133-112-11 showed *bi* values significantly different from unity (i.e., varied stability/adaptability), in oven method, while all of the same were found to be most stable (i.e., general adaptability) in hydrometer and seasand methods (*bi* approximating to 1.0; $p < 0.05$). Deviated values of stability parameters in oven method showed the superiority and accuracy of hydrometer and seasand methods.

4.1.2.6 Discussion

Tuber dry matter content determines the sensory perceived characteristics of potato (van Dijk et al., 2002). This is the first comprehensive study to demonstrate a comparison among standard TDM determination methods in multi-environment field trials. Practibility and reliability of methods were analysed using diverse 189 potato genotypes, with TDM range of 15.19% to 34.50%. Deviated results were observed with oven-dry method, while comparable findings were obtained with hydrometer and seasand methods. Hydrometer worked on the principle of under-water weight measurement (UWW). Kumar et al. (2005) noticed that 85% variance in TDM as response variable, was explained by regression model, using UWW/hydrometer as independent variable. A close relationship ($R^2=0.94$) was recorded between UWW and dry matter content in tubers (Haase, 2003). Moisture-drying on quartz seasand and oven-dry methods have been utilized solely to analyse the dry matter content of potatoes (AACC, 1993a; Haase, 2003, 2011; Caliskan et al., 2004; Bonierbale, 2007; Mebratie and Desta, 2018). Haase (2003, 2011) used moisture drying on quartz seasand (AACC, 1993a, 1993b) as reference method for NIRS estimating calibration equation to measure TDM. Calibration and validation models showed $R^2 = 0.99$, with seasand method (as reference method), disclosing the reliability of this method. Our findings were comparable to the studies mentioned earlier. Interpretation of regression and correlation results revealed a strong relationship between seasand and hydrometer methods in contrast to oven-dry method. The former two methods thus can be used interchangeably.

Seasand is an accurate, reliable, destructive method but offers some limitations in terms of laborious and time consuming. Alternatively, hydrometer is an automated, non-destructive, cheap and rapid method to calculate TDM of large number of tuber samples. It has wide applicability and practicability in laboratory as well as under field conditions for large number of samples (n). Nevertheless, it requires approximately 2500 g of clean raw tubers with minimum of 4-5 replications per sample. It can also estimate the specific gravity of tubers, simultaneously. Precision in dry weight measurements is inevitable for an estimation of water loss in tuber samples meant for dry matter content determination. Evaporative loss of water during measurement of TDM by oven-dry method might be responsible for its less precision. It can be overcome by putting the samples in desiccator and instant measurement of its weight after drying. Vacuum or freeze drying can be used alternatively. The current study thus allows the potato researcher/food analyst at industry to choose, either destructive (moisture-drying on quartz seasand) and/or non-destructive method (potato hydrometer) of TDM measurement. These methods gave stable results over range of environmental conditions.

AMMI analysis validates the presence of GEI indicating that genotypes respond differently in tested environments. Significant differences were present among test and check genotypes included in the study. Mebratie and Desta (2018) tested 105 potato genotypes and found significant variation among control, tests and test vs control genotypes for TDM. Konya standard water regime may be considered ideal for testing TDM of large number of genotypes. Our results were comparable to the findings of Rak et al. (2013). Drought conditions showed high dry matter content as compared to the standard water conditions in Hatay and Konya. Reports suggest that water deficit conditions reduce the tuber water contents, consequently tuber dry matter content increases (Kumar et al., 2007; Sharma et al., 2011). High temperatures reduce the starch contents in tubers. Since, starch and TDM can be used synonymously, high temperature thus decreases the tuber dry matter content (Van Eck, 2007). The decrease in average TDM under Konya standard water conditions compared to Hatay standard water circumstances might be due to relatively high temperature in Konya. AMMI analysis had been used extensively in yield stability studies, indicating most stable high yielding genotypes suitable to specific environments (Hassanpanah, 2010; Lenartowicz et al., 2019). The applicability of this analysis is debatable in current study to identify GEI

interactions for huge germplasm collections. Further stability statistical analysis might be helpful to unveil the stable GEI interactions.

Several statistical methods have been proposed for interpretation of GEI (Flores et al., 1998). Parametric stability methods like regression coefficient (bi ; Finlay and Wilkinson, 1963) and variance of deviations from the regression (S^2_{di} ; Eberhart and Russell, 1966) have been used primarily to assess the stability of genotype by associating an observed genotypic response (TDM; *in our case*) to environmental conditions (Pour-Aboughadareh et al., 2019). Reliability of methods can also be judged by stability statistics. Deviation in the stability parametric indices (bi and S^2_{di}) were found in oven method, while seasand and hydrometer indicated similar results, for the same genotypes within each tested environment. Stability parametric analysis disclosed candidate genotypes, depicting optimum stable TDM across the tested environments with three methods. These genotypes can be recommended as a useful genetic resource for breeding of processing cultivars, suitable to Mediterranean and Continental climatic conditions. Genotypes that maintain optimum mean TDM between 20% to 25% in varying environmental conditions are desirable for potato processing industry. Rak et al. (2013) identified desirable lines to extended cold conditions through stability analysis. Same stability parameters were discussed by Akcura et al. (2006) and Mohamed and Ali (2015). Overall, when making selection for optimum TDM, genotypes with too low and too high, mean TDM were eliminated regardless of their bi and S^2_{di} values equals to 1 and zero, respectively.

4.1.2.7 Conclusion

The current study concluded the comparative efficacy of both seasand and hydrometer methods in contrast to oven-dry method for the measurement of TDM. The seasand is an accurate, destructive method but offers some limitations in terms of laborious and time consuming. Alternatively, hydrometer is an automated, non-destructive, cheap and speedy method to calculate TDM of large number of tuber samples. Nevertheless, it requires approximately 2500 g of clean raw tubers with minimum of 4-5 replications per sample. A strong correlation and high goodness of fit was observed between seasand and hydrometer methods. The study also reinforce that environmental conditions have significant effect on TDM, and potato genotypes respond differently to environments. Konya standard water conditions prove to be the best among the three environments, for

obtaining optimum TDM with less environmental influence. Stability analysis revealed stable genotype clusters among the set of treatments. Certain genotypes were selected and docketed into stable category. These candidate genotypes would be exploited for further molecular studies and serve as a useful resource for breeding of processing cultivars.

4.1.3 Specific gravity (SG)

A detailed data of specific gravity for 192 genotypes measured across four environmental conditions is given in Appendix-B. The data elaborated the estimated values obtained after augmented design analysis (Appendix Q2) along with total and individual means of each genotype in four environments. Moreover, a descriptive statistic of SG is mentioned in Table 4.6. The range of specific gravity was found to be 1.067 to 1.127. The heritability estimates were similar to DMC and was found to be high with a H^2 value of 0.88. This indicates that genes contribute more towards the variation in SG compared to individual environment effects. AMMI analysis was performed for DMC and demonstrated that there were significant differences ($P < 0.001$) among genotypes, environments and genotype by environment interaction (GEI) (Table 4.7). Konya standard water conditions-2018 (1.088) and Hatay-2019 (1.089) were the best stable environments for determination of SG (Fig. S2). 15 most adaptable genotypes across all environments with an optimum specific gravity includes Hermes, Rumba, Lady Olympia, Wendy, DT14038.01, DT13085.01, 944-208-10, Borwina, Pelikan, Innara, 63-113-11, DT13143.54, Van Gogh, Albatros and DT14051.66. *bi* values of all genotypes are listed in Appendix B. Check cultivar Jelly and Alegria showed same pattern as observed for DMC.

4.1.4 Reducing sugars (RSS)

Reducing sugars (glucose and fructose) in the tubers were measured through HPLC. A detailed data set of reducing sugars (g/100g DW) calculated in four environmental conditions is given in Appendix C. ANOVA for augmented design analysis is given in Appendix Q3. Descriptive statistics showed that the reducing sugars in different genotypes ranged from 0.02 g/100g DW to 0.38 g/100g DW (Table 4.6). The heritability estimates predicted H^2 of 0.73, revealing the presence of 23% environmental variability. AMMI analysis showed that genotypes, environment and GEI

was highly significant (Table 4.7). Konya standard water conditions-2018 (0.10 g/100g DW) was found to be the stable environment (Fig. S3). Hatay-2019 recorded the maximum reducing sugars (0.16 g/100g DW), it may be due to genotype by environment interaction of some unstable genotypes or might be the effect of temperature. Finlay and Wilkinson (1963) regression coefficient (*bi*) stability estimates revealed 15 genotypes with average stability and low reducing sugar contents (i.e., lower than average 0.118 g/100g DW) including Rumba, Hermes, Alegria, Banba, DT14051.66, DT11088.01, Pomqueen, SFHIT, Terrana, 57-104-11, Maxilla, 146-103-11, DT14036.01, Beo and DT13124.21 (Appendix C). These genotypes could be important both for potato breeders and processing industry because of average stability in all environments and low reducing sugars.

4.1.5 Sucrose (SUC)

Sucrose contents in the tubers were measured through HPLC. A detailed data set of sucrose (g/100g DW) calculated in four environmental conditions is given in Appendix D. ANOVA for augmented design analysis is given in Appendix Q4. Descriptive statistics showed that the sucrose ranged from 0.03 g/100g DW to 0.37 g/100g DW (Table 4.6). The heritability estimates predicted H^2 of 0.65 revealing the presence of 35% environmental variability. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Hatay-2018 and Hatay-2019 were the stable environments with sucrose contents of 0.10 and 0.12 g/100g DW (Fig. S4). Konya standard water conditions recorded less sucrose contents (0.09 g/100g DW). Interestingly, drought conditions recorded higher sucrose concentration (0.13 g/100g DW). The same environment recorded less amount of reducing sugars (0.09 g/100g DW). High sucrose contents are not desirable by the processing industry as this disaccharide converts to the reducing sugars which acts as precursor for Maillard reaction. The concentration of sucrose in tubers increases with severity of drought stress (Bethke et al., 2009). The possible explanation of less reducing sugars under drought conditions is due to high dry matter content of genotypes as both are negatively correlated. Although less reducing sugars are desirable but drought conditions cannot be considered as best since the accumulation of high amount sucrose under water stress. This disaccharide will eventually undergo enzymatic hydrolysis to yield reducing sugars, thereby increasing its amount (Duarte-Delgado et al., 2016). *bi* adaptability index designated following 15

genotypes with average stability along with less amount of sucrose; i.e., Alegria, Rumba, 43-111-11, DT13085.01, Power, Terrana, 106-105-11, 68-105-11, DT14014.27, Zirve, Wendy, DT14069.13, DT13147.17, DT14057.36, DT13007.03 (Appendix D).

4.1.6 Free Asparagine (ASP)

Free asparagine in the tubers were measured through HPLC. A detailed data set of free asparagine (g/100g DW) calculated in four environmental conditions is given in Appendix E. ANOVA for augmented analysis is mentioned in Appendix Q5. Descriptive statistics showed that the ASP ranged from 0.07 g/100g DW to 0.22 g/100g DW (Table 4.6). The heritability estimates predicted H^2 of 0.66 revealing the presence of 34% environmental variability. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Konya standard water conditions (0.12 g/100g DW) was the stable environment (Fig. S5). Drought environment recorded the high free asparagine contents (0.14 g/100g DW). Free asparagine was almost doubled under drought stress in a study conducted by Muttucumaru et al. (2015). The GEI was explained through Finlay and Wilkinson stability model, which showed the genotypes with average stability and less free asparagine levels namely Prestige, Arkula, DT14051.66, Tokio, 860-201-10, Hermes, DT14011.18, 40-103-11, LOGO, 140-107-11, Birte, DT11007.01, DT11088.01, DT14038.01 and DT14069.13. Alegria was best adapted to unfavourable environment as it was less sensitive to environmental change ($bi=0.00$) and recorded less free asparagine (0.11 g/100g DW).

4.1.7 Tuber starch content (ST)

Polarimeter was used for measurement of tuber starch contents (%) and the complete data set disclosing the amount of starch (%) in 192 genotypes across four environments is given in Appendix F. ANOVA for augmented analysis is given in Appendix Q6. Starch contents in genotypes ranged from 67.55% to 86.96%. The heritability estimates predicted H^2 of 0.70 revealing the presence of 30% environmental variability. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Hatay-2019 (76.08%) considered as the stable environment (Fig. S6) with Konya standard water conditions recorded highest tuber starch (77%) contents. Drought stress environment recorded the minimum starch contents (72%). A significant reduction of

55% in starch was reported Rudack et al. (2017) under drought stress. Genotypes having average stability and high starch contents include Hermes, Albatros, Prestige, DT14006.07, Arkula, 878-202-10, DT14005.09, DT13037.31, Diplomat, Baltic cream, DT11007.01, Beo, Maxilla, 89-105-11 and 882-202-10 (Appendix F).

4.1.8 Beta-carotene (BCRT)

Beta-carotene content (ug/g DW) of tubers were measured with help of spectrophotometer and results were presented in Appendix G. ANOVA for augmented analysis is outlined in Appendix Q7. The beta-carotene content in tubers of various genotypes ranged from 4.59 ug/g DW to 23.02 ug/g DW (Table 4.6). The heritability estimates predicted H^2 of 0.56 revealing that 56% variation in the trait is due to genetic factors. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Hatay-2019 was found to be the stable environment (Fig. S7) with mean β -carotene of 11.62 ug/g DW, however the maximum beta-carotene was recorded under Konya standard water conditions (13.86 ug/g DW). Water stressed conditions exhibited minimum beta carotene contents (10.88 ug/g DW). The maximum amount of β -carotene under Konya standard water environment might be attributed to higher altitude as UV radiations and altitude are positively correlated for the synthesis of carotenoids (Hejtmánková et al., 2013). GEI was important for the variation in beta carotene. The genotypes possessing higher beta carotene contents along with average stability includes Alegria, Rumba, Allora, DT14069.13, 146-103-11, DT14016.34, DT14078.03, Borwina, DT14042.27, DT13147.17, DT14014.27, 63-113-11, Tacoma, DT14010.14 and DT13045.42 (Appendix G).

4.1.9 Total antioxidant activity (TAA)

The spectrophotometric results of total antioxidant activity (mg AAE/100 g DW) of 192 genotypes measured in four different environments is presented in Appendix H. ANOVA for augmented analysis is mentioned in Appendix Q8. Descriptive statistic revealed that TAA contents in various genotypes ranged from 26.04 to 40.95 mg ascorbic acid equivalent (AAE)/100g DW (Table 4.6). The heritability estimates predicted H^2 of 0.62 revealing that 62% variation in the trait is due to genetic factors. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Konya standard

water environment (30.97 mg AAE/100g DW) was found to be stable among the four (Fig. S8), while TAA was decreased under drought conditions (28.11 mg AAE/ 100g DW). Finlay and Wilkinson (1963) adaptability analysis showed genotypes with average adaptability coupled with high TAA. It includes Alegria, Rumba, Hermes, DT12068.21, DT14091.04, DT14054.11, DT14011.18, DT14006.07, DT13143.54, DT13045.103, Bonus, Tessa, Lady Olympia, Soraya and 141-104-11. Jelly was adaptable to unfavourable environments with $bi=0.36$, but recorded low TAA of 29.14 mg AAE/100g DW.

4.1.10 Total phenolic contents (TPC)

The spectrophotometric results of total phenolic contents (mg FAE/100 g DW) of 192 genotypes measured in four different environments is presented in Appendix I. ANOVA for augmented analysis is shown in Appendix Q9. Total phenolic contents in genotypes ranged from 62.13 to 298.64 (mg ferulic acid equivalent FAE/100g DW) Broad sense heritability was found to be 0.94, which means that 94% variability in a trait was caused by genetic differences among genotypes. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Konya standard water conditions (144.18 mg FAE/100g DW) recorded as the stable environment along with drought conditions (Fig. S9). However, total phenolics were decreased under water stressed environmental conditions (135.86 mg FAE/100g DW). Genotype adaptability was calculated through Finlay and Wilkinson model. Genotypes having average stability coupled with high total phenolics includes Madaleine, DT13143.58, DT13085.01, DT14006.07, Tucan, DT13049.50, Hermes, DT14090.11, DT13052.23, DT13143.49, DT13124.21, 68-105-11 and DT13100.02. Among check cultivars, Rumba and Alegria recorded high total phenolic contents of 193.24 and 171.83 mg FAE/100 g DW, respectively. Both of these genotypes were adapted to favourable environmental conditions owing to below average stability values ($bi=2.14$ and $bi=2.85$) (Appendix I).

4.1.11 Tuber Flesh colour “L* coordinate” (FCL)

The flesh colour of tubers was measured through CIELab chroma meter. It measures the colour in three coordinates L* (dark/light), a* (green/red) and b* (blue/yellow). The data pertaining to flesh colour L* coordinate/dimension (FCL) for 192 genotypes among four

environments is mentioned in Appendix J. ANOVA for augmented analysis is shown in Appendix Q10. The L* dimension clarifies that as the tuber flesh colour changes from dark yellow to white, the value of L (lightness) increases. The measurement of FCL in our population of 192 genotypes ranged from 62.16 (dark yellow) to 73.62 (white) (Table 4.6). Broad sense heritability was found to be 0.65, which means that 65% variability in a trait was caused by genetic variation among the genotypes. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Hatay 2019 was recorded as the stable environment recording FCL of 68.37 (Fig. S10). Konya drought environment exhibit higher FCL value of 69.67 (more light/white flesh colour). It might be due to differential response of genotypes to the accumulation of carotenoids and phenolics caused by water stress. Genotype adaptability was calculated through Finlay and Wilkinson model (1963). Genotypes having average stability includes Rumba (65.95), Birte (69.42), Soraya (67.30), Zirve (68.09), Fidelia (65.65), 944-208-10 (69.40), DT14026.04 (65.38), 43-118-11 (68.04), 878-202-10 (67.32), DT12068.21 (67.89), DT14003.01 (69.09), 868-201-10 (68.47) and 43-111-11 (71.25) (Appendix J).

4.1.12 Tuber flesh colour “b* coordinate” (FCb)

The data pertaining to flesh colour b* coordinate/dimension (FCb) for 192 genotypes among four environments is mentioned in Appendix K. ANOVA for augmented analysis is shown in Appendix Q11. The b* dimension clarifies that as the tuber flesh colour changes from white to yellow, the value of b* (yellowness) increases. The measurement of FCb in our population of 192 genotypes ranged from 13.57 to 29.52 (Table 4.6). L and b coordinates for potato flesh were highly correlated in our study and supported by the literature (Escurdeo et al., 2018). Our study revealed a significant negative correlation between flesh colour L* and b* coordinates ($r = -0.399^{**}$) (Table 4.8). Broad sense heritability was found to be 0.81, which means that 81% variability in a trait was caused by genetic variation among the genotypes. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Hatay 2019 (23.78) and Konya standard water conditions-2018 (23.83) were regarded as the stable environments (Fig. S11). Genotype adaptability was calculated through Finlay and Wilkinson model (1963). It revealed genotypes with average stability such as Rumba (23.09), Hermes (23.44), Karlana (25.01), DT14061.23 (26.72), DT13028.01 (25.76), Power (22.01), Romanze

(24.48), DT14085.03 (29.23), DT14027.08 (26.01), Soraya (26.22), DT13162.12 (24.54), Acapella (25.28), Adretta (23.81), Tokio (27.96) and Bettina (24.38).

4.1.13 Tuber flesh colour “a* coordinate” (FCa)

The data pertaining to flesh colour a* coordinate/dimension (FCa) for 192 genotypes among four environments is mentioned in Appendix L. ANOVA for augmented analysis is shown in Appendix Q12. The a* dimension describes the greenness and redness of tubers. The FCa measurements ranged from 0.13 to 3.11 (Table 4.6). Broad sense heritability was found to be 0.59, which means that 59% variability in a trait was caused by genetic variation among the genotypes. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Hatay 2019 was regarded as the stable environment among the tested four environments with flesh colour a* of 1.24 (Fig. S12). Genotype adaptability was calculated through Finlay and Wilkinson model (1963). Genotypes with average stability Kiwi (1.07), Rumba (1.57), 944-208-10 (1.42), Summer gold (1.34), 102-102-11 (1.34), 966-203-10 (1.37), DT13136.22 (0.79), DT13028.01 (1.61), Alegria (0.99), Tacoma (2.12), DT13130.48 (0.66), DT14085.03 (2.25), 139-101-11 (1.47), Logo (1.59) and DT14054.11 (0.40).

4.1.14 Tuber skin colour “L* coordinate” (SCL)

The data set illustrating the biological variation of tuber skin colour (L*) for 192 genotypes in four environmental conditions is shown in Appendix M. ANOVA for augmented analysis is shown in Appendix Q13. The L* dimension gives a marked indication as the tuber skin colour changes from dark red to light yellow by marked increase in the value of L (lightness). Descriptive statistics showed that SCL ranged from 47.34 (dark red skin) to 66.20 (light yellow skin) in current study (Table 4.6). Broad sense heritability was found to be 0.75, which means that 75% variability in a trait was caused by genetic variation among the genotypes. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Konya standard water conditions was found to be the best stable environment with SCL of 59.65 (Fig. S13). Genotype adaptability was calculated through Finlay and Wilkinson (1963) model. Genotypes having average stability includes DT14068.07 (62.98), Fasan (59.75), Adretta (58.83), Hermes (60.29), DT14051.66 (62.08), DT13083.01 (61.42), DT14062.08

(65.58), DT14026.04 (63.38), Rita (60.10), Talent (60.07), 89-105-11 (59.71), Fidelia (58.65), Mungo (58.50), 944-208-10 (59.45) and DT14004.17 (52.39) (Appendix M).

4.1.15 Tuber skin colour “b* coordinate” (SCb)

The data set showing the biological variation of tuber skin colour (b*) for 192 genotypes in four environmental conditions is shown in Appendix N. ANOVA for augmented analysis is shown in Appendix Q14. The b* dimension gives a marked indication as the tuber skin colour changes from dark red to light yellow by marked increase in the value of b (yellowness). A significant positive correlation was observed between SCL and SCb (0.584**) (Table 4.8). It means that b* coordinate of chroma meter is sensitive to detect yellow colour as some genotypes do have brown and red skin. Descriptive statistics showed that SCb ranged from 12.80 to 39.94 in current study (Table 4.6). Broad sense heritability was found to be 0.51, which means that 51% variability in a trait was caused by genetic variation among the genotypes. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Konya standard water conditions was found to be the best stable environment with SCb of 22.89 (Fig. S14). Genotype adaptability was calculated through Finlay and Wilkinson (1963) model. Genotypes having average stability includes Hermes (24.00), Rumba (24.80), DT14091.04 (29.20), DT14083.28 (25.50), DT13051.10 (26.97), DT13136.22 (25.70), Kutup (24.77), Privelige (26.46), Mungo (27.25), 735-102-09 (26.24), Solist (24.80), Tessa (25.18), 904-212-10 (28.05) and DT14004.17 (17.12) (Appendix N).

4.1.16 Tuber skin colour “a* coordinate” (SCa)

The data set showing the biological variation of tuber skin colour (a*) for 192 genotypes in four environmental conditions is shown in Appendix O. ANOVA for augmented analysis is shown in Appendix Q15. The a* dimension gives a marked indication as the tuber skin colour changes to red by showing an increase in the value of a (redness). A significant negative correlation was observed between SCL and SCa (-0.633**) exhibiting that less L* values (dark red skin colour) are equivalent to high a* values (indicator of redness) (Table 4.8). Descriptive statistics showed that SCa ranged from 4.32 to 12.03 (Table 4.6). Broad sense heritability was found to be 0.56, which means that 56% variability in a trait was caused by genetic variation among the genotypes.

AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Hatay-2018 was found to be the best stable environment with SCa of 7.33. (Fig. S15). Genotype adaptability was calculated through Finlay and Wilkinson (1963) model. Genotypes having average stability includes Alegria (7.35), Jelly (8.01), Rumba (7.20), Hermes (6.48), DT14034.03 (7.31), 89-105-11 (7.28), Fasan (7.23), Solist (6.94), Wendy (6.42), Electra (6.70), DT13007.03 (6.54), DT14078.03 (6.88), DT14046.19 (7.36), DT11088.01 (7.96), DT14063.12 (6.44), DT14004.17) (Appendix O).

The genotypes exhibiting dark skin colour (brown to red) includes DT13072.19, Romanze, Lady Rosetta, DT14004.17, Laura, DT14037.18, DT13028.01 with CIELab values of L* (47.34 to 55.39), b* (12 to 18) and a* (9 to 12), respectively. The same genotypes recorded tuber flesh colour CIELab values within the range of L* (66 to 68), b* (21 to 28) and a* (1 to 3), respectively. Similar trend was not observed for the trait tuber flesh colour (say L* values within range of 62 to 64, which is an indication of dark yellow tuber flesh colour). It might be due to the high environmental variation of tuber flesh colour which is caused by environmental fluctuations. Similar effect of environment on tuber flesh colour was also reported by Fogelman et al. (2019). Finlay and Wilkinson model also designated these genotypes either adapted to only favourable or unfavourable environments (below average or above average stability) (Appendix J-O). Hamouz et al. (2006) reported that the tuber flesh colour changes according to extrinsic features like cultivation year, location, fertility of soil and growing conditions.

4.1.17 Tuber skin (periderm) thickness (PT)

Tuber skin thickness was measured with help of optical stereo microscope (Leica 165C). The data pertaining to tuber periderm thickness (mm) for 192 genotypes in four environments is given in Appendix P. ANOVA for augmented analysis is shown in Appendix Q16. Tuber periderm thickness among 192 genotypes ranged from 0.037 to 0.120 mm. Broad sense heritability was found to be 0.94, which means that 94% variability in a trait was caused by genetic differences among the genotypes. AMMI analysis showed that genotypes, environment and GEI was highly significant (Table 4.7). Konya drought conditions recorded as the stable environment with higher average periderm thickness of 0.68 mm compared to other three environments (Fig. S16). It might be due to the reason that biotic and abiotic stress conditions activate stress responsive

pathways in the tissues of periderm. This enhances cell proliferation and cell wall synthesis through the activation of genes such as *StNAC* and *FHT*, in the phellogen layers resulting in suberin and wax deposition and thus increasing thickness (Verdaguer et al., 2016; Singh et al., 2020). Studies revealed that 63% of tuber skin periderm proteins were related to stress responses (Soler et al., 2011). Another study showed that 28% stress factors were linked with stress responsive suberin and lignin synthesis in periderm (Vulavala et al., 2019). Genotype adaptability was calculated through Finlay and Wilkinson model. Genotypes having average stability coupled with high periderm thickness includes Hermes, Rumba, DT13130.48, Kutup, DT14091.04, DT14042.27, DT13052.23, Madaleine, DT13083.01, 140-107-11, DT13037.31, 878-202-10, Nandu, 89-105-11 and DT14010.14.



Table 4.6. Descriptive statistics for all tuber quality traits of tested 192 genotypes across four environmental conditions.

Phenotypic Traits	H-18 Mean $\pm$ SEM	KN-18 Mean $\pm$ SEM	KD-18 Mean $\pm$ SEM	H-19 Mean $\pm$ SEM	Overall Mean $\pm$ SEM	Min	Max
DMC (%)	21.66 $\pm$ 0.19	21.98 $\pm$ 0.39	24.29 $\pm$ 0.37	22.19 $\pm$ 0.47	22.50 $\pm$ 0.160	17.52	30.00
SG	1.087 $\pm$ 0.0009	1.088 $\pm$ 0.0171	1.099 $\pm$ 0.0141	1.089 $\pm$ 0.0220	1.090 $\pm$ 0.0008	1.067	1.127
RSS (g/100g DW)	0.12 $\pm$ 0.0064	0.10 $\pm$ 0.0054	0.09 $\pm$ 0.0034	0.16 $\pm$ 0.0080	0.12 $\pm$ 0.0043	0.02	0.38
SUC (g/100 g DW)	0.10 $\pm$ 0.0041	0.09 $\pm$ 0.0046	0.13 $\pm$ 0.0061	0.12 $\pm$ 0.0049	0.12 $\pm$ 0.0034	0.03	0.37
ASP (g/100 g DW)	0.12 $\pm$ 0.0022	0.12 $\pm$ 0.0029	0.14 $\pm$ 0.0035	0.12 $\pm$ 0.0031	0.13 $\pm$ 0.0017	0.07	0.22
Starch (%)	75.66 $\pm$ 0.40	77.04 $\pm$ 1.03	72.00 $\pm$ 0.96	76.08 $\pm$ 1.52	75.17 $\pm$ 0.241	67.55	86.96
BCRT (ug/g DW)	11.21 $\pm$ 0.39	13.84 $\pm$ 0.39	10.88 $\pm$ 0.35	11.62 $\pm$ 0.43	11.89 $\pm$ 0.22	4.59	23.02
TAA (mg AAE/100 g DW)	32.31 $\pm$ 0.34	30.97 $\pm$ 0.55	28.11 $\pm$ 0.31	32.76 $\pm$ 0.74	31.03 $\pm$ 0.20	26.04	40.95
TPC (mg FAE/100g DW)	146.83 $\pm$ 4.86	144.18 $\pm$ 4.69	135.86 $\pm$ 4.13	141.53 $\pm$ 4.35	141.92 $\pm$ 3.79	62.13	298.64
FCL	66.60 $\pm$ 0.231	67.42 $\pm$ 1.075	69.67 $\pm$ 0.908	68.37 $\pm$ 1.391	67.97 $\pm$ 0.135	62.16	73.62
Fca	1.07 $\pm$ 0.063	1.37 $\pm$ 0.057	1.53 $\pm$ 0.060	1.24 $\pm$ 0.048	1.30 $\pm$ 0.036	0.13	3.11
FCb	18.65 $\pm$ 0.333	23.83 $\pm$ 0.454	24.83 $\pm$ 0.399	23.78 $\pm$ 0.534	22.66 $\pm$ 0.217	13.57	29.52
SCL	60.38 $\pm$ 0.271	59.65 $\pm$ 0.958	60.30 $\pm$ 0.805	63.08 $\pm$ 1.302	60.79 $\pm$ 0.186	47.34	66.20
Sca	7.33 $\pm$ 0.121	6.56 $\pm$ 0.137	6.96 $\pm$ 0.125	7.01 $\pm$ 0.192	6.985 $\pm$ 0.075	4.32	12.03
SCb	23.34 $\pm$ 0.419	22.89 $\pm$ 0.424	24.79 $\pm$ 0.490	30.38 $\pm$ 0.658	25.22 $\pm$ 0.214	12.80	39.94
PST (mm)	0.065 $\pm$ 0.0011	0.063 $\pm$ 0.0014	0.068 $\pm$ 0.0015	0.065 $\pm$ 0.0017	0.065 $\pm$ 0.0010	0.037	0.120

Abbreviations: H-18 (Hatay-2018), KN-18 (Konya standard water conditions-2018), KD-18 (Konya drought-2018), H-19 (Hatay-2019), SEM (Standard errors of mean), Min (minimum), Max (Maximum), DMC (Dry matter content), SG (Specific gravity), RSS (Reducing sugars), SUC (Sucrose), ASP (Free asparagine), BCRT (Beta-carotene), TAA (Total antioxidant activity), TPC (Total phenolic content), FC (Tuber flesh colour, L*a*b dimensions), SC (Tuber skin colour, L*a*b dimensions), PST (Periderm skin thickness).

DW (Dry weight); AAE (Ascorbic acid equivalent); FAE (Ferulic acid equivalent)

Table 4. 7. AMMI ANOVA describing degree of freedom and mean squares of genotypes, environment and genotype by environment interactions, along with genotypic variance, phenotypic variance and broad sense heritability (H^2) for all tuber quality traits of tested 192 genotypes across four environmental conditions.

Phenotypic Traits	Degrees of freedom			Mean squares			Heritability			
	DF_G	DF_E	DF_GE	MS_G	MS_E	MS_GE	Mse	GV	PV	H^2
DMC (%)	191	3	573	19.343**	257.447**	1.823**	1.138	4.380	4.836	0.91
SG	191	3	573	0.00043**	0.00577**	0.00005**	0.0000	0.0001	0.0001	0.88
RSS (g/100g DW)	191	3	573	0.01358**	0.13005**	0.0037**	0.0016	0.0025	0.0034	0.73
SUC (g/100 g DW)	191	3	573	0.00903**	0.0547**	0.00314**	0.0015	0.0015	0.0023	0.65
ASP (g/100 g DW)	191	3	573	0.00219**	0.03326**	0.00074**	0.0003	0.0004	0.0005	0.66
Starch (%)	191	3	573	43.870**	977.423**	13.28**	9.16	7.65	10.97	0.70
BCRT (ug/g DW)	191	3	573	39.04**	358.10**	17.35*	13.37	5.42	9.76	0.56
TAA (mg AAE/100 g DW)	191	3	573	30.43**	838.99**	11.62**	5.08	4.70	7.61	0.62
TPC (mg FAE/100g DW)	191	3	573	10584.51**	4458.68**	639.47**	328.63	2486.26	2646.13	0.94
FCL	191	3	573	13.91**	328.10**	4.83*	3.485	2.270	3.477	0.65
Fca	191	3	573	0.98**	7.40**	0.40**	0.303	0.145	0.246	0.59
FCb	191	3	573	36.60**	1429.30**	6.99**	2.740	7.403	9.150	0.81
SCL	191	3	573	26.38**	436.05**	6.53*	4.755	4.962	6.595	0.75
Sca	191	3	573	4.95**	19.30**	2.20**	0.943	0.686	1.236	0.56
SCb	191	3	573	33.360**	2213.91**	16.260**	7.188	4.275	8.340	0.51
PST (mm)	191	3	573	0.00081**	0.00085**	0.00005**	0.00002	0.00019	0.00020	0.94

Abbreviations: DF-G (Degree of freedom of genotypes), DF-E (Degree of freedom of environments), DF-GE (Degree of freedom of genotype by environment interaction), MSG (Mean square of genotypes), MSE (Mean square of environments), MSGE (Mean square of genotype by environment), Mse (Mean square error), GV (Genotypic variance), PV (Phenotypic variance), H^2 (Broad sense heritability) DMC (Dry matter content), SG (Specific gravity), RSS (Reducing sugars), SUC (Sucrose), ASP (Free asparagine), BCRT (Beta-carotene), TAA (Total antioxidant activity), TPC (Total phenolic content), FC (Tuber flesh colour, L*a*b dimensions), SC (Tuber skin colour, L*a*b dimensions), PST (Periderm skin thickness). DW (Dry weight); AAE (Ascorbic acid equivalent); FAE (Ferulic acid equivalent)

4.2 Correlation Analysis

Pearson correlation was performed through SPSS v.25 software using two tailed test (p value=0.01, (**) depicting highly significant correlations and p value=0.05 (*) showing significant correlations). The results of Pearson correlation coefficient (r) ($N=192$, Prob $> |r|$ under $H_0: \rho = 0$) for the studied tuber quality traits are summarized in Table 4.8. Results showed some interesting significant correlations among several traits. BLUPs (Best linear unbiased predictions) data was used for correlation analysis of all tuber quality traits. A significant strong positive correlation was observed between DMC and SG ($r=0.980^{**}$). DMC was also significantly correlated to starch ($r=0.307^{**}$). Similar significant relationship was observed between specific gravity and tuber starch content ($r=0.308^{**}$). Starch and DMC are thought to be synonymous terms in potato, since about 60 to 80% of the DMC is starch (Ek et al., 2012). It means that high dry matter content is synonymous to high tuber starch contents. Apart from DMC, processing industry is interested in amount of reducing sugars, sucrose and free asparagine. Since these are reactants in Maillard reaction for the synthesis of acrylamide (a potent carcinogenic substance) (Friedman et al., 1995). Correlation analysis revealed that reducing sugars were negatively correlated with DMC ($r=-0.526^{**}$) but significant positive correlation was observed between reducing sugars and free asparagine ($r=0.207^{**}$). Sucrose was not correlated to DMC and free asparagine; however, it was positively correlated to reducing sugars ($r=0.210^{**}$). Duarte-Delgado et al. (2016) also reported a strong positive correlation between disaccharide sucrose and reducing sugars. Free asparagine was also negatively correlated to DMC ($r=-0.257^{**}$). These results showed that instead of sucrose, reducing sugars react with free asparagine during Maillard reaction. Starch was also negatively associated with both reducing sugars and free asparagine ($r=-0.268^{**}$ and $r=-0.185^{**}$). Therefore, the amount of reducing sugars and free asparagine in the tubers decreases with an increase in dry matter content, starch and specific gravity. It has implications for the processing industry (French fries and chips) (Asmamaw et al., 2010).

A significant negative correlation was observed between tuber flesh colour (L^* dimension) and beta-carotene ($r=-0.854^{**}$), while the flesh colour dimension b^* depicted significant positive correlation with beta-carotene ($r=0.269^{**}$). The higher L^* values indicate lightness while the lower showed darkness, contrarily, higher b^* values specify yellow colour and vice versa. Light colour of tuber flesh (L^*) was positively associated

with less accumulation of yellow colour (b^*) in the flesh ($r = -0.399^{**}$). These results showed that amount of beta-carotene increases as the tuber flesh colour becomes dark or yellow. Beta carotene is an important carotenoid present in the tuber flesh. The carotenoid contents of white flesh potatoes are generally low in contrast to higher amounts present in the yellow fleshed varieties (Nesterenko and Sink, 2003). Furthermore, yellow colour of tuber flesh is due to the presence of beta-carotene (Lachman et al., 2016). Starch was not correlated to beta-carotene in our study. Similarly, no correlation was observed between starch and flesh colour (L^* and b^* dimensions). The results illustrated that white and yellow flesh colour of tubers is irrespective of starch but yellow colour of tuber flesh is due to the accumulation of carotenoids. White colour of tubers has more starch contents is a wrong perception.



Table 4. 8. Pearson correlation (r) analysis regarding all traits; DMC (dry matter content), SG (specific gravity), Free_ASP (free asparagine), Red.Sug (reducing sugars), sucrose, BCRT (beta carotene), Starch, TPC (total phenolic content), TAA (total antioxidant activity), FC L*a*b (tuber flesh colour dimensions), SC L*a*b (tuber skin colour dimensions) and PST (periderm skin thickness).

Pearson correlation coefficients, N = 192

Prob > |r| under H₀: $\rho = 0$

	DMC	SG	Free_Asp	Red.Sug	Sucrose	BCRT	STARCH	TPC	TAA	FCL	FCa	FCb	SCL	SCa	SCb	PST
DMC	1	.980**	-.257**	-.526**	-0.14	-.312**	.307**	-.323**	-.197**	.354**	0.10	-0.05	-0.14	0.09	0.07	-0.01
SG		1	-.282**	-.518**	-0.14	-.290**	.308**	-.298**	-.172*	.326**	0.08	-0.05	-.155*	0.10	0.06	0.00
Free_Asp			1	.207**	-0.01	0.09	-.185*	0.10	0.11	-.192**	0.00	0.03	-0.07	0.02	-0.09	0.01
Red.Sug				1	.210**	.262**	-.268**	.190**	.201**	-.228**	-.211**	-0.03	.190**	-0.13	0.08	0.00
Sucrose					1	-0.04	-0.13	0.00	0.00	0.06	-0.11	-0.05	.181*	-0.09	-0.08	-0.02
BCRT						1	-0.04	.604**	.543**	-.854**	0.07	.269**	-0.09	-0.09	-0.03	0.03
STARCH							1	-0.13	-0.11	0.04	0.05	0.05	-0.14	0.07	-0.03	0.05
TPC								1	.510**	-.660**	0.05	0.12	-0.08	-0.10	-0.04	0.12
TAA									1	-.546**	0.01	0.09	-0.04	-0.11	0.00	-0.01
FCL										1	-.177*	-.399**	.157*	0.03	0.05	-0.03
FCa											1	.543**	-.292**	.335**	0.01	0.04
FCb												1	-.246**	.203**	0.06	.152*
SCL													1	-.633**	.584**	-.214**
SCa														1	-.333**	0.11
SCb															1	-0.08
PST																1
**. Correlation is significant at the 0.01 level (2-tailed).																
*. Correlation is significant at the 0.05 level (2-tailed).																

Total phenolics and total antioxidant activity were negatively correlated with tuber flesh colour (L^* dimension) ($r = -0.660^{**}$ and $r = -0.546^{**}$). Beta-carotene was positively correlated to total antioxidant activity ($r = 0.543^{**}$). Likewise, total phenolics were also positively correlated ($r = 0.510^{**}$) with total antioxidant activity. The results were in line with the findings of Al-Weshahy and Rao (2009) who were of the view that carotenoids and phenolic compounds are well known antioxidants. A significant positive correlation was observed between tuber flesh colour and tuber skin colour (L^* dimension) ($r = 0.157^{**}$). Periderm skin thickness was negatively correlated to skin colour (L^* dimension) ($r = -0.214^{**}$). It indicates that darker skin colour tubers may have thick periderm. Suberin deposition in the skin offers resistance to tuber greening, and varietal periderm colour and thickness is considered as secondary resistance mechanisms against stress (Tanios et al., 2020).

4.3 Population Structure, Kinship and Clustering

Population structure of 192 potato genotypes were evaluated based on 13606 (64.10%) polymorphic and robust SNP markers obtained after removing monomorphic markers (35.90%) by adopting filtering approach with minor allele frequency (MAF) > 0.05 and missing data $\leq 10\%$. The delta $K = 4$ value obtained after structure analysis from STRUCTURE software revealed that the genotypes were grouped into four sub-populations or clusters (Fig. 4.6a and 4.7). The SNP HapMap numeric matrix with tetra-allelic SNP dosage (as explained in section 2.3) was used for PCA analysis to assess the genetic variation and diversity among potato genotypes using *Prcomp* package in R v. 3.6.3 (R core Team 2013). PCA results clearly grouped the genotypes into 4 clusters, which authenticates the results of structure analysis (Fig. 4.6b). PC1 and PC2 explained 13.10% and 11.59% variation in the genotypic data, respectively. The bar plot showed an estimated membership coefficient (Q) based on the Bayesian clustering approach, aligned in four colours; red, green, blue and yellow (clusters 1, 2, 3 and 4, respectively as shown in Fig 4b). Individuals having Q values ≥ 0.40 grouped in the same cluster, while those depicting Q values < 0.40 grouped as admixed (Fig. 4.7 and Table 4.9).

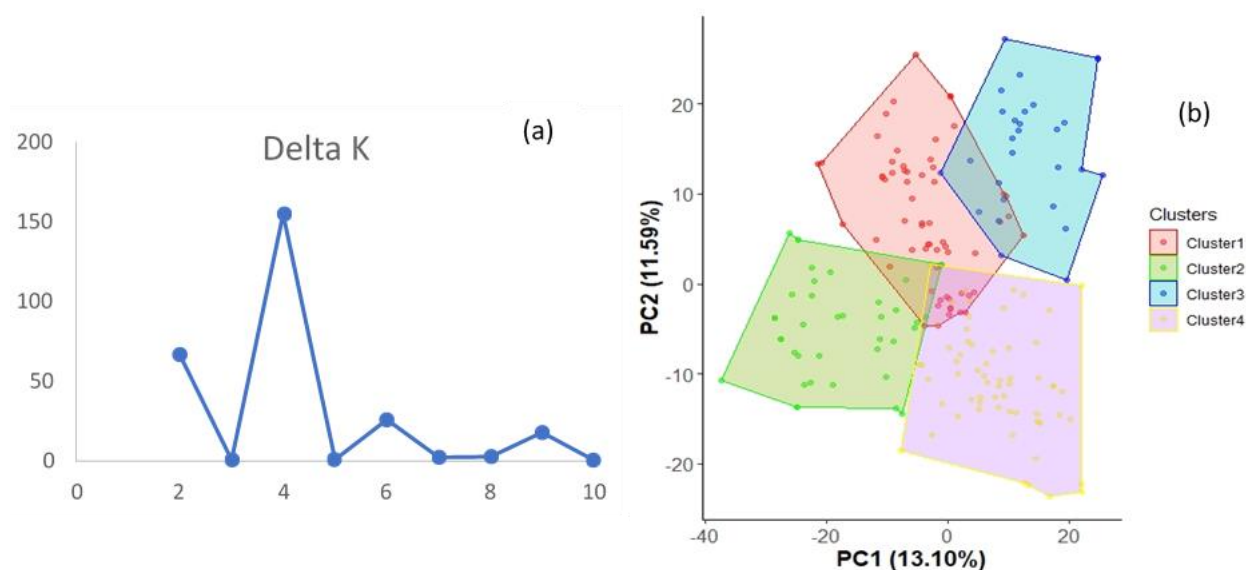


Figure 4. 6. Population structure of 192 potato genotypes based on SNP markers (a) Delta K values over 10 runs ($\Delta K=4$), (b) PCA scatter plot of the first two principal components (PC1 and PC2) depicting the clustering of genotypes into 4 clusters as indicated by delta K results from STRUCTURE.

Out of 192 genotypes, clusters 1 and 4 contained the highest number of genotypes (56, 29.16% and 57, 29.68%) followed by cluster 2 (33, 17.18%) and cluster 3 (26, 13.54%). 20 (10.41%) genotypes were categorized as admixed ($Q < 0.40$). More than 50% genotypes were assigned to clusters 1 and 4. Clusters 1, 2 and 3 mainly constitutes Turkish breeding lines with a relative percentage of 64.29%, 60.61% and 80.77%, respectively. Cluster 4 includes highest proportion of German varieties (52.63%) and German breeding lines (38.60%). Admixed group constitutes 40% German varieties, 30% German breeding lines, 15% Turkish breeding lines and 15% common varieties grown in both Germany and Turkey. Turkish breeding lines are more diverse due to varied and diverse pedigrees including CIP lines as parents from International Potato Centre, Peru (Table 3.1), while German breeding lines had a narrow genetic base as reported by Salimi et al. (2016).

The population structure was determined using the methods illustrated by Evanno et al. (2005) and Earl et al. (2012). Delta K values obtained after structure analysis were plotted against the number of runs (say 10) to obtain the K value. Population structure matrix “Q” of the designated K value was used for association mapping analysis as covariates. For instance, delta K=4 indicates the presence of four subpopulations or clusters, while delta K=2 showed no population structure or genetic similarity among the individuals in

a population. Higher delta K is an indication of genetic diversity or unrelatedness of individuals in an association panel. Careful estimation of population structure and kinship avoid spurious associations between marker and traits during GWAS studies, which could be possible either due to systemic variations in allele frequencies or differences in sample ancestry (Sharma et al., 2018). Variable number “clusters/sub-populations” or “Kinship groups” were identified in literature for GWAS, such as K = 6 (Rosyara et al., 2016), K= 3 (Vos et al., 2017), K=10 (Sharma et al., 2018), K =3 (Klassen et al., 2019) and K = 4 (Zia et al., 2020). The obtained four clusters in our study showed diverse segregation and some admixed distribution of the genotypes. These results indicated that population have a genetic diversity with different structural dimensions. It may be due to the reason that the crossing parents of the genotypes included in the study belongs to entirely different origin, such as diverse CIP lines and might be originated from some wild type species as well. Admixed genotypes were inter-mingled with each other and shared relatively common area exhibiting considerably similar origin with less number of meiotic recombination's. Detailed information of genotypes distribution in 4 clusters and admixed subpopulation is shown in Table 4.9.

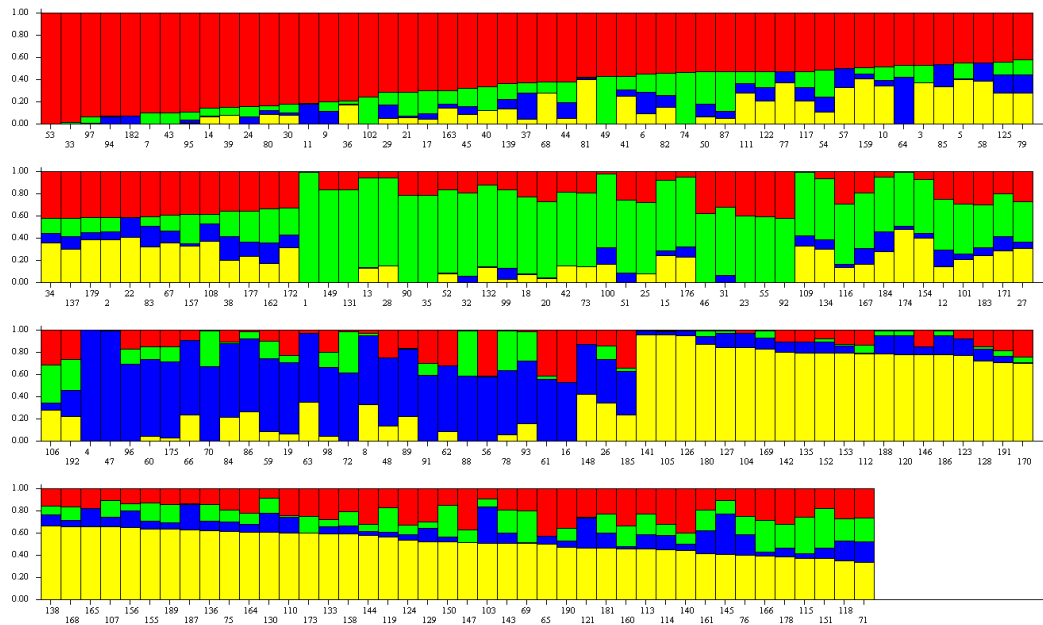


Figure 4. 7. Bar plot displaying population sub-structure of 192 genotypes (K=4). Sub-population clusters 1, 2, 3 and 4 were represented by colours red, green, blue and yellow, respectively according to the Q values (estimated membership covariates). X axis represents serial no. of genotypes corresponding to each individual bar plot as mentioned in Table 3.1, whereas y axis symbolizes Q values obtained from structure software.

Table 4. 9. Clustering of genotypes into admixed ($Q < 0.40$) and four clusters along with their relative distribution into several origins as common, DE_BL, DE_Var, TR_BL and TR_Var ($Q \geq 0.40$)

Clusters	Common	DE_BL	DE_Var	TR_BL	TR_Var	Total
Admixed	3	6	8	3	0	20
1	7	5	7	36	1	56
2	3	3	7	20	0	33
3	0	1	2	21	2	26
4	2	22	30	3	0	57
Total	15	37	54	83	3	192

Clustering in Percentage

Clusters	Common (%)	DE_BL (%)	DE_Var (%)	TR_BL (%)	TR_Var (%)
Admixed	15.00	30.00	40.00	15.00	0.00
1 (red)	12.50	8.93	12.50	64.29	1.79
2 (green)	9.09	9.09	21.21	60.61	0.00
3 (blue)	0.00	3.85	7.69	80.77	7.69
4 (yellow)	3.51	38.60	52.63	5.26	0.00

Common = Common genotypes in both DE and TR

DE_BL = German breeding lines

DE_Var = German varieties

TR_BL = Turkish breeding lines

TR_Var = Turkish varieties

4.4 Linkage disequilibrium (LD)

LD was performed on robust 13606 polymorphic SNP markers obtained by filtering monomorphic markers from a total set of 21226 SNPs using TASSEL software. After removal of N/A, NaN and unmapped chromosome “0”, the total markers used for LD was filtered to 13386 SNP markers. LD was calculated for each chromosome separately as shown in Table 4.10 and the mean r^2 value was observed to be 0.29. A non-linear trend line gives an assumptive estimate of LD decay, if plotted between variables r^2 and genetic distance (Mbp). A proposed marker data set showed LD decay at around 2.31 Mbp to an r^2 value of 0.29. (Fig. 4.8). Extent of LD appears to be between two groups; r^2 at 0.95 Mbp was 0.53 and declined to 0.05 at physical distance of 5.29 Mbp. It seems that after an initial relatively fast decline, decay of LD slows and is not as dramatic as in some other outcrossing species like maize. Extensive LD, small number of haplotypes with slow LD decay in potato could be due to vegetative mode of propagation of tetraploid potato, long breeding cycle and limited number of historical recombination's (Vos et al., 2017). Our results of population structure showed admixed group of genotypes probably separated

with few meiotic events owing to heterozygous autotetraploid nature of potato having a narrow genetic base with most species separated from each other by few meiotic generations (Gupta et al., 2005; Simko et al., 2006; Stich et al., 2005).

In order to enhance the power of marker-trait association, LD tests in conjunction with correction of population structure by taking into account accurate subpopulations leads to reliable GWAS results (Simko et al. 2004). Our results of LD were contrary to the study of Stich et al. (2013) who admonished that LD decay occurs with an intensity of 275 bp. Contrarily, Vos et al. (2017) used LD1/2,90 estimator with LD values ranged between 0.7 to 0.9 Mb. 2 to 4 Mb distance is the general trend for LD decay values in potato crop (Vos et al., 2017) as observed in the current study. LD decay of 1.22 Mbps to an r^2 value of 0.20 was reported by Zia et al. (2020). A population structure and marker density might have affected the LD in our study but still it is within the stipulated physical distance range with literature as 5 to 10 cM (equivalent to 2 to 4 Mbp) of LD decay has been reported by Björn et al. (2010), Simko et al. (2004) and Vos et al. (2017).

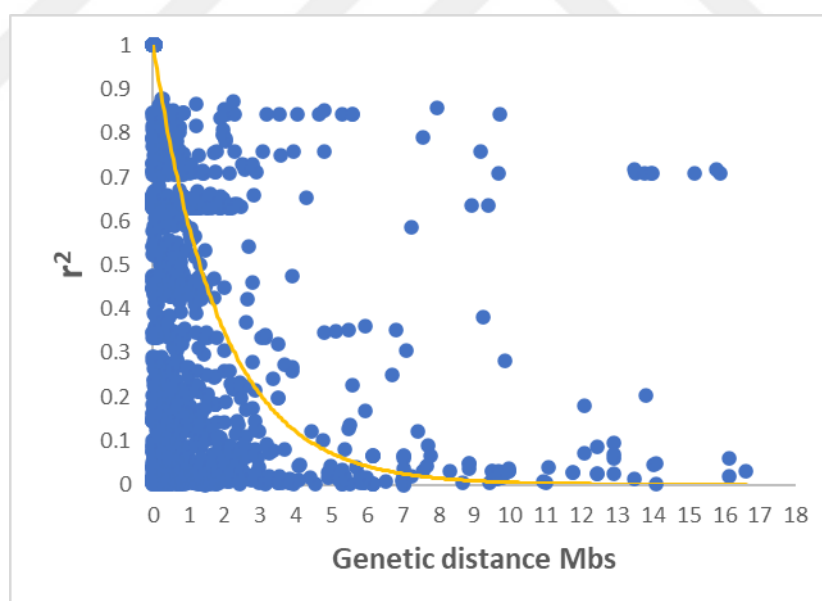


Figure 4. 8. Estimated LD (Linkage disequilibrium) decay plotted between r^2 and genetic distance (Mbs) with non-linear trend line. Mean estimated r^2 value is 0.29 with LD decay at 2.31 Mbs calculated from each chromosome as mentioned in Table 4.10.

Table 4. 10. Linkage disequilibrium in the tetraploid potato (*Solanum tuberosum* L.)

Chromosomes	No. of markers	Chr size Mbps	SNP markers/Mbp	r^2	LD decay (Mbps)
1	1050	88.58	11.85	0.26	2.2
2	453	48.49	9.34	0.21	1.6
3	2178	62.26	34.98	0.3	0.9
4	1489	72.14	20.64	0.29	2.5
5	631	51.99	12.14	0.31	1.0
6	983	59.36	16.55	0.3	2.6
7	1170	56.63	20.66	0.26	2.8
8	3650	56.80	64.26	0.3	1.8
9	485	61.46	7.89	0.21	1.8
10	510	59.67	8.54	0.46	6.0
11	495	45.42	10.89	0.27	2.2
12	292	61.14	4.77	0.3	2.4
Markers	13386	723.94	18.49	0.29	2.31

4.5 Association Mapping

An association mapping study was performed for twelve important quality traits of potato tuber using diverse 13606 polymorphic tetra-allelic SNPs panel of 192 genotypes. For each genotype, BLUPs (Best Linear Unbiased Predictions) extracted from multi-environment experiments (i.e., Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019) calculated for each trait were used to detect significant marker-trait associations. BLUPs estimate the random effects of a mixed model through the calculation of variance. The variance estimations of each trait for 192 genotypes across four environments were performed by REML (Restricted Maximum Likelihood) using *lme4* R package (R Core Team, 2014).

Association mapping was performed by using Q+K mixed linear model (MLM) in *GWASpoly* R package. MLM was used to avoid spurious marker-trait associations. Quantile-Quantile (Q-Q) plots and Manhattan plots were envisioned using two different gene action models (i.e., additive and general) using BLUPs for all traits. General model assumes that each genotype has its own effect and thus encompasses various gene actions. The degree of freedom of general model is 4df considering the five allele dosages (0, 1, 2, 3, 4) for tetraploid species. In general model, SNP effect of each genotypic class is arbitrary. Whereas, additive gene action was used with an assumption that the SNP effect is proportional to the minor allele dosage (Rosyara et al., 2016).

Q-Q plots illustrate the false positives, false negatives, family structure, and population stratification by a scale of $-\log_{10}(P)$ between observed and expected p values. The null hypothesis was accepted as true, if there is a uniform distribution (1:1 straight line without tailing on either side between expected and observed $-\log_{10}(P)$ values) meaning no significant associations or casual polymorphisms. The deviations of straight line at the tail indicated that null hypothesis was rejected with the presence of significant associations (i.e., significant p values are present in the tail which are found to be in LD (linkage disequilibrium) with a casual polymorphism). An early deflation of line upwards or downwards indicates false positives and false negatives, respectively. (Kaler et al., 2020). The normal distribution of the data was analysed through Q-Q plots and revealed normal distribution among all the traits. False positives and false negatives were appropriately controlled by the additive and general models in the study as depicted by sharp deviation of observed vs expected P values in the tail area. Few discrepancies were however observed in Q-Q plots between general and additive models for some traits. A detailed explanation of Q-Q plots between the two models (additive and general) for each studied trait is further illustrated in the following sections.

Manhattan plots were obtained by using both additive gene action and general models through *GWASpoly* R package, showing the significance threshold for each locus along with the location of SNPs corresponding to each phenotypic trait. Association mapping analysis revealing significant SNPs to each trait was taken with a P -value ≤ 0.001 . The dotted line in blue colour showed $-\log_{10}(P)$ threshold of ≥ 3.00 , which allows for identification of significant SNPs.

4.5.1 Dry matter content (DMC)

Dry matter content (DMC) is one of the important characteristics of processed tuber quality. It is an early determinant of tuber quality and influence the final yield of processed tuber products (chips/crisps and French fries). BLUPs calculated for DMC showed normal distribution as evident from the estimated BLUPs histogram. Moreover, the scatter plot highlighted the estimated predictive accuracy of BLUPs plotted against the mean of 192 genotypes calculated from four environmental conditions. BLUPs shrink the outliers towards the mean. A linear fitted regression line showed strong positive

relationship between BLUPs and mean data sets (Fig 4. 9). We observed that BLUPs were almost identical to means though the former offers adjustments for various random effects (genotypes and location by year) (Wang et al., 2017; Dong et al., 2018). Augmented analysis was performed to obtain estimated values of each genotype in each environment which could be the possible reason for strong relationship between BLUPs and mean values of four environments. Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the DMC trait additive model showed that the observed p values were normally or uniformly distributed as straight-line till $-\log_{10}(P)=2.5$, after that p values deviated indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviation was observed towards the normal at the tail avoiding false positives (Fig 4.10a). This is in accordance with the findings of Kaler et al. (2020), who were of the view that straight 1:1 line in Q-Q plot with sharp upward deviated tail depicted casual polymorphisms or true associations avoiding both false positives and false negatives. In general model, the observed p values followed normal distribution with expected p values till $-\log_{10}(P) = 3$, after that deviations were observed at the tail, which explains the presence of significant marker-trait associations.

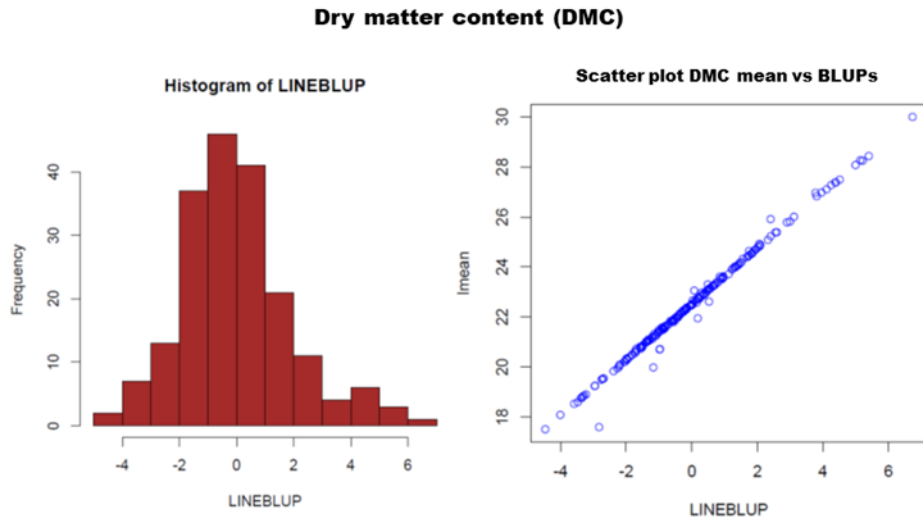


Figure 4.9. Histogram of LINEBLUPs for dry matter content. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

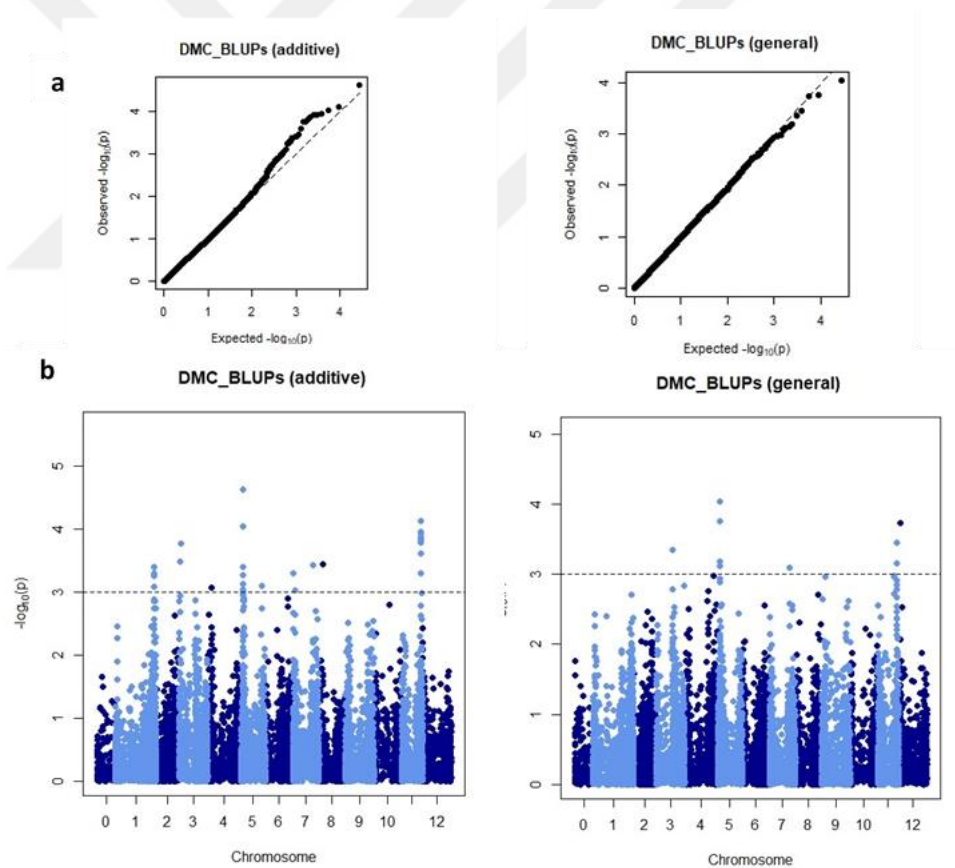


Figure 4.10. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing dry matter content (DMC) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Manhattan plots were formulated utilizing Q+K MLM in *GWASpoly R* to find marker-trait associations by employing two gene action models (Fig. 4.10b). 30 significant SNPs were found to be associated with DMC in additive model, while the general model revealed 9 significantly associated SNPs at $-\log_{10}(P) \geq 3$ ($P \leq 0.001$) (Table 4.11). The study found following significant SNPs associated with DMC with additive model i.e., *solcap_snp_c2_4898* (high mobility group nucleosome-binding domain-containing protein 5-like), *PotVar0035692* (Thioredoxin M3, chloroplastic), *PotVar0035772* (Longevity assurance factor), *PotVar0035775* (Longevity assurance factor), *PotVar0035852* (Conserved gene of unknown function), *PotVar0019336* (Conserved gene of unknown function), *solcap_snp_c1_15333* (uncharacterized), *solcap_snp_c2_3971826S* (proteasome non-ATPase regulatory subunit 12 homolog B-like), *PotVar0078561* (Sulfate/bicarbonate/oxalate exchanger and transporter sat-1), *solcap_snp_c2_22964* (intracellular ribonuclease), *PotVar0079081* (Transferase, transferring glycosyl groups), *PotVar0079374* (Conserved gene of unknown function), *PotVar0079652* (R2r3-myb transcription factor), *PotVar0079820* (Alpha-expansin 1), *PotVar0079948* (Oxygen evolving enhancer protein 3), *PotVar0079966* (NAC domain protein NAC2), *PotVar0033978* (Conserved gene of unknown function), *PotVar0022592* (1-acyl-sn-glycerol-3-phosphate acyltransferase), *solcap_snp_c2_46709* (4-coumarate--CoA ligase 2-like), *solcap_snp_c2_38634* (OBERON-like protein), *solcap_snp_c2_19643*, *solcap_snp_c1_4951*, *solcap_snp_c1_4949*, *solcap_snp_c1_4942* (uncharacterized), *PotVar0008207* (Kinase), *solcap_snp_c2_15340*, *solcap_snp_c2_15337*, *solcap_snp_c2_15336*, *solcap_snp_c2_15331* (auxin response factor 18) and *PotVar0008281* (Allene oxide synthase 2) present on chromosomes 1 (83.2-84.7Mbps), 3 (2.2 and 4.7 Mbps), 4 (7.8 Mbp), 5 (4.4-4.7 Mbps; 43.9 Mbp), 7 (0.79 Mbp, 4.87 Mbp and 44.3 Mbp), 8 (8.19 Mbp) and 11 (41.4-41.8 Mbps).

In general model, 9 significant SNPs were associated with DMC includes *PotVar0094670* (Nodulation receptor kinase), *solcap_snp_c2_22964* (intracellular ribonuclease), *PotVar0079374* (Conserved gene of unknown function), *PotVar0079652* (R2r3-myb transcription factor), *PotVar0079948* (Oxygen evolving enhancer protein 3), *solcap_snp_c2_38634* (OBERON-like protein), *solcap_snp_c1_4951*, *solcap_snp_c1_4949* (uncharacterized) and *PotVar0031068* (Sucrose synthase). These SNPs were located on chromosomes 3 (36.3 Mbp), 5 (4.4-4.7 Mbps), 7 (44.3 Mbp), 11 (41.4 Mbp) and 12 (3.08 Mbp).

Seven SNPs were found to be common in both gene action models namely; solcap_snp_c2_22964, PotVar0079374, PotVar0079652, PotVar0079948, solcap_snp_c2_38634, solcap_snp_c1_4951 and solcap_snp_c1_4949. These SNPs were present in the genes having putative functional roles as intracellular ribonuclease, R2r3-myb, transcription factor, oxygen evolving enhancer protein 3, OBERON-like protein and sucrose synthase. Some SNPs in the genes were found to be conserved with unknown functions or uncharacterized.

Our results were similar to the findings of Björn et al. (2008, 2014) who reported that the genomic regions associated with tuber dry matter content were located on chromosomes 1 (8.4, 9.2 & 24.9 cM), 4 (21.3 cM) and 5 (16.2 cM). The localization of SNPs on several chromosomes might be due to the polygenic nature of our traits, influenced by minor genes. Dry matter content is a polygenic trait, previous studies identified that genes linked to DMC were unequally distributed on all chromosomes and clusters between 0.5 to 4 Mbp width, with a putative regulatory and signalling functions (Schönhals et al., 2017). The identified SNP at chr 12 was associated with DMC with putative gene function of sucrose synthase. Sucrose synthase enzyme (*SuSy*) is a major determinant of sink strength in potato tubers, channelling the conversion of sucrose to complex polysaccharides such as starch. Overexpressed *SuSy* lines contain 35-55% more starch compared to control and significantly associated with tuber dry weight ratio, since major component of dry matter component is starch (Baroja-Fernández et al., 2009). An interesting SNP was present in the gene located on chr 5 with a putative function R2r3-myb transcription factor, important for anthocyanin biosynthesis in tuber skin (Jung et al., 2009). Another study proposes that total phenolics were positively correlated to tuber dry matter content (Tierno et al., 2015). Anthocyanin is a phenolic compound present in tuber flesh and skin and anthocyanin-based gene association with DMC is quite unique and needs further validation studies. The co-expression of starch genes was reported with transcription factors MYB and NAC, meaning that these TFs play important roles in starch biosynthesis (López-González, 2019). Genes of both these TFs carry SNPs linked with DMC as identified in present study located on chr 5 with genetic distance of 4.42-4.70 Mbp.

Table 4.11. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber dry matter content along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0094670	3	36318191	A/G	3.35	Nodulation receptor kinase
general	solcap_snp_c2_22964	5	4470491	A/C	3.19	intracellular ribonuclease
general	PotVar0079374	5	4495794	A/G	3.76	Conserved gene of unknown function
general	PotVar0079652	5	4548540	C/T	4.04	R2r3-myb transcription factor
general	PotVar0079948	5	4701617	G/T	3.12	Oxygen evolving enhancer protein 3
general	solcap_snp_c2_38634	7	44319895	A/C	3.09	OBERON-like protein
general	solcap_snp_c1_4951	11	41448369	A/G	3.15	uncharacterized
general	solcap_snp_c1_4949	11	41448481	A/G	3.46	uncharacterized
general	PotVar0031068	12	3089048	A/G	3.74	Sucrose synthase
						high mobility group nucleosome-binding
additive	solcap_snp_c2_4898	1	83283673	A/G	3.3	domain-containing protein 5-like
additive	PotVar0035692	1	84405289	A/G	3.39	Thioredoxin M3, chloroplastic
additive	PotVar0035772	1	84648780	C/T	3.25	Longevity assurance factor
additive	PotVar0035775	1	84648873	A/G	3.39	Longevity assurance factor
additive	PotVar0035852	1	84727400	A/G	3.08	Conserved gene of unknown function
additive	PotVar0019336	3	2236149	C/T	3.48	Conserved gene of unknown function
additive	solcap_snp_c1_15333	3	4732420	C/T	3.77	uncharacterized
						26S proteasome non-ATPase regulatory
additive	solcap_snp_c2_39718	4	7898214	A/G	3.07	subunit 12 homolog B-like
						Sulfate/bicarbonate/oxalate exchanger and
additive	PotVar0078561	5	4420610	A/G	3.02	transporter sat-1
additive	solcap_snp_c2_22964	5	4470491	A/C	3.4	intracellular ribonuclease
						Transferase, transferring glycosyl groups
additive	PotVar0079081	5	4489481	C/T	3	
additive	PotVar0079374	5	4495794	A/G	4.04	Conserved gene of unknown function
additive	PotVar0079652	5	4548540	C/T	4.63	R2r3-myb transcription factor
additive	PotVar0079820	5	4629401	A/G	3.04	Alpha-expansin 1
additive	PotVar0079948	5	4701617	G/T	3.27	Oxygen evolving enhancer protein 3
additive	PotVar0079966	5	4708417	A/G	3.12	NAC domain protein NAC2
additive	PotVar0033978	5	43920269	A/C	3.1	Conserved gene of unknown function
						1-acyl-sn-glycerol-3-phosphate acyltransferase
additive	PotVar0022592	7	795641	C/T	3.3	
additive	solcap_snp_c2_46709	7	4874797	A/G	3.02	4-coumarate--CoA ligase 2-like
additive	solcap_snp_c2_38634	7	44319895	A/C	3.43	OBERON-like protein
additive	solcap_snp_c2_19643	8	8193944	C/T	3.44	uncharacterized
additive	solcap_snp_c1_4951	11	41448369	A/G	3.83	uncharacterized
additive	solcap_snp_c1_4949	11	41448481	A/G	4.13	uncharacterized
additive	solcap_snp_c1_4942	11	41449440	G/T	3.61	uncharacterized
additive	PotVar0008207	11	41457873	A/C	3.96	Kinase
additive	solcap_snp_c2_15340	11	41585621	A/G	3.94	auxin response factor 18
additive	solcap_snp_c2_15337	11	41585906	C/T	3.92	auxin response factor 18
additive	solcap_snp_c2_15336	11	41585984	C/T	3.78	auxin response factor 18
additive	solcap_snp_c2_15331	11	41587672	G/T	3.87	auxin response factor 18
additive	PotVar0008281	11	41832374	G/T	3.3	Allene oxide synthase 2

****Score = List of data.frames, one for each trait. The data frame contains -log₁₀(P) results organized as markers x (additive) model (P values ≤ 0.001).***

4.5.2 Tuber specific gravity (SG)

Specific gravity (SG) was positively correlated to DMC and considered as an important characteristic for the potato breeder to enhance processed tuber quality. BLUPs calculated for SG showed normal distribution as evident from the estimated BLUPs histogram. Moreover, the scatter plot highlighted the estimated predictive accuracy of BLUPs plotted against the mean of 192 genotypes calculated from four environmental conditions. A strong positive correlation was observed between BLUPs and mean data sets (Fig. 11). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Same trend was found in Q-Q plot of specific gravity as observed in dry matter content for the additive and general models (Fig. 4.12a). Although observed vs expected p values showed sharp deviation after -log₁₀(p) value of 3, but the tail terminated with normal distribution. It indicates the presence of significant marker-trait associations similar to DMC.

Additive model identified 21 significant SNPs associated with SG located on chr 1 (83.28-84.64 Mbp), chr 2 (38.97 Mbp), chr 3 (2.23 and 4.73 Mbp), chr 5 (4.54 and 5.69 Mbp), chr 6 (49.7 Mbp), chr 7 (4.87 Mbp) and chr 11 (41.4-41.8 Mbps). While, the general model revealed 6 significantly associated SNPs located on chr 4 (54.61 Mbp), chr 5 (4.54 and 4.70 Mbp), chr 10 (43.66 Mbp), chr 11 (41.44 Mbp) and chr 12 (3.08 Mbp) (Fig. 4.12b and Table 4.12). The identified SNPs in both models along with their chromosome numbers, position and gene annotation are shown in Table 4.12. Interestingly, both models share 2 common SNPs i.e., PotVar0079652 (R2r3-myb transcription factor) and solcap_snp_c1_4949 (uncharacterized). The co-localization or association of SNPs with multi-traits is referred to as pleiotropy (Li et al., 2014). 21 pleiotropic SNPs were detected commonly associated with both DMC and SG. It strongly supports the idea that DMC and SG are synonymous terms, as the latter estimates the dry matter contents of tubers. In our study, the identified SNPs were in accordance with the

findings of Freyre and Douches (1994), McCord et al. (2011) and Urbany et al. (2011). They reported that genomic regions associated with specific gravity were positioned on chr 1, 2, 3, 5, 7 and 11. The SNPs associated with specific gravity were in synteny with SNPs of DMC except for few such as solcap_snp_c2_38273 located on chr 10 with putative gene function of cytochrome P450. These genes were responsible in biosynthesis of SGA (steroidal glycoalkaloids) in the tubers (Umemoto et al., 2016). Allene oxide synthase gene (*StAOS2*) was identified at chr 11 associated with specific gravity carrying SNP (PotVar0008281). *StAOS2* was responsible for the biosynthesis of jasmonates and involve in potential defence signalling against pathogens such as late blight, soft rot and black leg in potato (Pajerowska et al., 2008).

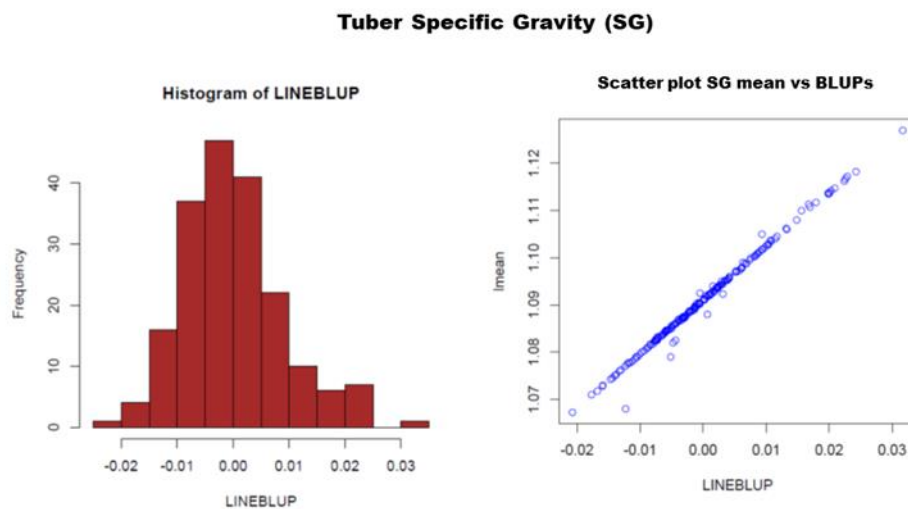


Figure 4.11. Histogram of LINEBLUPs for specific gravity. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

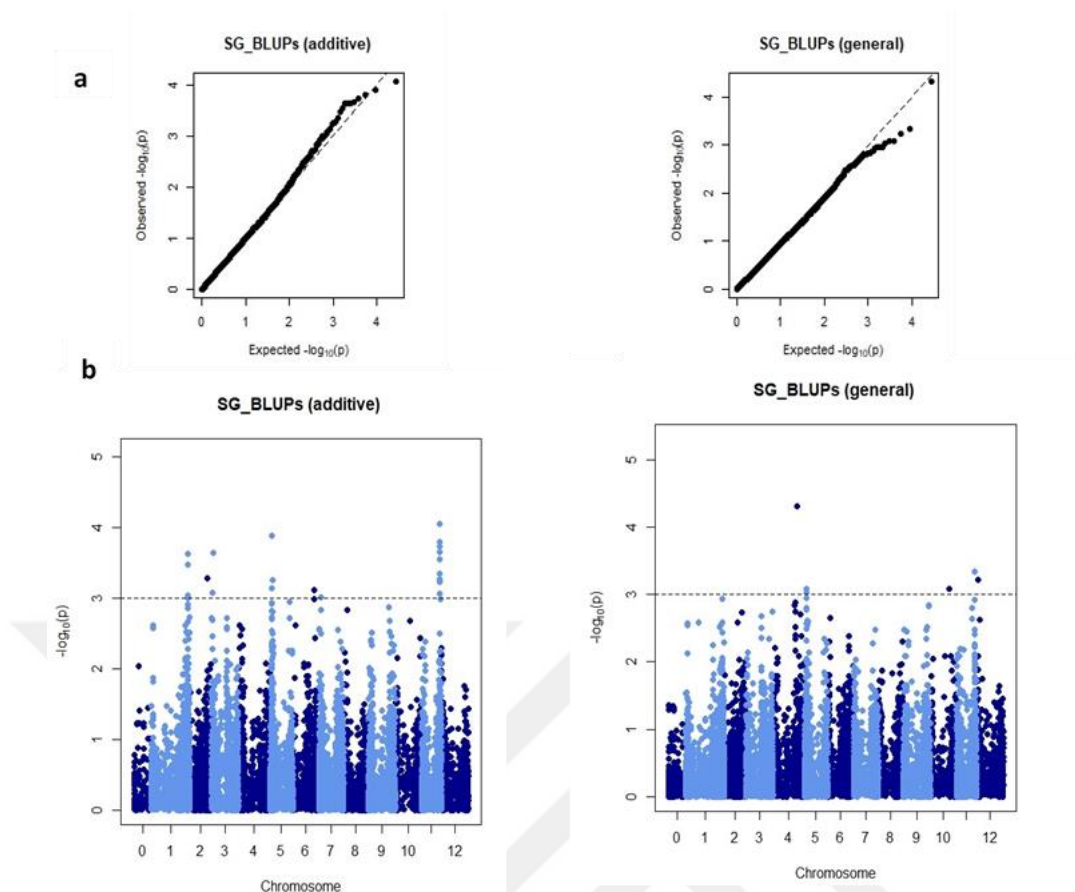


Figure 4.12. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing specific gravity (SG) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Table 4.12. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the specific gravity along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0133163	4	54619237	A/G	4.31	WRKY transcription factor
general	PotVar0079652	5	4548540	C/T	3.08	R2r3-myb transcription factor
general	PotVar0079966	5	4708417	A/G	3.03	NAC domain protein NAC2
general	solcap_snp_c2_38273	10	43666116	C/T	3.08	cytochrome P450 CYP72A219-like
general	solcap_snp_c1_4949	11	41448481	A/G	3.34	uncharacterized
general	PotVar0031068	12	3089048	A/G	3.22	Sucrose synthase
additive	solcap_snp_c2_4898	1	83283673	A/G	3.48	high mobility group nucleosome-binding domain-containing protein 5-like

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
additive	PotVar0035473	1	84052432	C/T	3.05	Tic21
additive	PotVar0035692	1	84405289	A/G	3.63	Thioredoxin M3, chloroplastic
additive	PotVar0035775	1	84648873	A/G	3.63	Longevity assurance factor Phospholipase D delta
additive	PotVar0010562	2	38970102	A/G	3.28	isoform 1a Conserved gene of unknown function
additive	PotVar0019336	3	2236149	C/T	3.08	uncharacterized
additive	solcap_snp_c1_15333	3	4732420	C/T	3.64	Conserved gene of unknown function
additive	PotVar0079374	5	4495794	A/G	3.14	uncharacterized
additive	PotVar0079652	5	4548540	C/T	3.89	R2r3-myb transcription factor
additive	PotVar0117354	5	5692838	A/G	3.26	Sucrose transporter
additive	solcap_snp_c1_10109	6	49795337	C/T	3.12	uncharacterized
additive	solcap_snp_c2_46709	7	4874797	A/G	3.02	4-coumarate--CoA ligase 2- like
additive	solcap_snp_c1_4951	11	41448369	A/G	3.66	uncharacterized
additive	solcap_snp_c1_4949	11	41448481	A/G	4.06	uncharacterized
additive	solcap_snp_c1_4942	11	41449440	G/T	3.27	uncharacterized
additive	PotVar0008207	11	41457873	A/C	3.74	Kinase
additive	solcap_snp_c2_15340	11	41585621	A/G	3.8	auxin response factor 18
additive	solcap_snp_c2_15337	11	41585906	C/T	3.55	auxin response factor 18
additive	solcap_snp_c2_15336	11	41585984	C/T	3.35	auxin response factor 18
additive	solcap_snp_c2_15331	11	41587672	G/T	3.24	auxin response factor 18
additive	PotVar0008281	11	41832374	G/T	3.06	Allene oxide synthase 2

****Score = List of data.frames, one for each trait. The data frame contains -log10(P) results organized as markers x (additive) model (P values ≤ 0.001).***

4.5.3 Reducing sugars (RS)

Low amount of reducing sugars with high dry matter content is desirable both for potato breeders and processing industry. In our study, a significant negative correlation was observed for both of these traits. Finding SNP markers associated with RS will be helpful for potato breeders in selection of genotypes with low RS and high DMC. BLUPs calculated for RS did not show normal distribution as evident from the estimated BLUPs histogram. Thus, log10 transformation was done in order to normalize the multi-environment RS data followed by the calculation of BLUPs. The scatter plot of transformed data exhibited less scattering and thus explains an enhanced estimated

predictive accuracy of BLUPs plotted against the mean of 192 genotypes calculated from four environmental conditions. A fitted linear regression line showed strong relationship between log transformed BLUPs and mean of RS (Fig. 4.13). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

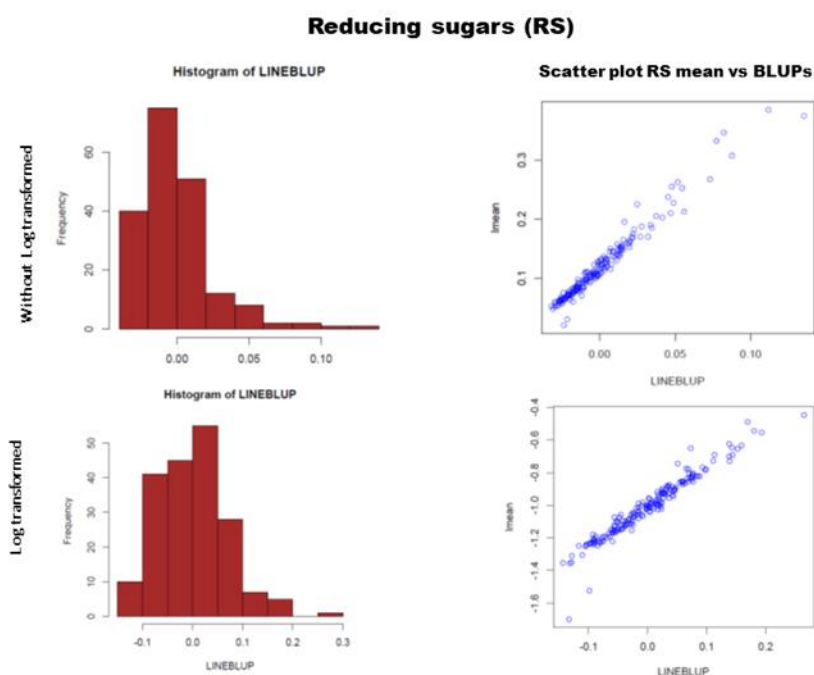


Figure 4.13. Histogram of LINEBLUPs for reducing sugars without and with log transformation. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” = genotypes included in the study)

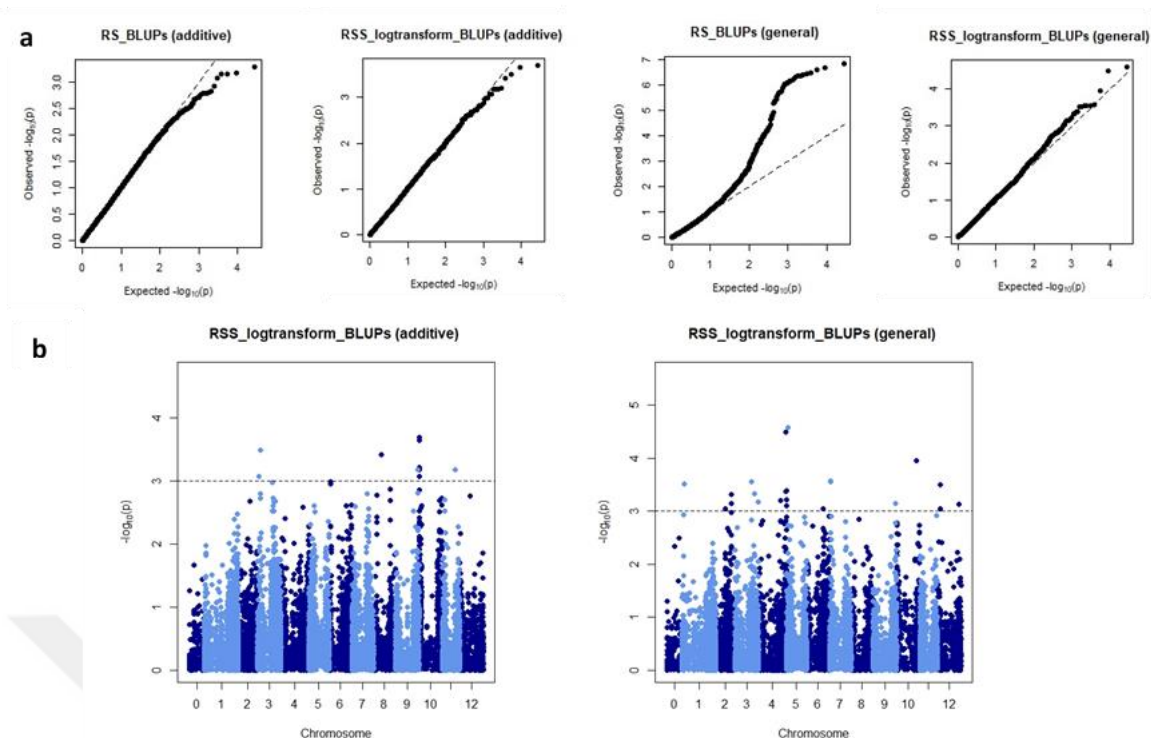


Figure 4.14. Q-Q plots of observed vs expected p values of non-transformed and log10 transform BLUPs (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing reducing sugars (RSS) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Results of Q-Q plot for the reducing sugar using additive model showed that the observed vs expected p values were uniformly distributed as straight-line till $-\log_{10}(P)=2.5$ in non-transformed data and $-\log_{10}(P)=3$ in transformed data. The deviations at the tail is an indication of significant associations. In general model with non-transformed data, Q-Q plots of RS depicted an early deflation at $-\log_{10}(P)=1$, which is an indication for the presence of false positives (i.e., the data is not normally distributed as a straight line). Therefore, log transformation of RS data was performed and the transformed data showed uniform distribution as shown in Q-Q plot of general model (log_transformed) (Fig. 4.14a). The observed p values deviated after $-\log_{10}(P)=2.5$, indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviation was observed towards the normal at the tail avoiding false positives. This is in accordance with the findings of Kaler et al. (2020), who were of the view that straight 1:1 line in Q-Q plot with sharp upward deviated tail depicted casual polymorphisms or true associations avoiding both false positives and false negatives. It is worthy to mention here that additive model control false positives even with non-transformed data.

Manhattan plots were created with log10 transformed RS BLUPs phenotypic data set considering 13606 SNP markers as a genotypic data in *GWASpoly R* (Fig. 4.14b). Results revealed that 10 SNP markers were significantly associated with reducing sugars within additive model, namely *solcap_snp_c1_15333* (uncharacterized), *solcap_snp_c2_54674* (nicotinate-phosphoribosyl transferase 1-like), *PotVar0076370* (Conserved gene of unknown function), *PotVar0011035* (DEAD-box ATP-dependent RNA helicase 13), *solcap_snp_c2_1447* (*kco1b* gene for K⁺ channel protein), *solcap_snp_c2_1475* (ethylene-responsive transcription factor 3-like), *PotVar0065371* (Ethylene-responsive transcription factor 3), *solcap_snp_c2_886* (integrator complex subunit 3), *PotVar0065119* (Gene of unknown function) and *solcap_snp_c2_50332* (serine/threonine-protein kinase UCN-like) located on chromosomes 3, 8, 9, 10 and 11 (Table 4.13).

Since, general model with non-transformed data lead to false positives as shown by the results of Q-Q plot, it was not considered for finding associations. Rather, a general model with log transformed data was presented and 23 significant marker-trait associations were detected by this model (Table 4.13). The locus accompanying with the gene containing the associated SNPs were positioned on all chromosomes except 8 and 11. The associated SNPs along with their putative functions includes *solcap_snp_c2_27878* (NDR1-like), *solcap_snp_c1_11122* (L-ascorbate oxidase homolog), *solcap_snp_c2_42126* (flavanone 3 beta-hydroxylase gene), *solcap_snp_c1_8118* (Uncharacterized), *PotVar0070281* (Plastid division regulator MinD), *solcap_snp_c2_1813* (callose synthase), *PotVar0021132* (RNA m5u methyltransferase), *solcap_snp_c1_16625* (probable caffeoyl-CoA O-methyltransferase), *solcap_snp_c1_4109* (3-ketoacyl-CoA synthase 4), *PotVar0015899* (Beta-fructofuranosidase), *PotVar0017413* (Glutamate receptor 3 plant), *solcap_snp_c2_10563* (3-hydroxy-3-methylglutaryl-coenzyme A reductase 1-like), *PotVar0017551* (Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha), *solcap_snp_c2_23056* (uncharacterized), *solcap_snp_c2_39576* (zinc finger protein ZAT4-like), *PotVar0095918* (Sucrose-phosphate-synthase), *solcap_snp_c2_55833* (sucrose-phosphate-synthase), *solcap_snp_c1_16221* (probable sucrose-phosphate synthase), *solcap_snp_c2_40078* (malate dehydrogenase, chloroplastic-like), *solcap_snp_c2_31395* (protein FAR-RED-ELONGATED HYPOCOTYL 1-LIKE), *solcap_snp_c2_24646* (cytochrome b6-f complex iron-sulfur

subunit), PotVar0061906 (Ethylene-responsive element binding factor) and solcap_snp_c2_6460 (low-temperature-induced cysteine proteinase-like).

Table 4.13. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the reducing sugars along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_27878	1	6071398	C/T	3.51	NDR1-like
general	solcap_snp_c1_11122	2	23799702	G/T	3.04	L-ascorbate oxidase homolog
general	solcap_snp_c2_42126	2	39369211	G/T	3.32	flavanone 3 beta-hydroxylase gene
general	solcap_snp_c1_8118	2	39940755	A/G	3.15	Uncharacterized
general	PotVar0070281	3	43922329	C/T	3.56	Plastid division regulator MinD
general	solcap_snp_c2_1813	3	51282166	A/G	3.32	callose synthase
general	PotVar0021132	3	60493682	A/C	3.17	RNA m5u methyltransferase probable caffeoyl-CoA O- methyltransferase
general	solcap_snp_c1_16625	4	57243271	C/T	3.2	3-ketoacyl-CoA synthase 4
general	solcap_snp_c1_4109	4	69830197	A/G	3.37	Beta-fructofuranosidase
general	PotVar0015899	4	70807391	C/T	4.49	Glutamate receptor 3 plant 3-hydroxy-3-methylglutaryl- coenzyme
general	PotVar0017413	4	71814793	C/T	3.21	A reductase 1-like Pyrophosphate--fructose 6- phosphate
general	solcap_snp_c2_10563	4	71956350	C/G	3.39	1-phosphotransferase subunit alpha
general	PotVar0017551	4	72024197	A/C	3.11	Uncharacterized
general	solcap_snp_c2_23056	5	4936615	C/T	4.58	zinc finger protein ZAT4-like
general	solcap_snp_c2_39576	6	43919744	G/T	3.04	Sucrose-phosphate-synthase
general	PotVar0095918	7	3889278	C/T	3.57	sucrose-phosphate-synthase probable sucrose-phosphate synthase
general	solcap_snp_c2_55833	7	3892715	C/T	3.55	malate dehydrogenase, chloroplastic-like
general	solcap_snp_c1_16221	7	3894102	A/T	3.55	protein FAR-RED-ELONGATED HYPOCOTYL 1-LIKE
general	solcap_snp_c2_40078	9	57518148	A/G	3.14	cytochrome b6-f complex iron- sulfur subunit
general	solcap_snp_c2_31395	10	51124055	A/G	3.95	Ethylene-responsive element binding factor
general	solcap_snp_c2_24646	12	6911438	C/T	3.04	low-temperature-induced cysteine proteinase-like
general	PotVar0061906	12	6983053	C/T	3.51	Uncharacterized nicotinate
general	solcap_snp_c2_6460	12	56495271	A/G	3.13	phosphoribosyltransferase 1-like
additive	solcap_snp_c1_15333	3	4732420	C/T	3.08	Conserved gene of unknown function
additive	solcap_snp_c2_54674	3	8390507	A/G	3.5	DEAD-box ATP-dependent RNA helicase 13
additive	PotVar0076370	8	19300737	G/T	3.42	kco1b gene for K ⁺ channel protein
additive	PotVar0011035	9	57167023	A/G	3.18	
additive	solcap_snp_c2_1447	10	1003208	G/T	3.65	

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
additive	solcap_snp_c2_1475	10	1121595	A/G	3.07	ethylene-responsive transcription factor 3-like
additive	PotVar0065371	10	1122487	A/C	3.21	Ethylene-responsive transcription factor 3
additive	solcap_snp_c2_886	10	1372642	A/G	3.18	integrator complex subunit 3
additive	PotVar0065119	10	1374955	A/C	3.69	Gene of unknown function serine/threonine-protein kinase
additive	solcap_snp_c2_50332	11	33927332	A/G	3.18	UCN-like

****Score = List of data.frames, one for each trait. The data frame contains -log₁₀(P) results organized as markers x (additive) model (P values ≤ 0.001).***

Literature suggested that significant QTLs were detected on chr 4, 5, 6, 10 and 11 associated with both fry colour and glucose. QTL in candidate gene was located on chr 5 with fry colour and function as "apoplastic invertases" (Massa et al., 2018). SNPs on same chromosomes were detected in present study. Menéndez et al. (2002) were of the view that QTLs of glucose and fructose were mapped on all chromosomes. The identified candidate genes in their study perform functional roles related to sucrose transports, sensor, sucrose synthase and invertases (Gebhardt et al., 2005). The present study detected SNPs in the genes of sucrose phosphate synthase located on chr 7. Sucrose phosphate synthase is involved in the synthesis of sucrose that were later hydrolyzed to glucose and fructose (Krause et al., 1998). It entails that this genomic region controls the regulation and accumulation of reducing sugars in potato tubers.

4.5.4 Sucrose (SUC)

Sucrose formed as a result of photosynthesis and accumulated in tubers as starch under normal tuber growing conditions. Conversely, the breakdown of starch occurs under stress (cold or sprouting) to sucrose, this disaccharide ultimately disintegrates to form glucose and fructose (undesirable products for processing industry). Finding SNP markers associated with SUC will be helpful for potato breeders in selection of genotypes with better sugar characteristics. BLUPs calculated for SUC did not show normal distribution as evident from the estimated BLUPs histogram. Thus, log₁₀ transformation was done in order to normalize the sucrose data of multi-environments followed by the calculation of BLUPs. The scatter plot of transformed data exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs plotted against the mean of 192 genotypes calculated from four environmental conditions. A fitted linear

regression line showed strong relationship between log transformed BLUPs and mean of SUC (Fig. 4.15). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the sucrose using additive model showed that the observed vs expected p values were uniformly distributed as straight-line till $-\log_{10}(P)=2.5$ in both non-transformed and log transformed data. The deviations at the tail is an indication of significant associations. In general model with non-transformed data, Q-Q plots of SUC depicted an early deflation at $-\log_{10}(P)=1.5$, which is a sign for the presence of false positives (i.e., the data is not normally

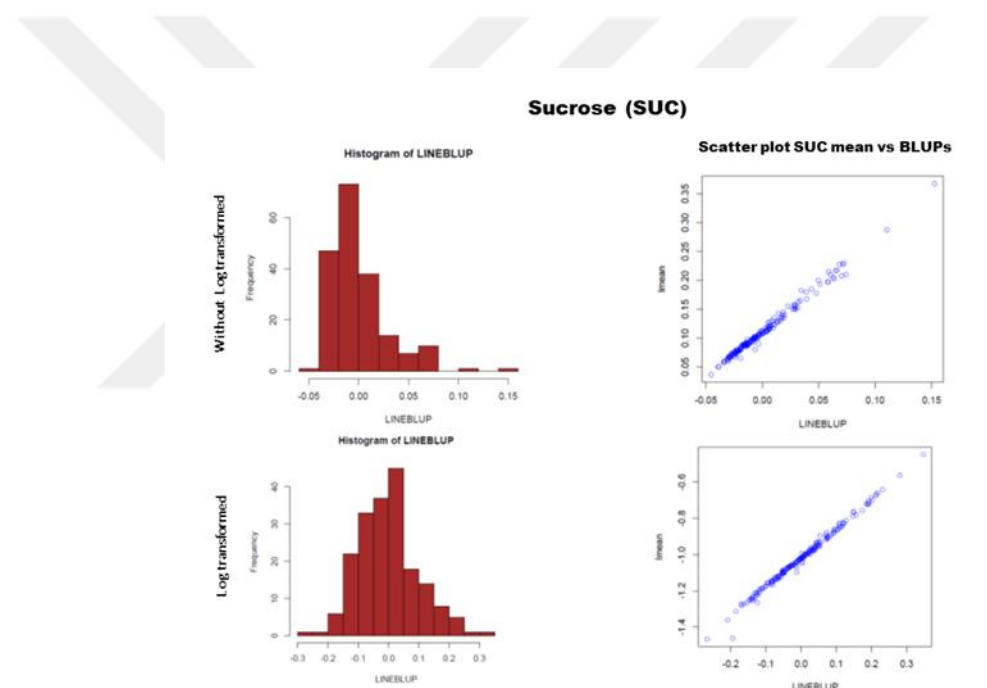


Figure 4.15. Histogram of LINEBLUPs for sucrose without and with log transformation. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” = genotypes included in the study)

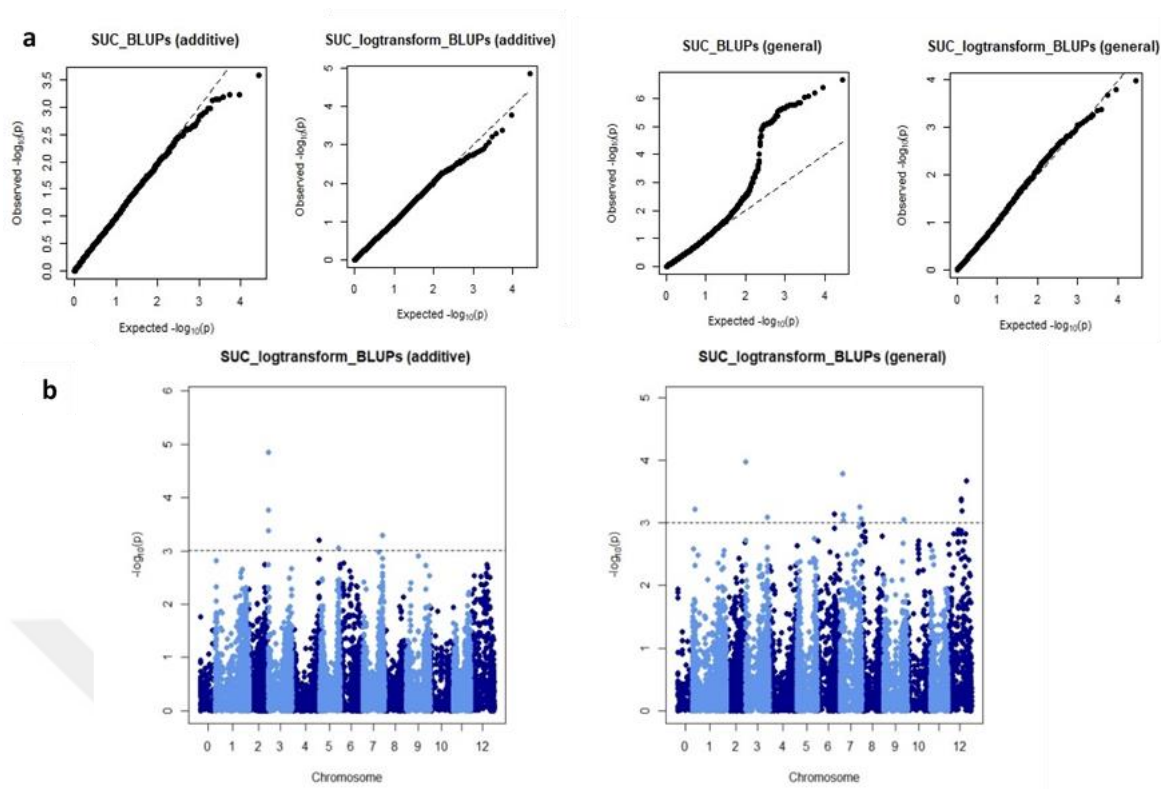


Figure 4.16. Q-Q plots of observed vs expected p values of non-transformed and $\log_{10}$ transform BLUPs (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing sucrose (SUC) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

distributed as a straight line). Therefore, log transformation of SUC data was performed and the transformed data showed uniform distribution as shown in Q-Q plot of general model (log_transformed) (Fig. 4.16a). The observed vs expected p values showed uniform distribution till $-\log_{10}(P)=3$, and start deviating at the tail roughly above p value of 3 indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviation was observed towards the normal at the tail avoiding false positives. This is in accordance with the findings of Kaler et al. (2020), who were of the view that straight 1:1 line in Q-Q plot with sharp upward deviated tail depicted casual polymorphisms or true associations avoiding both false positives and false negatives. It is worthy to mention here that in comparison to general model, additive model control false positives even with non-transformed data.

Manhattan plots were created with $\log_{10}$ transformed SUC BLUPs phenotypic data set considering 13606 polymorphic SNP markers as a genotypic data in *GWASpoly R* (Fig 4.16b). Results revealed that 6 SNP markers were significantly associated with sucrose

within the additive model. It includes solcap_snp_c1_12825 (serine/threonine-protein kinase HT1-like), solcap_snp_c2_52806 (neutral ceramidase 1), solcap_snp_c2_52813 (GDSL esterase/lipase At5g45910-like), solcap_snp_c1_4109 (3-ketoacyl-CoA synthase 4), PotVar0082101 (Phytochrome B2) and solcap_snp_c2_28222 (leucine-rich repeat receptor-like serine/threonine-protein kinase) positioned on chromosomes 3, 4, 5 and 7 (Table 4. 14).

Since, general model with non-transformed data lead to false positives as shown by the results of Q-Q plot, it is not considered for finding associations. Rather, a general model with log transformed data was presented and 14 significant marker-trait associations were detected by this model. The locus accompanying with the gene containing the associated SNPs were positioned on chromosomes 1, 3, 6, 7, 9 and 12 (Table 4.14). The associated SNPs along with their putative functions includes solcap_snp_c1_8608 (protein ETHYLENE INSENSITIVE 3-like), solcap_snp_c1_12825 (serine/threonine-protein kinase HT1-like), solcap_snp_c2_324 4-coumarate--CoA ligase 2), PotVar0133545 (3-isopropylmalate dehydrogenase small subunit), solcap_snp_c1_11942 (30S ribosomal protein S16), PotVar0127427 (Arabinose kinase), PotVar0028383 (similar to COP9 signalosome complex subunit 8), PotVar0044287 (Integral membrane family protein), solcap_snp_c1_8834 (E3 ubiquitin-protein ligase UPL1- like), PotVar0103851 (Glycosyltransferase, CAZy family GT8), PotVar0014978(uncharacterized), solcap_snp_c2_27771 (CBS domain-containing protein

Table 4.14. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the sucrose along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c1_8608	1	6144618	A/G	3.22	protein ETHYLENE INSENSITIVE 3-like
general	solcap_snp_c1_12825	3	872029	A/G	3.97	serine/threonine-protein kinase HT1-like
general	solcap_snp_c2_324	3	57569155	A/G	3.09	4-coumarate--CoA ligase 2
general	PotVar0133545	6	44031326	A/G	3.14	3-isopropylmalate dehydrogenase small subunit
general	solcap_snp_c1_11942	7	6046109	A/C	3.79	30S ribosomal protein S16
general	PotVar0127427	7	9118636	C/T	3.04	Arabinose kinase
general	PotVar0028383	7	9705677	C/T	3.12	similar to COP9 signalosome complex subunit 8

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0044287	7	52337121	C/T	3.25	Integral membrane family protein
general	solcap_snp_c1_8834	7	55678678	C/T	3.06	E3 ubiquitin-protein ligase UPL1-like
general	PotVar0103851	9	53048245	C/T	3.05	Glycosyltransferase, CAZy family GT8
general	PotVar0014978	12	35555783	A/G	3.35	Uncharacterized CBS domain-containing protein CBSCBSPB3
general	solcap_snp_c2_27771	12	35653078	A/G	3.39	RNA polymerase II C-terminal domain phosphatase-like 3
general	solcap_snp_c2_57702	12	36062717	A/G	3.19	
general	solcap_snp_c2_51049	12	48167367	A/C	3.68	NAP1-related protein 2-like
additive	solcap_snp_c1_12825	3	872029	A/G	4.84	serine/threonine-protein kinase HT1-like
additive	solcap_snp_c2_52806	3	1541622	A/G	3.77	neutral ceramidase 1
additive	solcap_snp_c2_52813	3	1611409	C/T	3.38	GDSL esterase/lipase At5g45910-like
additive	solcap_snp_c1_4109	4	69830197	A/G	3.2	3-ketoacyl-CoA synthase 4
additive	PotVar0082101	5	48661781	C/T	3.06	Phytochrome B2 leucine-rich repeat receptor-like serine/threonine-protein kinase
additive	solcap_snp_c2_28222	7	51604824	C/G	3.29	

****Score = List of data.frames, one for each trait. The data frame contains -log10(P) results organized as markers x (additive) model (P values ≤ 0.001).***

CBSCBSPB3), solcap_snp_c2_57702 (RNA polymerase II C-terminal domain phosphatase-like 3) and solcap_snp_c2_51049 (NAP1-related protein 2-like). Only 1 SNP was found to be common between additive and general models i.e., solcap_snp_c1_12825 (serine/threonine-protein kinase HT1-like). solcap_snp_c1_4109 with a plausible gene function as 3-ketoacyl-CoA synthase 4 was categorized as pleiotropic SNP commonly present in both reducing sugar and sucrose.

Arabinose kinases were involved in sugar signalling and signal transduction pathways (Ramon et al., 2008). SNPs with such putative roles were identified in our study located on chr 7. COP9 signalosome complex subunit was associated with carbohydrate metabolism and was present on chr 7 (Cao et al., 2019). These studies suggested that chr 7 is important for regulation and metabolism of sucrose.

4.5.5 Free asparagine (ASP)

High density SNP markers offer a valuable opportunity to accelerate selection for plant breeders in order to develop new potato cultivars with better processing quality (minimal reducing sugars and free asparagine, high dry matter content, high specific gravity and starch content). Free asparagine is an amino acid which acts a reactant along with reducing sugars in Maillard reaction for the synthesis of acrylamide (potential carcinogenic substance). Hence, SNPs associated with free asparagine allows the selection of potato genotypes with better processing quality. BLUPs calculated for ASP showed normal distribution as evident from the estimated BLUPs histogram. The scatter plot exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs plotted against the mean of 192 genotypes calculated from four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of ASP (Fig. 4.17). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the free asparagine using additive and general model demonstrated that the observed vs expected p values were normally or uniformly distributed as straight-line till $-\log_{10}(P)=3$ in both models. After that p values deviated indicating the presence of significant

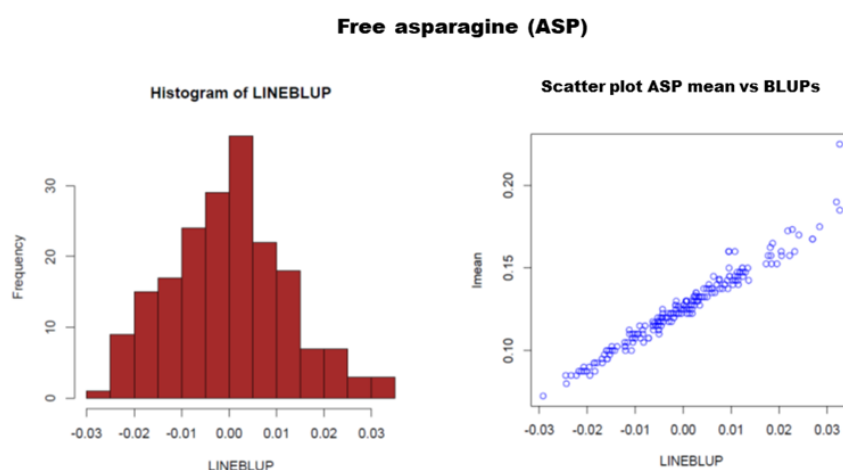


Figure 4.17. Histogram of LINEBLUPs for free asparagine. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

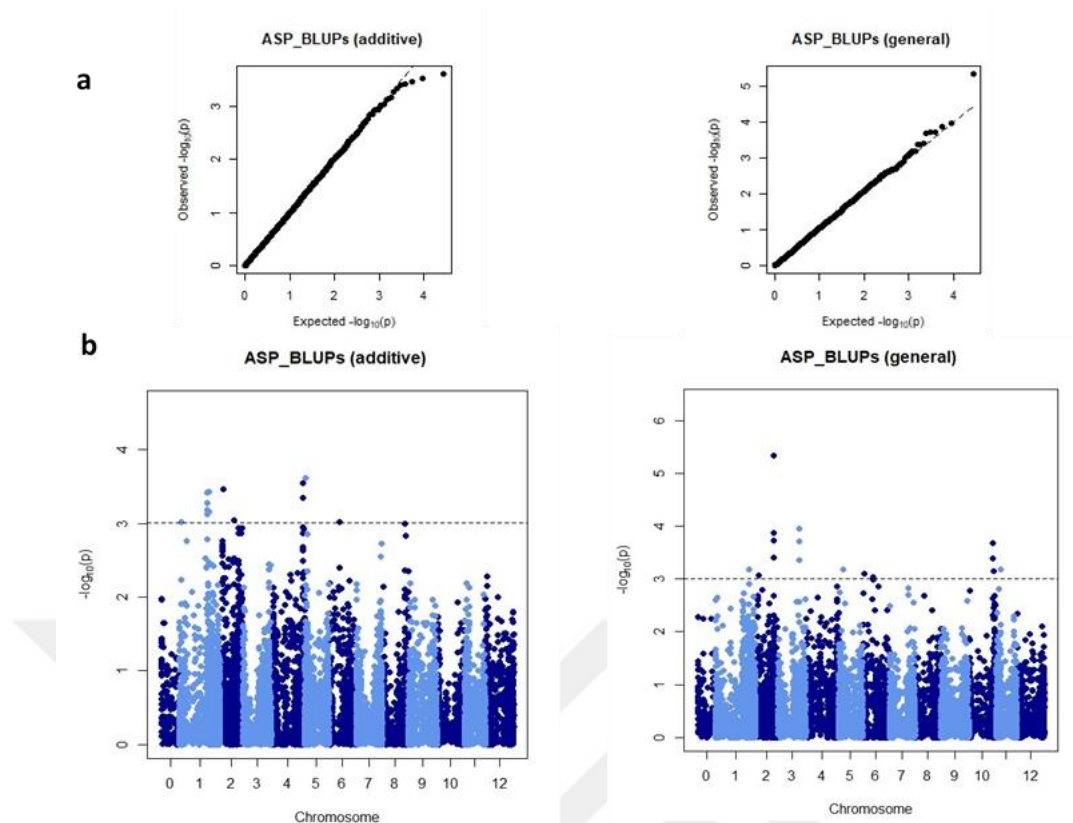


Figure 4.18. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing free asparagine (ASP) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

marker-trait associations. The p values were controlled by the model as sharp deviation was observed towards the normal at the tail avoiding false positives (Fig. 4.18a). This is in accordance with the findings of Kaler et al. (2020), who were of the view that straight 1:1 line in Q-Q plot with sharp upward deviated tail depicted casual polymorphisms or true associations avoiding both false positives and false negatives.

Manhattan plots were formulated utilizing Q+K MLM in *GWASpoly* R to find marker-trait associations by employing two gene action models. 13 significant SNPs were found to be associated with free asparagine in additive model (Fig. 4.18b and Table 4.15). The study found following significant SNPs associated with ASP with additive model i.e., solcap_snp_c1_6109 (uncharacterized), solcap_snp_c2_35480 (NtPRp27-like protein), solcap_snp_c2_35532 (ABC transporter C family member 14-like), solcap_snp_c2_35536 (ABC transporter C family member 14-like), solcap_snp_c2_35537 (ABC transporter C family member 14-like), PotVar0126039

(Expressed protein (matched with At)), solcap_snp_c2_40955 (Solyntus genome), solcap_snp_c1_3746 (COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB1, chloroplastic), PotVar0062483 (Cationic amino acid transporter), solcap_snp_c2_34862 (probable serine/threonine-protein kinase At1g01540), solcap_snp_c1_10424 (probable serine/threonine-protein kinase), solcap_snp_c2_11726 (putative late blight resistance protein homolog R1B-12) and solcap_snp_c2_12399 (uncharacterized). These SNPs were positioned on chromosomes 1, 2, 4, 5 and 6.

In general model, 16 significant SNPs were associated with ASP at chromosomes 1, 2, 3, 5, 6, 10 and 11. The associated SNPs along with their putative functions includes solcap_snp_c2_20053 (protein SDE2 homolog), solcap_snp_c1_3746 (protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB1, chloroplastic), solcap_snp_c2_40635 (peroxidase 64-like), PotVar0010377 (Conserved gene of unknown function), PotVar0010288 (Dehydroquinase synthase), PotVar0009857 (Galactinol synthase), solcap_snp_c2_11147 (Solyntus genome), PotVar0120195, PotVar0120301 (Dehydrogenase), solcap_snp_c2_43515 (putative late blight resistance protein homolog R1A-4), solcap_snp_c2_3108 (uncharacterized), solcap_snp_c2_12402 (AP3-complex subunit beta-A), PotVar0134670 (translin-like protein), solcap_snp_c2_53946 (phenylalanine ammonia-lyase), solcap_snp_c2_15577 (peroxiredoxin-2E-2, chloroplastic-like) and solcap_snp_c2_53273 (uncharacterized).

Table 4.15. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the free asparagine along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_20053	1	73377232	C/T	3.17	protein SDE2 homolog protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B
general	solcap_snp_c1_3746	2	7050595	C/T	3.07	CCB1, chloroplastic
general	solcap_snp_c2_40635	2	39073504	A/G	3.73	peroxidase 64-like Conserved gene of unknown
general	PotVar0010377	2	39080045	C/T	3.4	function
general	PotVar0010288	2	39156199	A/C	3.88	Dehydroquinase synthase
general	PotVar0009857	2	40242824	A/C	5.33	Galactinol synthase
general	solcap_snp_c2_11147	3	46806099	G/T	3.96	Solyntus
general	PotVar0120195	3	48350669	G/T	3.36	Dehydrogenase

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0120301	3	48359023	A/C	3.71	Dehydrogenase putative late blight resistance
general	solcap_snp_c2_43515	5	9144438	A/G	3.19	protein homolog R1A-4
general	solcap_snp_c2_3108	6	3974830	G/T	3.1	uncharacterized AP3-complex subunit beta-
general	solcap_snp_c2_12402	6	23933179	C/T	3.04	A
general	PotVar0134670	10	51909507	A/G	3.67	translin-like protein phenylalanine ammonia-
general	solcap_snp_c2_53946	10	51926832	C/T	3.39	lyase peroxiredoxin-2E-2,
general	solcap_snp_c2_15577	10	55503488	A/G	3.15	chloroplastic-like
general	solcap_snp_c2_53273	11	9576599	A/C	3.18	uncharacterized
additive	solcap_snp_c1_6109	1	3716735	A/G	3.02	uncharacterized
additive	solcap_snp_c2_35480	1	60259084	C/T	3.18	NtPRp27-like protein ABC transporter C family
additive	solcap_snp_c2_35532	1	60514625	C/T	3.41	member 14-like
additive	solcap_snp_c2_35536	1	60515967	A/G	3.28	ABC transporter C family member 14-like
additive	solcap_snp_c2_35537	1	60516974	A/G	3.12	ABC transporter C family member 14-like
additive	PotVar0126039	1	63841740	A/G	3.42	Expressed protein (Matched in At)
additive	solcap_snp_c2_40955	1	63874694	A/G	3.15	Solyntus COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT
additive	solcap_snp_c1_3746	2	7050595	C/T	3.47	B CCB1, chloroplastic Cationic amino acid
additive	PotVar0062483	2	29473499	G/T	3.04	transporter probable serine/threonine-
additive	solcap_snp_c2_34862	4	67984665	C/T	3.54	protein kinase probable serine/threonine-
additive	solcap_snp_c1_10424	4	67985201	C/T	3.34	protein kinase putative late blight resistance
additive	solcap_snp_c2_11726	5	2079223	A/C	3.61	protein homolog R1B-12
additive	solcap_snp_c2_12399	6	24508249	C/T	3.02	uncharacterized

***Score = List of data.frames, one for each trait. The data frame contains -log10(P) results organized as markers x (additive) model (P values ≤ 0.001).**

One SNP was found to be common in both gene action models namely; *solcap_snp_c1_3746* with a putative gene function as protein cofactor assembly of complex C subunit B CCB1.

Dehydrogenases are group of core enzymes involved in the synthesis and metabolism of asparagine (Raffan and Halford, 2019). The SNP having putative gene function of dehydrogenase was associated with free asparagine in our study at chr 3. Protein kinases such as *SnRK1* and *GCN2* regulate the gene expression of asparagine synthetase (Postles et al., 2016). Serine and threonine are important amino acids, another amino acid aspartate is derived from threonine. The interconversion between these and asparagine is controlled by asparagine synthetase requiring ATP. Thus, serine/threonine protein kinases may be important in the regulation of asparagine in tubers. A study concluded that silencing asparagine synthetase (Ast) reduce acrylamide potential of tubers by limiting asparagine levels (Chawla et al., 2012). The current study detected SNPs associated with free asparagine located on chr 4 with gene annotation of serine/threonine protein kinase.

4.5.6 Starch (ST)

Starch is the main polysaccharide and an important storage compound in potato tubers. Mapping of QTLs related to complex traits like potato starch helps in the identification of genes involved in carbohydrate transport and metabolism. BLUPs calculated for starch showed normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between ST mean and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of ST (Fig. 4.19). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for starch using additive and general models demonstrated that the observed vs expected *p* values were normally or uniformly distributed as straight-line till $-\log_{10}(P)=3$ in both models. After that *p* values deviated indicating the presence of significant marker-trait associations. The *p* values were controlled by the model as sharp deviation was observed towards the normal at the tail (Fig. 4.20a). A sharp deviation in the tail region from the expected *p* values (i.e., at high $-\log_{10}(P\text{-values})$) establish that

they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

Table 4.16. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber starch content along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0033086	1	64610871	C/T	3.6	Glycerol-3-phosphate dehydrogenase
general	PotVar0010401	2	39079631	A/G	3.47	Conserved gene of unknown function
general	PotVar0010209	2	39157230	G/T	4.08	Dehydroquinase synthase
general	solcap_snp_c2_13854	3	43779300	A/C	3.23	protein DETOXIFICATION 35-like
general	solcap_snp_c1_5766	3	44217284	C/T	3.15	uncharacterized
general	PotVar0042853	3	46457572	A/G	3.56	Catechol O-methyltransferase
general	solcap_snp_c2_23602	4	656465	C/T	3.7	phosphoenolpyruvate carboxylase 4
general	solcap_snp_c2_38556	4	66415083	G/T	4.22	Serine/threonine-protein kinase
general	PotVar0015526	4	70743432	A/C	3.28	Receptor expression-enhancing protein 3
general	solcap_snp_c2_33535	5	1437829	A/G	3.59	6-phosphogluconate dehydrogenase, decarboxylating 3
general	PotVar0083565	6	103682	C/T	3.13	Importin subunit alpha
general	PotVar0085064	6	50130132	C/T	3.25	DnaJ protein
general	solcap_snp_c2_8652	6	52986639	A/G	3.24	miraculin-like
general	PotVar0123578	10	44858010	A/G	3.79	Uncategorized
general	PotVar0057500	10	58303619	A/G	3.12	N-acetylneuraminate-9-phosphatase
general	PotVar0067014	11	2773828	G/T	3.68	Phospho-2-dehydro-3-deoxyheptonate aldolase 2
general	solcap_snp_c2_23250	12	53642804	A/G	3.32	uncharacterized
general	solcap_snp_c2_23251	12	53793893	G/T	3.36	6-phosphogluconate dehydrogenase, decarboxylating 2

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
additive	solcap_snp_c2_51057	1	68950624	A/G	3.17	probable DNA-directed RNA polymerase subunit delta
additive	solcap_snp_c1_4444	3	43602976	C/T	3.21	sec-independent protein translocase protein TATB
additive	solcap_snp_c1_5766	3	44217284	C/T	3.89	uncharacterized
additive	PotVar0000800	4	64802757	A/C	3.18	Polyprotein
additive	solcap_snp_c2_38556	4	66415083	G/T	3.56	G-type lectin S-receptor-like serine/threonine-protein kinase
additive	PotVar0015526	4	70743432	A/C	4.13	Receptor expression-enhancing protein 3
additive	solcap_snp_c2_35944	4	70878898	A/T	3.03	L-ascorbate oxidase homolog
additive	solcap_snp_c2_24297	6	35798871	C/T	3.09	ubiquinol-cytochrome-c reductase complex assembly factor 1

****Score = List of data.frames, one for each trait. The data frame contains -log10(P) results organized as markers x (additive) model (P values ≤ 0.001).***

Starch (ST_P)

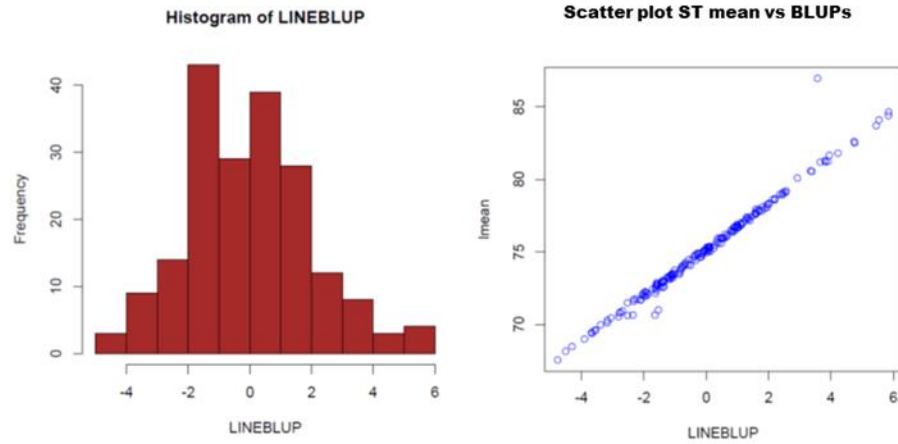


Figure 4.19. Histogram of LINEBLUPs for starch (percentage basis) and ST_DM (dry matter basis). Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

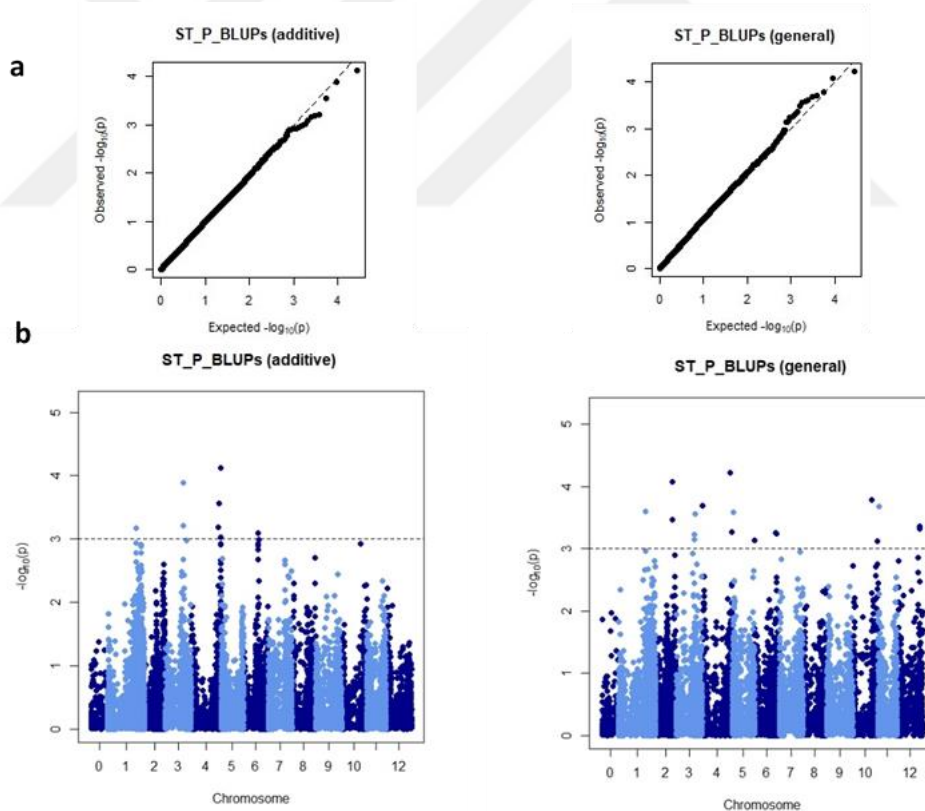


Figure 4.20. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing starch (ST_P “percentage basis”) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.

Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general models using BLUPs (Fig. 4.20b). The additive model showed 8 significant SNPs associated with starch located on chr 1 (68.9 Mbp), chr 3 (43.6 and 44.2 Mbp), chr 4 (64.8-70.8 Mbp) and chr 6 (35.79 Mbp) (Table 4.16). The associated SNPs along with their putative functions include *solcap_snp_c2_51057* (probable DNA-directed RNA polymerase subunit delta), *solcap_snp_c1_4444* (sec-independent protein translocase protein TATB), *solcap_snp_c1_5766* (uncharacterized), *PotVar0000800* (Polyprotein), *solcap_snp_c2_38556* G-type (lectin S-receptor-like serine/threonine-protein kinase), *PotVar0015526* (Receptor expression-enhancing protein 3), *solcap_snp_c2_35944* (L-ascorbate oxidase homolog) and *solcap_snp_c2_24297* (ubiquinol-cytochrome-c reductase complex assembly factor 1).

General model revealed 18 significant SNPs associated with starch located on chromosomes 1 (64.61 Mbp), 2 (39.0 and 39.1 Mbp), 3 (43.77-46.45 Mbps), 4 (0.65, 66.41, 7074 Mbps), 5 (1.43 Mbp), 6 (0.10, 50.13, 52.98 Mbps), 10 (44.85 and 58.30 Mbp), 11 (2.79 Mbp) and 12 (53.64 and 53.79 Mbp) (Table 4.16). The associated SNPs are present in the genes which perform putative functional roles related to glycerol-3-phosphate dehydrogenase (GPC), phosphoenolpyruvate carboxylase, G-type lectin S-receptor-like serine/threonine-protein kinase, 6-phosphogluconate dehydrogenase, phospho-2-dehydro-3-deoxyheptonate aldolase, DnaJ proteins and catechol O-methyltransferase. 3 SNPs were found to be common between additive and general models located on chr 3 (*solcap_snp_c1_5766*) and chr 4 (*solcap_snp_c2_38556* and *PotVar0015526*).

The gene annotation of the identified SNPS related to starch are involved in the regulation and metabolism of carbohydrate in potato. For instance, glycerol-3-phosphate dehydrogenase and phosphoenolpyruvate (PEP) carboxylase are important enzymes involved in carbohydrate metabolism such as sucrose synthesis and breakdown, starch degradation and glycolysis (Hajirezaei et al., 2006). DnaJ proteins play an important role as molecular chaperones and provides protection against heat stress by maintaining homeostasis (alleviate the degradation of Rubisco in calvin cycle) (Wang et al., 2015). The amino acid sequence examination of *StSnRK1* gene showed the existence serine/threonine-protein kinase. This gene is responsible for the transfer of carbon to

starch, inactivating sucrose phosphate synthase causing starch biosynthesis and accumulation (Wang et al., 2017).

Our results were supported by the studies conducted by Schonhals et al. (2016, 2017), who were of the view that QTLs associated with starch are positioned on chromosomes 1, 3, 4, 10, 11 and 12. 127 SNPs were identified using mixed linear model approach in 117 genes associated with tuber starch content. The identified genes were unequally distributed on all chromosomes and clusters between 0.5 to 4 Mbp width, with a putative regulatory and signalling functions (Schönhals et al., 2017). Both models in our study indicated the presence of SNPs within genes present on chromosomes 1, 2, 3, 4, 5, 6, 10, 11 and 12. 4 marker-trait associations were significant for starch positioned at chr 3 (61.49, 61.55, 61.55 and 61.89 Mbp) in a study conducted by Klassen et al. (2019). Genes associated with tuber starch content and its yield, quality of chips under cold storage, colocalized on chromosome 12. It plays a vital role in sugar metabolism converting starch into sugars and responsible for cold induced sweetening (CIS) (Fischer et al., 2013).

4.5.7 Beta-carotene (BCRT)

Beta-carotene (BCRT) is an important carotenoid imparting yellow colour to the tuber flesh (Andre et al., 2007). They have antioxidant properties and contribute to pro-vitamin activity in potato (Lachman et al., 2016). It is a wrong perception that tuber flesh colour is associated with starch content. In fact, the change in flesh colour of tuber depends on concentration of carotenoids not on the starch content as indicated by the results of correlation in the current study. Therefore, it is imperative to identify the SNP markers associated with carotenoids especially β -carotene for genetic gains in potato keeping in view the consumer preferability. BLUPs calculated for β -carotene showed normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between β -carotene mean and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of BCRT (Fig. 4.21). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

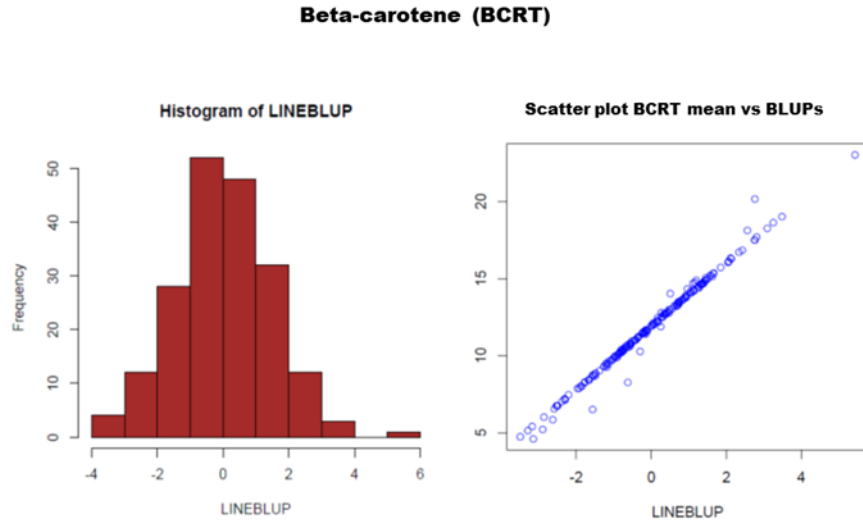


Figure 4.21. Histogram of LINEBLUPs for beta carotene. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

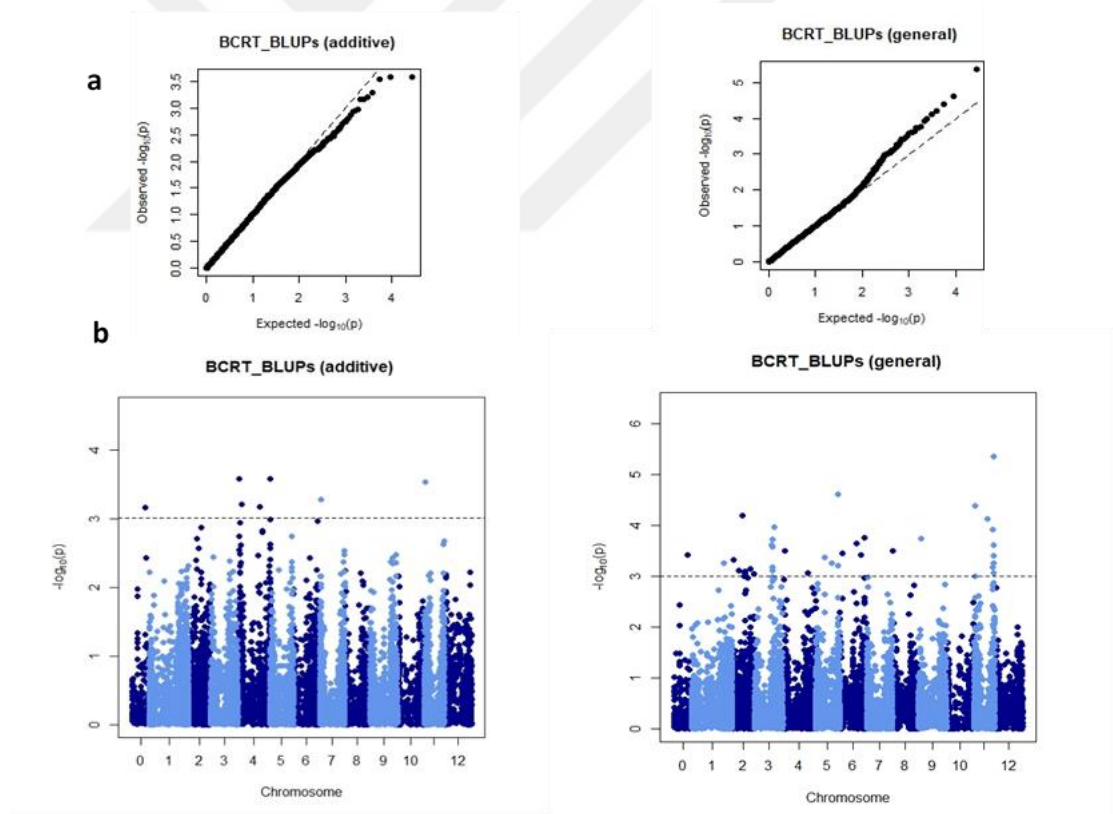


Figure 4.22. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing beta-carotene associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Table 4.17. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the beta-carotene content along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene annotation
general	solcap_snp_c2_53198	0	29279410	C/T	3.43	protease inhibitor-related protein (PI) mRNA
general	solcap_snp_c2_17192	1	70472766	A/G	3.26	arginase 1, mitochondrial
general	solcap_snp_c1_6462	2	2450782	G/T	3.32	uncharacterized protein PHLOEM PROTEIN 2-LIKE A9-like
general	solcap_snp_c2_54473	2	15060346	A/G	3.11	Conserved gene of unknown function
general	PotVar0038942	2	22153070	C/T	4.2	choline-phosphate cytidyltransferase 1-like
general	solcap_snp_c1_13459	2	27143975	A/G	3.09	UDP-N-acetylglucosamine pyrophosphorylase
general	PotVar0124112	2	27328113	A/C	3.04	Pyrroline-5-carboxylate reductase
general	PotVar0123993	2	27511390	A/C	3.01	2-oxo acid dehydrogenase, lipoyl-binding site
general	PotVar0123847	2	27602074	C/T	3.01	choline-phosphate cytidyltransferase 1-like
general	solcap_snp_c1_11556	2	28040094	A/C	3.03	Gamma-soluble nsf attachment protein
general	PotVar0062655	2	28751335	C/T	3.1	beta-galactosidase 3
general	solcap_snp_c1_8124	2	39969873	A/G	3.14	ethylene-responsive element-binding family protein
general	PotVar0003649	2	48262972	G/T	3.05	WD-repeat protein
general	PotVar0095359	3	38707513	A/G	3.62	trehalose-phosphate phosphatase A
general	solcap_snp_c1_14316	3	39221780	A/C	3.1	Tc vacuolar invertase
general	solcap_snp_c2_48370	3	39255317	A/G	3.73	(Pain-1) mRNA
general	solcap_snp_c2_48369	3	39257162	A/T	3.18	isolate P40d1 vacuolar invertase (Pain-1) mRNA
general	solcap_snp_c2_48360	3	39259017	A/C	3.58	beta-fructosidase (PAIN-1)
general	PotVar0070281	3	43922329	C/T	3.97	Beta-carotene hydroxylase
general	solcap_snp_c2_21858	4	5205905	A/G	3.49	rab GTPase-activating protein 1-like
general	solcap_snp_c2_45123	4	53994118	G/T	3.06	4-alpha-glucanotransferase, chloroplastic/amyloplastic-like
general	solcap_snp_c2_15730	5	19371368	A/G	3.36	protein OBERON 3-like
general	solcap_snp_c2_52870	5	34965675	C/T	3.26	uncharacterized
general	PotVar0081369	5	47989560	A/G	3.21	Phytochrome B2
general	PotVar0081749	5	48568302	A/G	4.6	Beta-1,3-galactosyltransferase 16
general	solcap_snp_c2_33933	6	6903541	C/T	3.45	uncharacterized

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene annotation
general	solcap_snp_c2_43093	6	37602254	A/G	3.65	scarecrow-like protein 8
general	PotVar0086011	6	47308739	C/T	3.42	WD-40 repeat protein
general	PotVar0040388	6	53750673	G/T	3.75	Fructokinase
general	solcap_snp_c2_54456	8	625053	C/T	3.5	uncharacterized
general	solcap_snp_c2_3986	9	5068865	C/T	3.74	uncharacterized
general	PotVar0067381	11	3072478	C/T	4.38	Acetolactate synthase arabinose-proton symporter
general	PotVar0061680	11	30153941	G/T	4.12	uncharacterized
general	solcap_snp_c2_15291	11	41722156	C/T	3.18	ATP-dependent zinc metalloprotease FTSH 4, mitochondrial-like
general	solcap_snp_c2_15268	11	42278941	A/G	3.92	uncharacterized
general	solcap_snp_c2_58364	11	42494182	C/T	3.07	protein EMBRYONIC FLOWER 1
general	solcap_snp_c2_30316	11	42589101	C/T	5.36	uncharacterized
general	solcap_snp_c2_30392	11	42657969	A/G	3.61	50S ribosomal protein L27-like
general	solcap_snp_c1_9204	11	42665808	C/T	3.25	Hyoscyamine 6- dioxygenase
general	PotVar0008668	11	43791440	C/T	3.41	protease inhibitor-related protein (PI) mRNA, GAGA-binding transcriptional activator
additive	solcap_snp_c2_53198	0	29279410	C/T	3.16	BBR/BPC1 acetyl-CoA acetyltransferase, cytosolic 1
additive	PotVar0076517	4	3547798	A/G	3.58	uncharacterized
additive	solcap_snp_c1_8341	4	9262447	C/T	3.2	Glutamate receptor 3 plant sucrose-phosphate- synthase (SPS)
additive	solcap_snp_c2_16712	4	48922939	C/T	3.17	Acetolactate synthase
additive	PotVar0017411	4	71814757	A/G	3.58	
additive	solcap_snp_c2_55831	7	3892550	C/T	3.28	
additive	PotVar0067381	11	3072478	C/T	3.53	

***Score = List of data.frames, one for each trait. The data frame contains -log₁₀(P) results organized as markers x (additive) model (P values ≤ 0.001).**

Results of Q-Q plot for the beta-carotene using additive model demonstrated that the observed vs expected *p* values were uniformly distributed as straight-line till -log₁₀(P)=2.5. After that *p* values deviated indicating the presence of significant marker-trait associations. The *p* values were controlled by the model as sharp deviation was observed towards the normal at the tail. A sharp deviation in the tail region from the expected *p* values (i.e., at high -log₁₀ (*P-values*)) establish that they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

In general model, the observed vs expected p values showed uniform distribution till $-\log_{10}(P)=2$, and start deviating at the tail roughly above p value of 3 indicating the presence of significant marker-trait associations. The false positives have been controlled by the model as the observed p values showed uniform distribution at the tail region with expected p values (Fig 4.22a).

Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general models using BLUPs data set of β -carotene (Fig. 4.22b). The additive model showed 7 SNPs significantly associated with β -carotene on chromosomes 4 (3.54, 9.26, 48.9 and 71.8 Mbps), 7 (3.89 Mbp) and 11 (3.07 Mbp). One SNP was present on unmapped chromosome. The identified SNPs along with the plausible functions includes PotVar0076517 (GAGA-binding transcriptional activator BBR/BPC1), solcap_snp_c1_8341 (acetyl-CoA acetyltransferase, cytosolic 1), solcap_snp_c2_16712 (uncharacterized), PotVar0017411 (Glutamate receptor 3 plant), solcap_snp_c2_55831 (sucrose-phosphate-synthase (SPS)) and PotVar0067381 (Acetolactate synthase) (Table 4.17).

General model, however revealed 40 significant marker-trait associations. The β -carotene associated SNPs were located on chromosomes 1 (70.47 Mbp), 2 (2.45, 15.06, 22.1-28.7, 39.96 and 48.26 Mbps), 3 (38.7-48.92 Mbps), 4 (5.2 and 53.99 Mbps), 5 (19.3, 34.96, 47.98, 48.56), 6 (6.90, 37.6-53.7 Mbps), 8 (0.62 Mbp), 9 (5.06 Mbp) and 11 (3.07, 30.15-43.79 Mbp) (Table 4.17). The associated SNPs are linked with the genes performing critical putative functions related to protease inhibitor-related protein (PI) mRNA arginase 1, mitochondrial, protein phloem protein 2-like A9-like, choline-phosphate cytidylyltransferase 1-like, UDP-N-acetylglucosamine pyrophosphorylase, pyrroline-5-carboxylate reductase, 2-oxo acid dehydrogenase, lipoyl-binding site, choline-phosphate cytidylyltransferase 1-like, gamma-soluble nsf attachment protein, beta-galactosidase 3, ethylene-responsive element-binding family protein, WD-repeat protein, trehalose-phosphate phosphatase A, vacuolar invertase (*Pain-1*) mRNA, beta-fructosidase (*PAIN-1*), beta-carotene hydroxylase, rab GTPase-activating protein 1-like, 4-alpha-glucanotransferase, chloroplastic/amyloplastic-like, Beta-1,3-galactosyltransferase 16, fructokinase, acetolactate synthase, arabinose-proton symporter and hyoscyamine 6-dioxygenase.

An important SNP (PotVar0070281) linked with β -carotene was identified in our study. It was present on chr 3 and genes containing that particular SNP has a putative function related to *beta-carotene hydroxylase*. Beta carotene hydroxylase 2 is referred to as *bch* or *chy2*, and literature revealed that this gene is responsible for converting white tuber flesh colour to yellow in potato (Brown et al., 2006). This gene is mapped on Y-locus of chr 3 in potato (Bonierbale et al., 1988). A nice illustration has been presented by Wolters et al. (2010) and Uitdewilligen et al. (2013) in tetraploid potato that *Chy2* allele 3 is in fact the key determining factor for flesh colour. Previous studies identified this genomic region associated with yellow tuber flesh colour, while the presence of the detected SNP in gene linked with β -carotene do support our hypothesis scientifically that beta-carotene is infact responsible for yellow flesh colour in potato. This SNP has a potential of becoming a selection marker for this particular trait in future breeding studies. Besides, ethylene-responsive element-binding family protein performs vital functions related to signalling in carotenoid biosynthesis in tomato (Cruz et al., 2018). WD protein domain is involved in biosynthesis of anthocyanin in *Medicago truncatula* (Li et al., 2016). Acetyl-CoA acetyltransferase is an important enzyme involved in carotenoid biosynthesis and metabolic pathways (Leng et al., 2017).

Our results depicted that no SNPs were detected on chromosomes 10 and 12. Contrastingly, the genes located on these chromosomes (10 (52-57 Mbp) and 12 (24.2 Mbp)) have functional roles related to the production of purple delphinidin-based pigments found on locus P (flavonoid 3',5'-hydroxylase-f3'5'h) for anthocyanin biosynthetic pathway converting phenylalanine to coumarate-CoA (Parra-Galindo et al., 2019).

4.5.8 Total antioxidant activity (TAA)

The total antioxidant activity of potatoes is linked with antioxidant compounds such as phenolics and carotenoids (Lachman et al., 2008). SNPs related to total antioxidant activity will indicate the presence of antioxidant compounds in potato which ultimately helps in selection process for improved potato cultivars having high radical scavenging activity. It provides a way to hunt for useful sources of genes for the accumulation of antioxidants in potato. BLUPs calculated for total antioxidant activity (TAA) showed

normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between TAA mean and BLUPs exhibited less

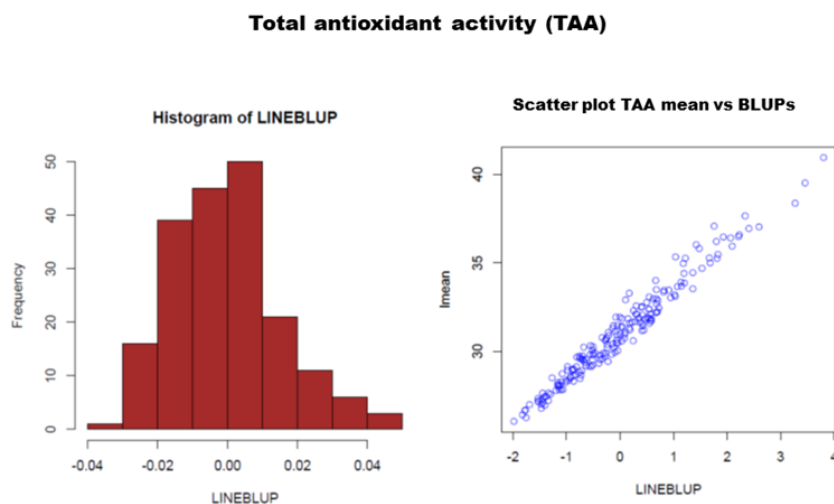


Figure 4.23. Histogram of LINEBLUPs for total antioxidant activity (TAA). Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

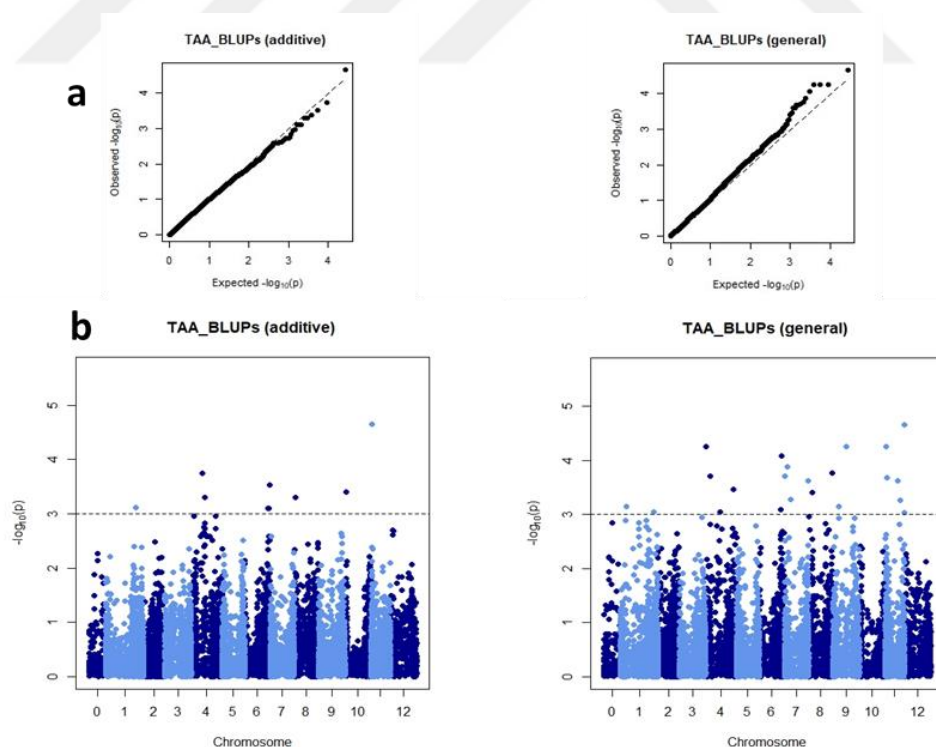


Figure 4.24. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing total antioxidant activity (TAA) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Table 4.18. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the total antioxidant activity along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c1_8908	1	13655916	A/G	3.15	mitochondrial outer membrane protein porin of 36 kDa-like (VDAC)
general	solcap_snp_c2_2531	1	77432643	A/G	3.04	tafazzin
general	solcap_snp_c2_54413	4	853209	A/T	4.26	Solyntus
general	solcap_snp_c2_54083	4	10969111	A/G	3.71	putative calcium-transporting ATPase 11, plasma membrane-type two-component response regulator-like PRR37
general	solcap_snp_c1_3443	4	32779431	C/T	3.04	uncharacterized
general	solcap_snp_c2_39448	4	63659421	C/T	3.47	DnaJ protein
general	PotVar0085064	6	50130132	C/T	3.09	Phytochrome-associated serine/threonine protein phosphatase 3
general	PotVar0040680	6	52929083	G/T	4.08	probable galacturonosyltransferase 6
general	solcap_snp_c2_46099	7	563754	A/G	3.7	xyloglucan endotransglycosylase
general	PotVar0097695	7	7481450	A/G	3.88	LeXET2 transcription factor
general	solcap_snp_c2_4342	7	14924207	C/T	3.27	bHLH68
general	solcap_snp_c2_18570	7	54961836	C/T	3.62	rab3 GTPase-activating protein catalytic subunit
general	solcap_snp_c2_47904	8	7795381	G/T	3.4	putative amidohydrolase YtcJ
general	solcap_snp_c1_5587	8	55187986	C/T	3.77	mitogen-activated protein kinase homolog MMK2-like
general	solcap_snp_c2_4404	9	13622577	C/T	3.14	uncharacterized chloroplast envelope quinone oxidoreductase homolog
general	solcap_snp_c2_22761	9	31630431	A/C	4.26	Acetolactate synthase
general	PotVar0067381	11	3072478	C/T	4.25	Protein tyrosine phosphatase
general	PotVar0106094	11	4346046	G/T	3.67	arabinose-proton symporter
general	PotVar0061680	11	30153941	G/T	3.62	probable magnesium transporter NIPA6
general	solcap_snp_c1_4385	11	36269574	C/T	3.26	phototropin-1
general	solcap_snp_c2_51273	11	44683272	A/G	4.66	Endoplasmic reticulum [ER]-type calcium ATPase
general	PotVar0118171	11	45420584	C/T	3.03	
additive	solcap_snp_c2_17592	1	69809843	A/C	3.11	uncharacterized
additive	solcap_snp_c2_55707	4	25320523	C/T	3.75	Solyntus
additive	solcap_snp_c1_3436	4	32229561	C/T	3.31	uncharacterized

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
additive	PotVar0039687	6	54085599	A/G	3.1	Hyoscyamine 6-dioxygenase
additive	PotVar0127587	6	55906509	C/T	3.1	Carbamoyl phosphate synthase large subunit
additive	PotVar0066099	6	59360561	C/T	3.53	Fiber protein Fb19
additive	PotVar0088677	8	2693867	G/T	3.3	Gene of unknown function Cmp-2-keto-3-deoctulosonate (Cmp-kdo)
additive	PotVar0116818	10	1912224	A/G	3.4	cytidyltransferase
additive	PotVar0067381	11	3072478	C/T	4.66	Acetolactate synthase

****Score = List of data.frames, one for each trait. The data frame contains -log₁₀(P) results organized as markers x (additive) model (P values ≤ 0.001).***

scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of TAA (Fig. 4.23). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the total antioxidant activity using additive and general models demonstrated that the observed vs expected *p* values were normally or uniformly distributed as straight-line till -log₁₀(P)=3 in both models (Fig. 4.24a). After that *p* values deviated indicating the presence of significant marker-trait associations. The *p* values were controlled by the model as sharp deviations were observed towards the normal at the tail. A sharp deviation in the tail region from the expected *p* values (i.e., at high -log₁₀ (*P*-values)) establish that they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general models using BLUPs (Fig. 4.24b). The additive model identified 9 significant SNPs associated with total antioxidant activity (TAA) located on chr 1 (69.80 Mbp), chr 4 (25.32 Mbp, 32.22 Mbp), chr 6 (54.08-59.36 Mbp), chr 8 (2.69 Mbp), chr 10 (1.91 Mbp) and chr 11 (3.07 Mbp) (Table. 4.18). General model revealed 22 significant SNPs linked with TAA positioned on chromosomes 1, 4, 6, 7, 8, 9 and 11. The detected SNPs were present in genes having plausible functions related to putative calcium-transporting

ATPase, two-component response regulator-like PRR37, DnaJ protein, phytochrome-associated serine/threonine protein phosphatase 3, probable galacturonosyltransferase 6, xyloglucan endotransglycosylase LeXET2, transcription factor bHLH68, rab3 GTPase-activating protein catalytic subunit, putative amidohydrolase YtcJ, mitogen-activated protein kinase homolog MMK2-like, chloroplast envelope quinone oxidoreductase homolog, acetolactate synthase, protein tyrosine phosphatase, arabinose-proton symporter, probable magnesium transporter NIPA6, phototropin-1, endoplasmic reticulum [ER]-type calcium ATPase and cmp-2-keto-3-deoctulosonate (Cmp-kdo) cytidyltransferase.

One SNP (PotVar0067381) at chromosome 11 was found to be common in both models with plausible gene function as acetolactate synthase. This is key enzyme for the synthesis of amino acids (branched chain) like valine, leucine and isoleucine. Studies reported that these amino acids inhibit lipid peroxidation and have antioxidant properties (Jin et al., 2015; Chang et al., 2020). Gene annotation showed that SNP named solcap_snp_c2_4342 located on chr 7 was present in the genes with putative function of transcription factor bHLH, associated with total antioxidant activity. This transcription factor played vital role in anthocyanin and flavonoid biosynthetic pathways in potato (Tai et al., 2013) and wheat (Zhao et al., 2020). Both of these phytochemicals possess antioxidant properties.

4.5.9 Total phenolic contents (TPC)

Phenolic compounds are another group of secondary metabolites and well-known antioxidants, which possess the ability of scavenging free radicals and therefore important in the reduction of diseases such as inflammatory disorders and cardiovascular diseases. Xu et al. (2009), Albishi et al. (2013) and Kim et al. (2019) reported that chlorogenic, p-coumaric, cryptochlorogenic, ferulic, caffeic, vanillic acids, and tryptophan were detected in the potato tuber flesh. BLUPs calculated for total phenolics (TPC) showed normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between TPC mean and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of TAA (Fig. 4.25). Q-Q plots were drawn between the observed and expected negative log (*P*) values

for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the total phenolics using additive and general models demonstrated that the observed vs expected p values were uniformly distributed as straight-line till $-\log_{10}(P)=3$ in both models. After that p values deviated indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviations were observed towards the normal at the tail (Fig. 4.26a). A sharp deviation in the tail region from the expected p values (i.e., at high $-\log_{10}(P\text{-values})$) establish that they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general models using BLUPs (Fig. 4.26b). The additive model showed that 11 significant SNPs were associated with total phenolics located on chr 3 (35.7-36.0 Mbp), chr 4 (6.2 Mbp), chr 7 (55.4-56.0 Mbp), chr 8 (3.21 Mbp) and chr 10 (3.97 Mbp). However, general model detected the presence of 17 SNPs significantly linked with TPC on chr 1 (70.5, 81.56 and 81.81 Mbp), chr 2 (32.11 and 35.11), chr 3 (22.5-36.0 Mbp), chr 4 (6.20 Mbp), chr 5 (51.70 Mbp), chr 7 (55.0, 56.0 and 56.62 Mbp) and chr 9 (2.47 Mbp). 7 SNPs were common in both models namely

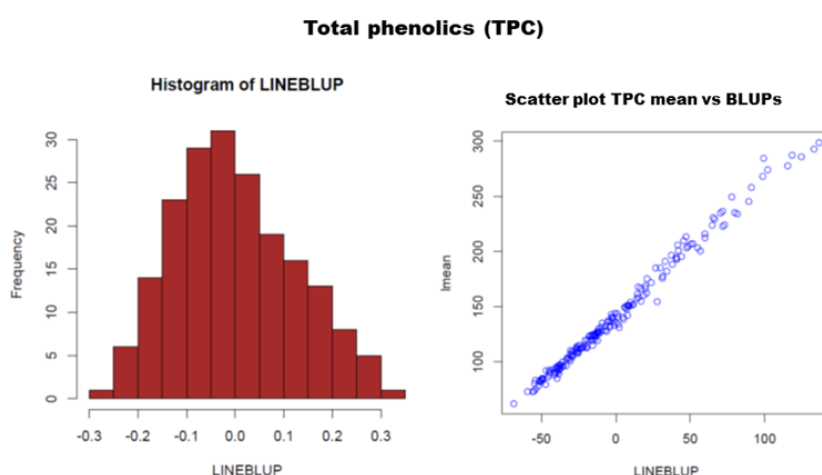


Figure 4.25. Histogram of LINEBLUPs for TPC. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

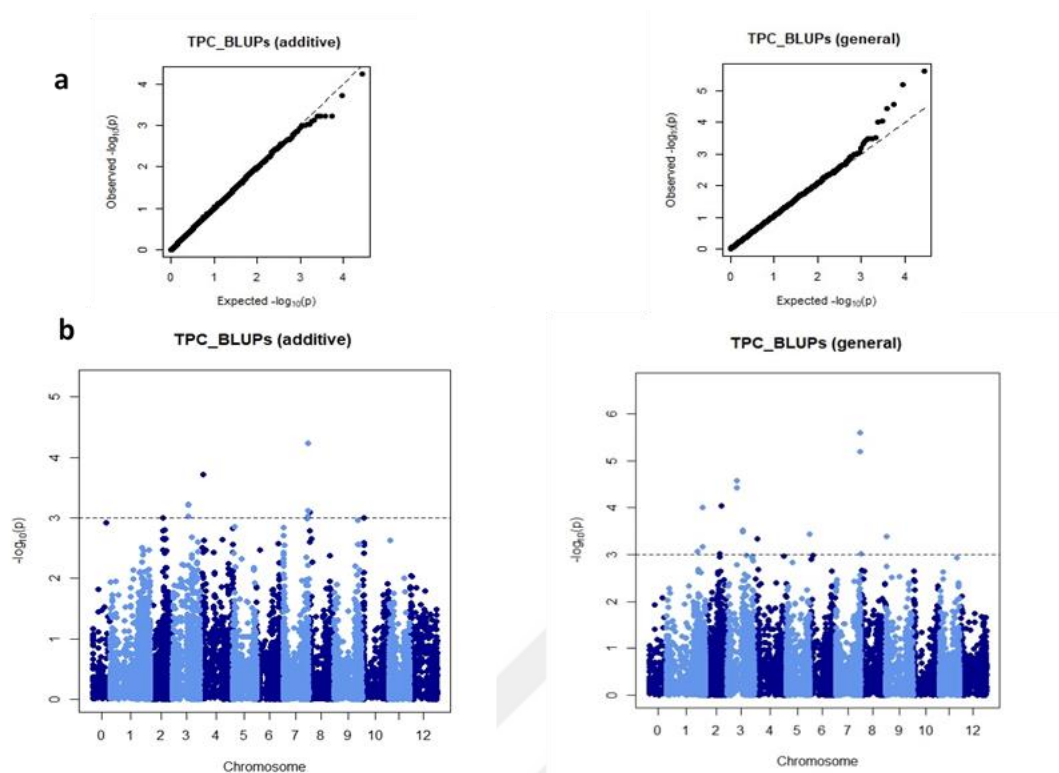


Figure 4.26. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing total phenolics (TPC) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Table 4.19. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the total phenolic contents along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_17192	1	70472766	A/G	3.06	vacuolar iron transporter
general	solcap_snp_c2_9892	1	81567297	C/T	3.17	homolog 4-like
general	PotVar0061043	1	81814306	A/G	4	Cationic peroxidase trihelix transcription factor
general	solcap_snp_c2_39178	2	32148414	A/G	3.01	ASIL2-like
general	PotVar0038725	2	35111438	A/G	4.04	Conserved gene of unknown function
general	solcap_snp_c2_1930	3	22534074	A/G	4.42	zinc finger CCCH domain- containing protein 30
general	solcap_snp_c2_1933	3	22535369	C/T	4.57	zinc finger CCCH domain- containing protein 30
general	PotVar0085728	3	35708053	A/C	3.52	Alpha amylase
general	PotVar0085760	3	35929651	A/C	3.49	Alpha amylase
general	solcap_snp_c2_35355	3	36000522	C/T	3.49	alpha-amylase-like
general	solcap_snp_c2_35350	3	36001002	A/T	3.49	alpha-amylase-like
general	solcap_snp_c2_11568	4	6210397	C/T	3.33	L-allo-threonine aldolase- related protein

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_3439	5	51709374	A/G	3.43	protein GPR107-like
general	PotVar0036966	7	55737035	A/G	5.2	Sucrase
general	PotVar0036767	7	56006235	A/C	5.6	Transducin family protein
general	solcap_snp_c2_33280	7	56628128	C/T	3.01	Uncharacterized Arginine biosynthesis
general	PotVar0011929	9	2475672	C/T	3.38	bifunctional protein
additive	PotVar0085728	3	35708053	A/C	3.03	Alpha amylase
additive	PotVar0085760	3	35929651	A/C	3.23	Alpha amylase
additive	solcap_snp_c2_35355	3	36000522	C/T	3.23	alpha-amylase-like
additive	solcap_snp_c2_35353	3	36000878	C/T	3.21	alpha-amylase-like
additive	solcap_snp_c2_35350	3	36001002	A/T	3.23	alpha-amylase-like L-allo-threonine aldolase-
additive	solcap_snp_c2_11568	4	6210397	C/T	3.72	related protein
additive	PotVar0037038	7	55469131	C/T	3.02	Cysteine synthase
additive	PotVar0036966	7	55737035	A/G	4.23	Sucrase
additive	PotVar0036767	7	56006235	A/C	3.12	Transducin family protein
additive	solcap_snp_c2_24407	8	3215967	A/C	3.09	beta-amylase 8 bifunctional epoxide
additive	solcap_snp_c1_13025	10	3970339	A/G	3.01	hydrolase 2-like

***Score = List of data.frames, one for each trait. The data frame contains -log₁₀(P) results organized as markers x (additive) model (P values ≤ 0.001).**

PotVar0085728 (alpha amylase), PotVar0085760 (alpha amylase), solcap_snp_c2_35355 (alpha-amylase-like), solcap_snp_c2_35350 (alpha-amylase-like), solcap_snp_c2_11568 (L-allo-threonine aldolase-related protein), PotVar0036966 (Sucrase) and PotVar0036767 (transducin family protein) (Table 4.19).

Literature suggests that association mapping study was not performed related to total phenolics in potato. Therefore, the identified genomic regions are of prime importance. The region between 35.70 Mbp to 36.00 Mbp on chr 3 carry four SNPs (PotVar0085728, PotVar0085760, solcap_snp_c2_35355, solcap_snp_c2_35350) detected by both models with putative functional roles as alpha-amylase. Alpha amylase is starch degrading enzyme, converting sugars to glucose and fructose. This enzyme is inhibited by the polyphenols present in tuber flesh of potatoes. A negative correlation was reported by Kalita et al. (2013) for tubers having high polyphenols with asparagine and acrylamide formation. Various transcription factors regulate the biosynthesis of secondary metabolites in plants such as phenolic compounds as they play an important role in plant stress response. Zinc finger CCCH gene family is involved in signal transduction during

abiotic stress in tomato and categorized as stress responsive genes (Xu et al., 2014). Genes carrying these SNPs were present on chr 3 in our study at 22.5 Mbp. Solcap_snp_c2_9892 SNP was present on chr 1 associated with total phenolics at 81.5Mbp. This SNP has a putative gene function of vacuolar iron transporter. The iron homeostasis in plants is controlled by vacuolar iron transporter (Legacy et al., 2012). An increased accumulation of phenolics were reported under Fe deficient conditions (Boamponsem et al., 2018).

4.5.10 Tuber flesh colour_L* coordinate (FCL)

Tuber flesh colour is a trait of vital value as the biological variation (white to yellow/dark yellow) in this variable indirectly relates to the carotenoids in tuber tissue. SNPs associated with this trait helps in the selection of tubers with better antioxidant activity due to accumulated carotenoids as well as anthocyanin pigments. Tuber flesh colour was measured with Konica Minolta chromameter CIELab in three dimensions/coordinates, L* indicating darkness/lightness, b* indicating yellow (+)/blue (-) while a* refers to red (+)/ green (-). In our study, correlation analysis showed that dark tuber flesh (less L values) has yellow colour (more b* values). a* coordinate is excluded for association mapping studies as it does not relate to the biological variation in tuber flesh colour in present study. Mapping of genomic regions associated with this trait will help to select

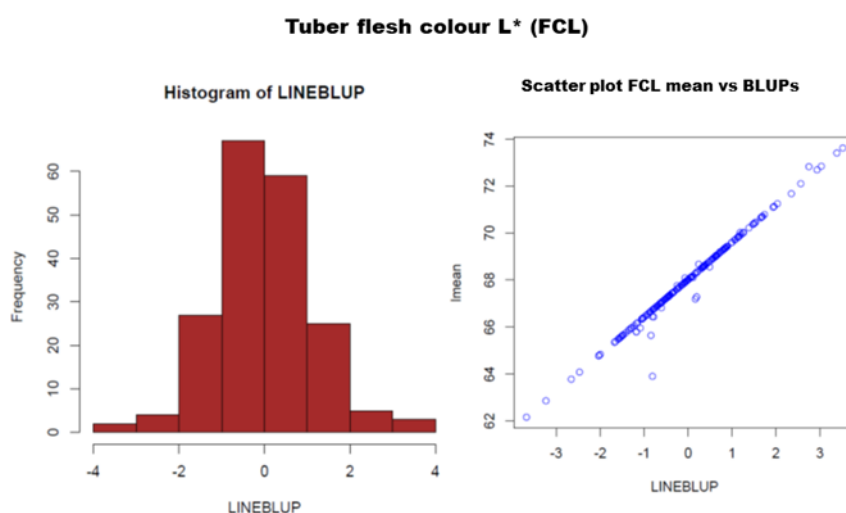


Figure 4.27. Histogram of LINEBLUPs for tuber flesh colour L* FCL. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

desirable flesh colour of tubers in a breeding programme efficiently, without rigorous selection in the field. BLUPs calculated for FCL showed normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between FCL mean and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of FCL (Fig. 4.27). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the FCL using additive model demonstrated that the observed vs expected p values were uniformly distributed as straight-line till $-\log_{10}(P)=3$. After that p values deviated indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviations were observed towards the normal at the tail. In general model, observed p values were also uniformly distributed with expected p values till $-\log_{10}(P)=2$, soon after the observed p values start deviating but still showed uniform distribution as sharp deviations were observed at the tail region towards the normal (Fig. 4.28a). A sharp deviation in the tail region from the expected p values (i.e., at high $-\log_{10}(P\text{-values})$) establish that they are in LD with casual polymorphism and produce significant marker-trait

Table 4.20. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber flesh colour L^* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c1_8358	1	49228392	C/T	3.09	uncharacterized
general	solcap_snp_c2_43285	1	57765672	A/G	3.19	uncharacterized
general	PotVar0036059	1	84985463	C/T	3.41	Cell division cycle protein Conserved gene of
general	PotVar0038942	2	22153070	C/T	3.67	unknown function
general	solcap_snp_c1_12339	2	27411239	A/G	3.73	uncharacterized
general	PotVar0070281	3	43922329	C/T	3.89	Beta-carotene hydroxylase DNA-directed RNA polymerases IV and V
general	solcap_snp_c2_1556	3	50573479	C/T	3.21	subunit 2-like Nucleic acid binding
general	PotVar0121379	3	56499714	A/G	3.26	protein
general	solcap_snp_c1_14440	4	55384468	C/T	3.56	systemin receptor SR160

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0071004	4	62730385	C/T	3.84	CAK associated cyclinH homolog
general	PotVar0070816	4	62734645	G/T	3.84	CAK associated cyclinH homolog
general	PotVar0081337	5	47989133	A/C	3.34	Phytochrome B2
general	PotVar0081369	5	47989560	A/G	3.39	Phytochrome B2
general	PotVar0081749	5	48568302	A/G	4.5	Beta-1,3-galactosyltransferase 16
general	solcap_snp_c2_43093	6	37602254	A/G	4.16	scarecrow-like protein 8
general	PotVar0040388	6	53750673	G/T	3.43	Fructokinase protein disulfide isomerase-like 2-3
general	solcap_snp_c1_10001	7	45239915	A/T	3.03	Stromal membrane-associated protein
general	PotVar0102858	7	53695441	A/C	3.04	haloacid dehalogenase-like hydrolase domain-containing protein Sgpp
general	solcap_snp_c2_32650	8	1141585	A/G	3.55	BTB/POZ domain-containing protein POB1-like
general	solcap_snp_c2_3986	9	5068865	C/T	3.62	like
general	PotVar0067381	11	3072478	C/T	3.1	Acetolactate synthase
general	PotVar0110452	11	3658852	A/G	4.05	GLYCEROL-3-PHOSPHATE DEHYDROGENASE
general	PotVar0110464	11	3659012	A/G	3.89	GLYCEROL-3-PHOSPHATE DEHYDROGENASE
general	solcap_snp_c2_30316	11	42589101	C/T	3.53	protein EMBRYONIC FLOWER 1
additive	solcap_snp_c2_54863	2	18520191	A/C	3.13	WD repeat-containing protein 55
additive	solcap_snp_c2_16682	3	3014439	C/T	3.49	3-hydroxy-3-methylglutaryl coenzyme A reductase
additive	solcap_snp_c1_13847	3	43465296	A/G	3.2	SKP1-like protein 21
additive	solcap_snp_c1_13843	3	43469293	A/C	3.02	SKP1-like protein 21
additive	solcap_snp_c2_46600	3	43478349	C/T	3.26	short-chain dehydrogenase TIC 32, chloroplastic-like
additive	solcap_snp_c2_46605	3	43497910	A/G	3.07	peroxidase P7-like
additive	PotVar0017171	4	71590429	C/T	3.03	1,4-alpha-glucan branching enzyme
additive	solcap_snp_c2_10681	4	71592572	A/G	3.22	1,4-alpha-glucan-branching enzyme-like
additive	PotVar0017411	4	71814757	A/G	3.27	Glutamate receptor 3 plant

***Score = List of data.frames, one for each trait. The data frame contains -log10(P) results organized as markers x (additive) model (P values ≤ 0.001).**

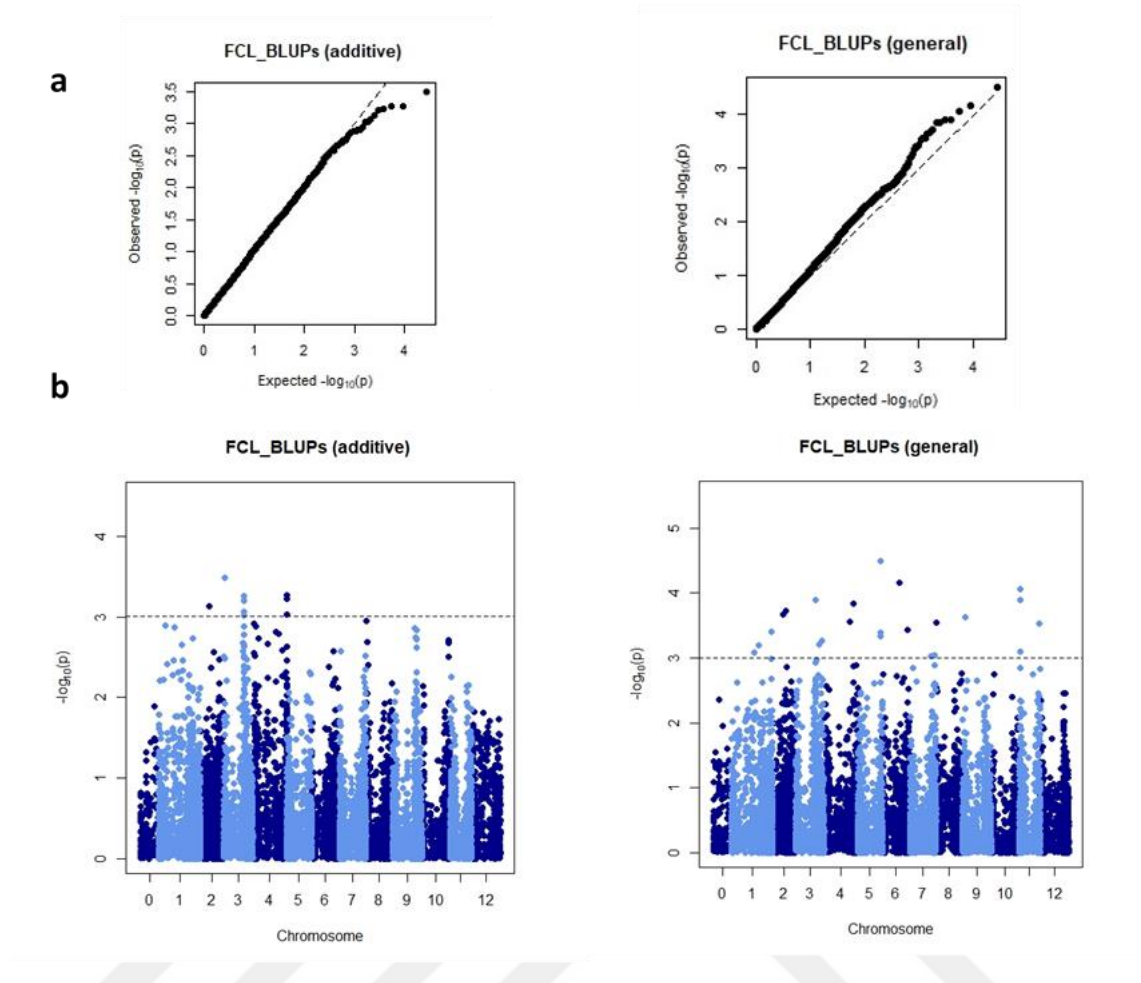


Figure 4.28. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing FCL associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.

associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

Manhattan plots were created by employing MLM in *GWASpoly R* with additive and general models using BLUPs (Fig. 4.28b). The additive model revealed that 9 SNPs were significantly associated with FCL located on chr 2 (18.5 Mbp), chr 3 (3.01 and 43.4 Mbp) and chr 4 (71.5 and 71.8 Mbp) (Table 4.20). The associated SNPs includes solcap_snp_c2_54863 (WD repeat-containing protein), solcap_snp_c2_16682 (3-hydroxy-3-methylglutaryl coenzyme A reductase), solcap_snp_c1_13847 (SKP1-like protein), solcap_snp_c1_13843 (SKP1-like protein), solcap_snp_c2_46600 (short-chain dehydrogenase TIC 32), solcap_snp_c2_46605 (peroxidase P7-like),

PotVar0017171 (1,4-alpha-glucan branching enzyme), solcap_snp_c2_10681 (1,4-alpha-glucan-branching enzyme-like) and PotVar0017411 (Glutamate receptor 3 plant). SKP-1 protein is a complex involved in signal transduction and plant defence response. Studies showed that it is part of SCF complex and respond to wounding in sweet potato (Weng et al., 2020)

General model detected 24 significant SNP markers associated with periderm thickness positioned on all chromosomes except 10 and 12 (Table 4.20). These results were in accordance with previous GWAS studies, which identified the genomic region between 8 cM to 38.5 cM associated with tuber flesh colour on chr 1, 3, 5, 6, 9, and 12 (Bjorn et al. 2014). In contrast to present study, chromosome 12 was associated with tuber flesh colour in a study by Sliwka et al. (2008). Björn et al. (2008) detected QTLs associated with flesh colour on chromosomes 1, 2, 3 (31.5 cM), 4, 6 and 7 (Björn et al. 2008). Both models in our study detected SNPs linked with tuber flesh colour on chromosomes 2, 3 and 4. Berdugo-Cely et al. (2017) used Infinium SolCAP 8k array for genotyping of 803 accessions of Central Colombian Collections to detect of marker-trait associations. The study dictated that 4 SNPs were associated with tuber flesh colour located on chromosomes 2, 4 and 7 with loci positions as 45.69 and 47.32 Mbp, 57.89 Mbp, and 53.07 Mbp, respectively.

General model revealed pleiotropic SNP (PotVar0070281) associated with both beta-carotene and tuber flesh colour detected on chr 3. This SNP is present in the gene related to *beta-carotene hydroxylase* (often referred to as *Chy2* or *Bch*), and responsible for the yellow colour of tuber flesh (Uitdewilligen et al. (2013). Hence based on current findings and available literature, chr 3 is linked with biological variation of tuber flesh colour. Moreover, yellow flesh colour in potato is mainly due to the presence of beta-carotene, positioned on chr 3 with loci position at 43.92 Mbp. This SNP has a potential of becoming a selection marker in future breeding studies. Our results were also supported by the findings of Campbell et al. (2013) who reported that QTLs linked with beta carotene was observed on chr 3 while chr 9 was not associated with any carotenoid biosynthetic genes. Furthermore, 10 SNPs were termed as pleiotropic SNPs as they were found to be common between beta-carotene and tuber flesh colour. These includes PotVar0038942 (Conserved gene of unknown function), PotVar0070281 (Beta-carotene hydroxylase), PotVar0081369 (Phytochrome B2), PotVar0081749 (Beta-1,3-galactosyltransferase)

solcap_snp_c2_43093 (scarecrow-like protein), PotVar0040388 (Fructokinase), solcap_snp_c2_3986 (BTB/POZ domain-containing protein POB1-like), PotVar0067381 (Acetolactate synthase), solcap_snp_c2_30316 (protein EMBRYONIC FLOWER 1) and PotVar0017411 (Glutamate receptor 3 plant). The photoperiodic control of tuberization is controlled by phytochrome B2 (*PHYB* gene). It is involved in the detection of far-red and red light, transcriptional regulation of photoreceptor activity in potato (Aksenova et al., 2005). Additive model detected tuber flesh colour associated SNP at chr 2 with plausible gene function as WD repeat protein. This class of proteins contains MYB transcription factors involved in synthesis of anthocyanins in tuber (Li et al., 2020).

4.5.11 Tuber flesh colour_b* coordinate (FCb)

BLUPs calculated for FCb showed normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between FCb mean and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of FCb (Fig. 4.29). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the FCb using additive model demonstrated that the observed vs expected p values were uniformly distributed as straight-line till $-\log_{10}(P)=2$. After that p values deviated indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviations were observed towards the normal at the tail. In general model, observed p values were also uniformly distributed with expected p values till $-\log_{10}(P)=2$, soon after the observed p values start deviating but still showed uniform distribution as sharp deviations were observed at the tail region towards the normal (Fig. 30a). A sharp deviation in the tail region from the expected p values (i.e., at high $-\log_{10}(P\text{-values})$) establish that they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020). Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general models using BLUPs. The additive model revealed 41 significant SNPs linked

with flesh colour b^* coordinate (Fig. 4.30b). These SNPs were located on chromosomes 1, 2, 3, 5, 6, 8, 9, 10 and 12. Contrarily, general model discovered 22 significant associated SNPs positioned on chromosomes 1, 2, 3, 6, 8, 9, 10, 11 and 12. Both models depicted 12 common SNPs positioned on chromosomes 1, 3, 6, 8 and 9. A detailed description of SNPs and their variants, chromosome number, position and gene annotation is described in Table 4.21. 12 SNPs were found to be common in both models performing vital biosynthetic and signalling processes.

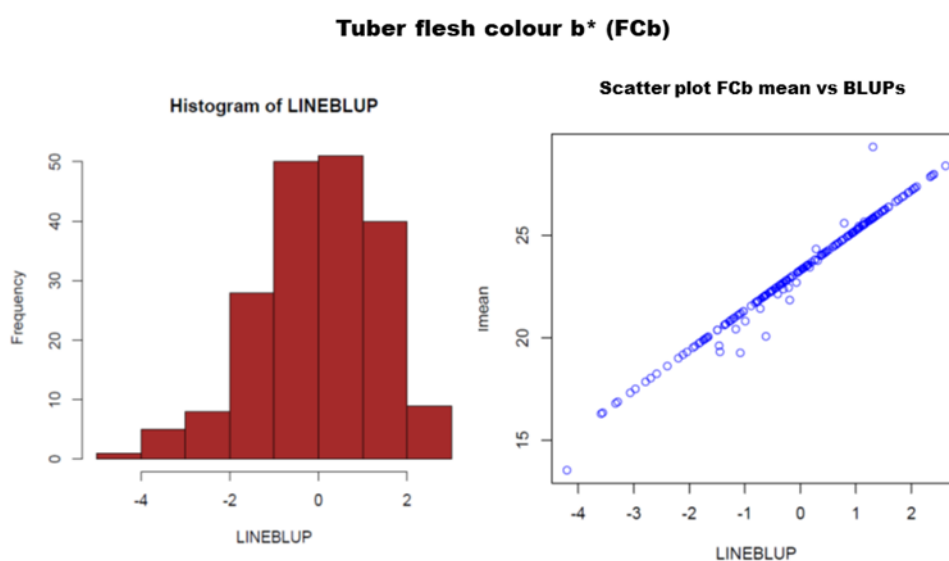


Figure 4.29. Histogram of LINEBLUPs for tuber flesh colour b^* FCb. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

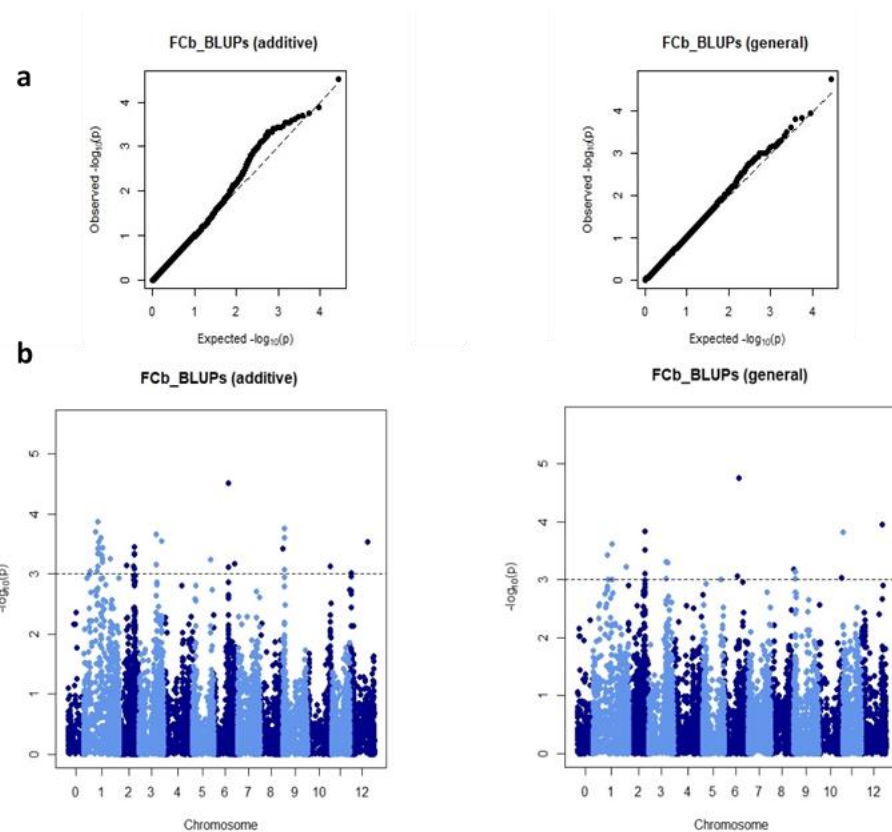


Figure 4.30. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing FCB associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Table 4.21. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber flesh colour b* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_46540	1	35678032	C/T	3.44	zinc finger protein VAR3,
general	solcap_snp_c2_27680	1	37067730	C/T	3.01	chloroplastic
general	solcap_snp_c1_8541	1	37276804	C/T	3.01	alkaline/neutral invertase
general	solcap_snp_c2_35218	1	47299905	C/T	3.01	A, mitochondrial
general	solcap_snp_c2_14939	1	47761676	G/T	3.62	uncharacterized
general	solcap_snp_c2_9921	1	81452360	A/G	3.22	peroxidase 40
general	solcap_snp_c2_40636	2	39073567	A/G	3.84	flowering time control
general	solcap_snp_c2_40637	2	39073604	C/T	3.52	protein FCA
general	PotVar0009178	2	40632942	A/C	3.1	probable helicase
						MAGATAMA 3
						peroxidase 64-like
						peroxidase 64-like
						U1 small nuclear
						ribonucleoprotein 70 kDa

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0070248	3	43921286	G/T	3.01	Plastid division regulator MinD
general	PotVar0070260	3	43921937	C/T	3.3	Plastid division regulator MinD
general	PotVar0120195	3	48350669	G/T	3.29	TF2B_KLULA
general	solcap_snp_c2_34002	6	32433877	C/T	3.06	Transcription initiation factor IIB
general	solcap_snp_c2_43093	6	37602254	A/G	4.75	Solyntus
general	PotVar0023392	8	56590329	A/G	3.18	scarecrow-like protein 8 LYS9_MAGGR
general	PotVar0023381	8	56624763	C/T	3.18	Saccharopine dehydrogenase [NADP+, L-glutamate-forming] (Saccharopine reductase)
general	PotVar0023148	8	56784173	A/G	3.18	Cystathionine gamma-synthase
general	PotVar0012114	9	3315213	A/G	3.14	Granule-bound starch synthase 1, chloroplastic/amyloplastic
general	solcap_snp_c2_4041	9	3689196	C/T	3.02	Arginine biosynthesis bifunctional protein ArgJ
general	PotVar0005644	10	56860555	A/G	3.03	beta chain
general	solcap_snp_c2_13473	11	922248	A/G	3.82	uncharacterized MYB domain class transcription factor
general	solcap_snp_c2_18855	12	51931824	A/G	3.95	uncharacterized oxidoreductase
additive	solcap_snp_c2_57176	1	16901062	A/G	3.05	At4g09670
additive	PotVar0122551	1	29683503	C/T	3.7	probable phospholipid-transporting ATPase 4
additive	PotVar0000060	1	32953922	A/G	3.05	importin-5-like
additive	solcap_snp_c1_14956	1	35477582	C/T	3.42	Regulator of chromosome condensation/beta-lactamase-inhibitor
additive	solcap_snp_c2_46540	1	35678032	C/T	3.88	protein II
additive	solcap_snp_c1_13816	1	35829489	A/G	3.13	Pentatricopeptide repeat-containing protein
additive	solcap_snp_c1_3693	1	36413189	A/C	3.34	boron transporter 1-like
additive	solcap_snp_c2_27680	1	37067730	C/T	3.44	zinc finger protein
additive	solcap_snp_c1_8534	1	37070639	C/T	3.53	VAR3, chloroplastic
additive	solcap_snp_c1_8541	1	37276804	C/T	3.44	30S ribosomal protein S1, chloroplastic-like
additive	solcap_snp_c2_54003	1	39325186	C/T	3.34	transcription factor
additive	solcap_snp_c1_11506	1	42861638	A/G	3.61	MYB108-like

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
additive	PotVar0095169	1	45757880	A/G	3.32	Phytochrome B
additive	solcap_snp_c2_35221	1	47297907	C/T	3.2	peroxidase 40
additive	solcap_snp_c2_35218	1	47299905	C/T	3.44	peroxidase 40
additive	solcap_snp_c2_14939	1	47761676	G/T	3.26	flowering time control protein FCA
additive	solcap_snp_c1_6485	1	67136074	C/T	3.25	beta-hexosaminidase 2 3-hydroxy-3- methylglutaryl-coenzyme A reductase 2
additive	solcap_snp_c1_15973	2	18501382	C/T	3.14	uncharacterized
additive	solcap_snp_c2_17816	2	36728587	A/G	3.12	60S ribosomal protein L10, mitochondrial
additive	PotVar0046627	2	36946881	A/G	3.33	Phytoene synthase 2
additive	PotVar0046766	2	36956651	A/G	3.33	Protease C56
additive	PotVar0046976	2	37015403	A/G	3.45	enhancer of polycomb- like protein 1
additive	solcap_snp_c2_42169	2	37438491	G/T	3.35	40S ribosomal protein S15-like
additive	solcap_snp_c2_42241	2	37676152	C/T	3.08	oxalate--CoA ligase-like
additive	solcap_snp_c1_9161	3	43024161	A/G	3.16	Plastid division regulator MinD
additive	PotVar0070248	3	43921286	G/T	3.66	GDP-mannose 4,6 dehydratase 1
additive	solcap_snp_c2_231	3	57934132	A/G	3.55	E3 ubiquitin-protein ligase SINAT5-like
additive	solcap_snp_c2_44375	5	44945205	C/T	3.25	protein SRC2-like
additive	solcap_snp_c2_37623	6	37560889	C/T	3.12	scarecrow-like protein 8
additive	solcap_snp_c2_43093	6	37602254	A/G	4.51	Beta-carotene hydroxylase
additive	PotVar0104776	6	37868566	C/T	3.12	short-chain type dehydrogenase/reductase- like
additive	solcap_snp_c2_8832	6	51913883	A/G	3.17	LYS9_MAGGR Saccharopine dehydrogenase [NADP+, L-glutamate-forming] (Saccharopine reductase)
additive	PotVar0023392	8	56590329	A/G	3.42	Cystathionine gamma- synthase
additive	PotVar0023381	8	56624763	C/T	3.42	Granule-bound starch synthase 1, chloroplastic/amyloplastic
additive	PotVar0023148	8	56784173	A/G	3.42	probable uridine nucleosidase 1
additive	solcap_snp_c2_54955	9	2931242	A/G	3.6	Arginine biosynthesis bifunctional protein ArgJ beta chain
additive	PotVar0012114	9	3315213	A/G	3.76	DM_SBEII
additive	PotVar0012538	9	3749280	A/G	3.08	OJ000223_09.10 protein
additive	PotVar0005644	10	56860555	A/G	3.12	Sucrose synthase
additive	PotVar0031147	12	3089924	C/T	3.01	zinc transporter 8-like
additive	solcap_snp_c2_42266	12	45024189	C/T	3.54	

***Score = List of data.frames, one for each trait. The data frame contains $-\log_{10}(P)$ results organized as markers x (additive) model (P values ≤ 0.001).**

4.5.12 Skin colour_L* coordinate (SCL)

Tuber skin colour is an important trait considered by the consumers while purchasing potatoes. It is also related to the several carotenoids and anthocyanin concentrations that contribute to human nutrition (Berdugo-Cely et al., 2017). Mapping of genomic regions associated with this trait can be helpful to select desirable skin colour of tubers in a breeding programme efficiently, without rigorous selection in the field. BLUPs calculated for SCL showed negatively skewed distribution as illustrated from the estimated BLUPs histogram. However, the scatter plot between SCL mean and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of SCL (Fig. 4.31). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

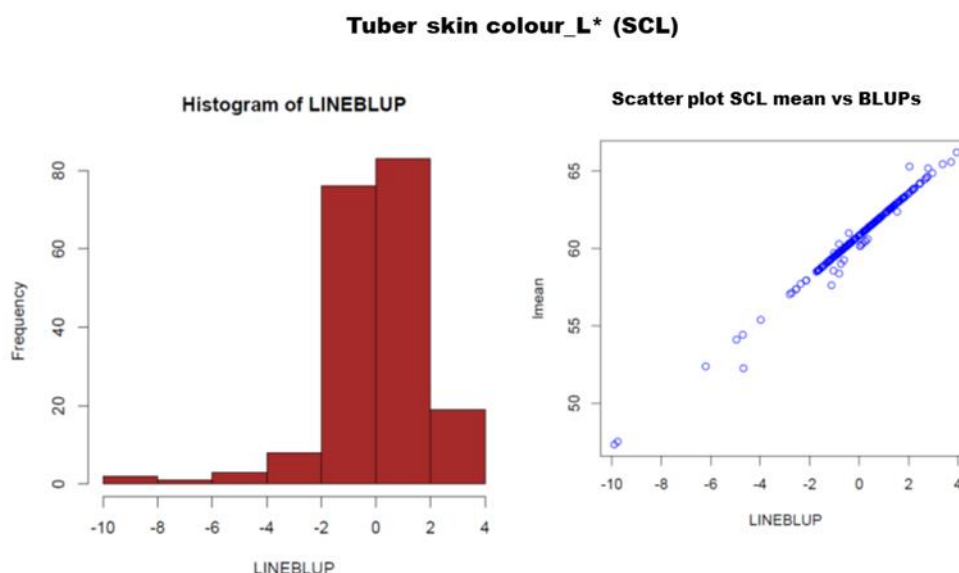


Figure 4.31. Histogram of LINEBLUPs for tuber skin colour L* SCL. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

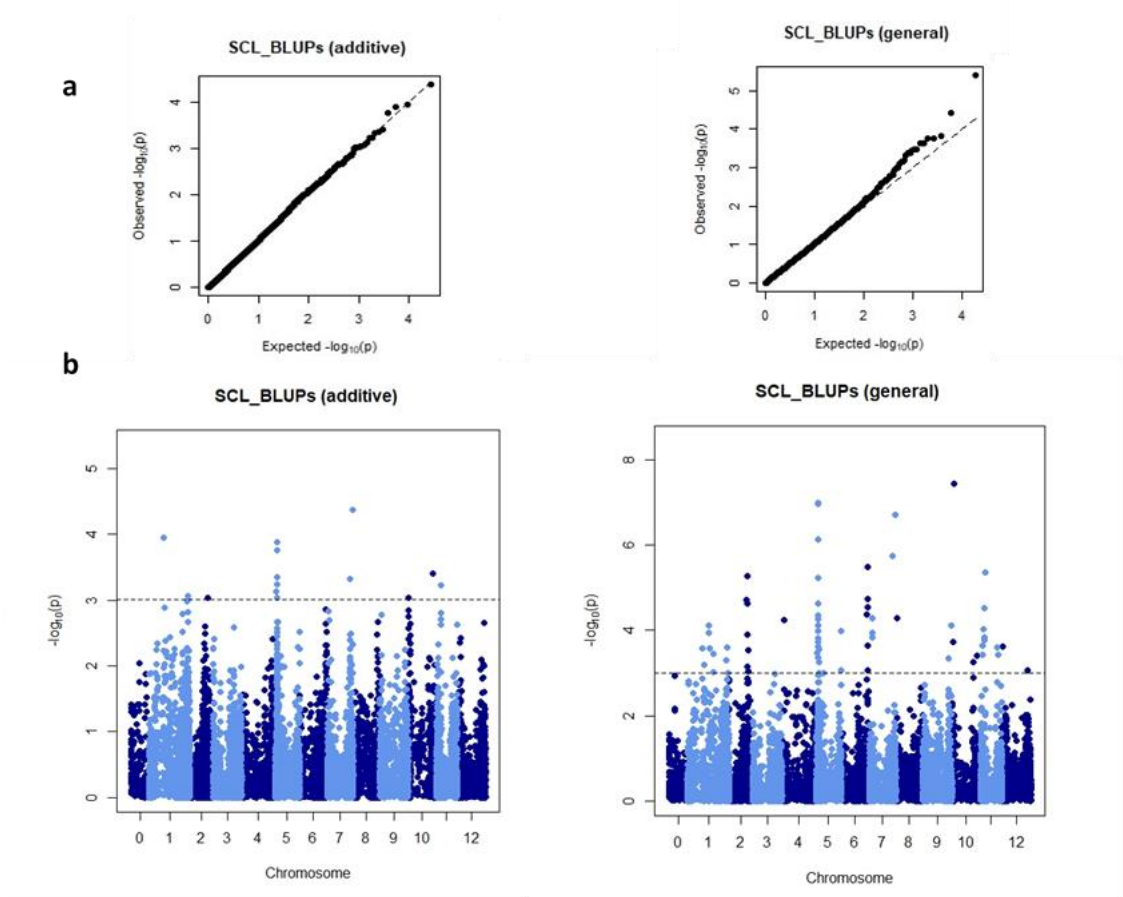


Figure 4. 32. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing SCL associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome.

Results of Q-Q plot for the SCL using additive model demonstrated that the observed vs expected p values were uniformly distributed as straight-line till $-\log_{10}(P)=3$. After that p values deviated indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviations were observed towards the normal at the tail. In general model, observed p values were also uniformly distributed with expected p values till $-\log_{10}(P)=2.5$, soon after the observed p values start deviating as sharp deviations were observed at the tail region (Fig. 4.32a). A sharp deviation in the tail region from the expected p values (i.e., at high $-\log_{10}(P\text{-values})$) establish that they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

Table 4.22. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber skin colour L* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_46231	1	32046995	C/T	3.59	protein kinase and PP2C-like domain-containing protein E3 ubiquitin-protein ligase
general	solcap_snp_c1_15961	1	36022417	A/G	3.18	UPL6
general	PotVar0095162	1	45757769	C/T	4.11	Phytochrome B
general	PotVar0095169	1	45757880	A/G	3.93	Phytochrome B peroxidase 40 (LOC102582765)
general	solcap_snp_c2_35220	1	47299582	A/G	3.57	
general	solcap_snp_c2_2872	1	55163541	C/T	3.45	TMV resistance protein N-like uncharacterized
general	solcap_snp_c2_55624	1	55426876	A/G	3.01	LOC102596256 endoplasmic reticulum-Golgi intermediate compartment protein 3-like
general	solcap_snp_c2_9791	1	81826022	A/C	3.29	
general	PotVar0035543	1	84053141	A/C	3.6	Tic21
general	PotVar0036159	1	85243972	A/G	3.01	Conserved gene of unknown function
general	PotVar0046416	2	36845853	A/C	4.71	Light-induced protein, chloroplastic
general	PotVar0046784	2	36956968	C/T	3.89	Phytoene synthase 2
general	PotVar0046936	2	36959370	A/G	3.14	Phytoene synthase 2
general	PotVar0047011	2	37015846	C/T	4.63	Protease C56 proteasome-like protein alpha subunit
general	solcap_snp_c2_55632	2	37474756	A/G	5.27	
general	PotVar0009827	2	40243261	A/G	3.54	Galactinol synthase
general	PotVar0009747	2	40251906	C/T	3.03	Endo-beta-mannanase
general	PotVar0101567	4	4925482	C/T	4.24	Conserved gene of unknown function
general	solcap_snp_c2_52084	5	1902218	A/C	3.46	aspartic proteinase nepenthesin-1
general	PotVar0025762	5	3817430	A/G	3.36	Fruit protein PKIWI502 (Di)nucleoside polyphosphate hydrolase
general	PotVar0026402	5	4337282	A/G	3.62	
general	PotVar0077897	5	4402263	C/T	3.62	Actin
general	PotVar0077965	5	4403822	A/C	3.74	Uridine cytidine kinase I
general	PotVar0078161	5	4410107	C/T	3.62	Actin
general	PotVar0078282	5	4413213	A/G	3.62	Actin
general	PotVar0078648	5	4432486	C/T	4.35	Actin
general	PotVar0078881	5	4442413	A/G	7	Actin

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0079044	5	4488591	C/T	6.97	Actin
general	PotVar0079086	5	4489590	A/C	5.23	Actin
general	PotVar0079450	5	4504555	A/G	6.13	Actin
general	PotVar0079478	5	4507537	A/G	4.26	Actin
general	PotVar0079559	5	4538967	C/T	4.11	Zinc finger protein
general	PotVar0079612	5	4541030	A/C	4.64	Zinc finger protein
general	PotVar0080186	5	4722081	A/G	3.82	Actin
general	PotVar0080614	5	4752243	A/G	3.98	Actin
general	PotVar0117267	5	5690944	C/T	3.55	Sucrose transporter
general	PotVar0117389	5	5693199	A/G	3.55	Sucrose transporter
general	solcap_snp_c1_14841	5	5693667	A/G	3.55	sucrose transport protein SUC3
general	PotVar0117438	5	5693945	C/T	3	Sucrose transporter
general	PotVar0117491	5	5694586	C/T	3.26	Sucrose transporter
general	PotVar0034560	5	51698390	C/T	3.99	Phenylalanine ammonia-lyase Arginine/serine-rich coiled coil protein
general	PotVar0034450	5	51893148	C/T	3.06	
general	PotVar0040287	6	53795163	A/G	4.37	Carbohydrate esterase
general	solcap_snp_c2_37350	6	56123395	A/G	4.54	Solyntus
general	solcap_snp_c2_28141	6	56290221	A/G	5.49	exocyst complex component EXO70A1-like
general	solcap_snp_c1_8673	6	56291313	C/T	3.06	exocyst complex component EXO70A1-like
general	solcap_snp_c2_28134	6	56315159	C/T	4.73	uncharacterized LOC102604525
general	solcap_snp_c2_50773	6	56878835	C/T	3.64	uncharacterized LOC102604525
general	PotVar0132505	7	7056259	C/T	4.29	26S proteasome subunit RPN7 xyloglucan
general	solcap_snp_c2_45800	7	7481006	C/G	3.94	endotransglucosylase/hydrolase protein 24-like
general	PotVar0097692	7	7481428	A/G	3.83	xyloglucan endotransglycosylase LeXET2
general	solcap_snp_c1_6228	7	49378419	G/T	5.74	ADP,ATP carrier protein 1, mitochondrial-like
general	solcap_snp_c2_18655	7	55207525	G/T	6.71	fimbrin-1
general	solcap_snp_c2_24403	8	3211341	A/G	4.3	beta-amylase 8 1,2-dihydroxy-3-keto-5- methylthiopentene dioxygenase
general	solcap_snp_c2_22041	9	54397297	C/T	3.35	1
general	PotVar0108663	9	59585980	G/T	4.12	NAD dependent epimerase
general	PotVar0104083	10	2646591	A/G	3.72	Glutathione S-transferase probable serine/threonine- protein kinase At1g54610
general	solcap_snp_c2_54140	10	3789697	A/G	7.45	

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0106287	10	45779117	C/T	3.25	Uncategorized
general	solcap_snp_c2_51204	10	52419848	C/T	3.4	Solyntus
general	solcap_snp_c2_6303	11	3943211	A/G	3.65	pullulanase 1, chloroplastic
general	solcap_snp_c2_6302	11	3943269	C/G	3.42	pullulanase 1, chloroplastic translation initiation factor
general	solcap_snp_c2_35856	11	7298363	A/C	4.03	eIF-2B subunit beta-like
general	solcap_snp_c2_12276	11	8651904	A/C	3.83	uncharacterized
general	solcap_snp_c1_3996	11	8660284	A/C	3.77	uncharacterized Pyruvate dehydrogenase E2 subunit
general	PotVar0059350	11	8822632	A/G	4.52	uncharacterized
general	solcap_snp_c2_29084	11	11081349	A/C	5.35	probable serine/threonine- protein kinase At5g41260
general	solcap_snp_c2_13591	11	35897776	A/G	3.59	Uncategorized
general	PotVar0111902	11	36668327	C/T	3.43	citrate synthase, glyoxysomal- like
general	solcap_snp_c2_25372	12	1324476	C/T	3.62	abscisic acid receptor PYL8- like
general	solcap_snp_c2_23235	12	53690152	A/C	3.05	protein kinase and PP2C-like domain-containing protein
additive	solcap_snp_c2_46231	1	32046995	C/T	3.94	protein TR11-like
additive	solcap_snp_c2_4608	1	83792878	A/G	3.01	Tic21
additive	PotVar0035543	1	84053141	A/C	3.06	probable E3 ubiquitin ligase SUD1
additive	solcap_snp_c1_1599	1	84246267	A/G	3.01	Phytoene synthase 2
additive	PotVar0046936	2	36959370	A/G	3.03	aspartic proteinase
additive	solcap_snp_c2_52084	5	1902218	A/C	3.13	nepenthesin-1
additive	solcap_snp_c2_11899	5	3776286	C/T	3.76	protein DETOXIFICATION 14-like
additive	PotVar0025762	5	3817430	A/G	3.88	Wall-associated kinase
additive	PotVar0026032	5	3876317	C/T	3.23	Membrane associated ring finger 1,8
additive	PotVar0078518	5	4419418	C/T	3.04	Actin
additive	PotVar0079086	5	4489590	A/C	3.35	Actin
additive	solcap_snp_c1_6228	7	49378419	G/T	3.32	ADP,ATP carrier protein 1, mitochondrial-like
additive	solcap_snp_c2_18655	7	55207525	G/T	4.36	not characterized
additive	solcap_snp_c2_1475	10	1121595	A/G	3.03	ethylene-responsive transcription factor 3-like
additive	solcap_snp_c2_51204	10	52419848	C/T	3.4	not characterized
additive	solcap_snp_c2_29087	11	11085125	C/T	3.23	chlorophyllide a oxygenase, chloroplastic-like

***Score = List of data.frames, one for each trait. The data frame contains -log10(P) results organized as markers x (additive) model (P values ≤ 0.001).**

Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general models using BLUPs. The additive model exhibited 16 significant SNPs associated with SCL positioned on chromosomes 1, 2, 5, 7, 10 and 11 (Fig. 4.32b). Out of 16, 6 SNPs were located on chr 5 with putative gene function linked with aspartic proteinase nepenthesin-1 (solcap_snp_c2_52084), protein DETOXIFICATION 14-like (solcap_snp_c2_11899), wall-associated kinase (PotVar0025762), membrane associated ring finger 1,8 (PotVar0026032) and Actin (PotVar0078518 and PotVar0079086). Contrarily, the general model indicated 71 significant SNPs linked with SCL. These SNPs were located on all chromosomes except 3. Interestingly 24 out 71 SNPs were positioned on chr 5. It entails that genes located on chr 5 have a possible connection with tuber skin colour (Table 4.22). Previous studies showed that genomic regions associated with skin colour were present on chromosomes 1, 4, 5, 7, 8, 10, 11 and 12 (Zia et al. 2020). Moreover, most of the identified SNPs have putative gene function as actin. This protein filament is involved in cell proliferation and protein synthesis, present in tuber skin or periderm (Barel and Ginzberg, 2008). Phytoene synthase encoding genes (*IbPSY1*) are group of carotenoids derived phytohormone playing vital role in carotenoid biosynthetic pathway in sweet potato (Shao et al., 2018). In our study, genes carrying these SNPs were present on chr 2 (36.95 Mbp) as detected by both models. Berdugo-Cely et al. (2017) reported that chromosomes 2 (25.05 Mbp), 7 (53.65 Mbp) and 10 (58.43 Mbp) were associated with tuber skin colour. The study highlighted the importance of SNPs located on chromosome 5 with a putative gene function of sucrose transport, besides a positive correlation was observed between sucrose and skin colour ($r=0.181^{**}$). Genes regulating sucrose transport (*StSUT1*, *StSUT2*) were involved in the transport and accumulation of sucrose from source to sink in potato (Chincinska et al., 2008). Sucrose also regulates and promotes carotenoid and anthocyanin biosynthesis in plants by upregulation of *PSY* genes (first gene involved in carotenoid biosynthesis) (Duran-Soria et al., 2020). The loci associated with this gene in our study indicates that genes regulating sucrose transport cross talk with carotenoid biosynthesis and affects the tuber skin colour. Ethylene-responsive transcription factors associated SNPs coordinate in stress signalling pathways (Heyman et al., 2018). Chlorophyllide a oxygenase (CAO) gene was involved in chlorophyll biosynthesis and associated with DEGs (differentially expressed genes) imparting green colour to cucumber skin (Wang et al., 2020).

4.5.13 Skin colour b^* coordinate (SCb)

Skin colour b^* coordinate was highly correlated with skin colour L^* coordinate. BLUPs calculated for SCb showed normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between SCb mean and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of SCb (Fig. 4.33). Q-Q plots were drawn between the observed and expected negative log (P) values across all markers for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

Results of Q-Q plot for the SCb using additive model demonstrated that the observed vs expected p values were uniformly distributed as straight-line till $-\log_{10}(P)=3$. After that p values deviated indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviations were observed towards the normal at the tail. In general model, observed p values were also uniformly distributed with expected p values till $-\log_{10}(P)=2$, soon after the observed p values start deviating as sharp deviations were observed at the tail region (Fig. 4.34a). A sharp deviation in the tail region from the expected p values (i.e., at high $-\log_{10}(P\text{-values})$) establish that they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

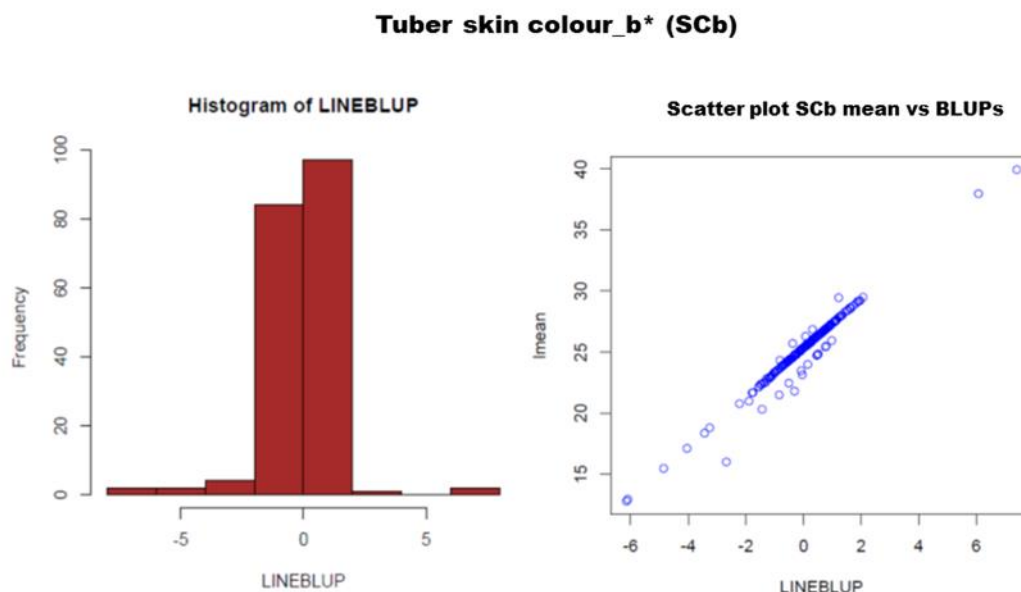


Figure 4.33. Histogram of LINEBLUPs for tuber skin colour b* (SCb). Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general model using BLUPs (Fig. 4.34b). The additive model revealed 7 significant SNPs associated with SCb, positioned on chromosomes 3, 4, 5, 6, 7 and 12 (Table 4.23). These SNPs include PotVar0085809 (alpha amylase), PotVar0000619 (argininosuccinate lyase), PotVar0000514 (argininosuccinate lyase), solcap_snp_c2_52084 (aspartic proteinase nepenthesin-1), PotVar0040287 (carbohydrate esterase), solcap_snp_c2_18655 (fimbrin-1) and PotVar0018388 (pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha). Skin of potato contain important enzymes such as carbohydrate esterase and pyrophosphate--fructose 6-phosphate 1-phosphotransferase, which were involved in glycolysis and sucrose breakdown (Barel and Ginzberg, 2008; Nakamura et al., 2017).

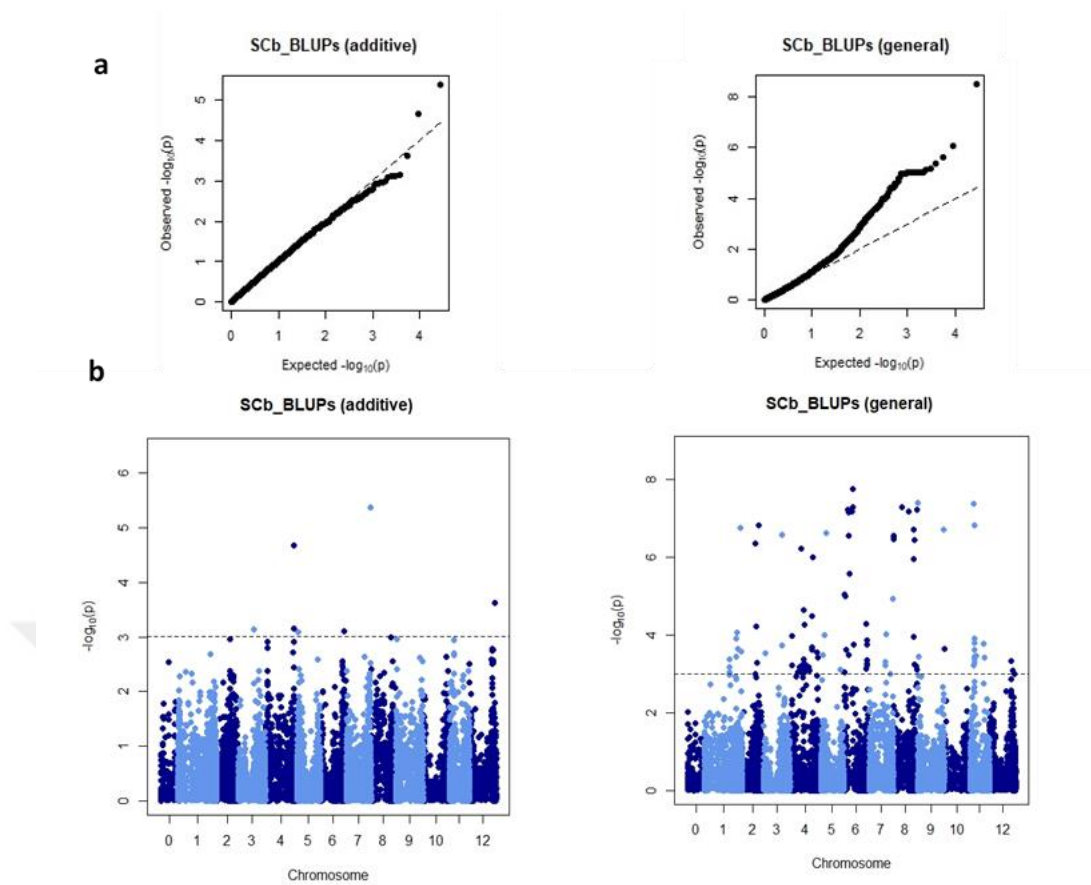


Figure 4.34. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing SCb associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Table 4.23. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber skin colour b^* coordinate along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_2723	1	58196772	A/G	3.17	protein SRC2-like
general	solcap_snp_c1_805	1	58567030	C/T	3.03	uncharacterized
general	solcap_snp_c1_779	1	58903714	A/C	3.36	proline-rich receptor-like
general	solcap_snp_c1_16401	1	73906470	A/G	3.91	protein kinase PERK15
general	PotVar0041585	1	74389555	C/T	3.44	homeobox-leucine zipper
general	PotVar0042709	1	75845003	G/T	4.06	protein ATHB-12
general	PotVar0029278	1	78346645	C/T	3.63	Gene trap locus 3
general	solcap_snp_c2_4909	1	83419073	A/G	6.75	VAP27-2
general	PotVar0036159	1	85243972	A/G	3.57	Conserved gene of unknown function

Model	Markers	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0082493	2	30396949	G/T	6.36	D1 protease
general	PotVar0094132	2	31350493	C/T	4.22	histidinol dehydrogenase
general	PotVar0038601	2	34813551	G/T	3.28	WD-repeat protein isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial-like
general	solcap_snp_c2_53035	2	38688398	A/G	6.83	1, mitochondrial-like
general	solcap_snp_c1_8974	3	5657114	A/G	3.54	protein BRICK 1 sec-independent protein
general	solcap_snp_c1_4444	3	43602976	C/T	6.58	translocase protein TATB Plastid division regulator
general	PotVar0070281	3	43922329	C/T	3.73	MinD
general	PotVar0100773	4	4578851	G/T	3.98	Pre-mRNA splicing factor Conserved gene of
general	PotVar0101567	4	4925482	C/T	3.22	unknown function
general	PotVar0082668	4	17527781	C/T	3.04	AFLP ADP-ribosylation factor 2-like
general	solcap_snp_c2_38247	4	21441266	A/G	3.18	VHS domain-containing protein At3g16270
general	solcap_snp_c1_859	4	26534587	A/G	6.22	protein At3g16270
general	PotVar0093363	4	27505089	C/T	3.01	AFLP 24 kDa vacuolar protein
general	PotVar0073742	4	28849480	A/G	3.12	VP24 protein SUPPRESSOR OF GENE SILENCING 3
general	solcap_snp_c2_32904	4	29010157	C/T	3.23	protein SUPPRESSOR OF GENE SILENCING 3
general	solcap_snp_c1_9837	4	29012392	C/T	3.1	OF GENE SILENCING 3
general	solcap_snp_c2_43763	4	29614371	C/T	3.07	uncharacterized
general	PotVar0007732	4	30717354	A/C	4.64	Alpha-glucosidase vacuolar protein sorting- associated protein 53 A
general	solcap_snp_c2_10460	4	32402884	C/T	3.38	two-component response regulator-like PRR37
general	solcap_snp_c1_3444	4	32777626	G/T	3.04	vesicle transport protein
general	solcap_snp_c2_58366	4	34230472	G/T	4.26	SFT2B ER membrane protein
general	solcap_snp_c2_37598	4	34826074	A/G	3.18	complex subunit 10 ER membrane protein
general	solcap_snp_c2_37596	4	34826609	A/G	3.23	complex subunit 10
general	solcap_snp_c2_41106	4	35757952	G/T	3.17	uncharacterized Acyl carrier protein (ACP)
general	PotVar0014800	4	36302675	A/C	3.18	uncharacterized
general	solcap_snp_c2_19423	4	36304058	A/G	3.18	uncharacterized
general	solcap_snp_c1_5081	4	37928038	A/G	3.18	uncharacterized DNA mismatch repair protein MLH1
general	solcap_snp_c2_33294	4	42331610	C/T	3.18	mismatch repair protein
general	solcap_snp_c2_33295	4	42353384	C/T	3.18	uncharacterized
general	solcap_snp_c1_15042	4	44312537	A/G	3.1	ASPARAGINE SYNTHETASE
general	PotVar0076141	4	50828150	A/C	4.48	SYNTHETASE
general	solcap_snp_c2_39847	4	50884547	C/T	3.62	uncharacterized
general	solcap_snp_c2_39848	4	50884571	G/T	3.69	uncharacterized

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_45035	4	53671782	C/T	5.99	cytochrome P450 CYP736A12-like
general	PotVar0071171	4	62419849	A/G	3.56	60S ribosomal protein L30
general	PotVar0000514	4	65000751	A/C	3.43	Argininosuccinate lyase
general	PotVar0078881	5	4442413	A/G	3.48	Actin
general	PotVar0079044	5	4488591	C/T	3.49	Actin
general	PotVar0085459	5	8808396	A/G	4	Pantothenate kinase family protein
general	PotVar0014564	5	11043844	A/G	6.62	Multidrug resistance protein 1, 2
general	PotVar0033952	5	43926714	C/T	3.1	Conserved gene of unknown function
general	solcap_snp_c2_53250	6	1801624	A/G	3.04	tetratricopeptide repeat protein 7A-like
general	solcap_snp_c2_27596	6	3153996	A/G	5.04	ran-binding protein 1 homolog a
general	solcap_snp_c2_27571	6	3469120	A/G	5.01	phosphomethylpyrimidine synthase
general	solcap_snp_c2_47002	6	6445075	C/T	3.62	putative pentatricopeptide repeat- containing protein
general	solcap_snp_c2_17377	6	10240158	A/G	7.21	At1g12700 mucin-1-like
general	solcap_snp_c2_17380	6	11038742	C/T	7.21	serine/threonine-protein phosphatase 6 regulatory subunit 3-like
general	solcap_snp_c2_26498	6	11223944	A/G	7.18	helicase protein MOM1- like
general	solcap_snp_c2_33105	6	12032376	A/C	3.48	pentatricopeptide repeat- containing protein At2g28050
general	PotVar0129007	6	12334133	A/G	7.16	Gene of unknown function
general	PotVar0086254	6	12568031	C/T	6.55	Uncategorized Gene of unknown function
general	PotVar0036584	6	14793319	A/G	5.58	probable magnesium transporter NIPA9
general	solcap_snp_c2_56793	6	20312642	A/G	7.18	Solyntus
general	solcap_snp_c1_16621	6	21067273	G/T	7.29	chaperone protein ClpB4, mitochondrial-like
general	solcap_snp_c2_33226	6	21482244	C/T	7.75	AP3-complex subunit
general	solcap_snp_c2_12402	6	23933179	C/T	3.74	beta-A probable protein S- acyltransferase 7
general	solcap_snp_c2_22388	6	53338313	C/T	4.28	uncharacterized COP9 signalosome
general	solcap_snp_c1_6997	6	53678569	A/G	3.13	complex subunit 5b-like
general	solcap_snp_c1_7005	6	53711466	C/T	3.75	Carbohydrate esterase
general	PotVar0040287	6	53795163	A/G	3.86	Biotin synthase
general	PotVar0039962	6	53985401	A/G	3.27	Biotin synthase
general	PotVar0039905	6	53988798	A/C	3.27	Biotin synthase

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0039697	6	54085434	A/C	3.23	Hyoscyamine 6-dioxygenase
general	solcap_snp_c2_24229	6	54218082	A/G	3.35	molybdopterin synthase catalytic subunit
general	solcap_snp_c1_506	7	37474267	C/T	3.31	uncharacterized
general	solcap_snp_c1_4465	7	38060656	A/G	3.21	uncharacterized
general	solcap_snp_c2_4459	7	39214976	C/T	4.02	uncharacterized
general	solcap_snp_c2_18655	7	55207525	G/T	4.94	fimbrin-1
general	solcap_snp_c1_8838	8	220082	C/T	6.54	uncharacterized
general	solcap_snp_c2_29043	8	494929	C/T	6.56	lactate dehydrogenase-2
general	solcap_snp_c2_29047	8	495260	A/G	6.47	dehydrogenase-2 (LDH-2)
general	PotVar0076370	8	19300737	G/T	7.28	Conserved gene of unknown function
general	solcap_snp_c2_49245	8	35651378	A/C	7.18	UDP-sulfoquinovose synthase, chloroplastic
general	solcap_snp_c2_51051	8	46390120	G/T	3.95	pectin acetyltransferase 8-AP-4 complex subunit
general	solcap_snp_c2_40295	8	47095975	C/T	5.95	epsilon
general	PotVar0103331	8	47376966	C/T	6.71	Carotenoid cleavage dioxygenase 4
general	solcap_snp_c2_28535	8	48171790	A/G	3.25	replication protein A 70 kDa DNA-binding subunit A-like
general	solcap_snp_c1_8769	8	48181310	C/T	6.43	uncharacterized
general	solcap_snp_c2_26631	8	53735510	A/G	3.21	PGR5-like protein 1A, chloroplastic
general	solcap_snp_c2_26655	8	54286342	C/T	7.21	osmotin-like protein OSML81
general	solcap_snp_c1_16495	8	54454507	C/T	3.11	protein LURP-one-related 4-like
general	solcap_snp_c2_3323	9	197357	A/G	7.41	uncharacterized
general	solcap_snp_c2_10956	9	2083608	C/G	3.43	eukaryotic translation initiation factor 3 subunit A-like
general	solcap_snp_c2_48041	9	59300365	C/T	6.7	beta-galactosidase 9
general	PotVar0065586	10	1098444	A/G	3.64	Transcription initiation factor ttfid
general	PotVar0065582	10	1098558	A/G	3.64	Transcription initiation factor ttfid
general	PotVar0059714	11	8972004	C/T	7.39	Sucrose transport protein
general	PotVar0059951	11	9057354	C/T	7.37	Sucrose transport protein
general	PotVar0060139	11	9379875	G/T	3.22	Nitrate reductase
general	solcap_snp_c2_33002	11	9631209	A/G	3.8	histone acetyltransferase of the MYST family 1-like
general	solcap_snp_c2_32999	11	9641316	C/T	3.62	histone acetyltransferase of the MYST family 1-like
general	solcap_snp_c2_33905	11	10681067	C/T	6.81	uncharacterized
general	solcap_snp_c2_33916	11	10773884	A/G	3.37	aminoacylase-1

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_29087	11	11085125	C/T	3.29	chlorophyllide a oxygenase, chloroplastic-like
general	solcap_snp_c2_29088	11	11085137	A/G	3.45	calcium-dependent protein kinase 11-like
general	solcap_snp_c2_29113	11	11175174	A/G	3.91	calcium-dependent protein kinase 11-like
general	PotVar0054079	11	14222467	G/T	3.47	Protein MYG1
general	solcap_snp_c2_4274	11	31441035	C/T	3.77	50S ribosomal protein L13, chloroplastic
general	solcap_snp_c2_29434	11	32899879	C/T	3.42	D-lactate dehydrogenase [cytochrome], mitochondrial
general	PotVar0037409	12	50391990	A/C	3.34	Heat shock 70 kDa protein
general	solcap_snp_c1_11668	12	54234293	A/G	3.08	pathogenesis-related protein R major form
additive	PotVar0085809	3	36000780	C/T	3.13	Alpha amylase
additive	PotVar0000619	4	64996828	G/T	3.16	Argininosuccinate lyase
additive	PotVar0000514	4	65000751	A/C	4.67	Argininosuccinate lyase
additive	solcap_snp_c2_52084	5	1902218	A/C	3.09	aspartic proteinase
additive	PotVar0040287	6	53795163	A/G	3.11	nepenthesin-1
additive	solcap_snp_c2_18655	7	55207525	G/T	5.38	Carbohydrate esterase
additive	PotVar0018388	12	57600615	C/T	3.63	fimbrin-1
						Pyrophosphate--fructose 6-phosphate 1-phosphotransferase
						subunit alpha

***Score = List of data.frames, one for each trait. The data frame contains -log₁₀(P) results organized as markers x (additive) model (P values ≤ 0.001).**

General model detected 110 significant SNPs associated with skin colour b* coordinate, present on all chromosomes (Table 4.23). Some important SNPs with a putative gene function related to skin colour pigmentation includes PotVar0038601 (WD repeat protein), PotVar0103331 (Carotenoid cleavage dioxygenase), solcap_snp_c2_29087 (chlorophyllide a oxygenase), and solcap_snp_c1_7005 (COP9 signalosome complex subunit 5b-like). Remaining SNPs were present in the genes performing roles related to signalling, transcription factors and metabolic regulation. WD repeat gene (*StAN11*) was connected to anthocyanin accumulation in tubers (Li et al., 2014), while carotenoid cleavage dioxygenase (*StCCD4*) has been found to inversely regulate the carotenoid synthesis in potato (Bruno et al., 2015). Chlorophyllide a oxygenase (CAO) gene was involved in chlorophyll biosynthesis and associated with DEGs (differentially expressed genes) imparting green colour to cucumber skin (Wang et al., 2020). COP9 signalosome complex subunit encompasses the metabolism of several carotenoids and

phenylpropanoids (Wei et al., 2018). The causative loci linked with these genes were positioned on chromosomes 2, 6, 8 and 11.

4.5.14 Skin (periderm) thickness (PT)

Tuber skin is termed as periderm (outermost layer of tissues), which acts as a barrier to biotic and abiotic stress conditions owing to processes of suberization and lignification. It maintains the skin impermeability and integrity of tubers. Finding SNP markers associated with periderm helps in the understanding of various processes linked to periderm formation and aids in selection of genotypes with better cell wall reinforcement against excoriation, pathogen attack and dehydration. BLUPs calculated for periderm thickness (PT) showed normal distribution as illustrated from the estimated BLUPs histogram. The scatter plot between PT means and BLUPs exhibited less scattering and thus explains an enhanced estimated predictive accuracy of BLUPs estimated across four environmental conditions. A fitted linear regression line showed strong relationship between BLUPs and mean of PT (Fig. 4.35). Q-Q plots were drawn between the observed and expected negative log (P) values for checking the validation of both models (additive and general) whether they control false positives, population stratification and family structure.

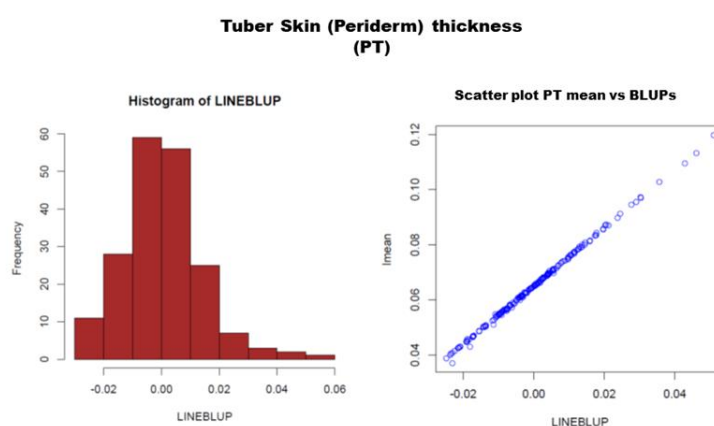


Figure 4.35. Histogram of LINEBLUPs for tuber skin (periderm) thickness. Scatter plot comparing estimated LINEBLUPs with mean of each genotype across all four environments (“LINE” here represents the genotypes included in the study)

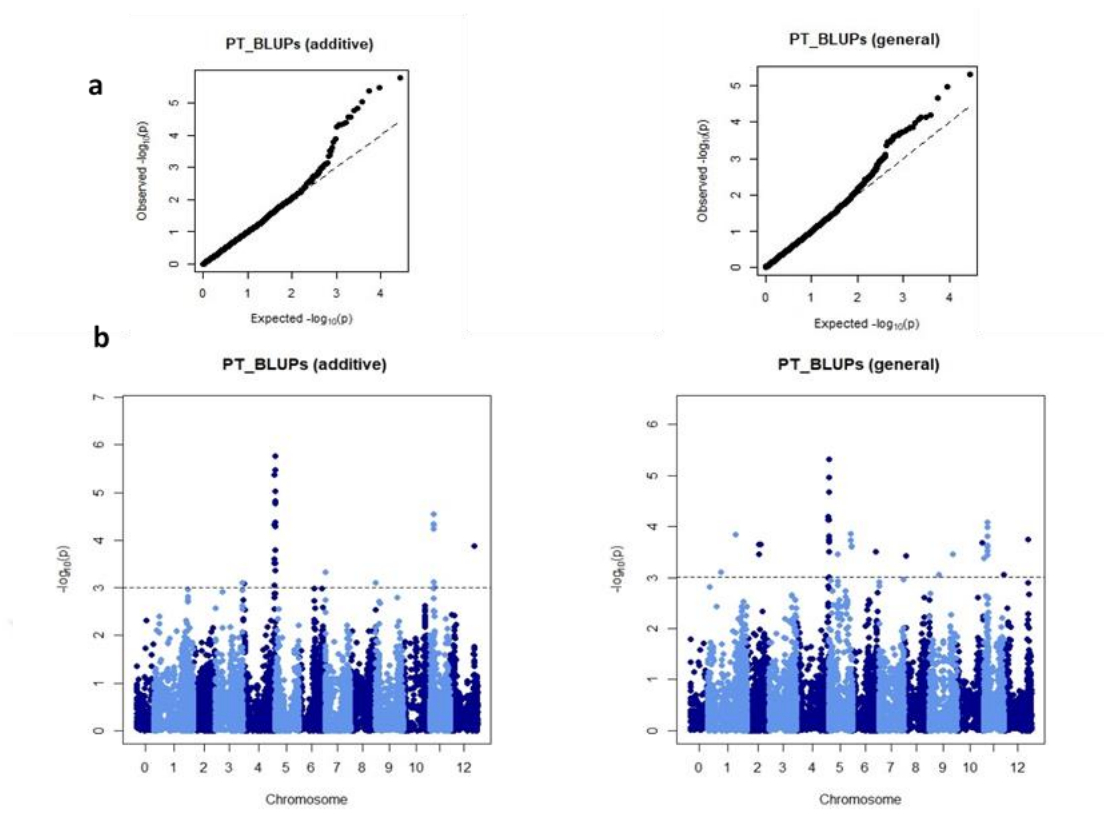


Figure 4.36. Q-Q plots of observed vs expected p values (a) Manhattan plots of threshold ($-\log_{10}(P) \geq 3$; $P \leq 0.001$) vs chromosomal location of SNP markers with additive and general models, showing periderm thickness (PT) associated SNPs from multi-environment BLUP estimates in the association mapping panel (b). Note: 0 refers to unmapped chromosome

Table 4.24. List of SNP variant (Ref/Alt), chromosome number and position (bp) of each identified significant SNP associated with the tuber skin (periderm) thickness along with their respective scores* (threshold: $-\log_{10}(P) \geq 3.23$; $P \leq 0.001$) and gene annotation

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0122473	1	29682264	A/G	3.11	Regulator of chromosome condensation/beta-lactamase-inhibitor protein II
general	PotVar0049334	1	62802628	C/T	3.85	WRKY transcription factor IIe-1
general	solcap_snp_c2_45308	2	27086756	C/T	3.64	Uncharacterized
general	PotVar0124248	2	27090334	C/T	3.45	Taz protein cation-chloride cotransporter 1
general	solcap_snp_c2_39107	2	29486591	A/G	3.65	receptor protein kinase
general	solcap_snp_c1_10714	4	70953672	A/T	4.13	CLAVATA1
general	solcap_snp_c1_3553	4	71359551	A/G	4.19	rop guanine nucleotide exchange factor 1-like
general	solcap_snp_c2_10799	4	71383530	A/C	5.31	L-ascorbate oxidase homolog

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	PotVar0016678	4	71428746	A/C	3.51	Scythe/bat3
general	PotVar0016791	4	71527582	A/G	3.74	Transducin family protein
general	PotVar0017410	4	71814632	A/G	4.68	Glutamate receptor 3 plant 3-hydroxy-3- methylglutaryl-coenzyme
general	solcap_snp_c2_10565	4	71955746	C/G	3	A reductase 1-like 3-hydroxy-3- methylglutaryl-coenzyme
general	solcap_snp_c1_3478	4	71956738	A/G	3.7	A reductase 1-like Pyrophosphate--fructose 6-phosphate 1- phosphotransferase
general	PotVar0017705	4	72026758	C/T	4.13	subunit alpha Pyrophosphate--fructose 6-phosphate 1- phosphotransferase
general	PotVar0017726	4	72027082	A/G	3.82	subunit alpha BZIP transcription factor
general	PotVar0017827	4	72031303	C/T	4.97	protein
general	solcap_snp_c1_15537	5	20390896	A/G	3.46	Uncharacterized
general	PotVar0082125	5	48662379	A/G	3.74	Phytochrome B2 DNA repair-
general	PotVar0123086	5	49243440	A/G	3.86	recombination protein
general	PotVar0034964	5	50252105	G/T	3.61	TSC13 protein
general	PotVar0034718	5	51320755	A/C	3.61	Flowering locus T protein protein EXECUTER 2,
general	solcap_snp_c2_8796	6	52275971	G/T	3.5	chloroplatic 1-aminocyclopropane-1-
general	solcap_snp_c2_30052	8	4911088	A/T	3.43	carboxylate synthase U-box domain-containing
general	solcap_snp_c1_16737	9	20846686	C/T	3.06	protein 9 U-box domain-containing
general	solcap_snp_c1_16738	9	20846752	C/T	3.06	protein 9 Multidrug resistance-
general	PotVar0101691	9	52570600	C/T	3.46	associated protein 2, 6 (Mrp2, 6), abc-transoprtter
general	solcap_snp_c2_42928	10	56673770	G/T	3.69	KHG/KDPG aldolase-like
general	Plocus_F35H_a1_LG11	11	0	C/T	3.37	NA
general	Plocus_F35H_a2_LG11	11	0	A/G	3.37	NA
general	PotVar0059350	11	8822632	A/G	3.45	Pyruvate dehydrogenase E2 subunit
general	PotVar0059554	11	8969994	C/T	3.81	Parallel spindle 1
general	PotVar0059581	11	8970321	A/G	4.09	Parallel spindle 1 Pyruvate dehydrogenase
general	PotVar0059692	11	8971755	G/T	3.61	E2 subunit Pyruvate dehydrogenase
general	PotVar0059736	11	8972279	A/G	3.53	E2 subunit
general	PotVar0059796	11	9052541	A/C	3.98	Sucrose transport protein
general	PotVar0059889	11	9055871	C/T	3.63	Sucrose transport protein Homogentisate 1,2-
general	PotVar0098373	12	364404	C/T	3.05	dioxygenase

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
general	solcap_snp_c2_39410	12	54234680	A/G	3.75	pathogenesis-related protein R major form
additive	PotVar0020426	3	61494119	C/T	3.11	Lipase class 3 protein zinc finger CCH
additive	solcap_snp_c2_45927	4	3562172	A/G	3.09	domain-containing protein receptor protein kinase
additive	solcap_snp_c1_10714	4	70953672	A/T	4.33	CLAVATA1
additive	solcap_snp_c1_10712	4	70954662	C/T	3.6	receptor protein kinase CLAVATA1
additive	PotVar0016251	4	71221277	A/G	3.06	CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa)
additive	PotVar0016254	4	71221298	A/G	3.53	CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa)
additive	solcap_snp_c1_3553	4	71359551	A/G	5.38	rop guanine nucleotide exchange factor 1-like
additive	solcap_snp_c2_10799	4	71383530	A/C	5.76	L-ascorbate oxidase homolog
additive	PotVar0016678	4	71428746	A/C	4.78	Scythe/bat3
additive	PotVar0016791	4	71527582	A/G	3.79	Transducin family protein
additive	PotVar0017410	4	71814632	A/G	5.04	Glutamate receptor 3 plant
additive	solcap_snp_c2_10565	4	71955746	C/G	3.51	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1-like
additive	solcap_snp_c1_3478	4	71956738	A/G	4.37	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1-like
additive	solcap_snp_c2_10546	4	72023252	A/G	4.29	Solyntus
additive	PotVar0017705	4	72026758	C/T	4.82	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha
additive	PotVar0017726	4	72027082	A/G	3.36	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha
additive	PotVar0017827	4	72031303	C/T	5.48	BZIP transcription factor protein
additive	PotVar0022719	7	637671	A/G	3.33	CBL-interacting serine/threonine-protein kinase
additive	solcap_snp_c2_3345	9	169527	C/T	3.11	protein argonaute 16-like
additive	solcap_snp_c2_11351	11	8968466	C/T	3.13	protein SENSITIVE TO PROTON
additive	PotVar0059554	11	8969994	C/T	4.56	RHIZOTOXICITY 1
additive	PotVar0059581	11	8970321	A/G	4.55	Parallel spindle 1
additive	PotVar0059692	11	8971755	G/T	4.33	Parallel spindle 1
						Pyruvate dehydrogenase E2 subunit

Model	Marker	Chrom	Position	Ref/Alt	Score	Gene Annotation
additive	PotVar0059736	11	8972279	A/G	4.25	Pyruvate dehydrogenase E2 subunit
additive	PotVar0059889	11	9055871	C/T	4.35	Sucrose transport protein
additive	solcap_snp_c2_29084	11	11081349	A/C	3.01	filament-like plant protein pathogenesis-related
additive	solcap_snp_c2_39410	12	54234680	A/G	3.88	protein R major form

****Score = List of data.frames, one for each trait. The data frame contains -log10(P) results organized as markers x (additive) model (P values ≤ 0.001).***

Results of Q-Q plot for the periderm thickness using additive and general models demonstrated that the observed vs expected p values were normally or uniformly distributed as straight-line till $-\log_{10}(P)=2.5$ in both models. After that p values deviated indicating the presence of significant marker-trait associations. The p values were controlled by the model as sharp deviations were observed towards the normal at the tail (Fig. 4.36a). A sharp deviation in the tail region from the expected p values (i.e., at high $-\log_{10}(P\text{-values})$) establish that they are in LD with casual polymorphism and produce significant marker-trait associations avoiding both false positives and false negatives (Stich et al., 2008; Kristensen et al., 2018; Kaler et al., 2020).

Manhattan plots were created by employing MLM in *GWASpoly* R with additive and general models using BLUPs (Fig. 4.36b). The additive model showed that 27 significant SNPs were associated with periderm thickness located on chr 3 (61.4 Mbp), chr 4 (3.5 Mbp, 70.95-72.03 Mbp), chr 7 (0.63 Mbp), chr 9 (0.16 Mbp), chr 11 (8.96-9.05 Mbp) and chr 12 (54.2 Mbp) (Table. 4.24). Out of 27 SNPs, a large agglomerative group of 16 SNPs were positioned on chr 4 showing that SNPs within the genes present on this chromosome have strong association with periderm thickness. The SNPs found in the candidate genes performed putative functional roles related to zinc finger CCCH domain-containing protein, receptor protein kinase CLAVATA1, CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa), rop guanine nucleotide exchange factor 1-like, L-ascorbate oxidase homolog, scythe/bat3, transducin family protein, glutamate receptor 3 plant, 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1-like, Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha and BZIP transcription factor protein. Wounding and abiotic stress conditions promotes the synthesis of suberin, a layer deposited in the periderm for protection against water loss and environmental stress. bZIP transcription factors are known to be involved in suberin biosynthesis in kiwi fruit

through abscisic acid (ABA) signalling pathways (Han et al., 2019). Transcriptome profiling of heat stress related transcriptomes in the periderm of potato revealed that zinc finger proteins are mainly expressed in the phellem tissues (a layer of periderm) under stress conditions (Ginzberg et al., 2009). Rey et al. (1998) showed that CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) accumulated in various tissues of potato in response to water deficit conditions. Drought environment was one of the treatments in the current study, these results endorse that the genomic region between 70.95-72.03 Mbp located on chr 4 is responsible for stress alleviated response in the periderm tissues of potato tuber. Furthermore, pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha (PFase) is involved in sucrose synthesis, glycolysis and starch metabolism in starchy crops like rice and potato (Chen et al., 2020). SNP marker solcap_snp_c2_39410 was detected at chr 12 linked with periderm thickness having a plausible function as pathogenesis-related protein R major form. This protein is involved in signal transduction during wounding and pathogenesis (Goyal et al., 2016).

General model detected 38 significant SNP markers associated with periderm thickness positioned on all chromosomes except 3 and 7 (Table 4.24). General model revealed that 11 SNPs were present on chr 4 similar to additive model. Besides, 17 associated SNPs were shared by both models present in the genes performing vital functional roles in the periderm as stated above. The proteome of potato skin is enriched with defence components. WRKY transcription factors are involved in plant defence signalling pathways, and cation-chloride cotransporter 1 (CCC1) provides resistance against *Pseudomonas syringae* (Han et al., 2020). The genes performing such putative functional roles contain the SNPs associated with periderm thickness on chr 1 (62.80 Mbp) and chr 2 (29.48 Mbp), respectively as disclosed by the general model. SNP (PotVar0123086) was present in the gene located on chr 5 (49.24 Mbp) with a putative function of DNA repair-recombination protein. Vulavala et al. (2019) stated that DNA and RNA related processes are responsible for periderm formation and maturation. The identified SNP on chr 5 might be responsible for DNA repair mechanisms in periderm. Tuber bruising related diagnostic markers were present on chr 2, chr 3 and chr 8 (Urbany et al., 201). We identified SNPs related to periderm thickness on chr 2 and chr 3. GWAS was not performed for the periderm thickness in the past, the current study provides valuable insights for the associated markers at several chromosomes along with their gene annotation, especially those located on chr 4.

CHAPTER V

CONCLUSION

The methodology of association mapping was initially developed for human genetics. Later the developments in the germplasm resources of plants and advancements in plant genomics courtesy to high-throughput sequencing methods made available the complete genome sequence in most plant species and potato has no exception. Genome sequencing in potato (Potato Genome Sequencing Consortium, 2011) and genotyping studies conducted by Hamilton et al. (2011) and Uitdewilligen et al. (2013) efficiently revolutionized the utilization of association mapping technique in potato. The current study was conducted with an objective to identify SNP markers associated with tuber quality traits in diverse panel of 192 genotypes utilizing the technique of association mapping. Promising SNP markers were detected which were found to be associated with all twelve important tuber quality traits. Tuber quality is a polygenic trait and controlled by complex genetic factors as well as GEI (Genotype by environment interaction). GEI analysis was performed and stable genotypes were detected for each tuber quality trait.

Stability and GEI analysis

Significant differences ($P < 0.01$) were observed among genotypes, environments and genotype by environment interactions. Konya standard water conditions was found to be the best stable environment, while drought conditions affected all tuber quality characteristics and showed a deviated behaviour. Drought conditions decreases starch contents, beta carotene, total antioxidant activity, total phenolics and causes the flesh colour to shift from yellow to white. It might be due to less accumulation of carotenoids and phenolic compounds under water stress. An increase in skin thickness under drought conditions might be attributed to the processes of suberization and wax deposition under stress environment. High accumulation of sucrose and free asparagine was noted under drought environment. Both these attributes are undesirable for processing industry.

The current study concluded the comparative efficacy of both seasand and hydrometer methods in contrast to oven-dry method for the measurement of tuber dry matter content (TDM). The seasand was found to be an accurate, destructive method but offers some

limitations in terms of laborious and time consuming. Alternatively, hydrometer was considered as an automated, non-destructive, cheap and speedy method to calculate TDM of large number of tuber samples. Nevertheless, it requires approximately 2500 g of clean raw tubers with minimum of 4-5 replications per sample

Finlay and Wilkinson (1963) stability and adaptability model revealed stable genotypes for each trait. These candidate genotypes would be exploited for further molecular studies and serve as a useful resource for breeding of processing and improved quality cultivars.

Association mapping

Genotyping of association mapping panel of 192 diverse genotypes were done with SolCAP 25K potato array, which includes tetraploid SNPs and utilizes ILMN'S (Illumina) new Genome Studio tetraploid calling. Tetraploid allelic combinations from nulliplex to quadriplex, with a total of diverse 21226 markers were obtained for each genotype. Population structure of 192 potato genotypes were evaluated based on 13606 (64.10%) polymorphic and robust SNP markers obtained after removing monomorphic markers (35.90%) by adopting filtering approach with minor allele frequency (MAF) > 0.05 and missing data $\leq 10\%$. The population structure was found to be diverse with four clusters, which could be either due to systemic variations in allele frequencies or differences in sample ancestry. A careful estimation of population structure and kinship was done to avoid spurious marker-trait associations during association mapping study. Linkage disequilibrium is a major principle of association mapping, and thus the results concludes that a proposed marker data set showed LD decay at around 2.31 Mbps to an r^2 threshold value of 0.29. A part of LD was preserved and found with linkage within 2 Mbps depicting no recombination.

Association mapping study was performed utilizing two gene action models i.e., additive and general in *GWASpoly* R package. SNPs associated with various quality traits were present on several chromosomes. The localization of SNPs on several chromosomes might be due to the polygenic nature of our traits, influenced by minor genes.

Dry matter content and specific gravity

Tuber dry matter content (DMC) was mainly associated with SNP markers located on chr 1 (83.2-84.7 Mbp), chr 5 (4.42-4.70 Mbp) and chr 11 (41.4-41.8). These SNPs were associated with genes of vital functions such as transcriptional regulation of starch biosynthesis in potato tubers. Allele oxide synthase genes (*StAOS2*) carry SNP (PotVar0008281) detected on chr 11 linked with DMC. It was found to be responsible for the biosynthesis of jasmonates and involve in potential defence signalling against pathogens such as late blight, soft rot and black leg in potato. Both gene action models detected SNPs on chr 5 and 11.

SNPs associated with tuber specific gravity (SG) were mainly present on chr 1, chr 5 and chr 11 similar to those observed for DMC. 21 pleiotropic SNPs were detected commonly associated with both DMC and SG. It strongly supports the idea that DMC and SG are synonymous terms, as the latter estimates the dry matter contents of tubers. A pleiotropic SNP (PotVar0031068) was identified at chr 12 (3.08 Mbp) associated with both DMC and SG with putative gene function of sucrose synthase. Sucrose synthase enzyme (*SuSy*) is a major determinant of sink strength in potato tubers, channelling the conversion of sucrose to complex polysaccharides such as starch.

Reducing sugars and sucrose

SNPs associated with reducing sugars and sucrose were detected on several chromosomes but important SNPs for both traits were located on chr 7. These SNPs have plausible functions related to sucrose phosphate synthase and arabinose kinase involved in sugar signalling and signal transduction pathways. COP9 signalosome complex subunit was associated with carbohydrate metabolism and SNP linked with it was present on chr 7. The study suggested that chr 7 is important for regulation and metabolism of sucrose and reducing sugars.

Free asparagine

Promising SNP markers were associated with free asparagine located on chromosomes 1, 2, 3, 4, 5, 6, 10 and 11. A major SNPs based on gene annotation was detected on chr 3 and chr 4 involved in regulation and metabolism of asparagine.

Tuber starch contents

In case of tuber starch contents, SNP markers associated with tuber starch contents were present on all chromosomes except 7, 8 and 9. SNPs located on chr 4 and 6 were of prime importance due to their role in regulation and metabolism of carbohydrate such as sucrose synthesis and breakdown, starch degradation and glycolysis.

Beta-carotene

An important SNP (PotVar0070281) linked with β -carotene was identified in our study. It was present on chr 3 and genes containing that particular SNP has a putative function related to *beta-carotene hydroxylase*. Beta carotene hydroxylase 2 is referred to as *bch* or *chy2*, and literature revealed that this gene is responsible for converting white tuber flesh colour to yellow and mapped on Y locus of chr 3 in potato. Besides, chr 2 and chr 4 also carry important SNPs associated with beta carotene which are part of genes involved in signalling pathways for biosynthesis of carotenoids.

Total antioxidant activity

An important SNPs were detected in current study positioned on chr 7 and chr 11 associated with total antioxidant activity. These SNPs were present in the genes of crucial amino-acids involved in antioxidant activity and includes bHLH transcription factor playing vital role in anthocyanin and flavonoid biosynthetic pathways in potato.

Total phenolic contents

The important SNPs linked to total phenolics were mainly present on chr 1 and 3. Gene annotation of those SNPs revealed that they act as transporters and perform signal

transduction during stress conditions. It might be due to the important role of phenolics as secondary metabolites to alleviate stress.

Tuber flesh colour

The SNP “PotVar0070281” was associated with both beta-carotene and tuber flesh colour L* detected on chr 3, hence termed as pleiotropic SNP marker. The current findings and available literature, suggested that chr 3 is linked with biological variation of tuber flesh colour. Moreover, yellow flesh colour in potato is mainly due to the presence of beta-carotene, positioned on chr 3 with loci position at 43.92 Mbp. Important SNP markers linked with tuber flesh colour L* was located on chr 5 having plausible gene function of phytochrome B2 related to the detection of far-red and red light, transcriptional regulation of photoreceptor activity in potato. Another associated SNP on chr 2 was present in genes of WD repeat protein consisting of MYB transcription factors involved in synthesis of anthocyanins in tuber. Similar SNPs were detected in flesh colour b* coordinate present in the genes involved that contains transcription factors like MYB (chr 1, 10) and zinc finger proteins (chr 1) regulating polyphenolic biosynthetic pathways and involve in stress signalling.

Tuber skin colour

The SNPs related to tuber skin colour were located on all chromosomes except 3. Important tuber skin colour associated SNPs were detected on chr 2 having a putative gene function of phytoene synthase encoding genes (*lPSY1*). These are group of carotenoids derived phytohormone playing vital role in carotenoid biosynthetic pathway in sweet potato. Chromosome 11 contains important SNPs in the genes of chlorophyllide a oxygenase (CAO) involved in chlorophyll biosynthesis and associated with DEGs (differentially expressed genes) imparting green colour to cucumber skin. These SNPs are of prime value due to their link with skin colour in plant species. Some important SNPs with a putative gene function related to skin colour pigmentation includes PotVar0038601 (WD repeat protein), PotVar0103331 (Carotenoid cleavage dioxygenase), solcap_snp_c2_29087 (chlorophyllide a oxygenase), and solcap_snp_c1_7005 (COP9 signalosome complex subunit 5b-like). COP9 signalosome complex subunit encompasses the metabolism of several carotenoids and

phenylpropanoids. The causative loci linked with these SNPs were positioned on chromosomes 2, 6, 8 and 11.

Tuber skin (periderm) thickness

A large agglomerative group of 16 SNPs were positioned on chr 4 showing that SNPs within the genes present on this chromosome have strong association with periderm thickness. The proteome of potato skin is enriched with defence components such as bZIP transcription factors and zinc finger proteins involved in suberin biosynthesis through abscisic acid (ABA) signalling pathways and mainly expressed in the phellem tissues (a layer of periderm) under stress conditions. Genomic region between 70.95-72.03 Mbp located on chr 4 is responsible for stress alleviated response in the periderm tissues of potato tuber and also responsible for periderm formation and maturation as indicated by gene annotation.

Comparison of additive and general gene action models for significant SNP associations

Altogether 215 significant SNPs were detected in additive model, while the general model suggested the presence of 430 significant SNPs associated with twelve important tuber quality traits. Gene action in polyploid crops especially tetraploid potato is of great importance. According to Ferrao et al. (2018) general model was the best as it takes into account the arbitrary gene actions, whereas Rosyara et al. (2016) obtained high statistical power with additive model. Nevertheless, the statistical power of gene action models depends upon the population size and number of markers used for GWAS analysis. In our study, both additive and general model controls false positives and population stratification as evident from the uniform distribution of observed vs expected *p* values, however the general model in some traits showed non-uniform behaviour. It might be due to the non-normal distribution of data and presence of outliers due to extreme values in some genotypes for a particular trait contributed by their performance across fluctuating environments. This ultimately contributes to genotype $\times$ marker effect. Since general model takes into consideration the effect of each individual genotypic class as arbitrary and statistically equivalent, it is more sensitive to the presence of outliers in data. Whereas, additive model anticipates the minor allele dosage. SNPs detected in both

models are valid as Rosyara et al. (2016) reported QTLs associated with vine maturity using both additive and general models. To my observation, Q-Q plot is the best deciding factor for delineating the associations in both models. Secondly, the gene annotation studies of associated SNPs will further help in the identification of true marker-trait association avoiding false positives. Future studies pertaining to the development of selection markers using allele specific KASP marker validation will be a breakthrough approach for marker assisted breeding of tuber quality traits.



REFERENCES

AACC (American Association of Cereal Chemistry)., “Approved method (Moisture-drying on quartz sand)”, *The Association* St. Paul, MN, 44-60, 1993a.

AACC (American Association of Cereal Chemistry)., “Approved method (Moisture-air oven methods)”, *The Association* St. Paul, MN, 44-15A, 1993b.

Achenbach, U., Paulo, J., Ilarionova, E., Lübeck, J., Strahwald, J., Tacke, E., Hofferbert, H.R. and Gebhardt, C., “Using SNP markers to dissect linkage disequilibrium at a major quantitative trait locus for resistance to the potato cyst nematode *Globodera pallida* on potato chromosome V”, *Theoretical and Applied Genetics* 118, 619, 2009.

Affleck, I., Sullivan, J.A., Tarn, R. and Falk, D.E., “Genotype by environment interaction effect on yield and quality of potatoes”, *Canadian Journal of Plant Science* 88, 1099-1107, 2008.

Afonnikov, D.A., Totsky, I.V. and Stasevski, Z., “Informational resources on potato germplasm collections”, *Vavilovskii Zhurnal Genetiki i Seleksii* 22, 115-121, 2018.

Ah-Hen, K., Fuenzalida, C., Hess, S., Contreras, A., Vega-Gálvez, A. and Lemus-Mondaca, R., “Antioxidant capacity and total phenolic compounds of twelve selected potato landrace clones grown in Southern Chile”, *Chilean Journal of Agricultural Research* 72, 3, 2012.

Aksenova, N.P., Konstantinova, T.N., Lozhnikova, V.N., Golyanovskaya, S.A., Gukasyan, I.A., Gatz, C. and Romanov, G.A., “Photoperiodic and hormonal control of tuberization in potato plants transformed with the PHYB gene from *Arabidopsis*”, *Russian Journal of Plant Physiology* 52, 623-628, 2005.

Albishi T., John J.A., Al-Khalifa A.S. and Shahidi F., “Phenolic content and antioxidant activities of selected potato varieties and their processing by-products”, *Journal of Functional Foods* 5, 590-600, 2013.

Allison, D.B., “Transmission-disequilibrium tests for quantitative traits”, ***American Journal of Human Genetics*** 60, 676, 1997.

Alqudah, A.M., Sallam, A., Baenziger, P.S. and Börner, A., “GWAS: Fast-forwarding gene identification and characterization in temperate Cereals: lessons from Barley–A review”, ***Journal of Advanced Research*** 22, 119-135, 2020.

Al-Weshahy, A. and Rao, A.V., “Isolation and characterization of functional components from peel samples of six potatoes varieties growing in Ontario”, ***Food Research International*** 42, 1062-1066, 2009.

Andre, C.M., Oufir, M., Guignard, C., Hoffmann, L., Hausman, J.F., Evers, D. and Larondelle, Y., “Antioxidant profiling of native Andean potato tubers (*Solanum tuberosum* L.) reveals cultivars with high levels of β -carotene, α -tocopherol, chlorogenic acid, and petanin”, ***Journal of Agricultural and Food Chemistry*** 55, 10839-10849, 2007.

Andrivon D., “Potato facing global challenges: how, how much, how well?” ***Potato Research*** 60, 389-400, 2017.

Anithakumari, A.M., Tang, J., van Eck, H.J., Visser, R.G.F., Leunissen, J.A.M., Vosman, B., van der Linden, C.G., “A pipeline for high throughput detection and mapping of SNPs from EST databases”, ***Molecular Breeding*** 26, 65-75, 2010.

Araus, J.L. and Cairns, J.E., “Field high-throughput phenotyping: the new crop breeding frontier”, ***Trends in Plant Science*** 19, 52-61, 2014.

Asmamaw, Y., Tekalign T. and Workneh. T.S., “Specific gravity, dry matter concentration, pH, and crisp-making potential of Ethiopian potato (*Solanum tuberosum* L.) cultivars as influenced by growing environment and length of storage under ambient conditions”, ***Potato Research*** 53, 95-109, 2010.

Aversano, R., Contaldi, F., Ercolano, M. R., Grosso, V., Iorizzo, M., Tatino, F. and Carputo, D., “The *Solanum commersonii* genome sequence provides insights into

adaptation to stress conditions and genome evolution of wild potato relatives”, *The Plant Cell* 27, 954-968, 2015.

Baldwin, S.J., Dodds, K.G., Auvray, B., Genet, R.A., Macknight, R.C. and Jacobs, J.M.E. Association mapping of cold-induced sweetening in potato using historical phenotypic data. *Annals of Applied Biology* 158, 248-256, 2011.

Barel, G. and Ginzberg, I., “Potato skin proteome is enriched with plant defence components”, *Journal of Experimental Botany* 59, 3347-3357, 2008.

Barker, L., Kühn, C., Weise, A., Schulz, A., Gebhardt, C., Hirner, B., Hellmann, H., Schulze, W., Ward, J.M. and Frommer, W.B., “A sucrose transporter homolog in sieve elements is a candidate gene for QTLs controlling starch and yield”, *The Plant Cell* 12, 1153-1164, 2000.

Baroja-Fernández, E., Muñoz, F.J., Montero, M., Etxeberria, E., Sesma, M.T., Ovecka, M., Bahaji, A., Ezquer, I., Li, J., Prat, S. and Pozueta-Romero, J. “Enhancing sucrose synthase activity in transgenic potato (*Solanum tuberosum* L.) tubers results in increased levels of starch, ADPglucose and UDPglucose and total yield”, *Plant and Cell Physiology* 50, 1651-1662, 2009.

Bates, D., Maechler, M. and Bolker, B., “Walker., S. Fitting linear mixed-effects models using *lme4*. *Journal of Statistical Software*”, 67, 1-48, 2015.

Bentley, D.R., Balasubramanian, S., Swerdlow, H.P., Smith, G.P., Milton, J., Brown, C.G., Hall, K.P., Evers, D.J., Barnes, C.L., Bignell, H.R. and Boutell, J.M., “Accurate whole human genome sequencing using reversible terminator chemistry,” *Nature* 456, 53-59, 2008.

Berdugo-Cely, J., Valbuena, R.I., Sánchez-Betancourt, E., Barrero, L.S. and Yockteng, R., “Genetic diversity and association mapping in the Colombian Central Collection of *Solanum tuberosum* L. Andigenum group using SNPs markers”, *PloS one* 12, e0173039, 2017.

Bethke, P.C., Sabba, R. and Bussan, A.J., “Tuber water and pressure potentials decrease and sucrose contents increase in response to moderate drought and heat stress”, ***American Journal of Potato Research***, 86, 519, 2009.

Biswas, A. K., Sahoo, J. and Chatli, M.K., “A simple UV-Vis spectrophotometric method for determination of β -carotene content in raw carrot, sweet potato and supplemented chicken meat nuggets”, ***LWT-Food Science and Technology*** 44, 1809-1813, 2011.

Björn, B., Keizer, P. L., Paulo, M.J., Visser, R. G., van Eeuwijk, F.A. and van Eck, H.J., “Identification of agronomically important QTL in tetraploid potato cultivars using a marker-trait association analysis”, ***Theoretical and Applied Genetics*** 127, 731-748, 2014.

Björn, B., Paulo, M. J., Mank, R. A., Van Eck, H. J. and Van Eeuwijk, F.A., “Association mapping of quality traits in potato (*Solanum tuberosum* L.)”, ***Euphytica*** 161, 47-60, 2008.

Björn, B., Paulo, M.J., Kowitwanich, K., Sengers, M., Visser, R.G., van Eck, H.J. and van Eeuwijk, F.A., “Population structure and linkage disequilibrium unravelled in tetraploid potato”, ***Theoretical and Applied Genetics*** 121, 1151-1170, 2010.

Boamponsem, G.A., Leung, D.W. and Lister, C., “Relationships among iron deficit-induced potato callus growth inhibition, Fe distribution, chlorosis, and oxidative stress amplified by reduced antioxidative enzyme activities”, ***Plant Cell, Tissue and Organ Culture (PCTOC)***, 132, 393-412, 2018.

Bonierbale, M., Grüneberg, W., Amoros, W., Burgos, G., Salas, E., Porras, E. and zum Felde, T., “Total and individual carotenoid profiles in *Solanum phureja* cultivated potatoes: II. Development and application of near-infrared reflectance spectroscopy (NIRS) calibrations for germplasm characterization”, ***Journal of Food Composition and Analysis*** 22, 509-516, 2009.

Bonierbale, M.W., Plaisted, R.L. and Tanksley, S.D., “RFLP maps based on a common set of clones reveal modes of chromosomal evolution in potato and tomato. ***Genetics*** 120, 1095-1103, 1988.

Bradbury, P.J., Zhang, Z., Kroon, D.E., Casstevens, T.M., Ramdoss, Y. and Buckler, E.S., “TASSEL: software for association mapping of complex traits in diverse samples”, *Bioinformatics* 23, 2633-2635, 2007.

Bradeen, J.M., Haynes, K.G. and Kole, C., “Introduction to potato”, *Genetics, Genomics and Breeding of Potato* 1-19, 2011.

Bradshaw, J.E. and Ramsay, G., “Utilisation of the Commonwealth Potato Collection in potato breeding”, *Euphytica* 146, 9-19, 2005.

Bradshaw, J.E., Hackett, C.A., Pande, B., Waugh, R. and Bryan, G.J., “QTL mapping of yield, agronomic and quality traits in tetraploid potato (*Solanum tuberosum* subsp. *tuberosum*)”, *Theoretical and Applied Genetics* 116, 193-211, 2008.

Brown, C.R., Kim, T.S., Ganga, Z., Haynes, K., De Jong, D., Jahn, M., Paran, I., De Jong, W., “Segregation of total carotenoid in high level potato germplasm and its relationship to beta-carotene hydroxylase polymorphism”, *American Journal of Potato Research* 83, 365-372, 2006.

Bruno, M., Beyer, P. and Al-Babili, S., “The potato carotenoid cleavage dioxygenase 4 catalyzes a single cleavage of β -ionone ring-containing carotenes and non-epoxidated xanthophylls”, *Archives of Biochemistry and Biophysics* 572, 126-133, 2015.

Brush, S., Kesseli, R., Ortega, R., Cisneros, P., Zimmerer, K. and Quiros, C., “Potato diversity in the Andean center of crop domestication”, *Conservation Biology* 9, 1189-1198, 1995.

Burgos, G., Auqui, S., Amoros, W., Salas, E. and Bonierbale, M., “Ascorbic acid concentration of native Andean potato varieties as affected by environment, cooking and storage”, *Journal of Food Composition and Analysis*, 22, 533-538, 2009.

Burlingame, B., Mouillé, B. and Charrondiere, R., “Nutrients, bioactive non-nutrients and anti-nutrients in potatoes”, *Journal of Food Composition and Analysis* 22, 494-502, 2009.

Byrne, S., Meade, F., Mesiti, F., Griffin, D., Kennedy, C. and Milbourne, D., “Genome-Wide Association and Genomic Prediction for Fry Color in Potato”, *Agronomy* 10, 90, 2010.

Çalışkan, M. E., Onaran, H. and Arioğlu, H., “Overview of the Turkish potato sector: challenges, achievements and expectations”, *Potato Research* 53, 255-266, 2010.

Camire, M. E., Kubow, S. and Donnelly, D.J., “Potatoes and human health”, *Critical Reviews in Food Science and Nutrition* 49, 823-840, 2009.

Campbell, R., Pont, S.D., Morris, J.A., McKenzie, G., Sharma, S. K., Hedley, P. E. and Taylor, M.A., “Genome-wide QTL and bulked transcriptomic analysis reveals new candidate genes for the control of tuber carotenoid content in potato (*Solanum tuberosum* L.). *Theoretical and Applied Genetics* 127, 1917-1933, 2014.

Cao, D., Damaris, R.N., Zhang, Y., Liu, M., Li, M. and Yang, P., “Proteomic analysis showing the signaling pathways involved in the rhizome enlargement process in *Nelumbo nucifera*”, *BMC Genomics* 20, 766, 2019.

Carputo, D. and L. Frusciante., “Classical genetics and traditional breeding”, In Genetics, genomics and breeding of potato (ed. James M. Bradeen and Chittaranjan Kole), Enfield: *Science Publishers* 20-40, 2011.

Chang, C.Y., Jin, J.D., Chang, H.L., Huang, K.C., Chiang, Y.F. and Hsia, S.M., “Physicochemical and Antioxidative Characteristics of Potato Protein Isolate Hydrolysate”, *Molecules* 25, 4450, 2020.

Chawla, R., Shakya, R. and Rommens, C.M., “Tuber-specific silencing of asparagine synthetase-1 reduces the acrylamide-forming potential of potatoes grown in the field without affecting tuber shape and yield”, *Plant Biotechnology Journal* 10, 913-924, 2012.

Chen, C., He, B., Liu, X., Ma, X., Liu, Y., Yao, H.Y., Zhang, P., Yin, J., Wei, X., Koh, H.J. and Yang, C., “Pyrophosphate-fructose 6-phosphate 1-phosphotransferase (PFP 1) regulates starch biosynthesis and seed development via heterotetramer formation in rice (*Oryza sativa* L.). **Plant Biotechnology Journal** 18, 83-95, 2020.

Chen, X., Salamini, F. and Gebhardt, C., “A potato molecular-function map for carbohydrate metabolism and transport. **Theoretical and Applied Genetics** 102, 284-295, 2001.

Chincinska, I.A., Liesche, J., Krügel, U., Michalska, J., Geigenberger, P., Grimm, B. and Kühn, C., “Sucrose transporter *StSUT4* from potato affects flowering, tuberization, and shade avoidance response”, **Plant Physiology** 146, 515-528, 2008.

Chun, O.K., Kim, D.O., Smith, N., Schroeder, D., Han, J.T. and Lee, C.Y., “Daily consumption of phenolics and total antioxidant capacity from fruit and vegetables in the American diet”, **Journal of the Science of Food and Agriculture** 85, 1715-1724, 2005.

Cruz, A.B., Bianchetti, R.E., Alves, F.R.R., Purgatto, E., Peres, L.E.P., Rossi, M. and Freschi, L., “Light, ethylene and auxin signaling interaction regulates carotenoid biosynthesis during tomato fruit ripening”, **Frontiers in Plant Science** 9, 1370, 2018.

De Haan, S., Burgos, G., Liria, R., Rodriguez, F., Creed-Kanashiro, H. and Bonierbale, M., “The Nutritional Contribution of Potato Varietal Diversity in Andean Food Systems: a Case Study”, **American Journal of Potato Research** 96, 151, 2019.

De Jong, H., “Inheritance of pigmented tuber flesh in cultivated diploid potatoes”, **American Potato Journal** 64, 337-343, 1987.

De Jong, W.S., De Jong, D.M., De Jong, H., Kalazich, J., Bodis, M., “An allele of dihydroflavonol 4-reductase associated with the ability to produce red anthocyanin pigments in potato (*Solanum tuberosum* L.)”, **Theoretical and Applied Genetics** 107, 1375-1383, 2003.

De Vleeschouwer, K., Van der Plancken, I., Van Loey, A. and Hendrickx, M.E., “Role of precursors on the kinetics of acrylamide formation and elimination under low moisture conditions using a multiresponse approach–Part II: Competitive reactions”, **Food Chemistry** 114, 535-546, 2009.

Devaux, A., Goffart, J.P., Petsakos, A., Kromann, P., Gatto, M., Okello, J. and Hareau, G., “Global Food Security, Contributions from Sustainable Potato Agri-Food Systems”, In *The Potato Crop* (pp. 3-35). **Springer**, Cham, 3-35, 2020.

Devaux, A., Kromann, P. and Ortiz, O., “Potatoes for sustainable global food security”, **Potato Research** 57, 185-199, 2014.

Dhingani, R.M., Umrana, V.V., Tomar, R.S., Parakhia, M.V. and Golakiya, B., “Introduction to QTL mapping in plants”, **Annals of Plant Sciences** 4, 1072-1079, 2015.

Dong, H., Wang, R., Yuan, Y., Anderson, J., Pumphrey, M., Zhang, Z. and Chen, J., “Evaluation of the potential for genomic selection to improve spring wheat resistance to Fusarium head blight in the Pacific Northwest”, **Frontiers in Plant Science** 9, 911, 2018

Douches, D.S., Maas, D., Jastrzebski, K. and Chase, R.W., “Assessment of potato breeding progress in the USA over the last century”, **Crop Science** 36, 1544-1552, 1996.

Duarte-Delgado, D., Núñez-López, C.E., Narváez-Cuenca, C.E., Restrepo-Sánchez, L.P., Melo, S.E., Sarmiento, F., Kushalappa, A.C. and Mosquera-Vásquez, T., “Natural variation of sucrose, glucose and fructose contents in Colombian genotypes of *Solanum tuberosum* Group Phureja at harvest”, **Journal of the Science of Food and Agriculture** 96, 4288-4294, 2016

Duran-Soria, S., Pott, D.M., Osorio, S. and Vallarino, J.G., “Sugar Signaling During Fruit Ripening”, **Frontiers in Plant Science**, 11, 564917, 2020.

Earl, D.A., “STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method”, **Conservation Genetics Resources** 4, 359-361, 2012.

Earl, D.A., “STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources* 4, 359-361, 2012.

Ek, K.L., Brand-Miller, J. and Copeland, L., “Glycemic effect of potatoes”, *Food Chemistry* 133, 1230-1240, 2012.

Ellis, D., Chavez, O., Coombs, J., Soto, J., Gomez, R., Douches, D. and Anglin, N.L., “Genetic identity in genebanks: application of the SolCAP 12K SNP array in fingerprinting and diversity analysis in the global in trust potato collection”, *Genome* 61, 523-537, 2018.

Escuredo, O., Seijo-Rodríguez, A., González-Martín, M.I., Rodríguez-Flores, M.S. and Seijo, M.C., “Potential of near infrared spectroscopy for predicting the physicochemical properties on potato flesh”, *Microchemical Journal* 141, 451-457, 2018.

Evanno, G., Regnaut, S. and Goudet, J., “Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study”, *Molecular Ecology* 14, 2611-2620, 2005.

FAOSTAT., “Statistical Division of the UN Food and Agriculture Organization of the United Nations”, <http://faostat.fao.org/>. accessed on 20 May 2020, 2020.

Felcher, K.J., Coombs, J.J., Massa, A.N., Hansey, C.N., Hamilton, J.P., Veilleux, R.E., Buell, C.R. and Douches, D.S., “Integration of two diploid potato linkage maps with the potato genome sequence”, *PloS one* 7, 36347, 2012.

Ferrão, L.F.V., Benevenuto, J., Oliveira, I.D.B., Cellon, C., Olmstead, J., Kirst, M., Resende Jr, M.F. and Munoz, P., “Insights into the genetic basis of blueberry fruit-related traits using diploid and polyploid models in a GWAS context”, *Frontiers in Ecology and Evolution* 6,107, 2018.

Finlay, K.W. and Wilkinson, G.N., “The analysis of adaptation in a plant-breeding programme”, *Australian Journal of Agricultural Research* 14, 742-754, 1963.

Fischer, M., Schreiber, L., Colby, T., Kuckenberg, M., Tacke, E., Hofferbert, H.R. and Gebhardt, C., “Novel candidate genes influencing natural variation in potato tuber cold sweetening identified by comparative proteomics and association mapping”, *BMC Plant Biology* 13, 113, 2013.

Flint-Garcia, S.A., Thornsberry, J.M. and Buckler IV, E.S., “Structure of linkage disequilibrium in plants”, *Annual Review of Plant Biology* 54, 357-374, 2003.

Fogelman, E., Oren-Shamir, M., Hirschberg, J., Mandolino, G., Parisi, B., Ovadia, R., Tanami, Z., Faigenboim, A. and Ginzberg, I., “Nutritional value of potato (*Solanum tuberosum*) in hot climates: anthocyanins, carotenoids, and steroidal glycoalkaloids”, *Planta* 249, 1143-1155, 2019.

Freyre, R. and Douches, D.S., “Development of a model for marker-assisted selection of specific gravity in diploid potato across environments”, *Crop Science* 34, 1361-1368, 1994.

Friedman, M., “Chemistry, biochemistry, and dietary role of potato polyphenols. A review”, *Journal of Agricultural and Food Chemistry* 45, 1523-1540, 1997.

Friedman, M., “Chemistry, biochemistry, and safety of acrylamide. A review”, *Journal of Agricultural and Food Chemistry* 51, 4504-4526, 2003.

Friedman, M., Lee, K. R., Kim, H. J., Lee, I. S. and Kozukue, N., “Anticarcinogenic effects of glycoalkaloids from potatoes against human cervical, liver, lymphoma, and stomach cancer cells”, *Journal of Agricultural and Food Chemistry* 53, 6162-6169, 2005.

Gauch, H.G. and Moran, D.R., “AMMISOFT for AMMI Analysis with Best Practices”, *BioRxiv* 1, 538454, 2019.

Gebhardt, C., “Molecular markers, maps and population genetics”, In Potato Biology and Biotechnology (pp. 77-89), **Elsevier Science BV**, 77-89, 2007.

Gebhardt, C., Menendez, C.M., Chen, X., Li, L., Schäfer-Pregl, R., Salamini, F., “Genomic approaches for the improvement of tuber quality traits in potato”, **Acta Horticulturae** 684, 85-92, 2005.

Ginzberg, I., Barel, G., Ophir, R., Tzin, E., Tanami, Z., Muddarangappa, T., De Jong, W. and Fogelman, E., “Transcriptomic profiling of heat-stress response in potato periderm”, **Journal of Experimental Botany** 60, 4411-4421, 2009.

Glendinning, D.R., “Potato Introductions and Breeding Up To the Early 20th Century”, **New Phytologist** 94, 479-505, 1983.

Goyal, R.K., Fatima, T., Topuz, M., Bernadec, A., Sicher, R., Handa, A.K. and Mattoo, A.K., “Pathogenesis-related protein 1b1 (*PR1b1*) is a major tomato fruit protein responsive to chilling temperature and upregulated in high polyamine transgenic genotypes”, **Frontiers in Plant Science** 7, 901, 2016.

Gupta, P.K., Rustgi, S. and Kulwal, P.L., “Linkage disequilibrium and association studies in higher plants: present status and future prospects”, **Plant Molecular Biology** 57, 461-485, 2005.

Haase, N.U., “Estimation of dry matter and starch concentration in potatoes by determination of under-water weight and near infrared spectroscopy”, **Potato Research** 46, 117-127 (2003)

Haase, N.U., “Prediction of potato processing quality by near infrared reflectance spectroscopy of ground raw tubers”, **Journal of Near Infrared Spectroscopy** 19, 37-45, 2011.

Hackett, C.A., Bradshaw, J.E. and Bryan, G.J., “QTL mapping in autotetraploids using SNP dosage information”, **Theoretical and Applied Genetics** 127, 1885-1904, 2014.

Hackett, C.A., McLean, K. and Bryan, G.J., “Linkage analysis and QTL mapping using SNP dosage data in a tetraploid potato mapping population”, *PLoS One* 8, 63939, 2013.

Hajirezaei, M.R., Biemelt, S., Peisker, M., Lytovchenko, A., Fernie, A.R. and Sonnewald, U., “The influence of cytosolic phosphorylating glyceraldehyde 3-phosphate dehydrogenase (GAPC) on potato tuber metabolism”, *Journal of Experimental Botany* 57, 2363-2377, 2006.

Hameed, A., Zaidi, S.S.E.A., Shakir, S. and Mansoor, S., “Applications of new breeding technologies for potato improvement”, *Frontiers in Plant Science* 9, 925, 2018.

Hamilton, J.P., Hansey, C.N., Whitty, B.R., Stoffel, K., Massa, A.N., Van Deynze, A. and Buell, C.R., “Single nucleotide polymorphism discovery in elite North American potato germplasm”, *BMC Genomics* 12, 1-12, 2011.

Hamouz K., Lachman J., Dvořák P., Jůzl M. and Pivec V., “The effect of site conditions, variety and fertilization on the content of polyphenols in potato tubers”, *Plant, Soil and Environment* 52, 407-412, 2006.

Han, B., Jiang, Y., Cui, G., Mi, J., Roelfsema, M.R.G., Mouille, G., Sechet, J., Al-Babili, S., Aranda, M. and Hirt, H., “CATION-CHLORIDE CO-TRANSPORTER 1 (CCC1) mediates plant resistance against *Pseudomonas syringae*”, *Plant Physiology* 182, 1052-1065, 2020.

Han, X., Mao, L., Lu, W., Wei, X., Ying, T. and Luo, Z., “Positive regulation of the transcription of AchnKCS by a bZIP transcription factor in response to ABA-stimulated suberization of kiwifruit”, *Journal of Agricultural and Food Chemistry* 67, 7390-7398, 2019.

Hardigan, M.A., Bamberg, J., Buell, C.R. and Douches, D.S., “Taxonomy and genetic differentiation among wild and cultivated germplasm of *Solanum* sect. *Petota*”, *The Plant Genome* 8, 1-16, 2015.

Hardigan, M.A., Laimbeer, F.P.E., Newton, L., Crisovan, E., Hamilton, J.P., Vaillancourt, B., Wiegert-Rininger, K., Wood, J.C., Douches, D.S., Farré, E.M. and Veilleux, R.E., “Genome diversity of tuber-bearing *Solanum* uncovers complex evolutionary history and targets of domestication in the cultivated potato”, ***Proceedings of the National Academy of Sciences*** 114, E9999-E10008, 2017.

Hawkes, J.G., “Origins of cultivated potatoes and species relationships”, In Potato genetics (ed. J.E. Bradshaw and G.R. Mackay), ***CAB International***, Wallingford, 3-42, 1994.

Hawkes, J.G., “The potato: evolution, biodiversity and genetic resources”, Belhaven Press, ***Smithsonian Institution Press*** Washington DC, USA, 1990.

Hejtmánková, K., Kotíková, Z., Hamouz, K., Pivec, V., Vacek, J. and Lachman, J., “Influence of flesh colour, year and growing area on carotenoid and anthocyanin content in potato tubers”, ***Journal of Food Composition and Analysis*** 32, 20-27, 2013.

Heyman, J., Canher, B., Bisht, A., Christiaens, F. and De Veylder, L., “Emerging role of the plant ERF transcription factors in coordinating wound defense responses and repair”, ***Journal of Cell Science*** 131, 2018.

Hijmans, R.J. and Spooner, D.M., “Geographic distribution of wild potato species”, ***American journal of Botany*** 88, 2101-2112, 2001.

Hijmans, R.J., Gavrilenko, T., Stephenson, S., Bamberg, J., Salas, A. and Spooner, D.M., “Geographical and environmental range expansion through polyploidy in wild potatoes (*Solanum* section *Petota*)”, ***Global Ecology and Biogeography*** 16, 485-495, 2007.

Hill, W.G. and Robertson, A., “Linkage disequilibrium in finite populations”, ***Theoretical and Applied Genetics*** 38, 226-231, 1968.

Huaman, Z. and Spooner, D.M., “Reclassification of landrace populations of cultivated potatoes (*Solanum* sect. *Petota*)”, ***American Journal of Botany*** 89, 947-965, 2002.

Huang, Y.C., Chang, Y.H. and Shao, Y.Y., “Effects of genotype and treatment on the antioxidant activity of sweet potato in Taiwan”, **Food Chemistry** 98, 529-538, 2006.

International Agency for Research on Cancer. “IARC monographs on the evaluation of carcinogenic risks to humans”, (pp. 389) **Some Industrial Chemicals** International Agency for Research on Cancer (IARC), Lyon, 1994.

Jacobs, J.M., van Eck, H.J., Horsman, K., Arens, P.F., Verkerk-Bakker, B., Jacobsen, E. and Stiekema, W.J., “Mapping of resistance to the potato cyst nematode *Globodera rostochiensis* from the wild potato species *Solanum vernei*”, **Molecular Breeding** 2, 51-60, 1996.

Jansen, G., Flamme, W., Schöler, K., Vandrey, M., “Tuber and starch quality of wild and cultivated potato species and cultivars”, **Potato Research** 44, 137-146, 2001.

Jansky, S., “Breeding for disease resistance in potato” **Plant Breed Reviews** 19, 69-155, 2000.

Jansky, S., “Overcoming hybridization barriers in potato”, **Plant Breeding** 125, 1-12, 2006.

Jansky, S.H. and Spooner, D.M., “The evolution of potato breeding”, **Plant Breeding Reviews** 41, 169-214, 2018.

Jin, H.J., Lee, J.H., Kim, K.T., Lee, G.W., Choi, S.J., Chang, P.S. and Paik, H.D., 2015. “Antioxidative and nitric oxide scavenging activity of branched-chain amino acids”, **Food Science and Biotechnology** 24, 1555-1558, 2015.

Jung, C.S., Griffiths, H.M., De Jong, D.M., Cheng, S., Bodis, M. and De Jong, W.S. “The potato P locus codes for flavonoid 3', 5'-hydroxylase”, **Theoretical and Applied Genetics** 110, 269-275, 2005.

Jung, C.S., Griffiths, H.M., De Jong, D.M., Cheng, S., Bodis, M., Kim, T.S. and De Jong, W.S., “The potato developer (D) locus encodes an R2R3 MYB transcription factor that

regulates expression of multiple anthocyanin structural genes in tuber skin”, ***Theoretical and Applied Genetics*** 120, 45-57, 2009.

Juzepczuk, S.W. and Bukasov. S.M., “A contribution to the question of the origin of the potato. Trudy Vsesoyuznogo S’zeda po Genetike i Selekcii Semenovodstvu i Plemennomu Zhivotnovodstvu”, ***Leningrad*** 3, 593–611, 1929.

Kaler, A.S., Gillman, J.D., Beissinger, T. and Purcell, L.C., “Comparing different statistical models and multiple testing corrections for association mapping in soybean and maize. ***Frontiers in Plant Science***, 10, 1794, 2020.

Kalita, D., Holm, D.G. and Jayanty, S.S., “Role of polyphenols in acrylamide formation in the fried products of potato tubers with colored flesh”, ***Food Research International*** 54, 753-759, 2013.

Kim, J., Soh, S.Y., Bae, H. and Nam, S.Y., “Antioxidant and phenolic contents in potatoes (*Solanum tuberosum* L.) and micropropagated potatoes”, ***Applied Biological Chemistry*** 62, 17, 2019.

Kim, S., Plagnol, V., Hu, T. T., Toomajian, C., Clark, R. M., Ossowski, S. and Nordborg, M., “Recombination and linkage disequilibrium in *Arabidopsis thaliana*. ***Nature Genetics*** 39, 1151-1155, 2007.

Klaassen, M.T., Willemsen, J.H., Vos, P.G., Visser, R.G., van Eck, H.J., Maliapaard, C. and Trindade, L.M., “Genome-wide association analysis in tetraploid potato reveals four QTLs for protein content”, ***Molecular Breeding*** 39, 151, 2019.

Krause, K.P., Hill, L., Reimholz, R., Hamborg Nielsen, T., Sonnewald, U. and Stitt, M., “Sucrose metabolism in cold-stored potato tubers with decreased expression of sucrose phosphate synthase”, ***Plant, Cell & Environment*** 21, 285-299, 1998.

Kuhl, J.C., Novy, R.G., Whitworth, J.L., Dibble, M.S., Schneider, B. and Hall, D., “Development of molecular markers closely linked to the potato leafroll virus resistance

gene, Rlr etb, for use in marker-assisted selection”, *American Journal of Potato Research* 93, 203-212, 2016.

Kumar, D., Singh, B. and Parveen, K., “An overview of the factors affecting sugar content of potatoes”, *Annals of Applied Biology* 145, 247-256, 2004.

Kumari, M., Kumar, M. and Solankey, S.S., “Breeding potato for quality improvement”. In *Potato-From Incas to all over the world*, *Intech Open* London, 37-59, 2018.

Lachman, J., Hamouz, K., Orsák, M. and Kotíková, Z., “Carotenoids in potatoes—a short overview”, *Plant, Soil and Environment* 62, 474-481, 2016.

Lachman, J., Hamouz, K., Orsák, M., Pivec, V. and Dvořák, P., “The influence of flesh colour and growing locality on polyphenolic content and antioxidant activity in potatoes”, *Scientia Horticulturae*, 117, 109-114, 2008.

Legay, S., Guignard, C., Ziebel, J. and Evers, D., “Iron uptake and homeostasis related genes in potato cultivated in vitro under iron deficiency and overload”, *Plant Physiology and Biochemistry* 60, 180-189, 2012.

Leng, X., Wang, P., Wang, C., Zhu, X., Li, X., Li, H., Mu, Q., Li, A., Liu, Z. and Fang, J., “Genome-wide identification and characterization of genes involved in carotenoid metabolic in three stages of grapevine fruit development”, *Scientific Reports* 7, 1-13, 2017.

Li, J., Wang, Y., Wen, G., Li, G., Li, Z., Zhang, R. and Xie, C., “Mapping QTL underlying tuber starch content and plant maturity in tetraploid potato. *The Crop Journal* 7, 261-272, 2019.

Li, L., Paulo, M.J., van Eeuwijk, F. and Gebhardt, C., “Statistical epistasis between candidate gene alleles for complex tuber traits in an association mapping population of tetraploid potato”, *Theoretical and Applied Genetics* 121, 1303-1310, 2010.

Li, L., Strahwald, J., Hofferbert, H. R., Lübeck, J., Tacke, E., Junghans, H. and Gebhardt, C., “DNA variation at the invertase locus *invGE/GF* is associated with tuber quality traits in populations of potato breeding clones”, ***Genetics*** 170, 813-821, 2005.

Li, L., Tacke, E., Hofferbert, H.R., Lübeck, J., Strahwald, J., Draffehn, A.M., Walkemeier, B. and Gebhardt, C., “Validation of candidate gene markers for marker-assisted selection of potato cultivars with improved tuber quality”, ***Theoretical and Applied Genetics*** 126, 1039-1052, 2013.

Li, N., Shi, J., Wang, X., Liu, G. and Wang, H., “A combined linkage and regional association mapping validation and fine mapping of two major pleiotropic QTLs for seed weight and silique length in rapeseed (*Brassica napus* L.)”, ***BMC Plant Biology*** 14, 114, 2014.

Li, P., Chen, B., Zhang, G., Chen, L., Dong, Q., Wen, J., Mysore, K.S. and Zhao, J., “Regulation of anthocyanin and proanthocyanidin biosynthesis by *Medicago truncatula* bHLH transcription factor MtTT8”, ***New Phytologist*** 210, 905-921, 2016.

Li, W., Wang, B., Wang, M., Chen, M., Yin, J.M., Kaleri, G.M., Zhang, R.J., Zuo, T.N., You, X. and Yang, Q., “Cloning and characterization of a potato StAN11 gene involved in anthocyanin biosynthesis regulation”, ***Journal of Integrative Plant Biology*** 56, 364-372, 2014.

Li, Y., Liang, J., Zeng, X., Guo, H., Luo, Y., Philip, K., Zhang, S. and Zhu, G., “Genome-wide Analysis of MYB Gene Family in Potato Provides Insights into Tissue-specific Regulation of Anthocyanin Biosynthesis”, ***Horticultural Plant Journal*** 1-13, 2021.

Lobato, M.C., Daleo, G.R., Andreu, A.B. and Olivieri, F.P., “Cell wall reinforcement in the potato tuber periderm after crop treatment with potassium phosphite”, ***Potato Research*** 61, 19-29, 2018.

López-González, C., Juárez-Colunga, S., Morales-Elías, N.C. and Tiessen, A., “Exploring regulatory networks in plants: transcription factors of starch metabolism”, ***PeerJ*** 7, 6841, 2019.

Lopez-Pardo, R., Barandalla, L., Ritter, E. and Ruiz de Galarreta, J.I., “Validation of molecular markers for pathogen resistance in potato”, ***Plant Breeding*** 132, 246-251, 2013.

Lu, W., Haynes, K., Wiley, E. and Clevidence, B., “Carotenoid content and color in diploid potatoes”, ***Journal of the American Society for Horticultural Science*** 126, 722-726, 2001.

Lutaladio, N. and Castaldi, L., “Potato: The hidden treasure”, ***Journal of Food Composition and Analysis*** 22, 491-493, 2009.

Machida-Hirano, R., “Diversity of potato genetic resources”, ***Breeding Science*** 65, 26-40, 2015.

Manrique-Carpintero, N.C., Coombs, J.J., Cui, Y., Veilleux, R.E., Buell, C.R. and Douches, D., “Genetic map and QTL analysis of agronomic traits in a diploid potato population using single nucleotide polymorphism markers”, ***Crop Science*** 55, 2566-2579, 2015.

Massa, A.N., Manrique-Carpintero, N.C., Coombs, J., Haynes, K.G., Bethke, P.C., Brandt, T.L. and Douches, D.S., “Linkage analysis and QTL mapping in a tetraploid russet mapping population of potato” ***BMC Genetics*** 19, 87, 2018.

Mau, J.L., Chang, C.N., Huang, S.J. and Chen, C.C., “Antioxidant properties of methanolic extracts from *Grifola frondosa*, *Morchella esculenta* and *Termitomyces albuminosus* mycelia. ***Food Chemistry*** 87, 111-118, 2004.

McCord, P.H., Sosinski, B.R., Haynes, K.G., Clough, M.E. and Yencho, G.C., “Linkage mapping and QTL analysis of agronomic traits in tetraploid potato (*Solanum tuberosum* subsp. *tuberosum*). ***Crop Science*** 51, 771-785, 2011.

McGregor, I., “The fresh potato market”, In *Potato biology and biotechnology: advances and perspectives* (eds. D. Vreugdenhil, J. Bradshaw, C. Gebhardt, F. Govers, M.A. Taylor, D.K. MacKerron and H.A. Ross), ***Elsevier Science BV***, 3-26, 2007.

Menéndez, C.M., Ritter, E., Schäfer-Pregl, R., Walkemeier, B., Kalde, A., Salamini, F. and Gebhardt, C., “Cold sweetening in diploid potato: mapping quantitative trait loci and candidate genes”, **Genetics** 162, 1423-1434, 2002.

Milbourne, D., Meyer, R.C., Collins, A.J., Ramsay, L.D., Gebhardt, C. and Waugh, R., “Isolation, characterisation and mapping of simple sequence repeat loci in potato”, **Molecular and General Genetics MGG** 259, 233-245, 1998.

Milczarek, D., Tatarowska, B., Plich, J., Podlewska-Przetakiewicz, A. and Flis, B., “*Solanum gourlayi*—a Source of Cyst Nematode Resistance in Potato Breeding”, **Potato Research** 63, 589-595, 2020.

Mitchell, G.A. “Methods of starch analysis”, **Starch-Starke** 42, 131-134, 1990.

Muthoni, J., Kabira, J., Shimelis, H. and Melis, R., “Tetrasomic inheritance in cultivated potato and implications in conventional breeding”, **Australian Journal of Crop Science**, 9, 185-190, 2015.

Muttucumaru, N., Powers, S.J., Elmore, J.S., Mottram, D.S. and Halford, N.G., “Effects of water availability on free amino acids, sugars, and acrylamide-forming potential in potato”, **Journal of Agricultural and Food Chemistry** 63, 2566-2575, 2015.

Myles S., Peiffer J., Brown P.J., Ersoz E.S., Zhang Z. and Costich D.E., “Association mapping: critical considerations shift from genotyping to experimental design”, **Plant Cell** 21, 2194-2202, 2009.

Nadeem, M.A., Nawaz, M.A., Shahid, M.Q., Doğan, Y., Comertpay, G., Yıldız, M. and Baloch, F.S., “DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. **Biotechnology & Biotechnological Equipment** 32, 261-285, 2018.

Naess, S.K., Bradeen, J.M., Wielgus, S.M., Haberlach, G.T., McGrath, J.M. and Helgeson, J.P., “Resistance to late blight in *Solanum bulbocastanum* is mapped to chromosome 8”, ***Theoretical and Applied Genetics*** 101, 697-704, 2000.

Nakamura, A.M., Nascimento, A.S. and Polikarpov, I., “Structural diversity of carbohydrate esterases”, ***Biotechnology Research and Innovation*** 1, 35-51, 2017.

Neele, A.E.F. and Louwes, K.M., “Early selection for chip quality and dry matter content in potato seedling populations in greenhouse or screenhouse”, ***Potato Research*** 32, 293-300, 1989.

Nesterenko, S. and Sink, K.C., “Carotenoid profiles of potato breeding lines and selected cultivars”, ***HortScience*** 38, 1173-1177, 2003.

Ogunniyan, D.J. and Olakojo, S.A., “Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). ***Nigerian Journal of Genetics*** 28, 24-28, 2014.

Ortiz, R. and Mihovilovich, E., “Genetics and Cytogenetics of the Potato”, In *The Potato Crop* (pp. 219-247). ***Springer*** Cham, 219-247, 2020.

Ortiz, R., “Genomic-led potato breeding for increasing genetic gains: achievements and outlook”, ***Genetics, Genomics and Breeding of Crop Plants*** 2, 1-25, 2020.

Pajerowska-Mukhtar, K.M., Mukhtar, M.S., Guex, N., Halim, V.A., Rosahl, S., Somssich, I.E. and Gebhardt, C., “Natural variation of potato allene oxide synthase 2 causes differential levels of jasmonates and pathogen resistance in *Arabidopsis*”, ***Planta*** 228, 293-306, 2008.

Parra-Galindo, M.A., Piñeros-Niño, C., Soto-Sedano, J.C. and Mosquera-Vasquez, T., “Chromosomes I and X Harbor Consistent Genetic Factors Associated with the Anthocyanin Variation in Potato”, ***Agronomy*** 9, 366, 2019.

PBI Solanum Project, “Solanaceae Source website., USA: Planetary Biodiversity Inventories (PBI)”, **National Science Foundation** 2014.

Pearsall, D.M., “Plant domestication and the shift to agriculture in the Andes”, In The handbook of South American archaeology (pp. 105-120), **Springer** New York, NY, 105-120, 2008.

Peiris, K.H.S., Dull, G.G., Leffler, R.G. and Kays, S.J., “Spatial variability of soluble solids or dry-matter content within individual fruits, bulbs, or tubers: implications for the development and use of NIR spectrometric techniques”, **HortScience** 34, 114-118, 1999.

Phan, H.T., Rybak, K., Bertazzoni, S., Furuki, E., Dinglasan, E., Hickey, L.T., Oliver, R.P. and Tan, K.C., “Novel sources of resistance to Septoria nodorum blotch in the Vavilov wheat collection identified by genome-wide association studies”, **Theoretical and Applied Genetics** 131, 1223-1238, 2018.

Piepho, H.P., Möhring, J., Melchinger, A.E. and Büchse, A., “BLUP for phenotypic selection in plant breeding and variety testing”, **Euphytica** 161, 209-228, 2008.

Pieterse, L. and Judd, J., “World Catalogue of Potato Varieties: Weltkatalog Der Kartoffelsorten. Erling Verlag”, 6th ed., **Agrimedia** New Zealand, 2014.

Plata-Guerrero, R., Guerra-Hernandez, E. and Garcia-Villanova, B., “Determination of reducing sugar and asparagine in potatoes”, **Journal of Liquid Chromatography & Related Technologies** 32, 2556-2568, 2009.

Po, E., Sinha, N. K. and Naeem, S., “Potato Production, Postharvest Quality, and Processed Products”, **Handbook of Vegetables and Vegetable Processing** 26, 785-809, 2018.

Postles, J., Curtis, T.Y., Powers, S.J., Elmore, J.S., Mottram, D.S. and Halford, N.G., “Changes in free amino acid concentration in rye grain in response to nitrogen and sulfur availability, and expression analysis of genes involved in asparagine metabolism”, **Frontiers in Plant Science** 7, 917, 2016.

Potato Genome Sequencing Consortium, “Genome sequence and analysis of the tuber crop potato”, ***Nature*** 475, 189-195, 2011.

Price, A. L., Patterson, N. J., Plenge, R. M., Weinblatt, M. E., Shadick, N. A. and Reich, D., “Principal components analysis corrects for stratification in genome-wide association studies”, ***Nature Genetics*** 38, 904-909, 2006.

Pritchard J.K., Stephens M. and Donnelly P., “Inference of population structure using multilocus genotype data”, ***Genetics*** 155, 945-959, 2000.

R Core Team, “A language and environment for statistical computing”, ***R Foundation for Statistical Computing*** Vienna, Austria, 2013.

Rady, A.M., Guyer, D.E., Kirk, W. and Donis-González, I.R., “The potential use of visible/near infrared spectroscopy and hyperspectral imaging to predict processing-related constituents of potatoes”, ***Journal of Food Engineering*** 135, 11-25, 2014.

Rafalski, J.A., “Association genetics in crop improvement”, ***Current Opinion in Plant Biology*** 13, 174-180, 2010.

Raffan, S. and Halford, N.G., “Acrylamide in food: Progress in and prospects for genetic and agronomic solutions”, ***Annals of Applied Biology*** 175, 259-281, 2019.

Rak, K., Bethke, P.C. and Palta, J.P., “QTL mapping of potato chip color and tuber traits within an autotetraploid family”, ***Molecular Breeding*** 37, 15, 2017.

Ramon, M., Rolland, F. and Sheen, J., “Sugar sensing and signaling”, ***The Arabidopsis book/American Society of Plant Biologists*** 6, 2008.

Rey, P., Pruvot, G., Becuwe, N., Eymery, F., Rumeau, D. and Peltier, G., “A novel thioredoxin-like protein located in the chloroplast is induced by water deficit in *Solanum tuberosum* L. plants”, ***The Plant Journal: for Cell and Molecular Biology*** 13, 97-107, 1998.

Riaz, A., Athiyannan, N., Periyannan, S.K., Afanasenko, O., Mitrofanova, O.P., Platz, G.J., Aitken, E.A., Snowdon, R.J., Lagudah, E.S., Hickey, L.T. and Voss-Fels, K.P., “Unlocking new alleles for leaf rust resistance in the Vavilov wheat collection”, ***Theoretical and Applied Genetics*** 131, 127-144, 2018.

Rodríguez Galdón, B., Ríos Mesa, D., Rodríguez Rodríguez, E. M. and Díaz Romero, C., “Influence of the cultivar on the organic acid and sugar composition of potatoes”, ***Journal of the Science of Food and Agriculture*** 90, 2301-2309, 2010.

Rosyara, U.R., De Jong, W.S., Douches, D.S. and Endelman, J.B., “Software for genome-wide association studies in autopolyploids and its application to potato”, ***The plant Genome*** 9, 1-10, 2016.

Rudack, K., Seddig, S., Sprenger, H., Köhl, K., Uptmoor, R. and Ordon, F., “Drought stress-induced changes in starch yield and physiological traits in potato”, ***Journal of Agronomy and Crop Science*** 203, 494-505, 2017.

Salimi, H., Bahar, M., Mirlohi, A. and Talebi, M., “Assessment of the genetic diversity among potato cultivars from different geographical areas using the genomic and EST microsatellites”, ***Iranian Journal of Biotechnology*** 14, 270, 2016.

Schäfer-Pregl, R., Ritter, E., Hesselbach, J., Lovatti, L., Walkemeier, B., Thelen, H., Salamini, F. and Gebhardt, C., “Analysis of quantitative trait loci (QTLs) and quantitative trait alleles (QTAs) for potato tuber yield and starch content”, ***Theoretical and Applied Genetics*** 97, 834-846, 1998.

Schönhals, E. M., Ortega, F., Barandalla, L., Aragonés, A., De Galarreta, J. R., Liao, J. C. and Gebhardt, C., “Identification and reproducibility of diagnostic DNA markers for tuber starch and yield optimization in a novel association mapping population of potato (*Solanum tuberosum* L.)”, ***Theoretical and Applied Genetics*** 129, 767-785, 2016.

Schönhals, E.M., Ding, J., Ritter, E., Paulo, M.J., Cara, N., Tacke, E., Hofferbert, H.R., Lübeck, J., Strahwald, J. and Gebhardt, C., “Physical mapping of QTL for tuber yield,

starch content and starch yield in tetraploid potato (*Solanum tuberosum* L.) by means of genome wide genotyping by sequencing and the 8.3 K SolCAP SNP array”, **BMC Genomics** 18, 1-20, 2017.

Schreiber, L., Nader-Nieto, A. C., Schönhals, E. M., Walkemeier, B. and Gebhardt, C., “SNPs in genes functional in starch-sugar interconversion associate with natural variation of tuber starch and sugar content of potato (*Solanum tuberosum* L.)”, **G3: Genes, Genomes, Genetics** 4, 1797-1811, 2014.

Segeberäck, D., Calleman, C.J., Schroeder, J.L., Costa, L.G. and Faustman, E.M., “Formation of N-7-(2-carbamoyl-2-hydroxyethyl) guanine in DNA of the mouse and the rat following intraperitoneal administration of [14C] acrylamide”, **Carcinogenesis** 16, 1161-1165, 1995.

Seo, J.H., Naing, A.H., Jeon, S.M. and Kim, C.K., “Anti-freezing-protein type III strongly influences the expression of relevant genes in cryopreserved potato shoot tips”, **Plant Molecular Biology** 97, 347-355, 2018.

Shao, H., Yong, B., Xu, P., Zheng, H., Liao, R., Wang, X., Li, X., Zhang, L. and Shen, J., “Phytoene Synthase Gene (PSY) from Sweet Potato (*Ipomoea batatas* Lam.) Enhances Tolerance to Abiotic Stress”, **Brazilian Archives of Biology and Technology** 61, 2018.

Sharma, S.K., MacKenzie, K., McLean, K., Dale, F., Daniels, S. and Bryan, G.J., “Linkage disequilibrium and evaluation of genome-wide association mapping models in tetraploid potato”, **G3: Genes, Genomes, Genetics** 8, 3185-3202, 2018.

Shendure, J. and Ji, H., “Next-generation DNA sequencing”, **Nature Biotechnology** 26, 1135-1145, 2008.

Shumbusha, D., Tusiime, G., Edema, R., Gibson, P., Adipala, E. and Mwanga, R.O.M., “Inheritance of root dry matter content in sweetpotato”, **African Crop Science Journal** 22, 69-78, 2014.

Simko, I., Costanzo, S., Haynes, K. G., Christ, B. J. and Jones, R.W., “Linkage disequilibrium mapping of a *Verticillium dahliae* resistance quantitative trait locus in tetraploid potato (*Solanum tuberosum*) through a candidate gene approach”, ***Theoretical and Applied Genetics*** 108, 217-224, 2004.

Simko, I., Haynes, K.G. and Jones, R.W., “Assessment of linkage disequilibrium in potato genome with single nucleotide polymorphism markers”, *Genetics* 173, 2237-2245, 2006

Singh, B., Bhardwaj, V., Kaur, K., Kukreja, S. and Goutam, U., “Potato Periderm is the First Layer of Defence against Biotic and Abiotic Stresses: a Review”, ***Potato Research*** 1-16, 2020.

Śliwka, J., Sołtys-Kalina, D., Szajko, K., Wasilewicz-Flis, I., Strzelczyk-Żyta, D., Zimnoch-Guzowska, E. and Marczewski, W., “Mapping of quantitative trait loci for tuber starch and leaf sucrose contents in diploid potato”, ***Theoretical and Applied Genetics*** 129, 131-140, 2016.

Sliwka, J., Wasilewicz-Flis, I., Jakuczun, H. and Gebhardt, C., “Tagging quantitative trait loci for dormancy, tuber shape, regularity of tuber shape, eye depth and flesh colour in diploid potato originated from six *Solanum* species”, ***Plant Breeding*** 127, 49-55, 2008.

Soler, M., Serra, O., Fluch, S., Molinas, M. and Figueras, M., “A potato skin SSH library yields new candidate genes for suberin biosynthesis and periderm formation”, ***Planta*** 233, 933-945, 2011.

Spooner, D.M., McLean, K., Ramsay, G., Waugh, R. and Bryan, G.J., “A single domestication for potato based on multilocus amplified fragment length polymorphism genotyping”, ***Proceedings of the National Academy of Sciences*** 102, 14694-14699, 2005.

Spooner, D.M., Nunez, J., Rodriguez, F., Naik, P. S. and Ghislain, M., “Nuclear and chloroplast DNA reassessment of the origin of Indian potato varieties and its implications

for the origin of the early European potato”, *Theoretical and Applied Genetics* 110, 1020-1026, 2005.

Stadler, R.H., Blank, I., Varga, N., Robert, F., Hau, J., Guy, P.A. and Riediker, S., “Acrylamide from Maillard reaction products”, *Nature* 419, 449-450, 2002.

Stefańczyk, E., Plich, J., Janiszewska, M., Smyda-Dajmund, P., Sobkowiak, S. and Śliwka, J., “Marker-assisted pyramiding of potato late blight resistance genes Rpi-rzc1 and Rpi-phu1 on di-and tetraploid levels”, *Molecular Breeding* 40, 1-12, 2020.

Stich, B., Melchinger, A.E., Frisch, M., Maurer, H.P., Heckenberger, M. and Reif, J.C., “Linkage disequilibrium in European elite maize germplasm investigated with SSRs”, *Theoretical and Applied Genetics* 111, 723-730, 2005.

Stich, B., Urbany, C., Hoffmann, P. and Gebhardt, C., “Population structure and linkage disequilibrium in diploid and tetraploid potato revealed by genome-wide high-density genotyping using the SolCAP SNP array”, *Plant Breeding* 132, 718-724, 2013.

Sulli, M., Mandolino, G., Sturaro, M., Onofri, C., Diretto, G., Parisi, B. and Giuliano, G., “Molecular and biochemical characterization of a potato collection with contrasting tuber carotenoid content”, *PLoS One* 12, e0184143, 2017.

Sverrisdóttir, E., Byrne, S., Sundmark, E.H.R., Johnsen, H.Ø., Kirk, H.G., Asp, T. and Nielsen, K.L., “Genomic prediction of starch content and chipping quality in tetraploid potato using genotyping-by-sequencing”, *Theoretical and Applied Genetics* 130, 2091-2108, 2017.

Swedish National Food Administration, “Opinion of the Scientific Committee on Food on new findings regarding the presence of acrylamide in food”, https://ec.europa.eu/food/sites/food/files/safety/docs/sci-com_scf_out131_en.pdf, accessed october 22, 2020, **Brussels** Belgium, 2002.

Tai, H.H., Goyer, C. and Murphy, A.M., “Potato *MYB* and *bHLH* transcription factors associated with anthocyanin intensity and common scab resistance”, *Botany* 91, 722-730, 2013.

Tamisier, L., Szadkowski, M., Nemouchi, G., Lefebvre, V., Szadkowski, E., Duboscq, R., Santoni, S., Sarah, G., Sauvage, C., Palloix, A. and Moury, B., “Genome-wide association mapping of QTLs implied in potato virus Y population sizes in pepper: evidence for widespread resistance QTL pyramiding”, *Molecular plant pathology* 21, 3-16, 2020.

Tanios, S., Thangavel, T., Eyles, A., Tegg, R.S., Nichols, D.S., Corkrey, R. and Wilson, C.R., “Suberin deposition in potato periderm: a novel resistance mechanism against tuber greening”, *New Phytologist* 225, 1273-1284, 2020.

Thudi, M., Li, Y., Jackson, S.A., May, G.D. and Varshney, R.K., “Current state-of-art of sequencing technologies for plant genomics research”, *Briefings in Functional Genomics* 11, 3-11, 2012.

Tierno, R., Hornero-Méndez, D., Gallardo-Guerrero, L., López-Pardo, R. and de Galarreta, J.I.R., “Effect of boiling on the total phenolic, anthocyanin and carotenoid concentrations of potato tubers from selected cultivars and introgressed breeding lines from native potato species”, *Journal of Food Composition and Analysis* 41, 58-65, 2015.

Tiwari, J. K., Siddappa, S., Singh, B. P., Kaushik, S. K., Chakrabarti, S. K., Bhardwaj, V. and Chandel, P., “Molecular markers for late blight resistance breeding of potato: an update”, *Plant Breeding* 132, 237-245, 2013.

Toker, C., Estimates of broad-sense heritability for seed yield and yield criteria in faba bean (*Vicia faba* L.)”, *Hereditas* 140, 222-225, 2004.

Uitdewilligen, J.G., Wolters, A.M.A., Bjorn, B., Borm, T.J., Visser, R.G. and Van Eck, H.J., “A next-generation sequencing method for genotyping-by-sequencing of highly heterozygous autotetraploid potato”, *PloS One* 8, e62355, 2013.

Umemoto, N., Nakayasu, M., Ohyama, K., Yotsu-Yamashita, M., Mizutani, M., Seki, H., Saito, K. and Muranaka, T., “Two cytochrome P450 monooxygenases catalyze early hydroxylation steps in the potato steroid glycoalkaloid biosynthetic pathway”, ***Plant Physiology*** 171,2458-2467, 2016.

UN, “World Population Prospects”, <https://population.un.org/wpp/>, 2019.

Urbany, C., Stich, B., Schmidt, L., Simon, L., Berding, H., Junghans, H. and Lübeck, J., “Association genetics in *Solanum tuberosum* provides new insights into potato tuber bruising and enzymatic tissue discoloration”, ***BMC Genomics*** 12, 7, 2011.

Van Eck, H.J., Jacobs, J.M.E., Van Den Berg, P.M.M.M., Stiekema, W.J., Jacobsen, E., “The inheritance of anthocyanin pigmentation in potato (*Solanum tuberosum* L.) and mapping of tuber skin colour loci using RFLPs”, ***Heredity*** 73, 410-421, 1994.

Van Eck, H.J., “Genetics of morphological and tuber traits”, In Potato biology and biotechnology: advances and perspectives (eds. D. Vreugdenhil, J. Bradshaw, C. Gebhardt, F. Govers, M.A. Taylor, D.K. MacKerron, H.A. Ross), ***Elsevier Science*** BV, 91-115, 2007.

Van Os, H., Andrzejewski, S., Bakker, E., Barrena, I., Bryan, G.J., Caromel, B., Ghareeb, B., Isidore, E., De Jong, W., Van Koert, P. and Lefebvre, V., “Construction of a 10,000-marker ultradense genetic recombination map of potato: providing a framework for accelerated gene isolation and a genome wide physical map”, ***Genetics*** 173, 1075-1087, 2006.

Verdaguer, R., Soler, M., Serra, O., Garrote, A., Fernández, S., Company-Arumí, D., Anticó, E., Molinas, M. and Figueras, M., “Silencing of the potato StNAC103 gene enhances the accumulation of suberin polyester and associated wax in tuber skin”, ***Journal of experimental botany*** 67, 5415-5427, 2016.

Vos, P.G., Paulo, M.J., Voorrips, R.E., Visser, R.G., van Eck, H.J. and van Eeuwijk, F.A., “Evaluation of LD decay and various LD-decay estimators in simulated and SNP-array data of tetraploid potato. *Theoretical and Applied Genetics* 130, 123-135, 2017.

Vos, P.G., Uitdewilligen, J.G., Voorrips, R.E., Visser, R. G. and van Eck, H.J., “Development and analysis of a 20K SNP array for potato (*Solanum tuberosum*): an insight into the breeding history”, *Theoretical and Applied Genetics* 128, 2387-2401, 2015.

Vulavala, V.K., Fogelman, E., Faigenboim, A., Shoseyov, O., and Ginzberg, I., “The transcriptome of potato tuber phellogen reveals cellular functions of cork cambium and genes involved in periderm formation and maturation”, *Scientific reports* 9, 1-14, 2019.

Wang, F., Ye, Y., Chen, X., Wang, J., Chen, Z. and Zhou, Q., “A sucrose non-fermenting-1-related protein kinase 1 gene from potato, StSnRK1, regulates carbohydrate metabolism in transgenic tobacco”, *Physiology and Molecular Biology of Plants* 23, 933-943, 2017.

Wang, G., Kong, F., Zhang, S., Meng, X., Wang, Y. and Meng, Q., “A tomato chloroplast-targeted DnaJ protein protects Rubisco activity under heat stress”, *Journal of experimental botany* 66, 3027-3040, 2015.

Wang, M., Chen, L., Liang, Z., He, X., Liu, W., Jiang, B., Yan, J., Sun, P., Cao, Z., Peng, Q. and Lin, Y.E., “Metabolome and transcriptome analyses reveal chlorophyll and anthocyanin metabolism pathway associated with cucumber fruit skin colour”, *BMC Plant Biology* 20, 1-13, 2020.

Wang, R., Chen, J., Anderson, J. A., Zhang, J., Zhao, W., Wheeler, J. and Dong, Y., “Genome-wide association mapping of Fusarium head blight resistance in spring wheat lines developed in the Pacific Northwest and CIMMYT”, *Phytopathology* 107, 1486-1495, 2017.

Wei, S., Li, X., Gruber, M.Y., Feyissa, B.A., Amyot, L. and Hannoufa, A., “COP9 signalosome subunit 5A affects phenylpropanoid metabolism, trichome formation and

transcription of key genes of a regulatory tri-protein complex in Arabidopsis”, **BMC Plant Biology** 18, 134, 2018.

Weng, S.T., Kuo, Y.W., King, Y.C., Lin, H.H., Tu, P.Y., Tung, K.S. and Jeng, S.T., “Regulation of microRNA2111 and its target *IbFBK* in sweet potato on wounding”, **Plant Science** 292, 110391, 2020.

Werij, J.S., Furrer, H., van Eck, H.J., Visser, R.G. and Bachem, C.W., “A limited set of starch related genes explain several interrelated traits in potato”, **Euphytica** 186, 501-516, 2012.

Wolfinger, R., Federer, W.T. and Cordero-Brana, O., “Recovering information in augmented designs, using SAS PROC GLM and PROC MIXED”, **Agronomy Journal** 89, 856-859, 1997.

Wolters, A.M.A., Uitdewilligen, J.G., Kloosterman, B.A., Hutten, R.C., Visser, R.G. and van Eck, H.J., “Identification of alleles of carotenoid pathway genes important for zeaxanthin accumulation in potato tubers”, **Plant Molecular Biology** 73(6), 659-671, 2010.

Xu, R., “Genome-wide analysis and identification of stress-responsive genes of the CCCH zinc finger family in *Solanum lycopersicum*”, **Molecular genetics and genomics** 289, 965-979, 2013.

Xu, X., Li, W., Lu, Z., Beta, T. and Hydamaka, A.W., “Phenolic content, composition, antioxidant activity, and their changes during domestic cooking of potatoes”, **Journal of Agricultural and Food Chemistry** 57, 10231-10238, 2009.

Xu, X., Li, W., Lu, Z., Beta, T. and Hydamaka, A.W., “Phenolic content, composition, antioxidant activity, and their changes during domestic cooking of potatoes”, **Journal of Agricultural and Food Chemistry** 57, 10231-10238, 2009.

Yu, J., Pressoir, G., Briggs, W.H., Vroh Bi, I., Yamasaki, M. and Doebley, J.F., “A unified mixed-model method for association mapping that accounts for multiple levels of relatedness”, *Nature Genetics* 38, 203-208, 2006.

Zhang, C., Wang, P., Tang, D., Yang, Z., Lu, F., Qi, J. and Huang, S., “The genetic basis of inbreeding depression in potato”, *Nature Genetics* 51, 374-378, 2019.

Zhang, Y., Jung, C.S. and De Jong, W.S., “Genetic analysis of pigmented tuber flesh in potato”, *Theoretical and Applied Genetics* 119, 143-150, 2009.

Zhao, K., Tung, C.W., Eizenga, G.C., Wright, M.H., Ali, M.L., Price, A.H. and McCouch, S.R., “Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*”, *Nature Communications* 2, 1-10, 2011.

Zhao, S., Xi, X., Zong, Y., Li, S., Li, Y., Cao, D. and Liu, B., “Overexpression of ThMYC4E Enhances Anthocyanin Biosynthesis in Common Wheat”, *International Journal of Molecular Sciences* 21, 137, 2020.

Zhu, Y.L., Song, Q.J., Hyten, D.L., Van Tassell, C.P., Matukumalli, L.K., Grimm, D.R., Hyatt, S.M., Fickus, E.W., Young, N.D. and Cregan, P.B., “Single-nucleotide polymorphisms in soybean”, *Genetics* 163, 1123-1134, 2003.

Zia, M.A.B., Naeem, M., Demirel, U., Caliskan, M.E., “Next Generation Breeding in Potato”, *Ekin Journal* 3,1-33, 2017.

Zia, M.A.B., Demirel, U., Nadeem, M.A. and Caliskan, M.E., “Genome-wide association study identifies various loci underlying agronomic and morphological traits in diversified potato panel”, *Physiology and Molecular Biology of Plants* 26, 1003-1020, 2020.

APPENDIX

APPENDIX-A Phenotypic data of tuber dry matter contents % (DMC) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). b_i correspond to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Codes	DMC_ H18	DMC_ KN18	DMC_ KD18	DMC_ H19	Mean DMC	b_i
1	JELLY	GENO2	21.07	20.00	21.36	NA	20.81	0.48
2	RUMBA	GENO3	23.32	22.42	25.10	NA	23.61	1.21
3	HERMES	GENO4	22.60	21.80	23.60	NA	22.67	0.83
4	ALEGRIA	GENO5	20.15	20.68	23.58	NA	21.47	1.88
5	ROYAL	GENO6	20.34	19.92	21.52	22.36	21.04	0.82
6	ELECTRA	GENO7	18.93	18.12	19.96	18.27	18.82	0.85
7	DT14003.01	GENO9	21.00	21.52	24.11	21.68	22.08	1.70
8	DT14038.01	GENO10	20.58	24.36	24.06	21.98	22.75	0.96
9	DT14010.18	GENO11	16.76	18.95	20.51	19.39	18.90	1.59
10	DT14004.17	GENO12	19.11	21.00	25.51	20.52	21.54	3.25
11	DT14010.14	GENO13	17.66	21.74	23.77	21.41	21.15	2.44
12	DT14085.03	GENO14	22.90	23.82	27.85	23.58	24.54	2.67
13	DT14013.15	GENO16	20.01	NA	NA	21.43	20.72	-12.3
14	DT14018.32	GENO18	15.81	17.25	19.66	17.34	17.52	1.87
15	DT14042.27	GENO19	22.69	18.47	23.41	21.67	21.56	1.66
16	DT14005.09	GENO20	19.48	20.69	25.72	22.07	21.99	3.35
17	DT14030.11	GENO21	22.05	22.70	25.16	21.67	22.90	1.66
18	DT14057.37	GENO22	20.72	21.69	25.10	21.32	22.21	2.32
19	DT14065.01	GENO23	21.61	23.19	29.13	NA	24.64	4.01
20	DT14016.01	GENO24	20.03	19.67	22.86	20.58	20.79	1.79
21	DT14016.34	GENO25	16.44	18.44	18.75	20.51	18.54	0.79
22	DT14078.03	GENO26	18.82	20.57	23.96	19.57	20.73	2.54
23	DT14028.03	GENO27	21.02	21.36	24.92	21.22	22.13	2.22
24	DT14054.11	GENO28	16.57	17.05	21.79	19.66	18.77	2.96
25	DT14037.18	GENO29	16.12	18.30	21.43	18.56	18.60	2.52
26	DT14091.04	GENO30	19.33	22.43	25.37	22.97	22.53	2.68
27	DT14083.28	GENO31	23.02	20.88	25.03	NA	22.98	1.82
28	DT14015.22	GENO32	21.82	19.05	25.11	19.82	21.45	2.76
29	DT14051.15	GENO33	20.03	22.68	21.61	20.77	21.27	0.17
30	DT14047.38	GENO34	19.73	18.26	22.93	21.08	20.50	2.33
31	DT14026.04	GENO35	21.55	19.45	22.45	20.59	21.01	1.15
32	DT14068.07	GENO36	22.86	18.75	19.31	22.02	20.74	-0.91
33	DT14063.12	GENO37	19.92	25.07	26.07	19.23	22.57	2.15
34	DT14036.01	GENO38	21.95	NA	NA	NA	21.95	-6.63
35	DT14055.25	GENO39	21.34	NA	NA	20.07	20.71	-12.3

36	LadyOlympia	GENO41	20.77	22.71	23.73	20.17	21.85	1.19
37	BANBA	GENO42	20.13	19.55	18.36	20.09	19.53	-0.88
38	VanGOGH	GENO43	21.10	22.38	24.81	20.88	22.29	1.83
39	DT14049.10	GENO44	19.29	22.42	22.28	NA	21.33	0.86
40	DT14061.23	GENO45	21.82	19.77	24.51	19.86	21.49	2.20
41	DT14006.07	GENO46	24.16	22.02	23.59	21.58	22.84	0.29
42	DT14046.19	GENO47	18.06	22.69	26.15	20.51	21.85	3.46
43	DT14014.27	GENO48	20.32	20.39	22.30	21.73	21.19	1.16
44	DT14011.18	GENO49	21.61	24.38	22.13	20.13	22.06	-0.50
45	DT14069.13	GENO50	22.05	21.64	25.79	20.43	22.48	2.34
46	DT14026.21	GENO52	22.03	24.45	26.71	21.67	23.72	2.07
47	DT14042.24	GENO53	19.92	20.23	23.77	21.52	21.36	2.20
48	DT14090.11	GENO54	20.09	21.27	22.91	21.36	21.41	1.33
49	DT14071.19	GENO55	16.67	19.60	23.04	20.46	19.94	2.93
50	DT14027.08	GENO56	23.66	21.68	24.46	22.82	23.16	1.05
51	DT14034.03	GENO57	21.60	20.65	23.83	20.66	21.69	1.60
52	DT14057.36	GENO58	22.81	20.79	25.40	22.74	22.94	2.13
53	DT14062.08	GENO59	18.23	21.05	21.77	NA	20.35	1.28
54	DT14079.02	GENO60	24.40	23.67	25.44	22.40	23.98	0.83
55	DT14053.03	GENO61	17.60	NA	NA	NA	17.60	-5.32
56	DT13088.03	GENO63	19.50	19.98	22.51	19.94	20.48	1.65
57	DT14051.66	GENO64	22.50	21.29	23.83	23.52	22.79	1.14
58	DT13100.02	GENO65	21.55	22.50	23.58	22.17	22.45	0.93
59	DT13162.15	GENO66	18.57	21.74	23.34	23.24	21.72	1.91
60	DT13162.12	GENO67	18.30	21.34	25.06	21.27	21.49	3.13
61	DT11107.01	GENO68	20.64	21.01	22.09	20.44	21.05	0.75
62	ZIRVE	GENO69	18.82	NA	24.53	19.98	21.11	-0.98
63	DT12012.02	GENO70	21.27	22.01	26.21	23.05	23.14	2.72
64	DT13136.22	GENO71	20.70	22.23	26.91	22.00	22.96	3.24
65	DT13045.74	GENO72	20.32	23.86	25.76	24.10	23.51	2.20
66	DT13124.21	GENO73	20.51	19.51	24.18	21.99	21.55	2.47
67	BORWINA	GENO74	19.06	18.60	20.51	20.02	19.55	1.00
68	BROOKE	GENO75	25.44	24.38	25.96	23.06	24.71	0.62
69	TESSA	GENO76	19.25	20.77	22.57	20.67	20.82	1.53
70	DT13143.49	GENO77	20.45	18.90	24.58	20.39	21.08	2.91
71	DT13130.48	GENO78	20.01	21.85	27.35	22.28	22.87	3.82
72	DT13143.54	GENO79	20.11	23.66	22.76	21.38	21.98	0.54
73	DT13007.03	GENO80	20.05	21.12	21.95	23.46	21.65	0.82
74	KUTUP	GENO81	23.26	23.60	26.88	22.99	24.18	2.05
75	DT13028.01	GENO82	22.52	20.94	24.01	23.28	22.69	1.35
76	DT13093.92	GENO83	19.12	20.16	24.17	23.00	21.61	2.70
77	DT13051.10	GENO84	24.50	20.59	21.85	20.42	21.84	-0.43
78	DT13143.58	GENO85	18.15	19.03	22.40	19.78	19.84	2.27

79	DT13026.10	GENO86	20.51	22.77	23.83	22.62	22.43	1.31
80	DT13049.50	GENO87	18.59	19.03	19.49	19.89	19.25	0.41
81	DT13072.19	GENO88	22.31	22.81	23.72	21.84	22.67	0.69
82	DT13083.01	GENO89	17.92	16.85	25.68	19.60	20.01	4.92
83	LadyRosetta	GENO90	21.00	NA	25.12	NA	23.06	-13.6
84	DT11007.01	GENO91	23.38	22.70	25.70	22.57	23.59	1.58
85	DT11108.02	GENO92	23.83	21.38	25.13	22.19	23.13	1.49
86	DORUK	GENO93	28.25	25.10	30.46	24.60	27.10	2.23
87	DT13085.01	GENO94	20.83	18.65	21.42	19.44	20.09	0.99
88	DT12068.21	GENO95	19.84	19.88	22.23	21.35	20.83	1.41
89	DT11088.01	GENO96	22.50	22.59	23.00	22.05	22.54	0.27
90	DT13045.42	GENO97	20.81	18.57	19.19	19.42	19.50	-0.31
91	DT13147.17	GENO98	20.28	20.81	20.95	19.23	20.32	0.24
92	DT13048.10	GENO99	18.53	20.77	23.64	20.22	20.79	2.38
93	DT13052.23	GENO100	19.75	22.28	25.91	21.94	22.47	2.92
94	DT13037.31	GENO101	23.78	21.02	24.98	22.50	23.07	1.52
95	DT13045.103	GENO102	19.61	19.27	24.46	18.95	20.57	2.98
96	DT13037.35	GENO103	18.70	24.20	24.45	19.80	21.79	1.81
97	DT13047.08	GENO104	21.19	22.19	24.98	22.66	22.76	1.96
98	DT13162.16	GENO105	19.46	20.15	21.70	19.50	20.20	1.13
99	DT13067.03	GENO106	18.63	19.74	22.42	20.45	20.31	1.93
100	SORAYA	GENO107	18.93	17.42	20.59	18.11	18.76	1.43
101	LAURA	GENO108	20.77	20.69	19.51	19.44	20.10	-0.73
102	SHEPODY	GENO109	20.09	18.88	21.86	21.59	20.61	1.41
103	43-111-11	GENO110	21.19	22.33	23.30	22.61	22.36	0.92
104	KARLENA	GENO111	24.00	24.83	25.07	23.66	24.39	0.39
105	139-101-11	GENO112	23.05	20.79	24.30	22.85	22.75	1.40
106	84-105-11	GENO113	20.68	21.79	23.44	21.64	21.89	1.32
107	NANDU	GENO114	26.24	27.43	27.23	NA	26.97	0.24
108	882-202-10	GENO115	23.36	22.92	26.16	21.14	23.40	1.79
109	TALENT	GENO116	25.02	23.40	24.56	22.83	23.95	0.20
110	57-104-11	GENO117	21.53	22.48	22.86	22.38	22.31	0.51
111	878-202-10	GENO118	23.15	22.65	24.27	24.43	23.63	0.81
112	146-103-11	GENO120	24.85	23.83	26.74	25.51	25.23	1.42
113	SALUTE	GENO121	20.34	21.07	21.87	21.12	21.10	0.70
114	68-105-11	GENO122	22.10	23.45	25.82	22.91	23.57	1.82
115	63-113-11	GENO123	19.99	20.77	21.65	21.77	21.05	0.76
116	106-105-11	GENO124	23.57	NA	23.52	22.83	23.31	-0.43
117	939-201-10	GENO125	19.23	23.29	25.50	25.15	23.29	2.54
118	NIXE	GENO126	22.92	21.44	22.50	21.71	22.14	0.18
119	51-109-11	GENO127	18.06	22.00	23.77	21.21	21.26	2.24
120	ETIKETSIZNORIKA	GENO128	23.38	25.25	20.71	24.79	23.53	-2.13
121	40-103-11	GENO130	23.34	20.86	22.67	22.13	22.25	0.33

122	99-115-11	GENO131	22.50	22.69	24.91	23.05	23.29	1.38
123	141-104-11	GENO132	24.27	24.97	24.70	24.66	24.65	0.05
124	89-105-11	GENO133	20.79	21.91	22.74	21.89	21.83	0.83
125	NAUTILUS	GENO134	25.93	21.86	25.01	24.51	24.33	0.64
126	157-103-11	GENO136	27.51	22.04	24.17	25.99	24.93	-0.39
127	133-112-11	GENO137	21.82	22.26	24.55	24.86	23.37	1.49
128	944-208-10	GENO138	25.72	24.58	26.83	26.01	25.79	0.99
129	PRIVELIGE	GENO139	19.61	21.08	25.23	22.93	22.21	2.91
130	966-203-10	GENO140	26.31	28.04	29.02	26.15	27.38	1.11
131	904-212-10	GENO141	23.30	24.36	23.14	22.12	23.23	-0.40
132	BETTINA	GENO142	22.14	20.30	21.32	20.17	20.98	0.05
133	125-104-11	GENO143	24.16	24.17	26.97	24.00	24.83	1.67
134	SWING	GENO144	19.99	NA	NA	NA	19.99	-6.04
135	758-109-09	GENO145	23.38	23.48	27.25	23.59	24.43	2.27
136	735-102-09	GENO146	25.67	24.78	26.38	24.69	25.38	0.68
137	99-102-11	GENO147	20.62	23.15	21.30	22.39	21.87	-0.33
138	TERRANA	GENO148	29.43	28.15	30.03	24.69	28.08	0.73
139	104-103-11	GENO149	18.51	21.80	23.96	22.06	21.58	2.28
140	SFHIT	GENO150	22.79	24.12	25.56	23.56	24.01	1.26
141	KIWI	GENO151	24.22	25.51	27.28	27.02	26.01	1.44
142	KIEBITZ	GENO152	25.06	23.00	27.27	23.50	24.71	1.91
143	BONUS	GENO153	21.86	22.98	25.36	22.75	23.24	1.75
144	509-104-09	GENO154	20.62	20.51	24.04	22.61	21.95	2.06
145	43-118-11	GENO155	20.43	20.60	23.66	24.81	22.38	1.87
146	BEO	GENO156	23.09	23.60	24.37	25.02	24.02	0.61
147	BALTICCREAM	GENO157	23.83	23.60	26.36	25.72	24.88	1.57
148	868-201-10	GENO158	22.90	23.64	24.49	24.56	23.90	0.73
149	860-201-10	GENO159	22.88	22.42	23.66	23.21	23.04	0.60
150	DUKATA	GENO160	19.44	22.38	23.89	23.66	22.34	1.79
151	84-107-11	GENO161	21.17	21.47	25.43	24.28	23.09	2.44
152	128-105-11	GENO162	28.18	26.65	26.57	26.51	26.98	-0.51
153	140-107-11	GENO163	25.86	25.09	27.83	22.78	25.39	1.40
154	PELIKAN	GENO164	21.88	21.89	23.57	21.95	22.32	1.00
155	KOLIBRI	GENO165	25.57	NA	26.25	NA	25.91	-15.4
156	82-119-11	GENO167	21.36	21.95	22.72	23.09	22.28	0.64
157	WENDY	GENO168	22.79	19.80	22.93	20.02	21.39	0.96
158	ROMANZE	GENO169	19.11	22.18	25.56	21.11	21.99	2.94
159	PRESTIGE	GENO170	25.00	24.44	24.91	24.84	24.80	0.11
160	MAXI	GENO171	22.71	25.71	29.13	25.70	25.81	2.94
161	FASAN	GENO172	21.95	23.57	26.54	24.14	24.05	2.25
162	Madaleine	GENO173	17.54	18.13	20.24	19.52	18.86	1.43
163	POMQUEEN	GENO174	21.96	22.35	24.76	20.79	22.47	1.55
164	MUNGO	GENO175	25.63	27.36	31.31	25.68	27.50	2.87

165	ALBATROS	GENO176	27.91	22.74	29.30	27.37	26.83	2.34
166	FIDELIA	GENO177	18.09	17.18	17.99	19.10	18.09	0.21
167	TACOMA	GENO178	23.00	17.73	23.18	20.11	21.01	1.65
168	BONZA	GENO179	29.35	29.56	33.07	28.01	30.00	2.15
169	ADRETTA	GENO180	22.98	23.46	27.07	22.83	24.09	2.29
170	POWER	GENO181	29.13	26.82	30.49	26.62	28.27	1.48
171	GOLDMARIE	GENO182	22.20	19.60	21.96	21.15	21.23	0.62
172	RITA	GENO183	20.81	22.21	22.49	22.52	22.01	0.59
173	SUMMERGOLD	GENO184	26.67	28.14	29.73	24.96	27.38	1.39
174	DIPLOMAT	GENO185	23.36	23.68	24.97	24.65	24.17	0.86
175	CASCADE	GENO186	21.88	21.59	22.07	21.03	21.64	0.20
176	SOLIST	GENO187	17.33	20.06	22.58	20.94	20.23	2.32
177	LOLITA	GENO188	21.91	19.11	22.78	19.75	20.89	1.33
178	KARATOP	GENO189	18.51	18.90	19.23	20.34	19.25	0.31
179	INARA	GENO190	21.04	20.94	22.76	NA	21.58	1.05
180	ACAPELLA	GENO191	22.64	22.27	26.39	22.86	23.54	2.34
181	ALLORA	GENO192	18.82	20.00	22.18	20.16	20.29	1.65
182	ARKULA	GENO193	25.02	20.33	NA	22.50	22.62	-0.13
183	TOKIO	GENO194	23.78	23.73	27.25	23.30	24.52	2.08
184	BIRTE	GENO195	20.93	20.13	21.20	20.38	20.66	0.39
185	900-205-10	GENO196	23.53	23.42	22.93	23.14	23.26	-0.32
186	MAXILLA	GENO197	25.23	24.01	26.11	22.52	24.47	0.88
187	TUCAN	GENO198	23.34	24.00	27.01	23.90	24.56	1.99
188	946-202-10	GENO199	24.30	23.96	28.53	23.55	25.09	2.61
189	KORMORAN	GENO200	24.28	29.12	33.47	26.88	28.44	4.05
190	JUMBO	GENO202	27.26	27.14	28.18	26.51	27.27	0.58
191	LOGO	GENO203	23.62	29.99	31.57	27.81	28.25	2.86
192	102-102-11	GENO204	19.04	20.57	21.50	20.43	20.39	1.02
		Mean	21.66	21.98	24.29	22.19	22.50	

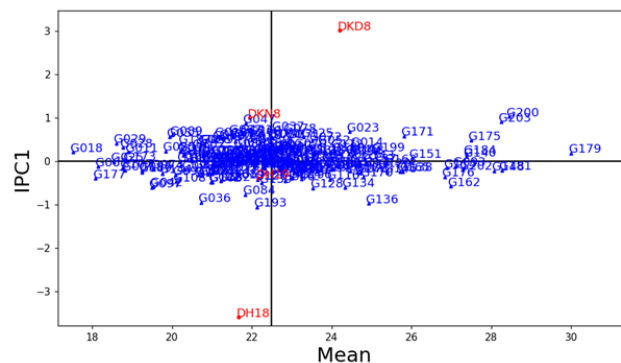


Fig.S1. Ammi biplot for mean of dry matter content of 192 genotypes across four environments (DH18, DKN18, DKD18, DH19) plotted against IPC1 (Interactive principal component).

APPENDIX-B Phenotypic data of specific gravity (SG) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). b_i corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S.No.	Genotype Names	Codes	SG H18	SG KN18	SG KD18	SG H19	Mean SG	b_i
1	JELLY	GENO2	1.084	1.080	1.090	NA	1.085	0.64
2	RUMBA	GENO3	1.095	1.090	1.100	NA	1.095	0.91
3	HERMES	GENO4	1.091	1.080	1.100	NA	1.090	1.14
4	ALEGRIA	GENO5	1.080	1.080	1.170	NA	1.110	7.59
5	ROYAL	GENO6	1.081	1.079	1.085	1.081	1.081	0.41
6	ELECTRA	GENO7	1.074	1.074	1.081	1.071	1.075	0.67
7	DT14003.01	GENO9	1.084	1.087	1.096	1.087	1.089	0.94
8	DT14038.01	GENO10	1.082	1.101	1.097	1.088	1.092	0.70
9	DT14010.18	GENO11	1.064	1.074	1.084	1.076	1.075	1.32
10	DT14004.17	GENO12	1.075	1.084	1.107	1.082	1.087	2.49
11	DT14010.14	GENO13	1.068	1.087	1.099	1.086	1.085	1.95
12	DT14085.03	GENO14	1.083	1.097	1.115	1.096	1.098	2.26
13	DT14013.15	GENO16	1.079	NA	NA	1.085	1.082	0.21
14	DT14018.32	GENO18	1.059	1.069	1.075	1.066	1.067	1.04
15	DT14042.27	GENO19	1.092	1.075	1.093	1.087	1.087	0.65
16	DT14005.09	GENO20	1.077	1.082	1.104	1.089	1.088	2.09
17	DT14030.11	GENO21	1.089	1.092	1.106	1.087	1.093	1.46
18	DT14057.37	GENO22	1.082	1.070	1.102	1.084	1.085	2.10
19	DT14065.01	GENO23	1.082	1.094	1.121	NA	1.099	2.88
20	DT14016.01	GENO24	1.079	1.077	1.091	1.082	1.082	1.08
21	DT14016.34	GENO25	1.062	1.071	1.075	1.084	1.073	0.58
22	DT14078.03	GENO26	1.073	1.081	1.096	1.077	1.082	1.76
23	DT14028.03	GENO27	1.084	1.085	1.104	1.085	1.090	1.74
24	DT14054.11	GENO28	1.063	1.065	1.086	1.077	1.073	1.79
25	DT14037.18	GENO29	1.061	1.070	1.084	1.072	1.072	1.63
26	DT14091.04	GENO30	1.076	1.094	1.101	1.093	1.091	1.46
27	DT14083.28	GENO31	1.093	1.083	1.100	NA	1.092	0.93
28	DT14015.22	GENO32	1.088	1.086	1.097	1.078	1.087	1.01
29	DT14051.15	GENO33	1.079	1.089	1.085	1.083	1.084	0.19
30	DT14047.38	GENO34	1.078	1.077	1.095	1.085	1.084	1.44
31	DT14026.04	GENO35	1.086	1.079	1.090	1.082	1.084	0.62
32	DT14068.07	GENO36	1.093	1.073	1.079	1.088	1.083	-0.60
33	DT14063.12	GENO37	1.079	1.098	1.077	1.076	1.082	-0.68
34	DT14036.01	GENO38	1.088	NA	NA	NA	1.088	0.24
35	DT14055.25	GENO39	1.085	NA	NA	1.080	1.082	0.01
36	LadyOlympia	GENO41	1.083	1.092	1.096	1.080	1.088	0.94
37	BANBA	GENO42	1.080	1.077	1.074	1.079	1.078	-0.43

38	VanGOGH	GENO43	1.084	1.090	1.100	1.083	1.089	1.27
39	DT14049.10	GENO44	1.076	1.090	1.088	NA	1.085	0.53
40	DT14061.23	GENO45	1.088	1.077	1.099	1.079	1.086	1.43
41	DT14006.07	GENO46	1.099	1.089	1.095	1.086	1.092	0.12
42	DT14046.19	GENO47	1.071	1.092	1.111	1.082	1.089	2.80
43	DT14014.27	GENO48	1.081	1.085	1.092	1.087	1.086	0.78
44	DT14011.18	GENO49	1.087	1.100	1.087	1.080	1.088	-0.27
45	DT14069.13	GENO50	1.089	1.087	1.104	1.081	1.090	1.51
46	DT14026.21	GENO52	1.089	1.100	1.113	1.087	1.097	1.85
47	DT14042.24	GENO53	1.079	1.080	1.099	1.086	1.086	1.65
48	DT14090.11	GENO54	1.079	1.085	1.089	1.086	1.085	0.62
49	DT14071.19	GENO55	1.063	1.077	1.091	1.081	1.078	1.83
50	DT14027.08	GENO56	1.096	1.087	1.099	1.092	1.093	0.59
51	DT14034.03	GENO57	1.082	1.082	1.100	1.082	1.087	1.61
52	DT14057.36	GENO58	1.092	1.083	1.107	1.092	1.094	1.60
53	DT14062.08	GENO59	1.072	1.084	1.089	NA	1.082	1.02
54	DT14079.02	GENO60	1.081	1.097	1.103	1.091	1.093	1.35
55	DT14053.03	GENO61	1.068	NA	NA	NA	1.068	-0.03
56	DT13088.03	GENO63	1.077	1.079	1.089	1.078	1.081	1.00
57	DT14051.66	GENO64	1.091	1.085	1.100	1.096	1.093	0.90
58	DT13100.02	GENO65	1.086	1.091	1.095	1.089	1.090	0.61
59	DT13162.15	GENO66	1.072	1.087	1.097	1.094	1.088	1.48
60	DT13162.12	GENO67	1.073	1.088	1.101	1.085	1.087	1.89
61	DT11107.01	GENO68	1.082	1.084	1.087	1.081	1.083	0.40
62	ZIRVE	GENO69	1.073	NA	1.101	1.079	1.084	2.09
63	DT12012.02	GENO70	1.085	1.088	1.107	1.094	1.094	1.74
64	DT13136.22	GENO71	1.082	1.090	1.110	1.089	1.093	2.17
65	DT13045.74	GENO72	1.081	1.097	1.105	1.098	1.095	1.43
66	DT13124.21	GENO73	1.081	1.077	1.097	1.088	1.086	1.44
67	BORWINA	GENO74	1.072	1.072	1.083	1.081	1.077	0.85
68	BROOKE	GENO75	1.105	1.100	1.110	1.094	1.102	0.75
69	TESSA	GENO76	1.075	1.083	1.090	1.082	1.083	1.01
70	DT13143.49	GENO77	1.081	1.074	1.103	1.081	1.085	2.17
71	DT13130.48	GENO78	1.079	1.088	1.112	1.090	1.092	2.52
72	DT13143.54	GENO79	1.080	1.096	1.094	1.086	1.089	0.70
73	DT13007.03	GENO80	1.079	1.084	1.091	1.096	1.087	0.68
74	KUTUP	GENO81	1.094	1.096	1.112	1.093	1.099	1.56
75	DT13028.01	GENO82	1.091	1.083	1.101	1.095	1.093	1.07
76	DT13093.92	GENO83	1.075	1.080	1.097	1.092	1.086	1.57
77	DT13051.10	GENO84	1.091	1.082	1.090	1.081	1.086	0.32
78	DT13143.58	GENO85	1.070	1.074	1.088	1.079	1.078	1.36
79	DT13026.10	GENO86	1.081	1.092	1.100	1.092	1.091	1.22
80	DT13049.50	GENO87	1.072	1.075	1.079	1.079	1.076	0.44

81	DT13072.19	GENO88	1.090	1.095	1.094	1.088	1.092	0.24
82	DT13083.01	GENO89	1.069	1.064	1.104	1.077	1.079	3.15
83	LadyRosetta	GENO90	1.084	NA	1.101	NA	1.093	1.17
84	DT11007.01	GENO91	1.095	1.092	1.105	1.091	1.096	1.04
85	DT11108.02	GENO92	1.097	1.087	1.102	1.089	1.094	0.85
86	DORUK	GENO93	1.124	1.103	1.127	1.101	1.114	1.21
87	DT13085.01	GENO94	1.083	1.072	1.088	1.077	1.080	0.85
88	DT12068.21	GENO95	1.078	1.078	1.088	1.086	1.083	0.78
89	DT11088.01	GENO96	1.091	1.089	1.096	1.089	1.091	0.53
90	DT13045.42	GENO97	1.083	1.074	1.078	1.076	1.078	-0.08
91	DT13147.17	GENO98	1.080	1.083	1.086	1.075	1.081	0.52
92	DT13048.10	GENO99	1.071	1.083	1.094	1.086	1.083	1.49
93	DT13052.23	GENO100	1.078	1.090	1.105	1.088	1.090	1.92
94	DT13037.31	GENO101	1.097	1.084	1.105	1.091	1.094	1.18
95	DT13045.103	GENO102	1.077	1.076	1.103	1.074	1.082	2.39
96	DT13037.35	GENO103	1.073	1.099	1.099	1.078	1.087	1.50
97	DT13047.08	GENO104	1.085	1.089	1.101	1.092	1.092	1.21
98	DT13162.16	GENO105	1.076	1.079	1.090	1.076	1.080	1.16
99	DT13067.03	GENO106	1.094	1.078	1.089	1.081	1.086	0.21
100	SORAYA	GENO107	1.074	1.067	1.090	1.070	1.075	1.69
101	LAURA	GENO108	1.083	1.082	1.075	1.076	1.079	-0.58
102	SHEPODY	GENO109	1.079	1.074	1.092	1.087	1.083	1.19
103	43-111-11	GENO110	1.085	1.090	1.097	1.093	1.091	0.81
104	KARLENA	GENO111	1.098	1.102	1.106	1.097	1.101	0.61
105	139-101-11	GENO112	1.093	1.082	1.103	1.092	1.093	1.22
106	84-105-11	GENO113	1.082	1.087	1.098	1.087	1.089	1.21
107	NANDU	GENO114	1.109	1.114	1.111	NA	1.111	0.00
108	882-202-10	GENO115	1.095	1.093	1.106	1.084	1.095	1.20
109	TALENT	GENO116	1.103	1.095	1.098	1.093	1.097	-0.07
110	57-104-11	GENO117	1.086	1.091	1.091	1.090	1.089	0.24
111	878-202-10	GENO118	1.094	1.092	1.098	1.100	1.096	0.33
112	146-103-11	GENO120	1.102	1.097	1.110	1.105	1.103	0.81
113	SALUTE	GENO121	1.081	1.084	1.088	1.084	1.084	0.49
114	68-105-11	GENO122	1.089	1.095	1.104	1.093	1.095	1.11
115	63-113-11	GENO123	1.079	1.082	1.090	1.088	1.085	0.76
116	106-105-11	GENO124	1.096	NA	1.094	1.092	1.094	-0.06
117	939-201-10	GENO125	1.075	1.094	1.107	1.106	1.096	1.85
118	NIXE	GENO126	1.093	1.086	1.089	1.087	1.089	-0.07
119	51-109-11	GENO127	1.070	1.091	1.094	1.085	1.085	1.32
120	ETIKETSIZNORIKA	GENO128	1.095	1.104	1.080	1.102	1.095	-1.70
121	40-103-11	GENO130	1.095	1.084	1.094	1.089	1.091	0.32
122	99-115-11	GENO131	1.091	1.092	1.105	1.093	1.095	1.19
123	141-104-11	GENO132	1.101	1.102	1.103	1.101	1.102	0.15

124	89-105-11	GENO133	1.083	1.088	1.096	1.088	1.089	0.94
125	NAUTILUS	GENO134	1.107	1.088	1.105	1.100	1.100	0.47
126	157-103-11	GENO136	1.115	1.089	1.103	1.108	1.104	-0.22
127	133-112-11	GENO137	1.088	1.091	1.099	1.102	1.095	0.69
128	944-208-10	GENO138	1.106	1.101	1.110	1.108	1.106	0.47
129	PRIVELIGE	GENO139	1.077	1.086	1.102	1.093	1.089	1.74
130	966-203-10	GENO140	1.109	1.117	1.125	1.108	1.115	1.21
131	904-212-10	GENO141	1.095	1.100	1.093	1.089	1.094	-0.24
132	BETTINA	GENO142	1.089	1.082	1.084	1.083	1.085	-0.16
133	125-104-11	GENO143	1.099	1.099	1.109	1.098	1.101	0.91
134	SWING	GENO144	1.079	NA	NA	NA	1.079	0.46
135	758-109-09	GENO145	1.097	1.096	1.112	1.096	1.100	1.38
136	735-102-09	GENO146	1.106	1.102	1.109	1.101	1.105	0.46
137	99-102-11	GENO147	1.082	1.094	1.084	1.090	1.087	-0.29
138	TERRANA	GENO148	1.124	1.118	1.125	1.100	1.117	0.61
139	104-103-11	GENO149	1.072	1.088	1.101	1.089	1.087	1.88
140	SFHIT	GENO150	1.092	1.097	1.103	1.096	1.097	0.78
141	KIWI	GENO151	1.099	1.105	1.116	1.112	1.108	1.15
142	KIEBITZ	GENO152	1.103	1.093	1.112	1.096	1.101	1.19
143	BONUS	GENO153	1.088	1.093	1.102	1.092	1.094	1.05
144	509-104-09	GENO154	1.082	1.081	1.096	1.091	1.088	1.15
145	43-118-11	GENO155	1.081	1.081	1.095	1.102	1.090	0.94
146	BEO	GENO156	1.094	1.096	1.102	1.103	1.099	0.52
147	BALTICCREAM	GENO157	1.097	1.097	1.112	1.106	1.103	1.21
148	868-201-10	GENO158	1.093	1.096	1.098	1.101	1.097	0.24
149	860-201-10	GENO159	1.093	1.090	1.099	1.094	1.094	0.61
150	DUKATA	GENO160	1.076	1.091	1.096	1.096	1.090	1.06
151	84-107-11	GENO161	1.085	1.089	1.107	1.096	1.094	1.69
152	128-105-11	GENO162	1.118	1.111	1.108	1.110	1.112	-0.57
153	140-107-11	GENO163	1.107	1.103	1.114	1.092	1.104	0.96
154	PELIKAN	GENO164	1.088	1.088	1.099	1.090	1.091	0.95
155	KOLIBRI	GENO165	1.105	NA	1.105	NA	1.105	-0.01
156	82-119-11	GENO167	1.085	1.088	1.094	1.095	1.091	0.57
157	WENDY	GENO168	1.092	1.078	1.093	1.079	1.085	0.68
158	ROMANZE	GENO169	1.075	1.089	1.107	1.084	1.089	2.32
159	PRESTIGE	GENO170	1.103	1.100	1.106	1.102	1.103	0.37
160	MAXI	GENO171	1.092	1.106	1.120	1.106	1.106	1.89
161	FASAN	GENO172	1.088	1.096	1.109	1.099	1.098	1.48
162	Madaleine	GENO173	1.067	1.070	1.083	1.077	1.074	1.19
163	POMQUEEN	GENO174	1.088	1.088	1.101	1.083	1.090	1.23
164	MUNGO	GENO175	1.106	1.114	1.128	1.106	1.113	1.73
165	ALBATROS	GENO176	1.117	1.092	1.120	1.114	1.111	1.03
166	FIDELIA	GENO177	1.070	1.067	1.072	1.075	1.071	0.19

167	TACOMA	GENO178	1.093	1.067	1.092	1.079	1.083	0.87
168	BONZA	GENO179	1.123	1.124	1.144	1.117	1.127	1.93
169	ADRETTA	GENO180	1.093	1.096	1.110	1.092	1.098	1.44
170	POWER	GENO181	1.122	1.111	1.125	1.111	1.117	0.75
171	GOLDMARIE	GENO182	1.087	1.077	1.084	1.085	1.083	0.05
172	RITA	GENO183	1.083	1.089	1.091	1.091	1.089	0.42
173	SUMMERGOLD	GENO184	1.111	1.116	1.125	1.103	1.114	1.22
174	DIPLOMAT	GENO185	1.095	1.097	1.105	1.101	1.099	0.75
175	CASCADE	GENO186	1.088	1.086	1.091	1.084	1.087	0.38
176	SOLIST	GENO187	1.066	1.077	1.090	1.083	1.079	1.58
177	LOLITA	GENO188	1.088	1.075	1.091	1.078	1.083	0.79
178	KARATOP	GENO189	1.072	1.074	1.077	1.081	1.076	0.26
179	INARA	GENO190	1.084	1.084	1.093	NA	1.087	0.76
180	ACAPELLA	GENO191	1.092	1.090	1.108	1.093	1.096	1.47
181	ALLORA	GENO192	1.073	1.079	1.086	1.080	1.079	0.88
182	ARKULA	GENO193	1.103	1.083	NA	1.091	1.092	-0.23
183	TOKIO	GENO194	1.097	1.097	1.112	1.095	1.100	1.37
184	BIRTE	GENO195	1.083	1.082	1.083	1.081	1.082	0.06
185	900-205-10	GENO196	1.096	1.095	1.091	1.094	1.094	-0.39
186	MAXILLA	GENO197	1.104	1.098	1.109	1.091	1.101	0.81
187	TUCAN	GENO198	1.095	1.098	1.114	1.100	1.102	1.54
188	946-202-10	GENO199	1.099	1.098	1.118	1.096	1.103	1.77
189	KORMORAN	GENO200	1.099	1.121	1.141	1.112	1.118	2.92
190	JUMBO	GENO202	1.113	1.113	1.121	1.110	1.114	0.76
191	LOGO	GENO203	1.096	1.127	1.126	1.116	1.116	1.49
192	102-102-11	GENO204	1.074	1.084	1.085	1.081	1.081	0.59
		Mean	1.087	1.088	1.099	1.089	1.091	

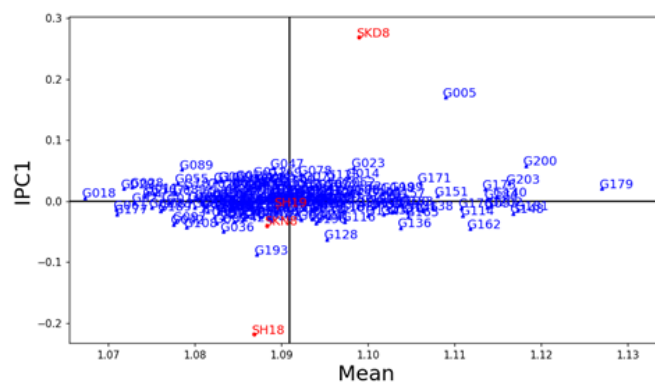


Fig.S2. Ammi biplot for mean of specific gravity of 192 genotypes across four environments (SH18, SKN18, SKD18, SH19) plotted against IPC1 (Interactive principal component)

APPENDIX-C Phenotypic data of reducing sugars “g/100 g dry weight” (RSS) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Codes	RSS_H18	RSS_KN18	RSS_KD18	RSS_H19	Mean RSS	b_i
1	JELLY	GENO2	0.10	0.11	0.10	NA	0.11	-0.06
2	RUMBA	GENO3	0.09	0.08	0.08	NA	0.08	0.82
3	HERMES	GENO4	0.10	0.09	0.11	NA	0.10	1.27
4	ALEGRIA	GENO5	0.11	0.10	0.10	NA	0.10	0.88
5	ROYAL	GENO6	0.05	0.02	0.13	0.08	0.07	-2.42
6	ELECTRA	GENO7	0.23	0.12	0.13	0.34	0.20	3.88
7	DT14003.01	GENO9	0.04	0.09	0.10	0.09	0.08	-2.23
8	DT14038.01	GENO10	0.16	0.04	0.04	0.20	0.11	4.58
9	DT14010.18	GENO11	0.45	0.12	0.08	0.40	0.26	13.90
10	DT14004.17	GENO12	0.17	0.12	0.09	0.15	0.13	2.88
11	DT14010.14	GENO13	0.06	0.07	0.10	0.08	0.08	-1.35
12	DT14085.03	GENO14	0.05	0.06	0.10	0.07	0.07	-1.68
13	DT14013.15	GENO16	0.25	NA	NA	0.20	0.22	8.39
14	DT14018.32	GENO18	0.32	0.10	0.05	0.48	0.24	10.03
15	DT14042.27	GENO19	0.05	0.05	0.05	0.09	0.06	0.00
16	DT14005.09	GENO20	0.11	0.41	0.14	0.19	0.21	-2.71
17	DT14030.11	GENO21	0.03	0.08	0.06	0.09	0.07	-1.26
18	DT14057.37	GENO22	0.05	0.13	0.08	0.22	0.12	-1.44
19	DT14065.01	GENO23	0.11	0.07	0.06	NA	0.08	1.85
20	DT14016.01	GENO24	0.23	0.04	0.11	0.25	0.16	4.99
21	DT14016.34	GENO25	0.30	0.56	0.39	0.25	0.38	-4.42
22	DT14078.03	GENO26	0.22	0.05	0.10	0.29	0.17	4.87
23	DT14028.03	GENO27	0.05	0.07	0.11	0.06	0.07	-2.06
24	DT14054.11	GENO28	0.54	0.35	0.06	0.59	0.38	16.66
25	DT14037.18	GENO29	0.15	0.06	0.10	0.31	0.15	2.14
26	DT14091.04	GENO30	0.21	0.09	0.15	0.16	0.15	2.64
27	DT14083.28	GENO31	0.05	0.23	0.09	NA	0.12	-2.34
28	DT14015.22	GENO32	0.12	0.14	0.17	0.18	0.15	-1.74
29	DT14051.15	GENO33	0.07	0.05	0.06	0.07	0.06	0.44
30	DT14047.38	GENO34	0.20	0.23	0.15	0.23	0.20	1.45
31	DT14026.04	GENO35	0.09	0.19	0.11	0.05	0.11	-1.23
32	DT14068.07	GENO36	0.12	0.14	0.12	0.19	0.14	-0.12
33	DT14063.12	GENO37	0.04	0.10	0.15	0.14	0.11	-3.91
34	DT14036.01	GENO38	0.03	NA	NA	NA	0.03	1.15
35	DT14055.25	GENO39	0.12	NA	NA	0.27	0.20	3.02
36	LadyOlympia	GENO41	0.19	0.09	0.04	0.17	0.12	5.44
37	BANBA	GENO42	0.11	0.09	0.09	0.07	0.09	0.76
38	VanGOGH	GENO43	0.10	0.14	0.02	0.14	0.10	2.36

39	DT14049.10	GENO44	0.07	0.11	0.10	NA	0.09	-1.20
40	DT14061.23	GENO45	0.04	0.03	0.11	0.09	0.07	-2.21
41	DT14006.07	GENO46	0.07	0.07	0.11	0.21	0.11	-1.30
42	DT14046.19	GENO47	0.17	0.10	0.06	0.25	0.15	3.97
43	DT14014.27	GENO48	0.16	0.09	0.07	0.21	0.13	3.32
44	DT14011.18	GENO49	0.08	0.12	0.06	0.19	0.12	0.42
45	DT14069.13	GENO50	0.09	0.05	0.12	0.13	0.10	-0.74
46	DT14026.21	GENO52	0.11	0.10	0.14	0.21	0.14	-0.91
47	DT14042.24	GENO53	0.05	0.13	0.13	0.21	0.13	-3.06
48	DT14090.11	GENO54	0.06	0.08	0.11	0.08	0.08	-1.74
49	DT14071.19	GENO55	0.34	0.37	0.12	0.40	0.30	6.96
50	DT14027.08	GENO56	0.07	0.07	0.09	0.06	0.07	-0.65
51	DT14034.03	GENO57	0.10	0.16	0.13	0.08	0.12	-1.32
52	DT14057.36	GENO58	0.04	0.22	0.13	0.07	0.11	-3.96
53	DT14062.08	GENO59	0.12	0.05	0.06	NA	0.08	2.35
54	DT14079.02	GENO60	0.08	0.07	0.10	0.18	0.11	-0.59
55	DT14053.03	GENO61	0.07	NA	NA	NA	0.07	2.67
56	DT13088.03	GENO63	0.22	0.10	0.10	0.28	0.17	4.58
57	DT14051.66	GENO64	0.10	0.07	0.08	0.13	0.10	0.82
58	DT13100.02	GENO65	0.07	0.05	0.08	0.09	0.07	-0.21
59	DT13162.15	GENO66	0.11	0.05	0.12	0.15	0.11	0.02
60	DT13162.12	GENO67	0.19	0.06	0.06	0.22	0.13	4.97
61	DT11107.01	GENO68	0.09	0.09	0.10	0.10	0.09	-0.32
62	ZIRVE	GENO69	0.38	NA	0.19	0.47	0.35	-1.82
63	DT12012.02	GENO70	0.07	0.14	0.16	0.05	0.10	-3.32
64	DT13136.22	GENO71	0.26	0.08	0.10	0.29	0.18	6.23
65	DT13045.74	GENO72	0.04	0.12	0.13	0.11	0.10	-3.38
66	DT13124.21	GENO73	0.10	0.06	0.07	0.10	0.08	1.20
67	BORWINA	GENO74	0.12	0.07	0.09	0.17	0.11	1.26
68	BROOKE	GENO75	0.05	0.10	0.06	0.07	0.07	-0.61
69	TESSA	GENO76	0.07	0.11	0.12	0.25	0.14	-1.85
70	DT13143.49	GENO77	0.28	0.22	0.15	0.26	0.23	4.56
71	DT13130.48	GENO78	0.08	0.09	0.07	0.09	0.08	0.27
72	DT13143.54	GENO79	0.18	0.04	0.07	0.22	0.13	4.38
73	DT13007.03	GENO80	0.08	0.11	0.10	0.04	0.08	-0.82
74	KUTUP	GENO81	0.13	0.05	0.15	0.16	0.12	-0.19
75	DT13028.01	GENO82	0.15	0.04	0.06	0.14	0.10	3.55
76	DT13093.92	GENO83	0.09	0.07	0.10	0.15	0.10	-0.21
77	DT13051.10	GENO84	0.16	0.11	0.12	0.26	0.16	1.59
78	DT13143.58	GENO85	0.24	0.09	0.14	0.28	0.19	4.11
79	DT13026.10	GENO86	0.10	0.08	0.09	0.07	0.09	0.44
80	DT13049.50	GENO87	0.16	0.09	0.20	0.18	0.16	-0.89
81	DT13072.19	GENO88	0.06	0.09	0.09	0.07	0.08	-1.15
82	DT13083.01	GENO89	0.11	0.08	0.07	0.29	0.13	1.47
83	LadyRosetta	GENO90	0.10	NA	0.14	NA	0.12	3.01
84	DT11007.01	GENO91	0.08	0.08	0.14	0.17	0.12	-1.95

85	DT11108.02	GENO92	0.10	0.08	0.12	0.09	0.10	-0.53
86	DORUK	GENO93	0.04	0.07	0.12	0.09	0.08	-2.77
87	DT13085.01	GENO94	0.15	0.09	0.09	0.20	0.13	2.29
88	DT12068.21	GENO95	0.16	0.07	0.15	0.22	0.15	0.84
89	DT11088.01	GENO96	0.09	0.05	0.07	0.12	0.08	0.88
90	DT13045.42	GENO97	0.07	0.07	0.06	0.30	0.12	0.32
91	DT13147.17	GENO98	0.35	0.12	0.16	0.38	0.25	7.49
92	DT13048.10	GENO99	0.15	0.10	0.09	0.27	0.15	2.23
93	DT13052.23	GENO100	0.17	0.07	0.06	0.14	0.11	4.14
94	DT13037.31	GENO101	0.06	0.04	0.07	0.07	0.06	-0.21
95	DT13045.103	GENO102	0.05	0.14	0.17	0.32	0.17	-4.41
96	DT13037.35	GENO103	0.17	0.09	0.13	0.28	0.17	1.76
97	DT13047.08	GENO104	0.07	0.04	0.13	0.17	0.10	-1.77
98	DT13162.16	GENO105	0.12	0.09	0.09	0.29	0.15	1.15
99	DT13067.03	GENO106	0.24	0.04	0.10	0.22	0.15	5.70
100	SORAYA	GENO107	0.17	0.29	0.07	0.15	0.17	2.55
101	LAURA	GENO108	0.09	0.13	0.09	0.12	0.11	-0.23
102	SHEPODY	GENO109	0.12	0.05	0.09	0.11	0.09	1.38
103	43-111-11	GENO110	0.19	0.07	0.09	0.17	0.13	3.94
104	KARLENA	GENO111	0.04	0.10	0.05	0.03	0.05	-0.67
105	139-101-11	GENO112	0.21	0.10	0.11	0.16	0.14	3.88
106	84-105-11	GENO113	0.05	0.09	0.09	0.09	0.08	-1.53
107	NANDU	GENO114	0.04	0.06	0.09	NA	0.06	-1.74
108	882-202-10	GENO115	0.03	0.04	0.11	0.03	0.05	-2.65
109	TALENT	GENO116	0.07	0.10	0.11	0.12	0.10	-1.47
110	57-104-11	GENO117	0.09	0.07	0.06	0.08	0.08	1.09
111	878-202-10	GENO118	0.16	0.13	0.12	0.19	0.15	1.47
112	146-103-11	GENO120	0.09	0.12	0.05	0.06	0.08	1.12
113	SALUTE	GENO121	0.11	0.09	0.08	0.14	0.11	1.09
114	68-105-11	GENO122	0.06	0.06	0.08	0.06	0.07	-0.65
115	63-113-11	GENO123	0.17	0.07	0.30	0.20	0.18	-3.64
116	106-105-11	GENO124	0.05	NA	0.06	0.06	0.06	-0.38
117	939-201-10	GENO125	0.05	0.07	0.05	0.07	0.06	-0.12
118	NIXE	GENO126	0.04	0.11	0.06	0.09	0.08	-1.05
119	51-109-11	GENO127	0.12	0.09	0.08	0.23	0.13	1.47
120	ETIKETSIZNORIK	GENO128	0.09	0.05	0.12	0.08	0.09	-0.74
121	40-103-11	GENO130	0.11	0.17	0.07	0.19	0.14	0.95
122	99-115-11	GENO131	0.04	0.10	0.06	0.05	0.06	-1.00
123	141-104-11	GENO132	0.17	0.06	0.06	0.14	0.11	4.20
124	89-105-11	GENO133	0.05	0.05	0.10	0.10	0.07	-1.62
125	NAUTILUS	GENO134	0.09	0.07	0.05	0.10	0.08	1.41
126	157-103-11	GENO136	0.09	0.04	0.04	0.07	0.06	1.91
127	133-112-11	GENO137	0.12	0.04	0.04	0.10	0.08	3.06
128	944-208-10	GENO138	0.08	0.14	0.06	0.14	0.10	0.30
129	PRIVELIGE	GENO139	0.16	0.07	0.13	0.13	0.12	1.49

130	966-203-10	GENO140	0.06	0.20	0.03	0.13	0.11	0.16
131	904-212-10	GENO141	0.08	0.14	0.10	0.09	0.10	-1.00
132	BETTINA	GENO142	0.06	0.08	0.07	0.07	0.07	-0.44
133	125-104-11	GENO143	0.04	0.03	0.08	0.06	0.05	-1.24
134	SWING	GENO144	0.02	NA	NA	NA	0.02	0.76
135	758-109-09	GENO145	0.07	0.08	0.15	0.13	0.11	-2.65
136	735-102-09	GENO146	0.04	0.06	0.12	0.09	0.08	-2.71
137	99-102-11	GENO147	0.13	0.08	0.10	0.18	0.12	1.26
138	TERRANA	GENO148	0.07	0.06	0.04	0.09	0.06	1.03
139	104-103-11	GENO149	0.08	0.10	0.07	0.09	0.09	0.21
140	SFHIT	GENO150	0.07	0.07	0.04	0.05	0.06	0.97
141	KIWI	GENO151	0.13	0.14	0.12	0.20	0.15	0.27
142	KIEBITZ	GENO152	0.11	0.09	0.10	0.14	0.11	0.44
143	BONUS	GENO153	0.23	0.14	0.14	0.17	0.17	3.44
144	509-104-09	GENO154	0.04	0.05	0.18	0.07	0.08	-4.60
145	43-118-11	GENO155	0.05	0.15	0.09	0.08	0.09	-1.88
146	BEO	GENO156	0.11	0.08	0.08	0.08	0.09	1.15
147	BALTICCREAM	GENO157	0.06	0.10	0.04	0.05	0.06	0.42
148	868-201-10	GENO158	0.08	0.05	0.16	0.09	0.10	-2.42
149	860-201-10	GENO159	0.14	0.13	0.09	0.15	0.13	1.68
150	DUKATA	GENO160	0.12	0.10	0.08	0.09	0.10	1.41
151	84-107-11	GENO161	0.17	0.09	0.09	0.14	0.12	3.06
152	128-105-11	GENO162	0.06	0.10	0.14	0.04	0.08	-2.82
153	140-107-11	GENO163	0.09	0.12	0.09	0.06	0.09	-0.17
154	PELIKAN	GENO164	0.14	0.07	0.03	0.20	0.11	3.97
155	KOLIBRI	GENO165	0.06	NA	0.06	NA	0.06	1.95
156	82-119-11	GENO167	0.08	0.05	0.11	0.09	0.08	-0.80
157	WENDY	GENO168	0.19	0.28	0.02	0.27	0.19	4.99
158	ROMANZE	GENO169	0.21	0.08	0.06	0.23	0.15	5.61
159	PRESTIGE	GENO170	0.09	0.06	0.04	0.08	0.07	1.79
160	MAXI	GENO171	0.19	0.06	0.11	0.15	0.13	3.35
161	FASAN	GENO172	0.08	0.09	0.10	0.11	0.09	-0.71
162	Madaleine	GENO173	0.61	0.15	0.07	0.50	0.33	20.17
163	POMQUEEN	GENO174	0.07	0.08	0.04	0.06	0.06	0.91
164	MUNGO	GENO175	0.06	0.07	0.07	0.05	0.06	-0.38
165	ALBATROS	GENO176	0.04	0.09	0.05	0.06	0.06	-0.61
166	FIDELIA	GENO177	0.23	0.36	0.09	0.39	0.27	3.79
167	TACOMA	GENO178	0.02	0.07	0.09	0.10	0.07	-2.56
168	BONZA	GENO179	0.06	0.06	0.11	0.04	0.07	-1.62
169	ADRETTA	GENO180	0.14	0.17	0.09	0.16	0.14	1.45
170	POWER	GENO181	0.08	0.08	0.03	0.02	0.05	1.62
171	GOLDMARIE	GENO182	0.17	0.16	0.08	0.23	0.16	2.98
172	RITA	GENO183	0.15	0.12	0.11	0.11	0.12	1.47
173	SUMMERGOLD	GENO184	0.05	0.07	0.06	0.08	0.06	-0.44
174	DIPLOMAT	GENO185	0.05	0.05	0.06	0.09	0.06	-0.32

175	CASCADA	GENO186	0.18	0.10	0.11	0.23	0.15	2.73
176	SOLIST	GENO187	0.17	0.19	0.05	0.24	0.16	3.77
177	LOLITA	GENO188	0.06	0.16	0.05	0.28	0.14	-0.25
178	KARATOP	GENO189	0.09	0.15	0.03	0.16	0.11	1.60
179	INARA	GENO190	0.15	0.10	0.09	NA	0.11	2.23
180	ACAPELLA	GENO191	0.20	0.11	0.04	0.16	0.12	5.71
181	ALLORA	GENO192	0.42	0.05	0.08	0.47	0.26	13.16
182	ARKULA	GENO193	0.14	0.09	NA	0.18	0.14	-1.01
183	TOKIO	GENO194	0.06	0.12	0.06	0.04	0.07	-0.35
184	BIRTE	GENO195	0.19	0.29	0.14	0.22	0.21	1.04
185	900-205-10	GENO196	0.17	0.14	0.08	0.20	0.15	3.09
186	MAXILLA	GENO197	0.08	0.06	0.05	0.17	0.09	1.09
187	TUCAN	GENO198	0.05	0.04	0.08	0.07	0.06	-0.91
188	946-202-10	GENO199	0.06	0.09	0.10	0.05	0.08	-1.47
189	KORMORAN	GENO200	0.03	0.07	0.06	0.03	0.05	-1.20
190	JUMBO	GENO202	0.05	0.06	0.12	0.06	0.07	-2.33
191	LOGO	GENO203	0.08	0.11	0.06	0.04	0.07	0.47
192	102-102-11	GENO204	0.07	0.07	0.07	0.06	0.07	0.00
		Mean	0.12	0.10	0.09	0.16	0.12	

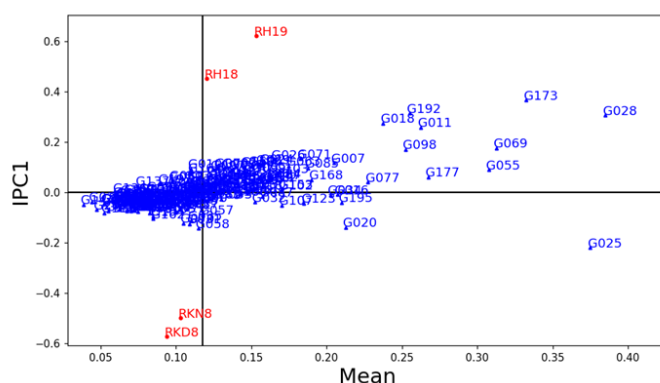


Fig.S3. Ammi biplot for mean of reducing sugars of 192 genotypes across four environments (RH18, RKN18, RKD18, RH19) plotted against IPC1 (Interactive principal component)

APPENDIX-D Phenotypic data of sucrose “g/100g dry weight” (SUC) showing the estimated values measured across four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Codes	SUC_ H18	SUC_ KN18	SUC_ KD18	SUC_ H19	Mean SUC	b_i
1	JELLY	GENO2	0.09	0.11	0.12	NA	0.11	0.54
2	RUMBA	GENO3	0.13	0.10	0.14	NA	0.12	1.03
3	HERMES	GENO4	0.10	0.18	0.14	NA	0.14	-0.53
4	ALEGRIA	GENO5	0.08	0.08	0.12	NA	0.09	1.24
5	ROYAL	GENO6	0.12	0.04	0.09	0.11	0.09	0.86
6	ELECTRA	GENO7	0.24	0.06	0.23	0.27	0.20	3.86
7	DT14003.01	GENO9	0.06	0.07	0.05	0.12	0.07	-0.57
8	DT14038.01	GENO10	0.11	0.03	0.06	0.12	0.08	0.19
9	DT14010.18	GENO11	0.08	0.06	0.15	0.16	0.11	2.81
10	DT14004.17	GENO12	0.06	0.08	0.24	0.11	0.12	5.56
11	DT14010.14	GENO13	0.07	0.07	0.08	0.10	0.08	0.33
12	DT14085.03	GENO14	0.09	0.06	0.08	0.09	0.08	0.36
13	DT14013.15	GENO16	0.01	NA	NA	0.12	0.06	-2.90
14	DT14018.32	GENO18	0.11	0.10	0.33	0.37	0.23	7.60
15	DT14042.27	GENO19	0.12	0.02	0.12	0.11	0.09	2.33
16	DT14005.09	GENO20	0.06	0.01	0.14	0.09	0.08	3.84
17	DT14030.11	GENO21	0.06	0.12	0.12	0.19	0.12	0.61
18	DT14057.37	GENO22	0.09	0.07	0.20	0.11	0.12	4.15
19	DT14065.01	GENO23	0.12	0.07	0.16	NA	0.12	2.50
20	DT14016.01	GENO24	0.17	0.11	0.16	0.12	0.14	1.06
21	DT14016.34	GENO25	0.05	0.02	0.11	0.09	0.07	2.71
22	DT14078.03	GENO26	0.11	0.14	0.16	0.13	0.13	0.97
23	DT14028.03	GENO27	0.14	0.05	0.09	0.09	0.10	0.42
24	DT14054.11	GENO28	0.02	0.04	0.05	0.09	0.05	0.54
25	DT14037.18	GENO29	0.06	0.04	0.06	0.19	0.09	0.47
26	DT14091.04	GENO30	0.03	0.07	0.15	0.10	0.09	3.08
27	DT14083.28	GENO31	0.09	0.02	0.09	NA	0.07	1.63
28	DT14015.22	GENO32	0.10	0.06	0.12	0.11	0.10	1.60
29	DT14051.15	GENO33	0.12	0.20	0.28	0.19	0.20	3.49
30	DT14047.38	GENO34	0.02	0.07	0.14	0.11	0.09	2.85
31	DT14026.04	GENO35	0.07	0.12	0.07	0.13	0.10	-1.17
32	DT14068.07	GENO36	0.13	0.05	0.15	0.19	0.13	2.53
33	DT14063.12	GENO37	0.10	0.14	0.08	0.09	0.10	-1.60
34	DT14036.01	GENO38	0.09	NA	NA	NA	0.09	-0.91
35	DT14055.25	GENO39	0.08	NA	NA	0.13	0.10	-3.84
36	LadyOlympia	GENO41	0.10	0.13	0.18	0.10	0.13	1.98
37	BANBA	GENO42	0.10	0.01	0.09	0.09	0.08	1.76
38	VanGOGH	GENO43	0.10	0.09	0.10	0.10	0.10	0.23
39	DT14049.10	GENO44	0.08	0.34	0.16	NA	0.19	-3.38

40	DT14061.23	GENO45	0.10	0.09	0.18	0.11	0.12	2.91
41	DT14006.07	GENO46	0.05	0.03	0.05	0.11	0.06	0.47
42	DT14046.19	GENO47	0.19	0.09	0.13	0.21	0.15	0.32
43	DT14014.27	GENO48	0.06	0.05	0.09	0.09	0.07	1.24
44	DT14011.18	GENO49	0.06	0.11	0.11	0.12	0.10	0.51
45	DT14069.13	GENO50	0.06	0.05	0.08	0.11	0.07	0.90
46	DT14026.21	GENO52	0.10	0.18	0.10	0.09	0.12	-1.87
47	DT14042.24	GENO53	0.06	0.09	0.03	0.08	0.07	-1.70
48	DT14090.11	GENO54	0.09	0.04	0.04	0.12	0.07	-0.51
49	DT14071.19	GENO55	0.39	0.34	0.25	0.49	0.37	-3.52
50	DT14027.08	GENO56	0.12	0.07	0.13	0.11	0.11	1.50
51	DT14034.03	GENO57	0.17	0.23	0.30	0.11	0.20	2.95
52	DT14057.36	GENO58	0.07	0.07	0.10	0.12	0.09	1.00
53	DT14062.08	GENO59	0.09	0.13	0.12	NA	0.11	0.07
54	DT14079.02	GENO60	0.14	0.07	0.14	0.12	0.12	1.63
55	DT14053.03	GENO61	0.11	NA	NA	NA	0.11	-1.12
56	DT13088.03	GENO63	0.09	0.13	0.22	0.10	0.13	3.42
57	DT14051.66	GENO64	0.08	0.04	0.05	0.10	0.07	-0.07
58	DT13100.02	GENO65	0.13	0.06	0.13	0.19	0.13	1.63
59	DT13162.15	GENO66	0.08	0.04	0.19	0.11	0.11	4.61
60	DT13162.12	GENO67	0.06	0.10	0.15	0.12	0.11	2.08
61	DT11107.01	GENO68	0.12	0.06	0.12	0.15	0.11	1.40
62	ZIRVE	GENO69	0.03	NA	0.11	0.12	0.09	1.15
63	DT12012.02	GENO70	0.09	0.02	0.64	0.09	0.21	20.04
64	DT13136.22	GENO71	0.20	0.17	0.20	0.34	0.23	0.70
65	DT13045.74	GENO72	0.09	0.11	0.07	0.10	0.09	-1.14
66	DT13124.21	GENO73	0.05	0.04	0.04	0.07	0.05	-0.10
67	BORWINA	GENO74	0.06	0.03	0.14	0.05	0.07	3.38
68	BROOKE	GENO75	0.09	0.10	0.07	0.10	0.09	-0.90
69	TESSA	GENO76	0.09	0.10	0.02	0.10	0.08	-2.58
70	DT13143.49	GENO77	0.27	0.17	0.41	0.30	0.28	7.02
71	DT13130.48	GENO78	0.10	0.04	0.18	0.10	0.11	4.08
72	DT13143.54	GENO79	0.06	0.05	0.04	0.12	0.07	-0.44
73	DT13007.03	GENO80	0.04	0.07	0.10	0.10	0.08	1.29
74	KUTUP	GENO81	0.06	0.08	0.09	0.09	0.08	0.54
75	DT13028.01	GENO82	0.10	0.06	0.07	0.10	0.08	-0.07
76	DT13093.92	GENO83	0.03	0.03	0.27	0.12	0.11	8.03
77	DT13051.10	GENO84	0.10	0.02	0.06	0.12	0.08	0.53
78	DT13143.58	GENO85	0.14	0.07	0.34	0.12	0.17	8.33
79	DT13026.10	GENO86	0.16	0.16	0.20	0.09	0.15	1.34
80	DT13049.50	GENO87	0.07	0.04	0.24	0.12	0.12	6.39
81	DT13072.19	GENO88	0.09	0.08	0.07	0.11	0.09	-0.44
82	DT13083.01	GENO89	0.08	0.12	0.08	0.11	0.10	-0.93
83	LadyRosetta	GENO90	0.09	NA	0.09	NA	0.09	-3.01
84	DT11007.01	GENO91	0.07	0.05	0.05	0.06	0.06	-0.20
85	DT11108.02	GENO92	0.04	0.03	0.14	0.20	0.10	3.58

86	DORUK	GENO93	0.09	0.25	0.07	0.10	0.13	-4.40
87	DT13085.01	GENO94	0.11	0.07	0.11	0.12	0.10	0.93
88	DT12068.21	GENO95	0.14	0.14	0.09	0.11	0.12	-1.67
89	DT11088.01	GENO96	0.09	0.09	0.07	0.10	0.09	-0.67
90	DT13045.42	GENO97	0.21	0.04	0.28	0.21	0.19	6.31
91	DT13147.17	GENO98	0.06	0.05	0.08	0.12	0.08	0.90
92	DT13048.10	GENO99	0.04	0.09	0.23	0.29	0.16	5.19
93	DT13052.23	GENO100	0.19	0.10	0.18	0.25	0.18	1.76
94	DT13037.31	GENO101	0.10	0.24	0.17	0.10	0.15	-0.92
95	DT13045.103	GENO102	0.06	0.04	0.14	0.12	0.09	3.14
96	DT13037.35	GENO103	0.05	0.05	0.13	0.12	0.09	2.68
97	DT13047.08	GENO104	0.10	0.06	0.08	0.11	0.09	0.26
98	DT13162.16	GENO105	0.26	0.16	0.15	0.29	0.21	-1.35
99	DT13067.03	GENO106	0.07	0.16	0.17	0.26	0.16	1.25
100	SORAYA	GENO107	0.16	0.21	0.09	0.17	0.16	-3.51
101	LAURA	GENO108	0.05	0.03	0.08	0.09	0.06	1.47
102	SHEPODY	GENO109	0.09	0.06	0.08	0.10	0.08	0.36
103	43-111-11	GENO110	0.08	0.09	0.11	0.12	0.10	0.77
104	KARLENA	GENO111	0.09	0.06	0.15	0.12	0.11	2.71
105	139-101-11	GENO112	0.14	0.26	0.23	0.19	0.21	0.21
106	84-105-11	GENO113	0.07	0.05	0.07	0.17	0.09	0.47
107	NANDU	GENO114	0.09	0.05	0.14	NA	0.09	2.61
108	882-202-10	GENO115	0.09	0.06	0.07	0.09	0.08	0.03
109	TALENT	GENO116	0.09	0.08	0.12	0.12	0.10	1.24
110	57-104-11	GENO117	0.04	0.04	0.09	0.10	0.07	1.67
111	878-202-10	GENO118	0.17	0.06	0.10	0.18	0.13	0.22
112	146-103-11	GENO120	0.10	0.04	0.10	0.13	0.09	1.40
113	SALUTE	GENO121	0.09	0.07	0.18	0.10	0.11	3.48
114	68-105-11	GENO122	0.13	0.08	0.13	0.09	0.11	1.17
115	63-113-11	GENO123	0.07	0.14	0.13	0.11	0.11	0.38
116	106-105-11	GENO124	0.04	NA	0.02	0.05	0.03	0.80
117	939-201-10	GENO125	0.04	0.04	0.06	0.09	0.06	0.67
118	NIXE	GENO126	0.10	0.07	0.21	0.10	0.12	4.38
119	51-109-11	GENO127	0.08	0.08	0.16	0.15	0.12	2.68
120	ETIKETSIZNORIK	GENO128	0.06	0.06	0.03	0.11	0.06	-1.00
121	40-103-11	GENO130	0.06	0.15	0.12	0.11	0.11	-0.09
122	99-115-11	GENO131	0.08	0.08	0.10	0.09	0.09	0.67
123	141-104-11	GENO132	0.42	0.04	0.13	0.14	0.18	-0.85
124	89-105-11	GENO133	0.11	0.07	0.13	0.08	0.10	1.60
125	NAUTILUS	GENO134	0.13	0.19	0.42	0.09	0.21	8.31
126	157-103-11	GENO136	0.07	0.09	0.12	0.09	0.09	1.21
127	133-112-11	GENO137	0.08	0.03	0.06	0.10	0.07	0.50
128	944-208-10	GENO138	0.04	0.08	0.04	0.09	0.06	-0.93
129	PRIVELIGE	GENO139	0.17	0.12	0.27	0.28	0.21	4.51
130	966-203-10	GENO140	0.05	0.19	0.07	0.09	0.10	-2.59

131	904-212-10	GENO141	0.05	0.20	0.15	0.20	0.15	-0.15
132	BETTINA	GENO142	0.06	0.05	0.15	0.09	0.09	3.25
133	125-104-11	GENO143	0.07	0.12	0.17	0.09	0.11	2.18
134	SWING	GENO144	0.08	NA	NA	NA	0.08	-0.81
135	758-109-09	GENO145	0.09	0.05	0.04	0.10	0.07	-0.74
136	735-102-09	GENO146	0.09	0.04	0.07	0.08	0.07	0.50
137	99-102-11	GENO147	0.11	0.04	0.05	0.11	0.08	-0.38
138	TERRANA	GENO148	0.10	0.10	0.13	0.10	0.11	1.00
139	104-103-11	GENO149	0.07	0.14	0.08	0.10	0.10	-1.30
140	SFHIT	GENO150	0.10	0.06	0.04	0.19	0.10	-1.08
141	KIWI	GENO151	0.07	0.07	0.12	0.10	0.09	1.67
142	KIEBITZ	GENO152	0.11	0.06	0.09	0.10	0.09	0.50
143	BONUS	GENO153	0.07	0.07	0.09	0.11	0.08	0.67
144	509-104-09	GENO154	0.19	0.05	0.29	0.09	0.16	6.61
145	43-118-11	GENO155	0.12	0.06	0.06	0.10	0.08	-0.61
146	BEO	GENO156	0.11	0.17	0.13	0.05	0.12	-0.73
147	BALTICCREAM	GENO157	0.07	0.08	0.06	0.09	0.08	-0.57
148	868-201-10	GENO158	0.10	0.11	0.07	0.10	0.09	-1.24
149	860-201-10	GENO159	0.10	0.06	0.06	0.09	0.08	-0.41
150	DUKATA	GENO160	0.12	0.07	0.06	0.10	0.09	-0.84
151	84-107-11	GENO161	0.07	0.07	0.08	0.09	0.08	0.33
152	128-105-11	GENO162	0.06	0.06	0.09	0.03	0.06	1.00
153	140-107-11	GENO163	0.06	0.08	0.06	0.09	0.07	-0.47
154	PELIKAN	GENO164	0.05	0.09	0.07	0.10	0.07	-0.26
155	KOLIBRI	GENO165	0.09	NA	0.18	NA	0.14	-5.11
156	82-119-11	GENO167	0.09	0.12	0.22	0.09	0.13	3.65
157	WENDY	GENO168	0.11	0.07	0.12	0.11	0.10	1.27
158	ROMANZE	GENO169	0.03	0.08	0.04	0.11	0.06	-0.83
159	PRESTIGE	GENO170	0.10	0.14	0.07	0.09	0.10	-1.94
160	MAXI	GENO171	0.26	0.09	0.09	0.13	0.14	-1.73
161	FASAN	GENO172	0.08	0.10	0.08	0.12	0.10	-0.47
162	Madaleine	GENO173	0.06	0.06	0.05	0.12	0.07	-0.33
163	POMQUEEN	GENO174	0.08	0.05	0.05	0.09	0.07	-0.30
164	MUNGO	GENO175	0.10	0.12	0.27	0.11	0.15	5.22
165	ALBATROS	GENO176	0.07	0.18	0.11	0.09	0.11	-1.23
166	FIDELIA	GENO177	0.15	0.07	0.13	0.10	0.11	1.20
167	TACOMA	GENO178	0.08	0.08	0.18	0.09	0.11	3.35
168	BONZA	GENO179	0.12	0.06	0.13	0.09	0.10	1.73
169	ADRETTA	GENO180	0.09	0.09	0.05	0.10	0.08	-1.34
170	POWER	GENO181	0.08	0.08	0.11	0.11	0.10	1.00
171	GOLDMARIE	GENO182	0.20	0.14	0.17	0.12	0.16	0.39
172	RITA	GENO183	0.10	0.05	0.11	0.09	0.09	1.50
173	SUMMERGOLD	GENO184	0.08	0.14	0.18	0.14	0.14	1.95
174	DIPLOMAT	GENO185	0.06	0.07	0.06	0.10	0.07	-0.23
175	CASCADA	GENO186	0.23	0.20	0.22	0.27	0.23	0.36

176	SOLIST	GENO187	0.24	0.28	0.15	0.20	0.22	-3.95
177	LOLITA	GENO188	0.09	0.10	0.11	0.09	0.10	0.44
178	KARATOP	GENO189	0.07	0.05	0.06	0.09	0.07	0.13
179	INARA	GENO190	0.22	0.18	0.25	NA	0.21	1.94
180	ACAPELLA	GENO191	0.07	0.06	0.08	0.10	0.08	0.57
181	ALLORA	GENO192	0.22	0.09	0.15	0.12	0.15	0.69
182	ARKULA	GENO193	0.12	0.22	NA	0.11	0.15	-2.67
183	TOKIO	GENO194	0.11	0.12	0.06	0.11	0.10	-1.91
184	BIRTE	GENO195	0.14	0.23	0.24	0.18	0.20	1.25
185	900-205-10	GENO196	0.12	0.11	0.19	0.10	0.13	2.58
186	MAXILLA	GENO197	0.05	0.05	0.04	0.10	0.06	-0.33
187	TUCAN	GENO198	0.08	0.06	0.11	0.10	0.09	1.47
188	946-202-10	GENO199	0.05	0.05	0.10	0.09	0.07	1.67
189	KORMORAN	GENO200	0.04	0.14	0.20	0.09	0.11	3.02
190	JUMBO	GENO202	0.11	0.06	0.09	0.09	0.09	0.50
191	LOGO	GENO203	0.11	0.26	0.22	0.12	0.18	0.18
192	102-102-11	GENO204	0.07	0.14	0.10	0.09	0.10	-0.63
		Mean	0.10	0.09	0.13	0.12	0.11	

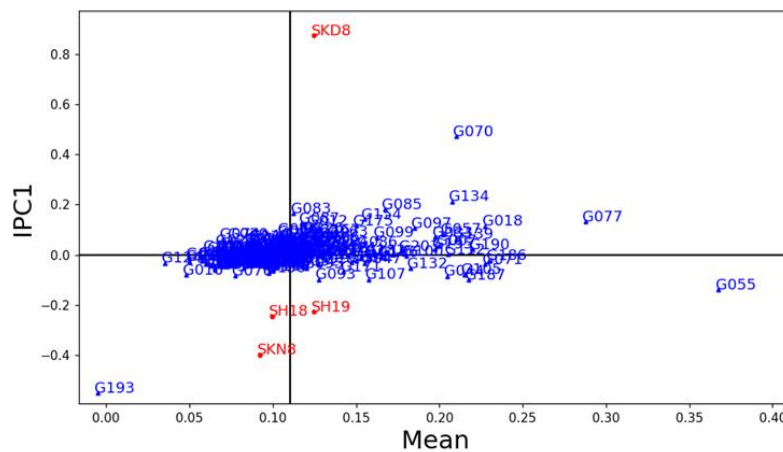


Fig. S4. Ammi biplot for mean of sucrose of 192 genotypes across four environments (SH18, SKN18, SKD18, SH19) plotted against IPC1 (Interactive principal component).

APPENDIX-E Phenotypic data of free asparagine “g/100 g dry weight” (ASP) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S.No.	Genotype Names	Codes	ASP_H18	ASP_KN18	ASP_KD18	ASP_H19	Mean ASP	b_i
1	JELLY	GENO2	0.13	0.08	0.15	NA	0.12	3.03
2	RUMBA	GENO3	0.13	0.09	0.16	NA	0.13	3.18
3	HERMES	GENO4	0.15	0.11	0.14	NA	0.13	1.04
4	ALEGRIA	GENO5	0.11	0.11	0.11	NA	0.11	0.00
5	ROYAL	GENO6	0.13	0.06	0.11	0.11	0.11	1.68
6	ELECTRA	GENO7	0.11	0.12	0.12	0.13	0.12	0.14
7	DT14003.01	GENO9	0.12	0.10	0.14	0.13	0.12	1.86
8	DT14038.01	GENO10	0.13	0.11	0.14	0.13	0.13	1.23
9	DT14010.18	GENO11	0.15	0.12	0.15	0.15	0.14	1.18
10	DT14004.17	GENO12	0.12	0.16	0.11	0.09	0.12	-2.11
11	DT14010.14	GENO13	0.08	0.07	0.11	0.10	0.09	2.00
12	DT14085.03	GENO14	0.11	0.08	0.08	0.09	0.09	-0.42
13	DT14013.15	GENO16	0.22	NA	NA	0.23	0.22	-2.14
14	DT14018.32	GENO18	0.16	0.10	0.09	0.15	0.12	-1.38
15	DT14042.27	GENO19	0.17	0.18	0.16	0.12	0.16	-0.93
16	DT14005.09	GENO20	0.11	0.11	0.07	0.06	0.09	-2.14
17	DT14030.11	GENO21	0.13	0.11	0.10	0.14	0.12	-0.82
18	DT14057.37	GENO22	0.11	0.15	0.19	0.12	0.14	2.70
19	DT14065.01	GENO23	0.11	0.10	0.14	NA	0.11	2.00
20	DT14016.01	GENO24	0.09	0.17	0.19	0.11	0.14	2.20
21	DT14016.34	GENO25	0.15	0.12	0.18	0.15	0.15	2.78
22	DT14078.03	GENO26	0.16	0.10	0.20	0.14	0.15	4.50
23	DT14028.03	GENO27	0.13	0.13	0.13	0.13	0.13	0.00
24	DT14054.11	GENO28	0.10	0.19	0.24	0.14	0.17	3.95
25	DT14037.18	GENO29	0.16	0.17	0.23	0.18	0.18	3.35
26	DT14091.04	GENO30	0.12	0.14	0.17	0.06	0.12	1.89
27	DT14083.28	GENO31	0.15	0.12	0.16	NA	0.14	1.71
28	DT14015.22	GENO32	0.19	0.10	0.13	0.16	0.15	0.33
29	DT14051.15	GENO33	0.12	0.13	0.12	0.12	0.12	-0.39
30	DT14047.38	GENO34	0.17	0.14	0.10	0.13	0.14	-2.56
31	DT14026.04	GENO35	0.16	0.08	0.16	0.12	0.13	3.14
32	DT14068.07	GENO36	0.11	0.10	0.15	0.10	0.11	2.53
33	DT14063.12	GENO37	0.12	0.14	0.25	0.12	0.16	6.16
34	DT14036.01	GENO38	0.16	NA	NA	NA	0.16	-2.26
35	DT14055.25	GENO39	0.16	NA	NA	0.10	0.13	-6.19
36	LadyOlympia	GENO41	0.14	0.09	0.11	0.12	0.12	0.36
37	BANBA	GENO42	0.12	0.07	0.11	0.09	0.10	1.43
38	VanGOGH	GENO43	0.13	0.13	0.14	0.13	0.13	0.53

39	DT14049.10	GENO44	0.16	0.16	0.20	NA	0.17	2.14
40	DT14061.23	GENO45	0.12	0.13	0.19	0.11	0.14	3.35
41	DT14006.07	GENO46	0.07	0.14	0.13	0.09	0.11	0.46
42	DT14046.19	GENO47	0.14	0.11	0.16	0.14	0.14	2.25
43	DT14014.27	GENO48	0.14	0.17	0.14	0.11	0.14	-1.18
44	DT14011.18	GENO49	0.12	0.11	0.13	0.10	0.12	0.93
45	DT14069.13	GENO50	0.13	0.11	0.14	0.13	0.13	1.23
46	DT14026.21	GENO52	0.14	0.09	0.15	0.14	0.13	2.50
47	DT14042.24	GENO53	0.13	0.18	0.21	0.09	0.15	2.31
48	DT14090.11	GENO54	0.18	0.15	0.16	0.16	0.16	0.11
49	DT14071.19	GENO55	0.09	0.12	0.08	0.13	0.10	-1.71
50	DT14027.08	GENO56	0.11	0.10	0.18	0.12	0.13	4.13
51	DT14034.03	GENO57	0.13	0.16	0.19	0.15	0.16	2.03
52	DT14057.36	GENO58	0.13	0.17	0.25	0.09	0.16	4.84
53	DT14062.08	GENO59	0.12	0.09	0.15	NA	0.12	2.78
54	DT14079.02	GENO60	0.14	0.08	0.16	0.11	0.12	3.43
55	DT14053.03	GENO61	0.16	NA	NA	NA	0.16	-2.26
56	DT13088.03	GENO63	0.09	0.15	0.19	0.13	0.14	2.99
57	DT14051.66	GENO64	0.12	0.11	0.13	0.14	0.12	0.93
58	DT13100.02	GENO65	0.12	0.13	0.18	0.11	0.13	2.81
59	DT13162.15	GENO66	0.14	0.12	0.11	0.12	0.12	-0.82
60	DT13162.12	GENO67	0.14	0.11	0.11	0.07	0.11	-0.42
61	DT11107.01	GENO68	0.13	0.11	0.17	0.12	0.13	2.92
62	ZIRVE	GENO69	0.14	NA	0.16	0.08	0.13	-3.99
63	DT12012.02	GENO70	0.08	0.18	0.24	0.13	0.16	4.62
64	DT13136.22	GENO71	0.14	0.09	0.08	0.09	0.10	-1.24
65	DT13045.74	GENO72	0.11	0.09	0.06	0.08	0.09	-1.89
66	DT13124.21	GENO73	0.14	0.15	0.12	0.11	0.13	-1.46
67	BORWINA	GENO74	0.13	0.16	0.15	0.15	0.15	-0.11
68	BROOKE	GENO75	0.13	0.11	0.10	0.13	0.12	-0.82
69	TESSA	GENO76	0.13	0.11	0.12	0.10	0.12	0.25
70	DT13143.49	GENO77	0.09	0.09	0.18	0.09	0.11	4.81
71	DT13130.48	GENO78	0.13	0.09	0.08	0.10	0.10	-1.10
72	DT13143.54	GENO79	0.09	0.17	0.21	0.10	0.14	3.27
73	DT13007.03	GENO80	0.13	0.08	0.19	0.08	0.12	5.17
74	KUTUP	GENO81	0.12	0.10	0.15	0.19	0.14	2.39
75	DT13028.01	GENO82	0.12	0.11	0.12	0.12	0.12	0.39
76	DT13093.92	GENO83	0.14	0.16	0.16	0.14	0.15	0.28
77	DT13051.10	GENO84	0.14	0.14	0.17	0.13	0.15	1.60
78	DT13143.58	GENO85	0.17	0.19	0.17	0.15	0.17	-0.79
79	DT13026.10	GENO86	0.12	0.09	0.21	0.07	0.12	5.99
80	DT13049.50	GENO87	0.11	0.17	0.17	0.10	0.14	0.85
81	DT13072.19	GENO88	0.12	0.13	0.17	0.12	0.13	2.28
82	DT13083.01	GENO89	0.12	0.06	0.20	0.11	0.13	6.63
83	LadyRosetta	GENO90	0.11	NA	0.15	NA	0.13	-7.45
84	DT11007.01	GENO91	0.09	0.07	0.10	0.09	0.09	1.22

85	DT11108.02	GENO92	0.12	0.15	0.12	0.04	0.11	-1.18
86	DORUK	GENO93	0.08	0.09	0.07	0.11	0.09	-0.93
87	DT13085.01	GENO94	0.15	0.11	0.18	0.14	0.14	3.18
88	DT12068.21	GENO95	0.13	0.07	0.16	0.11	0.12	3.96
89	DT11088.01	GENO96	0.09	0.07	0.10	0.08	0.09	1.23
90	DT13045.42	GENO97	0.14	0.10	0.14	0.11	0.12	1.57
91	DT13147.17	GENO98	0.20	0.16	0.14	0.19	0.17	-1.63
92	DT13048.10	GENO99	0.12	0.13	0.10	0.12	0.12	-1.46
93	DT13052.23	GENO100	0.13	0.11	0.16	0.13	0.13	2.39
94	DT13037.31	GENO101	0.13	0.13	0.08	0.11	0.11	-2.67
95	DT13045.103	GENO102	0.14	0.11	0.21	0.11	0.14	4.92
96	DT13037.35	GENO103	0.14	0.05	0.17	0.12	0.12	5.14
97	DT13047.08	GENO104	0.15	0.13	0.15	0.07	0.12	0.79
98	DT13162.16	GENO105	0.13	0.15	0.17	0.13	0.14	1.35
99	DT13067.03	GENO106	0.10	0.10	0.19	0.12	0.13	4.81
100	SORAYA	GENO107	0.15	0.10	0.11	0.08	0.11	-0.17
101	LAURA	GENO108	0.15	0.13	0.17	0.12	0.14	1.86
102	SHEPODY	GENO109	0.10	0.11	0.12	0.13	0.11	0.68
103	43-111-11	GENO110	0.10	0.09	0.10	0.09	0.10	0.39
104	KARLENA	GENO111	0.18	0.11	0.14	0.17	0.15	0.61
105	139-101-11	GENO112	0.09	0.12	0.15	0.11	0.12	2.03
106	84-105-11	GENO113	NA	0.11	0.14	0.11	0.12	-1.18
107	NANDU	GENO114	0.12	0.10	0.17	NA	0.13	3.46
108	882-202-10	GENO115	0.07	0.13	0.14	0.08	0.11	1.38
109	TALENT	GENO116	0.10	0.14	0.13	0.12	0.12	0.03
110	57-104-11	GENO117	0.10	0.13	0.10	0.09	0.10	-1.18
111	878-202-10	GENO118	0.11	0.18	0.19	0.13	0.15	1.52
112	146-103-11	GENO120	0.09	0.12	0.19	0.11	0.13	4.17
113	SALUTE	GENO121	0.14	0.14	0.17	0.14	0.15	1.60
114	68-105-11	GENO122	0.14	0.12	0.16	0.11	0.13	1.86
115	63-113-11	GENO123	0.14	0.14	0.16	0.15	0.15	1.07
116	106-105-11	GENO124	0.07	NA	0.14	0.09	0.10	-1.68
117	939-201-10	GENO125	0.07	0.12	0.07	0.09	0.09	-1.97
118	NIXE	GENO126	0.14	0.09	0.09	0.12	0.11	-0.71
119	51-109-11	GENO127	0.16	0.15	0.11	0.13	0.14	-2.28
120	ETIKETSIZNORIK	GENO128	0.14	0.15	0.13	0.14	0.14	-0.93
121	40-103-11	GENO130	0.13	0.13	0.15	0.11	0.13	1.07
122	99-115-11	GENO131	0.09	0.11	0.10	0.08	0.10	-0.25
123	141-104-11	GENO132	0.07	0.09	0.12	0.09	0.09	1.89
124	89-105-11	GENO133	0.16	0.08	0.14	0.13	0.13	2.08
125	NAUTILUS	GENO134	0.09	0.12	0.12	0.14	0.12	0.42
126	157-103-11	GENO136	0.11	0.07	0.13	0.08	0.10	2.64
127	133-112-11	GENO137	0.14	0.12	0.13	0.14	0.13	0.25
128	944-208-10	GENO138	0.16	0.15	0.06	0.12	0.12	-4.95
129	PRIVELIGE	GENO139	0.11	0.13	0.11	0.08	0.11	-0.79
130	966-203-10	GENO140	0.09	0.12	0.16	0.10	0.12	2.56

131	904-212-10	GENO141	0.08	0.10	0.04	0.07	0.07	-2.92
132	BETTINA	GENO142	0.21	0.14	0.16	0.15	0.17	0.08
133	125-104-11	GENO143	0.09	0.07	0.11	0.10	0.09	1.86
134	SWING	GENO144	0.16	NA	NA	NA	0.16	-2.26
135	758-109-09	GENO145	0.09	0.07	0.12	0.13	0.10	2.39
136	735-102-09	GENO146	0.12	0.09	0.12	0.10	0.11	1.18
137	99-102-11	GENO147	0.10	0.10	0.17	0.12	0.12	3.74
138	TERRANA	GENO148	0.14	0.11	0.07	0.14	0.11	-2.56
139	104-103-11	GENO149	0.10	0.11	0.14	0.12	0.12	1.74
140	SFHIT	GENO150	0.13	0.11	0.18	0.11	0.13	3.46
141	KIWI	GENO151	0.09	0.15	0.15	0.11	0.13	0.85
142	KIEBITZ	GENO152	0.13	0.14	0.14	0.14	0.14	0.14
143	BONUS	GENO153	0.14	0.16	0.15	0.11	0.14	-0.25
144	509-104-09	GENO154	0.13	0.11	0.20	0.11	0.14	4.53
145	43-118-11	GENO155	0.08	0.09	0.10	0.10	0.09	0.68
146	BEO	GENO156	0.14	0.17	0.17	0.10	0.14	0.42
147	BALTICCREAM	GENO157	0.09	0.12	0.09	0.08	0.10	-1.18
148	868-201-10	GENO158	0.11	0.10	0.20	0.12	0.13	5.20
149	860-201-10	GENO159	0.13	0.12	0.14	0.11	0.12	0.93
150	DUKATA	GENO160	0.17	0.16	0.21	0.10	0.16	2.53
151	84-107-11	GENO161	0.14	0.12	0.16	0.13	0.14	1.86
152	128-105-11	GENO162	0.07	0.10	0.12	0.06	0.09	1.49
153	140-107-11	GENO163	0.09	0.10	0.12	0.10	0.10	1.21
154	PELIKAN	GENO164	0.14	0.10	0.09	0.11	0.11	-1.10
155	KOLIBRI	GENO165	0.13	NA	0.19	NA	0.16	-9.31
156	82-119-11	GENO167	0.10	0.14	0.15	0.11	0.12	1.10
157	WENDY	GENO168	0.09	0.15	0.07	0.10	0.10	-3.43
158	ROMANZE	GENO169	0.14	0.13	0.16	0.15	0.14	1.46
159	PRESTIGE	GENO170	0.13	0.11	0.13	0.15	0.13	0.79
160	MAXI	GENO171	0.11	0.06	0.07	0.10	0.08	-0.17
161	FASAN	GENO172	0.15	0.11	0.11	0.14	0.13	-0.57
162	Madaleine	GENO173	0.13	0.10	0.14	0.17	0.13	1.71
163	POMQUEEN	GENO174	0.15	0.10	0.15	0.15	0.14	1.97
164	MUNGO	GENO175	0.14	0.12	0.21	0.10	0.14	4.53
165	ALBATROS	GENO176	0.08	0.06	0.22	0.13	0.12	8.27
166	FIDELIA	GENO177	0.12	0.11	0.15	0.15	0.13	2.00
167	TACOMA	GENO178	0.10	0.11	0.09	0.10	0.10	-0.93
168	BONZA	GENO179	0.10	0.08	0.17	0.10	0.11	4.53
169	ADRETTA	GENO180	0.14	0.20	0.20	0.16	0.18	0.85
170	POWER	GENO181	0.08	0.14	0.18	0.09	0.12	2.99
171	GOLDMARIE	GENO182	0.20	0.16	0.19	0.21	0.19	1.04
172	RITA	GENO183	0.11	0.08	0.12	0.13	0.11	1.71
173	SUMMERGOLD	GENO184	0.08	0.17	0.24	0.12	0.15	5.01
174	DIPLOMAT	GENO185	0.07	0.13	0.09	0.05	0.09	-1.29
175	CASCADA	GENO186	0.12	0.14	0.14	0.12	0.13	0.28
176	SOLIST	GENO187	0.06	0.11	0.18	0.09	0.11	4.45

177	LOLITA	GENO188	0.09	0.10	0.17	0.09	0.11	3.88
178	KARATOP	GENO189	0.12	0.10	0.09	0.09	0.10	-0.82
179	INARA	GENO190	0.13	0.13	0.13	NA	0.13	0.00
180	ACAPELLA	GENO191	0.10	0.10	0.13	0.11	0.11	1.60
181	ALLORA	GENO192	0.12	0.10	0.17	0.14	0.13	3.46
182	ARKULA	GENO193	0.10	0.08	0.10	0.09	0.09	0.79
183	TOKIO	GENO194	0.09	0.08	0.10	0.13	0.10	0.93
184	BIRTE	GENO195	0.14	0.15	0.17	0.13	0.15	1.21
185	900-205-10	GENO196	0.08	0.08	0.09	0.07	0.08	0.53
186	MAXILLA	GENO197	0.11	0.10	0.11	0.10	0.11	0.39
187	TUCAN	GENO198	0.15	0.07	0.09	0.14	0.11	-0.06
188	946-202-10	GENO199	0.13	0.15	0.18	0.13	0.15	1.89
189	KORMORAN	GENO200	0.10	0.18	0.25	0.14	0.17	4.87
190	JUMBO	GENO202	0.10	0.12	0.14	0.10	0.11	1.35
191	LOGO	GENO203	0.11	0.11	0.13	0.05	0.10	1.07
192	102-102-11	GENO204	0.13	0.11	0.16	0.10	0.12	2.39
		Mean	0.12	0.12	0.14	0.12	0.13	

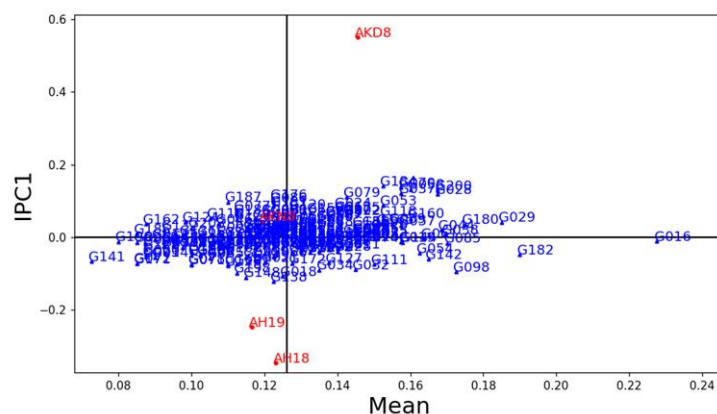


Fig.S5. Ammi biplot for mean of free asparagine of 192 genotypes across four environments (AH18, AKN18, AKD18, AH19) plotted against IPC1 (Interactive principal component)

APPENDIX-F Phenotypic data of starch % (ST) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Names	ST_H18	ST_KN18	ST_KD18	ST_H19	Mean ST	b_i
1	JELLY	GENO2	78.96	79.28	70.83	NA	76.36	1.39
2	RUMBA	GENO3	80.86	81.48	72.41	NA	78.25	1.47
3	HERMES	GENO4	78.52	80.01	71.50	NA	76.68	1.31
4	ALEGRIA	GENO5	72.88	74.64	76.51	NA	74.68	-0.46
5	ROYAL	GENO6	73.76	76.24	69.01	74.18	73.30	1.01
6	ELECTRA	GENO7	71.07	72.16	74.28	73.76	72.82	-0.45
7	DT14003.01	GENO9	69.78	82.49	73.02	73.19	74.62	0.54
8	DT14038.01	GENO10	73.22	83.32	71.44	78.57	76.64	1.16
9	DT14010.18	GENO11	70.93	75.88	65.27	71.11	70.80	1.38
10	DT14004.17	GENO12	80.71	77.81	69.02	71.79	74.83	1.72
11	DT14010.14	GENO13	92.05	80.67	78.41	85.28	84.10	1.32
12	DT14085.03	GENO14	71.39	72.97	73.12	73.19	72.67	-0.16
13	DT14013.15	GENO16	66.91	NA	NA	74.39	70.65	11.89
14	DT14018.32	GENO18	69.36	74.13	74.12	78.12	73.93	-0.39
15	DT14042.27	GENO19	79.65	80.21	68.43	73.21	75.38	1.93
16	DT14005.09	GENO20	85.80	74.54	74.18	75.00	77.38	0.99
17	DT14030.11	GENO21	73.12	81.12	68.31	80.36	75.73	1.49
18	DT14057.37	GENO22	82.31	78.37	66.25	63.57	72.62	2.36
19	DT14065.01	GENO23	72.46	73.82	70.16	NA	72.15	0.50
20	DT14016.01	GENO24	73.04	75.30	71.02	77.19	74.14	0.53
21	DT14016.34	GENO25	73.12	74.34	64.24	77.33	72.26	1.60
22	DT14078.03	GENO26	79.92	76.73	65.50	75.71	74.47	2.15
23	DT14028.03	GENO27	72.54	78.15	70.23	74.44	73.84	0.87
24	DT14054.11	GENO28	68.80	69.30	64.31	70.22	68.16	0.80
25	DT14037.18	GENO29	70.45	75.33	70.10	77.78	73.42	0.48
26	DT14091.04	GENO30	73.72	70.54	68.88	75.71	72.21	0.54
27	DT14083.28	GENO31	73.12	69.71	69.05	NA	70.63	0.39
28	DT14015.22	GENO32	85.63	78.50	69.94	86.29	80.09	2.03
29	DT14051.15	GENO33	75.35	76.28	68.78	71.74	73.04	1.18
30	DT14047.38	GENO34	67.23	75.19	63.33	70.22	68.99	1.34
31	DT14026.04	GENO35	71.19	75.19	71.34	69.98	71.93	0.32
32	DT14068.07	GENO36	71.43	78.18	78.01	72.19	74.95	-0.53
33	DT14063.12	GENO37	72.08	78.40	74.16	74.64	74.82	0.19
34	DT14036.01	GENO38	70.65	NA	NA	NA	70.65	5.83
35	DT14055.25	GENO39	81.64	NA	NA	63.57	72.61	12.18
36	LadyOlympia	GENO41	79.23	74.01	74.04	77.61	76.22	0.43
37	BANBA	GENO42	72.38	79.36	74.82	71.11	74.42	0.19

38	VanGOGH	GENO43	79.34	83.01	72.02	80.28	78.66	1.55
39	DT14049.10	GENO44	80.19	79.00	68.33	82.10	77.40	1.89
40	DT14061.23	GENO45	80.96	78.11	69.84	70.71	74.91	1.63
41	DT14006.07	GENO46	75.00	81.83	73.47	80.30	77.65	0.84
42	DT14046.19	GENO47	67.98	83.12	77.01	74.29	75.60	-0.22
43	DT14014.27	GENO48	73.70	70.27	69.94	74.29	72.05	0.34
44	DT14011.18	GENO49	78.34	72.08	69.16	75.39	73.75	1.01
45	DT14069.13	GENO50	76.61	76.79	76.57	78.10	77.02	0.02
46	DT14026.21	GENO52	76.06	78.76	70.35	75.34	75.13	1.19
47	DT14042.24	GENO53	80.19	83.51	71.12	78.57	78.35	1.81
48	DT14090.11	GENO54	86.58	79.94	66.38	78.81	77.93	2.83
49	DT14071.19	GENO55	77.26	73.82	67.92	72.01	72.75	1.28
50	DT14027.08	GENO56	75.98	75.40	69.10	73.28	73.44	1.11
51	DT14034.03	GENO57	70.12	72.55	65.34	70.21	69.56	1.01
52	DT14057.36	GENO58	75.00	68.90	67.31	70.00	70.31	0.77
53	DT14062.08	GENO59	72.88	77.30	70.20	NA	73.46	0.83
54	DT14079.02	GENO60	72.06	79.29	76.42	82.50	77.57	-0.11
55	DT14053.03	GENO61	71.00	NA	NA	NA	71.00	5.86
56	DT13088.03	GENO63	71.71	71.23	69.11	71.28	70.83	0.40
57	DT14051.66	GENO64	75.35	77.20	73.02	78.20	75.94	0.55
58	DT13100.02	GENO65	70.12	74.70	67.40	78.93	72.79	0.85
59	DT13162.15	GENO66	71.04	82.74	76.67	78.19	77.16	0.06
60	DT13162.12	GENO67	72.06	72.49	67.75	74.64	71.74	0.76
61	DT11107.01	GENO68	70.78	74.55	69.09	78.57	73.25	0.61
62	ZIRVE	GENO69	72.41	NA	NA	73.93	73.17	12.31
63	DT12012.02	GENO70	79.89	76.61	71.49	73.21	75.30	1.13
64	DT13136.22	GENO71	83.42	80.09	70.01	78.21	77.93	1.97
65	DT13045.74	GENO72	68.79	70.19	76.76	74.29	72.51	-1.22
66	DT13124.21	GENO73	79.33	77.70	70.11	79.64	76.69	1.41
67	BORWINA	GENO74	73.05	65.59	70.12	78.21	71.74	-0.15
68	BROOKE	GENO75	91.56	81.36	75.12	77.14	81.29	1.89
69	TESSA	GENO76	75.96	75.79	70.20	74.64	74.15	0.95
70	DT13143.49	GENO77	70.83	73.63	64.01	73.33	70.45	1.39
71	DT13130.48	GENO78	72.41	80.27	78.16	70.20	75.26	-0.29
72	DT13143.54	GENO79	71.81	78.38	73.14	73.11	74.11	0.34
73	DT13007.03	GENO80	77.61	80.42	77.22	80.71	78.99	0.31
74	KUTUP	GENO81	93.07	77.01	75.48	81.10	81.67	1.58
75	DT13028.01	GENO82	71.30	69.69	71.51	71.23	70.93	-0.17
76	DT13093.92	GENO83	80.06	74.51	79.11	76.18	77.47	-0.32
77	DT13051.10	GENO84	71.48	76.39	75.01	72.00	73.72	-0.17
78	DT13143.58	GENO85	67.56	78.65	67.14	78.57	72.98	1.02
79	DT13026.10	GENO86	64.55	74.56	64.30	66.79	67.55	0.90
80	DT13049.50	GENO87	74.00	73.29	74.74	72.10	73.53	-0.19

81	DT13072.19	GENO88	78.46	71.64	76.57	80.28	76.74	-0.27
82	DT13083.01	GENO89	67.81	70.50	65.44	74.12	69.47	0.63
83	LadyRosetta	GENO90	88.93	74.02	64.92	NA	75.96	2.76
84	DT11007.01	GENO91	81.87	77.99	73.30	79.29	78.11	1.11
85	DT11108.02	GENO92	79.60	70.47	70.33	70.71	72.78	0.78
86	DORUK	GENO93	75.37	76.54	72.23	76.07	75.05	0.63
87	DT13085.01	GENO94	71.04	77.94	68.95	75.55	73.37	0.94
88	DT12068.21	GENO95	77.98	75.39	69.11	73.57	74.01	1.27
89	DT11088.01	GENO96	78.02	78.37	72.11	75.19	75.92	1.02
90	DT13045.42	GENO97	70.50	71.61	67.30	68.12	69.39	0.63
91	DT13147.17	GENO98	78.69	79.95	74.28	68.93	75.46	0.85
92	DT13048.10	GENO99	75.35	79.76	74.21	79.64	77.24	0.57
93	DT13052.23	GENO100	75.28	78.61	79.90	78.19	77.99	-0.49
94	DT13037.31	GENO101	80.93	75.30	72.00	79.29	76.88	1.02
95	DT13045.103	GENO102	80.19	70.11	65.30	64.29	69.97	1.64
96	DT13037.35	GENO103	66.85	78.45	73.98	70.20	72.37	-0.21
97	DT13047.08	GENO104	70.97	72.20	69.11	68.21	70.12	0.42
98	DT13162.16	GENO105	67.23	75.01	69.10	77.33	72.17	0.35
99	DT13067.03	GENO106	77.70	68.64	70.40	71.81	72.14	0.45
100	SORAYA	GENO107	72.31	72.99	71.63	72.86	72.45	0.17
101	LAURA	GENO108	78.24	73.47	64.86	75.00	72.90	1.84
102	SHEPODY	GENO109	71.67	79.08	74.30	69.29	73.58	0.19
103	43-111-11	GENO110	69.44	79.77	79.52	71.43	75.04	-0.81
104	KARLENA	GENO111	79.57	79.99	78.76	78.10	79.11	0.17
105	139-101-11	GENO112	74.00	72.99	70.88	81.67	74.88	0.44
106	84-105-11	GENO113	79.59	75.01	74.58	76.76	76.49	0.45
107	NANDU	GENO114	82.52	73.50	66.20	NA	74.07	1.97
108	882-202-10	GENO115	84.48	87.62	78.83	83.87	83.70	1.22
109	TALENT	GENO116	76.95	72.99	69.90	79.27	74.78	0.85
110	57-104-11	GENO117	76.92	73.63	71.92	78.87	75.33	0.56
111	878-202-10	GENO118	75.74	76.98	70.62	77.43	75.19	0.97
112	146-103-11	GENO120	79.68	82.29	71.06	82.87	78.98	1.67
113	SALUTE	GENO121	74.63	74.83	75.51	76.28	75.31	-0.13
114	68-105-11	GENO122	77.62	81.02	72.93	79.81	77.85	1.08
115	63-113-11	GENO123	74.13	76.08	67.01	79.87	74.27	1.36
116	106-105-11	GENO124	80.12	78.53	71.63	75.71	76.50	1.29
117	939-201-10	GENO125	74.11	69.13	70.44	72.71	71.60	0.19
118	NIXE	GENO126	75.54	78.60	72.36	77.14	75.91	0.80
119	51-109-11	GENO127	76.96	67.69	65.56	75.73	71.49	1.12
120	ETIKETSIZNORIK	GENO128	80.90	70.07	74.24	78.57	75.94	0.19
121	40-103-11	GENO130	71.78	81.81	73.73	80.00	76.83	0.53
122	99-115-11	GENO131	70.43	72.23	65.31	70.55	69.63	1.02
123	141-104-11	GENO132	81.53	85.73	72.07	82.86	80.55	1.95

124	89-105-11	GENO133	78.43	79.92	72.01	80.52	77.72	1.21
125	NAUTILUS	GENO134	83.80	81.18	73.21	78.28	79.12	1.56
126	157-103-11	GENO136	73.02	73.63	70.52	74.86	73.00	0.47
127	133-112-11	GENO137	74.03	74.86	77.94	76.98	75.95	-0.59
128	944-208-10	GENO138	76.21	82.89	72.11	79.98	77.79	1.26
129	PRIVELIGE	GENO139	72.80	76.78	70.63	80.11	75.08	0.71
130	966-203-10	GENO140	78.23	79.56	70.57	78.29	76.66	1.40
131	904-212-10	GENO141	77.96	85.13	73.12	79.53	78.93	1.43
132	BETTINA	GENO142	79.23	75.27	76.13	78.13	77.19	0.18
133	125-104-11	GENO143	74.68	74.99	69.60	74.81	73.52	0.88
134	SWING	GENO144	86.96	NA	NA	NA	86.96	7.17
135	758-109-09	GENO145	78.66	76.82	72.94	78.93	76.84	0.80
136	735-102-09	GENO146	95.00	83.09	74.94	85.58	84.65	2.35
137	99-102-11	GENO147	69.77	76.58	72.44	69.28	72.02	0.13
138	TERRANA	GENO148	78.34	79.08	70.46	80.17	77.01	1.39
139	104-103-11	GENO149	72.80	77.27	78.76	71.43	75.06	-0.62
140	SFHIT	GENO150	74.68	78.32	74.57	81.79	77.34	0.33
141	KIWI	GENO151	72.72	79.99	75.36	74.38	75.61	0.18
142	KIEBITZ	GENO152	76.05	74.97	72.37	74.64	74.51	0.53
143	BONUS	GENO153	71.82	78.32	76.11	78.21	76.12	-0.16
144	509-104-09	GENO154	72.80	76.14	69.84	77.50	74.07	0.78
145	43-118-11	GENO155	79.01	76.97	70.76	77.14	75.97	1.21
146	BEO	GENO156	85.11	85.42	78.13	81.79	82.61	1.20
147	BALTICCREAM	GENO157	75.71	80.72	72.12	79.12	76.92	1.03
148	868-201-10	GENO158	77.45	78.73	73.42	74.25	75.96	0.79
149	860-201-10	GENO159	76.72	71.03	71.73	80.18	74.92	0.35
150	DUKATA	GENO160	65.50	79.06	73.46	75.00	73.26	-0.18
151	84-107-11	GENO161	72.05	80.42	74.58	79.77	76.70	0.29
152	128-105-11	GENO162	72.89	81.72	76.92	79.76	77.82	0.08
153	140-107-11	GENO163	73.49	81.08	78.92	78.78	78.07	-0.26
154	PELIKAN	GENO164	75.99	80.27	69.91	75.00	75.29	1.39
155	KOLIBRI	GENO165	78.67	72.73	66.26	NA	72.56	1.58
156	82-119-11	GENO167	70.91	79.72	70.13	80.71	75.37	0.89
157	WENDY	GENO168	77.56	81.34	71.49	80.36	77.69	1.34
158	ROMANZE	GENO169	68.80	76.63	75.72	71.32	73.12	-0.49
159	PRESTIGE	GENO170	79.08	82.63	73.11	78.37	78.30	1.31
160	MAXI	GENO171	78.91	71.32	77.97	79.10	76.83	-0.49
161	FASAN	GENO172	73.36	75.94	72.49	71.87	73.42	0.37
162	Madaleine	GENO173	66.17	81.36	71.02	74.29	73.21	0.49
163	POMQUEEN	GENO174	76.96	81.63	75.30	80.44	78.58	0.68
164	MUNGO	GENO175	69.86	79.76	67.21	71.07	71.97	1.29
165	ALBATROS	GENO176	82.51	77.55	75.47	78.93	78.61	0.76
166	FIDELIA	GENO177	89.54	87.83	77.48	82.73	84.40	1.88

167	TACOMA	GENO178	68.44	74.97	73.11	70.22	71.68	-0.23
168	BONZA	GENO179	78.90	74.70	70.12	75.00	74.68	1.12
169	ADRETTA	GENO180	84.68	82.01	79.69	80.87	81.81	0.61
170	POWER	GENO181	81.86	78.65	80.56	83.78	81.21	-0.06
171	GOLDMARIE	GENO182	68.34	81.38	66.37	70.76	71.71	1.45
172	RITA	GENO183	72.79	76.38	69.29	75.19	73.41	0.90
173	SUMMERGOLD	GENO184	73.05	79.53	75.27	76.43	76.07	0.18
174	DIPLOMAT	GENO185	82.96	79.61	75.12	84.64	80.58	1.03
175	CASCADA	GENO186	73.40	77.42	69.12	73.19	73.28	1.06
176	SOLIST	GENO187	76.72	79.93	72.84	77.42	76.73	0.93
177	LOLITA	GENO188	70.80	72.07	76.94	71.79	72.90	-0.92
178	KARATOP	GENO189	68.22	74.78	72.44	66.73	70.54	-0.15
179	INARA	GENO190	66.99	74.56	76.32	NA	72.62	-0.92
180	ACAPELLA	GENO191	71.24	76.20	70.78	75.22	73.36	0.50
181	ALLORA	GENO192	73.22	78.49	77.11	76.92	76.43	-0.20
182	ARKULA	GENO193	79.74	81.39	75.02	80.66	79.20	0.94
183	TOKIO	GENO194	83.80	85.33	77.59	78.21	81.23	1.18
184	BIRTE	GENO195	75.30	72.54	72.63	71.17	72.91	0.21
185	900-205-10	GENO196	73.86	78.01	77.19	76.82	76.47	-0.20
186	MAXILLA	GENO197	72.47	80.45	69.39	78.57	75.22	1.20
187	TUCAN	GENO198	80.10	89.12	78.34	82.48	82.51	1.07
188	946-202-10	GENO199	74.83	78.42	74.29	72.98	75.13	0.40
189	KORMORAN	GENO200	64.54	69.80	64.24	75.37	68.49	0.50
190	JUMBO	GENO202	86.76	80.10	72.01	85.88	81.19	1.91
191	LOGO	GENO203	72.44	77.72	70.38	80.71	75.31	0.80
192	102-102-11	GENO204	71.30	74.83	75.94	77.86	74.98	-0.48
		Mean	75.66	77.04	72.00	76.08	75.17	

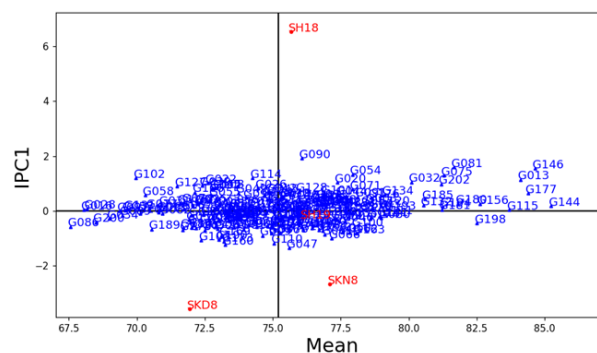


Fig.S6. Amami biplot for mean of starch of 192 genotypes across four environments (SH18, SKN18, SKD18, SH19) plotted against IPC1 (Interactive principal component)

APPENDIX-G Phenotypic data of beta-carotene “ug/g dry weight” (BCRT) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Codes	BCRT_H18	BCRT_KN18	BCRT_KD18	BCRT_H19	Mean BCRT	b_i
1	JELLY	GENO2	7.28	11.41	9.08	NA	9.26	0.37
2	RUMBA	GENO3	14.01	15.77	14.88	NA	14.89	0.89
3	HERMES	GENO4	9.12	11.78	10.76	NA	10.55	0.50
4	ALEGRIA	GENO5	17.7	15.61	10.76	NA	14.69	1.00
5	ROYAL	GENO6	3.77	11.14	4.78	11.81	7.88	2.27
6	ELECTRA	GENO7	15.66	21.86	12.89	20.34	17.69	2.80
7	DT14003.01	GENO9	4.1	14.86	16.88	10.51	11.59	0.52
8	DT14038.01	GENO10	9.31	13.65	19.87	14.88	14.43	-1.12
9	DT14010.18	GENO11	3.05	22.77	15.89	3.88	11.40	3.57
10	DT14004.17	GENO12	14.89	18.75	14.88	18.32	16.71	1.32
11	DT14010.14	GENO13	14.17	19.86	16.98	13.17	16.05	1.25
12	DT14085.03	GENO14	9.95	11.87	7.78	9.72	9.83	1.19
13	DT14013.15	GENO16	5.26	NA	NA	7.76	6.51	2.15
14	DT14018.32	GENO18	10.54	16.77	16.76	14.51	14.65	0.59
15	DT14042.27	GENO19	14.27	15.68	11.86	14.38	14.05	1.08
16	DT14005.09	GENO20	10.93	20.81	9.87	4.19	11.45	3.64
17	DT14030.11	GENO21	9.99	9.87	16.76	14.14	12.69	-1.71
18	DT14057.37	GENO22	7.4	15.13	11.99	15.56	12.52	1.51
19	DT14065.01	GENO23	17.46	8.88	16.65	NA	14.33	-2.73
20	DT14016.01	GENO24	13.7	9.98	10.88	15.42	12.50	-0.57
21	DT14016.34	GENO25	13.87	14.86	11.41	10.51	12.66	0.95
22	DT14078.03	GENO26	15.6	15.61	11.73	9.16	13.03	0.96
23	DT14028.03	GENO27	8.26	19.76	7.81	6.89	10.68	4.04
24	DT14054.11	GENO28	16.67	20.87	9.67	15.67	15.72	3.16
25	DT14037.18	GENO29	10.63	19.86	14.71	5.87	12.77	2.15
26	DT14091.04	GENO30	17.39	21.89	9.51	4.67	13.37	3.48
27	DT14083.28	GENO31	1.39	5.38	8.88	NA	5.22	-0.49
28	DT14015.22	GENO32	10.29	6.99	9.98	13.67	10.23	-1.05
29	DT14051.15	GENO33	3.74	12.15	19.86	3.78	9.88	-1.11
30	DT14047.38	GENO34	19.31	26.87	21.89	23.99	23.02	1.95
31	DT14026.04	GENO35	14.06	15.88	15.87	10.84	14.16	0.18
32	DT14068.07	GENO36	11.03	20.86	5.31	14.13	12.83	4.77
33	DT14063.12	GENO37	9.02	13.88	6.88	10.61	10.10	2.19
34	DT14036.01	GENO38	14.02	NA	NA	NA	14.02	-1.33
35	DT14055.25	GENO39	28.54	NA	NA	11.78	20.16	1.32
36	LadyOlympia	GENO41	13.19	10.87	18.71	16.92	14.92	-2.16
37	BANBA	GENO42	15.15	21.76	11.78	9.78	14.62	3.09
38	VanGOGH	GENO43	13.03	16.81	4.87	8.28	10.75	3.31

39	DT14049.10	GENO44	13.59	15.31	6.87	11.82	11.90	2.25
40	DT14061.23	GENO45	12.43	12.78	10.88	14.78	12.72	0.50
41	DT14006.07	GENO46	19.13	19.88	10.77	6.56	14.09	2.32
42	DT14046.19	GENO47	14.1	19.86	7.88	16.67	14.63	3.50
43	DT14014.27	GENO48	17.89	16.88	11.88	12.67	14.83	1.14
44	DT14011.18	GENO49	13.32	10.87	11.31	17.41	13.23	-0.34
45	DT14069.13	GENO50	19.82	19.76	16.77	16.67	18.26	0.73
46	DT14026.21	GENO52	14.86	11.31	5.76	6.67	9.65	1.03
47	DT14042.24	GENO53	12.39	16.76	20.76	17.44	16.84	-0.57
48	DT14090.11	GENO54	15.85	18.71	13.76	11.62	14.99	1.49
49	DT14071.19	GENO55	4.65	19.87	6.99	9.32	10.21	4.62
50	DT14027.08	GENO56	4.14	10.88	6.88	6.72	7.16	1.63
51	DT14034.03	GENO57	13.52	14.67	9.91	6.42	11.13	1.28
52	DT14057.36	GENO58	9.05	11.75	13.86	13.67	12.08	-0.26
53	DT14062.08	GENO59	13.34	11.73	7.87	NA	10.98	0.80
54	DT14079.02	GENO60	8.51	12.75	4.87	9.32	8.86	2.35
55	DT14053.03	GENO61	12.79	NA	NA	NA	12.79	-1.21
56	DT13088.03	GENO63	13.4	17.88	7.76	11.67	12.68	2.92
57	DT14051.66	GENO64	11.38	9.87	15.77	11.72	12.19	-1.60
58	DT13100.02	GENO65	18.6	9.86	5.88	3.68	9.51	0.15
59	DT13162.15	GENO66	3.59	9.88	5.54	14.14	8.29	1.67
60	DT13162.12	GENO67	13.56	10.88	11.87	8.32	11.16	-0.50
61	DT11107.01	GENO68	5.08	6.76	3.65	3.47	4.74	0.93
62	ZIRVE	GENO69	19.53	NA	10.89	12.77	14.40	-1.28
63	DT12012.02	GENO70	2.2	13.76	8.76	11.39	9.03	2.33
64	DT13136.22	GENO71	16.7	12.61	9.76	16.51	13.90	0.32
65	DT13045.74	GENO72	11.04	4.77	7.86	5.13	7.20	-1.36
66	DT13124.21	GENO73	12.5	11.76	19.86	14.78	14.73	-2.07
67	BORWINA	GENO74	16.3	12.65	6.99	18	13.49	1.05
68	BROOKE	GENO75	3.15	11.87	5.88	5.28	6.55	2.31
69	TESSA	GENO76	11.7	20.76	18.75	9.32	15.13	1.36
70	DT13143.49	GENO77	17.68	16.65	4.28	15.51	13.53	2.96
71	DT13130.48	GENO78	10.73	8.88	8.88	3.66	8.04	-0.18
72	DT13143.54	GENO79	3.29	10.76	9.98	9.62	8.41	0.90
73	DT13007.03	GENO80	8.57	10.76	7.87	5.78	8.25	0.92
74	KUTUP	GENO81	17.24	10.88	5.38	8.61	10.53	0.75
75	DT13028.01	GENO82	13.54	7.87	9.71	17.43	12.14	-0.99
76	DT13093.92	GENO83	17.82	17.76	15.86	13.67	16.28	0.46
77	DT13051.10	GENO84	15.62	13.81	11.81	12.56	13.45	0.32
78	DT13143.58	GENO85	16.51	15.98	21.86	NA	18.12	-1.50
79	DT13026.10	GENO86	10.02	9.61	15.76	6.71	10.53	-1.56
80	DT13049.50	GENO87	11.12	5.56	11.75	22.32	12.69	-2.06
81	DT13072.19	GENO88	15.76	9.86	10.81	8.42	11.21	-0.79
82	DT13083.01	GENO89	7.03	13.65	7.86	16.44	11.25	2.06
83	LadyRosetta	GENO90	11.77	NA	8.77	NA	10.27	1.88

84	DT11007.01	GENO91	10.5	13.87	13.86	11.71	12.49	0.32
85	DT11108.02	GENO92	3.52	15.71	4.77	10.32	8.58	3.86
86	DORUK	GENO93	4.24	5.76	6.76	3.78	5.14	-0.10
87	DT13085.01	GENO94	14.09	10.88	7.71	15.51	12.05	0.48
88	DT12068.21	GENO95	16.01	9.98	6.75	7.13	9.97	0.23
89	DT11088.01	GENO96	7.19	10.76	6.75	21.39	11.52	1.33
90	DT13045.42	GENO97	19.96	17.13	10.87	11.44	14.85	1.28
91	DT13147.17	GENO98	20.54	19.53	14.76	19.67	18.63	1.08
92	DT13048.10	GENO99	9.73	14.68	10.77	5.78	10.24	1.43
93	DT13052.23	GENO100	25.44	10.76	9.87	4.67	12.69	-1.17
94	DT13037.31	GENO101	4.98	6.75	2.78	15.33	7.46	1.15
95	DT13045.103	GENO102	10.56	15.76	6.61	4.18	9.28	2.75
96	DT13037.35	GENO103	22.41	9.67	8.87	19.31	15.07	-1.01
97	DT13047.08	GENO104	1.23	22	7.71	3.81	8.69	5.50
98	DT13162.16	GENO105	5.08	8.76	10.13	13.28	9.31	0.01
99	DT13067.03	GENO106	11.27	13.76	5.93	8.87	9.96	2.17
100	SORAYA	GENO107	15.37	9.91	15.88	10.61	12.94	-1.99
101	LAURA	GENO108	6.98	13.67	10.76	23.71	13.78	1.35
102	SHEPODY	GENO109	6.87	6.28	4.68	3.78	5.40	0.34
103	43-111-11	GENO110	4.23	14.88	12.51	6.18	9.45	1.60
104	KARLENA	GENO111	14.06	11.67	7.61	13.11	11.61	0.78
105	139-101-11	GENO112	14.36	12.65	13.67	5.32	11.50	-0.41
106	84-105-11	GENO113	4.68	10.88	6.75	4.67	6.75	1.61
107	NANDU	GENO114	3.99	8.78	4.76	NA	5.84	1.45
108	882-202-10	GENO115	5.87	14.78	5.68	14.78	10.28	3.09
109	TALENT	GENO116	10.54	16.87	11.87	22.13	15.35	1.83
110	57-104-11	GENO117	17.76	18.76	20.76	12.71	17.50	-0.40
111	878-202-10	GENO118	7.47	10.81	11.67	11.46	10.35	0.10
112	146-103-11	GENO120	6.85	17.77	18.81	15.32	14.69	0.78
113	SALUTE	GENO121	12.96	17.76	5.61	6.78	10.78	3.45
114	68-105-11	GENO122	19.05	10.77	4.88	9.12	10.96	0.67
115	63-113-11	GENO123	13.34	14.99	10.87	4.78	11.00	1.17
116	106-105-11	GENO124	13.09	NA	11.87	10.67	11.88	0.18
117	939-201-10	GENO125	18.76	11.75	5.76	15.67	12.99	0.81
118	NIXE	GENO126	19.39	11.77	13.87	15.78	15.20	-1.24
119	51-109-11	GENO127	16.33	14.88	13.81	16.31	15.33	0.13
120	ETIKETSIZNORIK	GENO128	9.2	9.71	6.97	17.42	10.83	0.72
121	40-103-11	GENO130	13.67	15.88	9.77	9.51	12.21	1.72
122	99-115-11	GENO131	8.77	14.72	9.86	10.76	11.03	1.76
123	141-104-11	GENO132	11.09	10.77	16.77	14.76	13.35	-1.51
124	89-105-11	GENO133	14.7	11.86	10.88	9.37	11.70	-0.03
125	NAUTILUS	GENO134	10.04	11.76	9.86	17.45	12.28	0.63
126	157-103-11	GENO136	13.88	14.77	8.88	15.77	13.33	1.54
127	133-112-11	GENO137	9.67	18.67	14.86	9.78	13.25	1.79
128	944-208-10	GENO138	5.51	10.76	5.88	15.76	9.48	1.70
129	PRIVELIGE	GENO139	16.1	12.78	8.65	8.32	11.46	0.70

130	966-203-10	GENO140	8.82	12.89	5.88	13.61	10.30	2.12
131	904-212-10	GENO141	2.02	13.75	10.13	6.13	8.01	2.01
132	BETTINA	GENO142	12.1	21.86	9.61	11.51	13.77	3.95
133	125-104-11	GENO143	4.14	14.76	7.71	7.17	8.45	2.75
134	SWING	GENO144	8.26	NA	NA	NA	8.26	-0.78
135	758-109-09	GENO145	3.52	15.55	6.76	14.67	10.13	3.31
136	735-102-09	GENO146	16.38	13.28	14.79	16.32	15.19	-0.67
137	99-102-11	GENO147	6.71	9.77	16.87	7.98	10.33	-1.46
138	TERRANA	GENO148	13.63	7.88	3.76	16.33	10.40	0.47
139	104-103-11	GENO149	24.26	6.1	13.65	12.67	14.17	-3.59
140	SFHIT	GENO150	5.03	16.77	7.81	9.32	9.73	3.33
141	KIWI	GENO151	9.91	14.81	6.81	14.67	11.55	2.44
142	KIEBITZ	GENO152	8.55	6.61	7.76	5.16	7.02	-0.47
143	BONUS	GENO153	11.62	17.87	9.98	18.67	14.54	2.54
144	509-104-09	GENO154	14.5	12.89	11.77	7.32	11.62	0.12
145	43-118-11	GENO155	9.92	13.76	20.77	4.21	12.17	-1.37
146	BEO	GENO156	5.85	17.54	15.76	13.67	13.21	1.55
147	BALTICCREAM	GENO157	7.48	19.86	7.55	12.81	11.93	4.21
148	868-201-10	GENO158	5.04	14.76	5.88	9.67	8.84	3.11
149	860-201-10	GENO159	4.06	13.86	11.14	4.58	8.41	1.60
150	DUKATA	GENO160	11.42	5.89	15.68	7.67	10.17	-2.94
151	84-107-11	GENO161	15.22	14.71	8.77	15.32	13.51	1.42
152	128-105-11	GENO162	3.7	20.87	5.81	9.68	10.02	5.35
153	140-107-11	GENO163	13.45	13.76	17.87	13.67	14.69	-0.99
154	PELIKAN	GENO164	10.63	17.68	14.77	13.72	14.20	1.39
155	KOLIBRI	GENO165	10.8	NA	18.67	NA	14.74	5.36
156	82-119-11	GENO167	3.62	18.77	13.75	6.13	10.57	2.68
157	WENDY	GENO168	12.6	9.76	9.65	14.67	11.67	-0.24
158	ROMANZE	GENO169	15.21	9.76	11.28	19.38	13.91	-0.89
159	PRESTIGE	GENO170	10.88	24.76	16.56	17.77	17.49	3.34
160	MAXI	GENO171	14.46	10.87	5.65	11.81	10.70	0.95
161	FASAN	GENO172	5.22	20.55	6.1	16.16	12.01	5.02
162	Madaleine	GENO173	21.42	11.81	14.76	17.32	16.33	-1.64
163	POMQUEEN	GENO174	15.9	7.28	7.76	11.65	10.65	-0.94
164	MUNGO	GENO175	5.51	5.93	5.76	9.79	6.75	0.08
165	ALBATROS	GENO176	14.74	19.76	9.76	14.14	14.60	2.94
166	FIDELIA	GENO177	15.8	11.87	16.76	10.31	13.69	-1.58
167	TACOMA	GENO178	14.69	21.88	19.86	19.61	19.01	1.18
168	BONZA	GENO179	18.41	10.87	14.79	13	14.27	-1.68
169	ADRETTA	GENO180	19.05	13.65	11.55	10.37	13.66	0.01
170	POWER	GENO181	4.61	9.81	10.68	3.37	7.12	0.28
171	GOLDMARIE	GENO182	11.41	12.87	8.67	6.67	9.91	1.18
172	RITA	GENO183	4.79	8.87	15.53	8.32	9.38	-1.26
173	SUMMERGOLD	GENO184	3.92	14.79	7.55	5.29	7.89	2.82
174	DIPLOMAT	GENO185	6.49	10.68	3.65	3.25	6.02	2.13
175	CASCADA	GENO186	18.12	11.55	10.87	10.67	12.80	-0.46

176	SOLIST	GENO187	10.34	17.51	10.76	15.71	13.58	2.35
177	LOLITA	GENO188	9.27	16.76	16.88	15.61	14.63	0.68
178	KARATOP	GENO189	14.54	16.56	14.72	13.77	14.90	0.65
179	INARA	GENO190	3.7	18.81	14.86	NA	12.46	2.41
180	ACAPELLA	GENO191	7.56	11.86	5.56	16.81	10.45	1.96
181	ALLORA	GENO192	6.78	16.98	18	22.67	16.11	0.72
182	ARKULA	GENO193	1.18	9.08	NA	3.52	4.59	2.12
183	TOKIO	GENO194	8.62	7.71	12.78	16.56	11.42	-1.34
184	BIRTE	GENO195	6.75	15.88	9.76	10.67	10.77	2.38
185	900-205-10	GENO196	10.85	10.88	12.15	4.81	9.67	-0.31
186	MAXILLA	GENO197	5.85	24.51	7.28	15.75	13.35	6.02
187	TUCAN	GENO198	15.33	20.76	15.61	12.67	16.09	1.79
188	946-202-10	GENO199	5.03	14.79	9.76	14.55	11.03	2.17
189	KORMORAN	GENO200	7.81	8.65	6.77	3.67	6.73	0.54
190	JUMBO	GENO202	5.85	7.71	6.76	14.62	8.74	0.41
191	LOGO	GENO203	4.65	10.81	9.76	9.61	8.71	0.84
192	102-102-11	GENO204	15.68	16.97	10.88	11.67	13.80	1.63
		Mean	11.21	13.84	10.88	11.62	11.88	

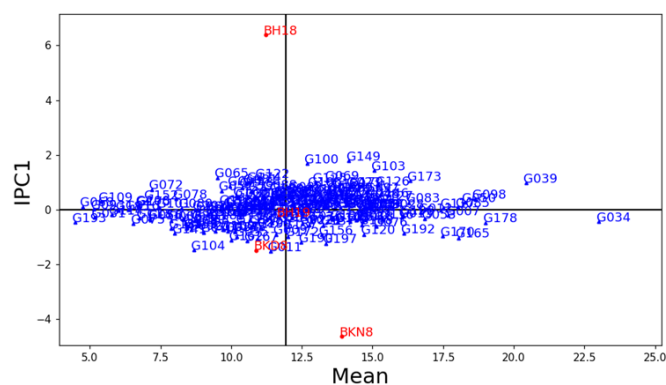


Fig.S7. Ammi biplot for mean of beta carotene of 192 genotypes across four environments (BH18, BKN18, BKD18, BH19) plotted against IPC1 (Interactive principal component)

APPENDIX-H Phenotypic data of total antioxidant activity “mg ascorbic acid equivalent (AAE)/ 100 g dry weight” (TAA) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Codes	TAA_H18	TAA_KN18	TAA_KD18	TAA_H19	Means TAA	b_i
1	JELLY	GENO2	27.08	33.76	26.58	NA	29.14	0.36
2	RUMBA	GENO3	28.30	30.80	26.87	NA	28.66	0.82
3	HERMES	GENO4	33.76	34.59	28.26	NA	32.20	1.28
4	ALEGRIA	GENO5	27.95	41.75	26.85	NA	32.18	0.77
5	ROYAL	GENO6	32.50	31.12	24.67	34.25	30.63	1.73
6	ELECTRA	GENO7	46.75	40.33	31.61	45.10	40.95	3.20
7	DT14003.01	GENO9	26.26	28.33	25.21	29.17	27.25	0.32
8	DT14038.01	GENO10	30.88	32.74	33.65	29.61	31.72	-0.56
9	DT14010.18	GENO11	30.41	34.98	26.24	27.92	29.89	1.12
10	DT14004.17	GENO12	26.19	30.23	29.90	35.34	30.41	-0.69
11	DT14010.14	GENO13	31.75	31.26	29.62	31.61	31.06	0.47
12	DT14085.03	GENO14	25.11	28.46	26.93	27.53	27.01	-0.29
13	DT14013.15	GENO16	27.43	NA	32.27	30.43	30.04	-0.50
14	DT14018.32	GENO18	38.37	NA	29.08	38.32	35.26	-0.34
15	DT14042.27	GENO19	27.74	28.12	26.42	30.16	28.11	0.31
16	DT14005.09	GENO20	29.33	25.76	27.93	29.90	28.23	0.18
17	DT14030.11	GENO21	25.74	31.79	26.31	27.55	27.85	0.10
18	DT14057.37	GENO22	28.42	27.24	26.64	28.28	27.65	0.36
19	DT14065.01	GENO23	27.71	27.31	25.84	NA	26.95	0.41
20	DT14016.01	GENO24	34.10	32.19	29.18	34.05	32.38	1.05
21	DT14016.34	GENO25	32.24	28.53	25.23	32.22	29.56	1.45
22	DT14078.03	GENO26	25.58	30.90	25.73	29.17	27.85	0.16
23	DT14028.03	GENO27	30.32	36.14	25.15	30.30	30.48	1.39
24	DT14054.11	GENO28	35.94	35.79	31.84	36.41	34.99	0.93
25	DT14037.18	GENO29	31.49	37.62	27.64	29.00	31.44	1.10
26	DT14091.04	GENO30	37.59	36.08	33.50	40.59	36.94	0.87
27	DT14083.28	GENO31	25.45	27.19	27.72	NA	26.79	-0.45
28	DT14015.22	GENO32	30.47	29.26	27.72	31.65	29.78	0.58
29	DT14051.15	GENO33	27.37	26.57	30.41	29.15	28.38	-0.72
30	DT14047.38	GENO34	31.47	36.79	31.44	41.32	35.25	0.21
31	DT14026.04	GENO35	36.21	36.40	30.08	36.07	34.69	1.40
32	DT14068.07	GENO36	28.42	36.80	25.28	28.37	29.72	1.03
33	DT14063.12	GENO37	28.44	29.07	29.01	30.23	29.19	-0.11
34	DT14036.01	GENO38	35.81	NA	28.40	NA	32.11	7.85
35	DT14055.25	GENO39	41.40	NA	29.69	40.13	37.07	-0.15
36	LadyOlympia	GENO41	33.70	29.44	29.35	31.19	30.92	0.83
37	BANBA	GENO42	35.16	34.49	25.69	36.55	32.97	2.12
38	VanGOGH	GENO43	31.64	28.21	24.55	34.05	29.61	1.48

39	DT14049.10	GENO44	35.15	26.19	29.62	32.05	30.75	0.92
40	DT14061.23	GENO45	28.97	29.81	26.50	28.95	28.56	0.59
41	DT14006.07	GENO46	32.86	38.40	28.34	32.81	33.10	1.23
42	DT14046.19	GENO47	28.90	36.11	26.62	30.71	30.58	0.79
43	DT14014.27	GENO48	36.25	28.76	26.50	34.37	31.47	1.93
44	DT14011.18	GENO49	35.17	29.62	29.00	34.54	32.08	1.19
45	DT14069.13	GENO50	40.62	32.65	29.18	42.38	36.20	2.30
46	DT14026.21	GENO52	35.12	37.61	27.61	35.10	33.86	1.80
47	DT14042.24	GENO53	39.41	32.13	28.59	33.27	33.35	2.18
48	DT14090.11	GENO54	31.42	35.34	29.23	33.83	32.45	0.64
49	DT14071.19	GENO55	27.76	33.75	30.13	27.71	29.84	-0.31
50	DT14027.08	GENO56	27.73	28.46	25.93	27.68	27.45	0.44
51	DT14034.03	GENO57	33.77	27.79	25.47	31.90	29.73	1.66
52	DT14057.36	GENO58	28.10	28.14	27.91	29.27	28.35	0.04
53	DT14062.08	GENO59	33.86	25.12	25.94	NA	28.31	1.47
54	DT14079.02	GENO60	27.77	27.85	25.28	27.72	27.16	0.57
55	DT14053.03	GENO61	33.29	NA	NA	NA	33.29	6.31
56	DT13088.03	GENO63	37.89	36.46	28.94	37.82	35.28	1.98
57	DT14051.66	GENO64	34.54	29.07	27.59	33.27	31.12	1.37
58	DT13100.02	GENO65	32.31	31.80	28.95	32.26	31.33	0.74
59	DT13162.15	GENO66	35.43	28.33	26.05	35.38	31.30	1.86
60	DT13162.12	GENO67	31.66	31.33	30.30	31.61	31.23	0.30
61	DT11107.01	GENO68	27.39	25.09	25.71	29.78	26.99	0.30
62	ZIRVE	GENO69	34.04	NA	28.17	35.22	32.48	-0.49
63	DT12012.02	GENO70	25.67	32.59	24.98	28.06	27.82	0.42
64	DT13136.22	GENO71	37.13	27.77	27.99	30.71	30.90	1.73
65	DT13045.74	GENO72	31.66	27.67	26.92	34.05	30.07	0.93
66	DT13124.21	GENO73	31.74	34.93	35.76	31.71	33.54	-0.79
67	BORWINA	GENO74	42.24	27.66	29.71	40.26	34.97	2.30
68	BROOKE	GENO75	26.59	26.48	30.09	29.82	28.25	-0.80
69	TESSA	GENO76	33.12	34.25	29.10	39.15	33.90	0.95
70	DT13143.49	GENO77	30.29	30.07	26.26	40.77	31.85	0.91
71	DT13130.48	GENO78	30.48	27.26	24.74	26.85	27.33	1.18
72	DT13143.54	GENO79	34.98	32.41	29.11	34.96	32.86	1.24
73	DT13007.03	GENO80	30.44	31.19	25.44	30.39	29.37	1.16
74	KUTUP	GENO81	28.59	33.70	24.75	28.57	28.90	1.06
75	DT13028.01	GENO82	37.15	25.08	27.44	31.61	30.32	1.75
76	DT13093.92	GENO83	39.81	32.42	33.65	39.76	36.41	1.12
77	DT13051.10	GENO84	40.79	30.69	29.62	32.71	33.45	2.16
78	DT13143.58	GENO85	34.05	41.09	35.96	NA	37.03	-0.17
79	DT13026.10	GENO86	33.72	29.07	25.26	27.92	28.99	1.75
80	DT13049.50	GENO87	35.95	26.62	27.66	34.05	31.07	1.53
81	DT13072.19	GENO88	37.79	31.12	25.61	37.75	33.07	2.52
82	DT13083.01	GENO89	30.55	31.20	28.53	30.50	30.19	0.48
83	LadyRosetta	GENO90	33.87	NA	29.97	NA	31.92	7.54

84	DT11007.01	GENO91	34.10	27.05	26.69	35.27	30.78	1.42
85	DT11108.02	GENO92	26.45	26.83	26.08	29.36	27.18	0.10
86	DORUK	GENO93	26.78	26.52	24.74	28.56	26.65	0.45
87	DT13085.01	GENO94	36.51	27.67	26.73	36.46	31.84	1.89
88	DT12068.21	GENO95	36.03	37.41	32.46	37.84	35.94	0.86
89	DT11088.01	GENO96	33.52	33.63	26.98	33.38	31.88	1.49
90	DT13045.42	GENO97	41.59	39.38	34.91	42.18	39.51	1.43
91	DT13147.17	GENO98	39.04	37.33	31.00	38.97	36.59	1.76
92	DT13048.10	GENO99	33.07	29.40	27.60	35.47	31.39	1.10
93	DT13052.23	GENO100	42.70	28.98	28.90	42.65	35.81	2.62
94	DT13037.31	GENO101	28.00	26.49	24.91	27.34	26.69	0.65
95	DT13045.103	GENO102	34.90	32.59	29.07	37.29	33.46	1.24
96	DT13037.35	GENO103	45.29	28.33	27.04	43.42	36.02	3.51
97	DT13047.08	GENO104	26.81	38.57	25.78	28.62	29.95	0.67
98	DT13162.16	GENO105	26.86	27.48	26.37	28.66	27.34	0.13
99	DT13067.03	GENO106	33.41	31.20	30.92	35.21	32.68	0.48
100	SORAYA	GENO107	37.83	31.33	33.35	35.25	34.44	0.77
101	LAURA	GENO108	28.91	27.60	26.25	27.01	27.44	0.55
102	SHEPODY	GENO109	36.76	25.76	25.47	39.74	31.93	2.15
103	43-111-11	GENO110	27.52	30.58	31.28	28.91	29.57	-0.74
104	KARLENA	GENO111	25.70	26.31	25.26	37.65	28.73	0.12
105	139-101-11	GENO112	32.54	28.61	27.63	33.73	30.63	0.97
106	84-105-11	GENO113	37.50	31.98	24.67	39.80	33.48	2.71
107	NANDU	GENO114	33.77	29.97	24.88	NA	29.54	1.88
108	882-202-10	GENO115	29.34	30.11	28.19	30.51	29.53	0.29
109	TALENT	GENO116	27.78	27.13	31.57	39.86	31.58	-0.88
110	57-104-11	GENO117	33.27	35.19	28.47	37.71	33.66	1.16
111	878-202-10	GENO118	34.75	33.64	31.61	34.73	33.68	0.67
112	146-103-11	GENO120	26.52	32.74	30.99	36.11	31.59	-0.78
113	SALUTE	GENO121	26.49	40.49	24.67	26.06	29.43	0.94
114	68-105-11	GENO122	42.77	27.48	25.58	40.19	34.00	3.33
115	63-113-11	GENO123	30.47	28.34	26.45	30.40	28.91	0.83
116	106-105-11	GENO124	27.33	35.83	26.38	27.80	29.34	0.53
117	939-201-10	GENO125	37.24	37.48	29.97	37.21	35.47	1.66
118	NIXE	GENO126	32.31	33.64	26.85	29.84	30.66	1.31
119	51-109-11	GENO127	32.03	28.46	31.14	34.94	31.64	0.07
120	ETIKETSIZNORIKA	GENO128	34.74	28.12	27.61	28.82	29.82	1.37
121	40-103-11	GENO130	31.54	29.62	30.03	32.71	30.98	0.27
122	99-115-11	GENO131	33.77	25.70	25.61	33.62	29.68	1.55
123	141-104-11	GENO132	34.16	33.20	29.72	29.46	31.63	0.97
124	89-105-11	GENO133	33.49	34.85	31.00	33.45	33.20	0.62
125	NAUTILUS	GENO134	30.72	24.69	29.71	33.09	29.55	0.00
126	157-103-11	GENO136	31.02	27.69	27.95	31.56	29.55	0.57
127	133-112-11	GENO137	31.33	35.60	24.95	34.84	31.68	1.61
128	944-208-10	GENO138	28.32	30.07	26.97	29.11	28.62	0.37
129	PRIVELIGE	GENO139	30.09	25.76	29.02	28.23	28.28	0.08

130	966-203-10	GENO140	46.02	25.95	25.93	43.44	35.33	3.81
131	904-212-10	GENO141	24.70	31.19	29.43	28.54	28.46	-0.83
132	BETTINA	GENO142	33.57	34.88	26.36	34.72	32.38	1.69
133	125-104-11	GENO143	28.68	29.18	28.33	28.54	28.68	0.10
134	SWING	GENO144	32.91	NA	NA	NA	32.91	6.24
135	758-109-09	GENO145	28.99	34.85	24.87	30.39	29.78	1.15
136	735-102-09	GENO146	36.08	29.40	28.04	36.62	32.54	1.58
137	99-102-11	GENO147	32.33	26.62	24.68	32.89	29.13	1.52
138	TERRANA	GENO148	34.93	25.98	27.59	37.30	31.45	1.33
139	104-103-11	GENO149	34.14	25.55	24.67	36.56	30.23	1.83
140	SFHIT	GENO150	27.13	28.14	27.67	28.21	27.79	-0.08
141	KIWI	GENO151	30.18	33.26	29.49	30.04	30.74	0.27
142	KIEBITZ	GENO152	26.55	27.74	27.47	26.73	27.12	-0.16
143	BONUS	GENO153	32.90	33.64	27.51	34.09	32.04	1.25
144	509-104-09	GENO154	37.44	25.98	26.31	29.17	29.73	2.10
145	43-118-11	GENO155	29.26	35.19	31.59	28.62	31.16	-0.31
146	BEO	GENO156	25.37	26.97	24.95	28.35	26.41	0.16
147	BALTICCREAM	GENO157	33.94	39.24	27.64	26.14	31.74	1.63
148	868-201-10	GENO158	30.82	33.69	27.67	31.62	30.95	0.82
149	860-201-10	GENO159	29.87	31.98	24.67	27.56	28.52	1.26
150	DUKATA	GENO160	35.11	24.69	29.23	31.99	30.26	0.95
151	84-107-11	GENO161	31.50	27.53	29.50	31.06	29.90	0.31
152	128-105-11	GENO162	29.39	33.33	26.86	29.98	29.89	0.72
153	140-107-11	GENO163	36.90	24.69	31.16	36.46	32.30	0.85
154	PELIKAN	GENO164	34.39	24.48	25.16	29.98	28.50	1.73
155	KOLIBRI	GENO165	33.45	27.05	30.17	NA	30.22	0.51
156	82-119-11	GENO167	28.38	28.15	27.04	26.73	27.57	0.30
157	WENDY	GENO168	29.48	26.92	27.51	28.44	28.09	0.35
158	ROMANZE	GENO169	30.14	24.48	32.66	38.32	31.40	-0.78
159	PRESTIGE	GENO170	41.07	42.78	35.60	34.02	38.37	1.29
160	MAXI	GENO171	32.24	33.75	28.38	27.53	30.47	0.93
161	FASAN	GENO172	28.10	40.97	26.25	29.50	31.21	0.90
162	Madaleine	GENO173	37.42	33.02	24.86	35.76	32.77	2.69
163	POMQUEEN	GENO174	29.81	25.98	26.55	33.42	28.94	0.60
164	MUNGO	GENO175	30.00	25.98	25.78	28.76	27.63	0.81
165	ALBATROS	GENO176	39.39	39.14	29.65	37.73	36.48	2.20
166	FIDELIA	GENO177	25.77	27.06	29.69	26.33	27.21	-0.84
167	TACOMA	GENO178	33.66	33.64	31.80	33.02	33.03	0.42
168	BONZA	GENO179	40.89	31.98	30.93	42.04	36.46	1.93
169	ADRETTA	GENO180	42.68	29.92	31.75	33.28	34.41	2.00
170	POWER	GENO181	27.78	28.33	26.33	34.05	29.12	0.35
171	GOLDMARIE	GENO182	36.45	26.41	29.18	25.87	29.48	1.28
172	RITA	GENO183	25.52	26.31	24.81	27.53	26.04	0.19
173	SUMMERGOLD	GENO184	27.68	28.39	26.92	29.36	28.09	0.20
174	DIPLOMAT	GENO185	30.89	31.19	25.14	32.28	29.88	1.32

175	CASCADA	GENO186	42.61	33.05	30.32	44.62	37.65	2.43
176	SOLIST	GENO187	29.99	32.59	33.08	31.75	31.85	-0.60
177	LOLITA	GENO188	28.78	29.43	26.24	27.54	28.00	0.60
178	KARATOP	GENO189	32.86	33.09	30.39	31.00	31.83	0.57
179	INARA	GENO190	28.02	33.26	34.31	NA	31.86	-1.23
180	ACAPELLA	GENO191	35.76	33.03	25.93	37.16	32.97	2.13
181	ALLORA	GENO192	31.11	31.80	33.79	32.28	32.25	-0.58
182	ARKULA	GENO193	25.76	27.92	NA	25.08	26.25	0.24
183	TOKIO	GENO194	34.06	27.85	30.09	36.43	32.11	0.67
184	BIRTE	GENO195	28.02	31.76	26.32	29.17	28.82	0.53
185	900-205-10	GENO196	31.44	30.77	27.68	31.61	30.37	0.83
186	MAXILLA	GENO197	28.52	42.04	25.17	26.67	30.60	1.27
187	TUCAN	GENO198	28.26	37.60	29.19	31.29	31.59	0.14
188	946-202-10	GENO199	25.45	35.09	25.28	31.04	29.21	0.40
189	KORMORAN	GENO200	38.14	26.87	28.18	37.10	32.57	1.84
190	JUMBO	GENO202	29.95	27.90	26.77	31.35	28.99	0.65
191	LOGO	GENO203	28.15	30.90	28.66	28.94	29.16	-0.01
192	102-102-11	GENO204	37.93	27.24	25.67	36.89	31.93	2.38
		Mean	32.31	30.97	28.11	32.76	31.03	

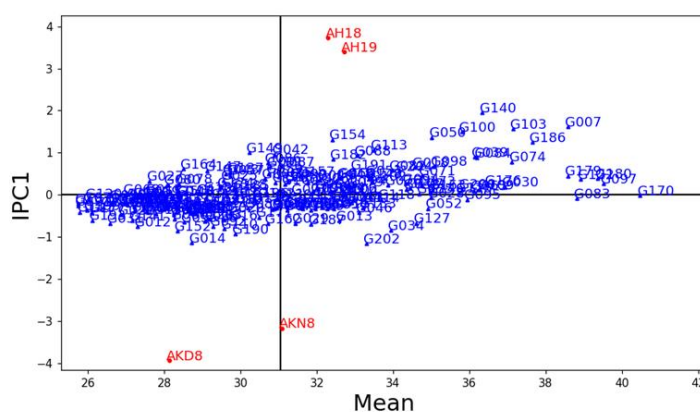


Fig. S8. Ammi biplot for mean of total antioxidant activity of 192 genotypes across four environments (AH18, AKN18, AKD18, AH19) plotted against IPC1 (Interactive principal component).

APPENDIX-I Phenotypic data of total phenolics “mg ferulic acid equivalent (FAE)/ 100 g dry weight” (TPC) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Codes	TPC_H18	TPC_KN18	TPC_KD18	TPC_H19	Mean TPC	b_i
1	JELLY	GENO2	105.11	108.27	100.84	NA	104.74	0.32
2	RUMBA	GENO3	206.82	198.64	174.25	NA	193.24	2.14
3	HERMES	GENO4	128.18	131.00	114.77	NA	124.65	0.94
4	ALEGRIA	GENO5	188.30	181.73	145.45	NA	171.83	2.85
5	ROYAL	GENO6	104.90	115.36	105.53	124.86	112.66	0.05
6	ELECTRA	GENO7	275.31	294.65	271.97	268.47	277.60	0.41
7	DT14003.01	GENO9	120.94	151.41	105.87	153.52	132.94	1.31
8	DT14038.01	GENO10	118.16	134.14	122.73	130.21	126.31	-0.16
9	DT14010.18	GENO11	63.44	138.08	62.09	118.32	95.48	0.78
10	DT14004.17	GENO12	139.80	155.36	135.97	160.24	147.84	0.40
11	DT14010.14	GENO13	243.67	297.78	224.53	180.24	236.55	1.80
12	DT14085.03	GENO14	63.57	71.41	65.84	91.83	73.16	-0.08
13	DT14013.15	GENO16	121.80	NA	NA	108.32	115.06	8.16
14	DT14018.32	GENO18	109.07	93.74	111.78	112.82	106.85	-0.33
15	DT14042.27	GENO19	155.39	138.28	158.78	119.23	142.92	-0.39
16	DT14005.09	GENO20	79.80	104.36	74.87	80.65	84.92	0.56
17	DT14030.11	GENO21	118.12	129.19	110.06	101.24	114.65	0.65
18	DT14057.37	GENO22	74.58	83.77	76.87	117.63	88.21	-0.07
19	DT14065.01	GENO23	100.85	101.01	125.84	NA	109.23	-1.70
20	DT14016.01	GENO24	150.89	146.46	156.09	151.82	151.32	-0.39
21	DT14016.34	GENO25	82.66	99.19	93.84	99.52	93.81	-0.61
22	DT14078.03	GENO26	118.54	90.81	114.87	103.27	106.87	-0.01
23	DT14028.03	GENO27	87.21	86.27	102.97	86.32	90.69	-1.08
24	DT14054.11	GENO28	269.12	271.01	214.87	167.32	230.58	3.71
25	DT14037.18	GENO29	89.80	106.87	88.98	95.90	95.39	0.21
26	DT14091.04	GENO30	259.80	208.28	254.44	130.89	213.35	-0.11
27	DT14083.28	GENO31	85.39	96.50	88.75	NA	90.21	-0.13
28	DT14015.22	GENO32	111.62	70.50	109.75	118.54	102.60	-0.25
29	DT14051.15	GENO33	61.62	126.46	111.73	68.67	92.12	-2.81
30	DT14047.38	GENO34	319.94	320.72	247.77	306.13	298.64	4.92
31	DT14026.04	GENO35	236.39	245.27	175.78	233.81	222.81	4.20
32	DT14068.07	GENO36	147.08	169.81	108.62	115.46	135.24	2.83
33	DT14063.12	GENO37	97.99	129.60	106.44	110.65	111.17	-0.28
34	DT14036.01	GENO38	284.48	NA	NA	NA	284.48	16.73
35	DT14055.25	GENO39	243.62	NA	NA	142.23	192.93	15.64
36	LadyOlympia	GENO41	154.90	136.18	148.75	168.31	152.04	0.25
37	BANBA	GENO42	300.76	305.59	255.21	210.52	268.02	3.14
38	VanGOGH	GENO43	162.35	142.54	129.97	139.76	143.65	2.02

39	DT14049.10	GENO44	240.71	163.45	103.75	158.23	166.54	8.60
40	DT14061.23	GENO45	157.21	168.28	170.75	148.37	161.15	-0.82
41	DT14006.07	GENO46	239.07	228.28	226.84	128.88	205.77	0.73
42	DT14046.19	GENO47	104.48	115.56	115.53	101.23	109.20	-0.65
43	DT14014.27	GENO48	117.26	103.77	105.75	126.32	113.28	0.66
44	DT14011.18	GENO49	270.85	161.95	210.73	206.32	212.46	3.09
45	DT14069.13	GENO50	231.27	172.63	222.75	137.77	191.10	0.04
46	DT14026.21	GENO52	113.57	133.54	122.06	123.65	123.21	-0.39
47	DT14042.24	GENO53	111.62	158.99	100.62	142.22	128.36	1.18
48	DT14090.11	GENO54	237.21	198.31	216.75	174.37	206.66	1.03
49	DT14071.19	GENO55	108.16	164.65	109.78	112.68	123.82	0.41
50	DT14027.08	GENO56	99.07	108.28	97.87	109.23	103.62	0.17
51	DT14034.03	GENO57	194.35	191.04	141.62	148.56	168.89	3.56
52	DT14057.36	GENO58	127.26	136.50	120.53	127.42	127.93	0.54
53	DT14062.08	GENO59	228.12	213.74	229.53	NA	223.80	-0.23
54	DT14079.02	GENO60	89.07	94.36	88.78	89.65	90.47	0.07
55	DT14053.03	GENO61	96.39	NA	NA	NA	96.39	5.67
56	DT13088.03	GENO63	126.72	141.95	111.45	117.87	124.50	1.18
57	DT14051.66	GENO64	237.99	179.19	180.96	142.41	185.14	3.34
58	DT13100.02	GENO65	204.35	142.63	179.51	139.85	166.58	1.12
59	DT13162.15	GENO66	116.35	103.54	135.62	135.52	122.76	-1.43
60	DT13162.12	GENO67	144.53	147.78	154.78	129.27	144.09	-0.67
61	DT11107.01	GENO68	98.90	81.04	96.67	106.90	95.88	-0.01
62	ZIRVE	GENO69	171.62	NA	129.01	146.42	149.02	1.32
63	DT12012.02	GENO70	117.26	135.36	113.67	158.53	131.20	0.41
64	DT13136.22	GENO71	237.21	167.09	172.78	176.23	188.33	3.74
65	DT13045.74	GENO72	84.53	85.27	86.78	96.56	88.29	-0.15
66	DT13124.21	GENO73	151.76	154.68	133.78	165.85	151.52	1.25
67	BORWINA	GENO74	322.76	259.90	271.53	288.94	285.78	2.91
68	BROOKE	GENO75	87.13	93.45	91.65	61.56	83.45	-0.25
69	TESSA	GENO76	192.17	188.08	191.11	129.85	175.30	0.03
70	DT13143.49	GENO77	256.30	241.72	237.51	245.68	245.30	1.14
71	DT13130.48	GENO78	84.35	85.59	81.87	80.46	83.07	0.18
72	DT13143.54	GENO79	86.30	152.86	110.07	161.51	127.69	-1.00
73	DT13007.03	GENO80	74.53	76.27	77.06	128.54	89.10	-0.16
74	KUTUP	GENO81	80.85	88.99	80.78	115.42	91.51	0.08
75	DT13028.01	GENO82	131.62	120.13	132.41	184.65	142.20	-0.16
76	DT13093.92	GENO83	177.26	196.27	193.76	234.84	200.53	-0.95
77	DT13051.10	GENO84	281.76	263.74	279.84	206.65	258.00	-0.04
78	DT13143.58	GENO85	150.85	168.28	142.89	NA	154.01	0.70
79	DT13026.10	GENO86	105.44	91.92	100.62	101.56	99.89	0.20
80	DT13049.50	GENO87	146.72	151.92	134.50	186.65	154.95	0.88
81	DT13072.19	GENO88	190.71	200.50	157.78	179.25	182.06	2.33
82	DT13083.01	GENO89	70.89	127.78	119.87	158.75	119.32	-2.81
83	LadyRosetta	GENO90	103.49	NA	98.60	NA	101.05	6.99
84	DT11007.01	GENO91	127.26	148.31	93.43	138.69	126.92	2.49

85	DT11108.02	GENO92	66.39	101.01	78.68	88.65	83.68	-0.52
86	DORUK	GENO93	59.80	66.50	59.45	62.77	62.13	0.09
87	DT13085.01	GENO94	275.44	208.08	255.87	177.95	229.33	0.71
88	DT12068.21	GENO95	135.39	120.10	119.76	166.88	135.53	0.92
89	DT11088.01	GENO96	115.48	104.68	108.51	195.85	131.13	0.37
90	DT13045.42	GENO97	227.21	192.63	179.83	182.54	195.55	2.90
91	DT13147.17	GENO98	313.99	319.90	256.53	205.77	274.05	3.96
92	DT13048.10	GENO99	92.53	108.69	127.76	106.90	108.97	-2.25
93	DT13052.23	GENO100	294.35	265.36	273.87	164.51	249.52	1.13
94	DT13037.31	GENO101	108.90	82.83	114.21	115.88	105.45	-0.60
95	DT13045.103	GENO102	138.90	144.65	144.61	132.56	140.18	-0.34
96	DT13037.35	GENO103	329.80	328.31	203.46	309.52	292.77	8.58
97	DT13047.08	GENO104	108.12	123.74	111.90	105.86	112.40	-0.11
98	DT13162.16	GENO105	59.94	81.92	59.62	138.52	85.00	0.22
99	DT13067.03	GENO106	243.26	175.59	228.78	180.85	207.12	0.36
100	SORAYA	GENO107	137.30	126.50	145.10	139.42	137.08	-0.63
101	LAURA	GENO108	133.08	118.91	136.84	173.42	140.56	-0.39
102	SHEPODY	GENO109	141.27	134.36	115.87	138.69	132.55	1.66
103	43-111-11	GENO110	61.67	81.63	63.56	94.65	75.38	0.06
104	KARLENA	GENO111	134.40	139.81	125.19	126.67	131.52	0.68
105	139-101-11	GENO112	203.26	215.59	195.56	164.88	194.82	0.64
106	84-105-11	GENO113	123.67	91.92	99.20	138.99	113.45	1.37
107	NANDU	GENO114	110.94	105.96	126.78	NA	114.56	-1.12
108	882-202-10	GENO115	152.71	178.00	134.47	175.99	160.29	1.47
109	TALENT	GENO116	116.22	127.41	127.47	183.62	138.68	-0.66
110	57-104-11	GENO117	316.22	291.63	293.46	247.70	287.25	1.32
111	878-202-10	GENO118	90.54	120.13	90.43	129.68	107.69	0.28
112	146-103-11	GENO120	120.41	129.19	105.43	181.35	134.09	1.10
113	SALUTE	GENO121	110.41	107.17	105.62	115.67	109.72	0.30
114	68-105-11	GENO122	229.12	211.63	213.46	149.69	200.97	0.90
115	63-113-11	GENO123	239.45	212.32	193.21	140.90	196.47	2.89
116	106-105-11	GENO124	82.76	NA	79.01	110.58	90.78	-1.93
117	939-201-10	GENO125	131.44	89.90	116.65	138.98	119.24	0.62
118	NIXE	GENO126	265.08	221.41	154.75	171.79	203.26	7.10
119	51-109-11	GENO127	225.48	235.27	200.31	235.56	224.16	1.80
120	ETIKETSIZNORIK	GENO128	116.22	105.59	127.87	127.58	119.31	-0.89
121	40-103-11	GENO130	134.53	168.00	141.11	159.38	150.75	-0.14
122	99-115-11	GENO131	109.12	144.68	111.62	132.18	124.40	0.16
123	141-104-11	GENO132	103.49	72.32	81.65	128.38	96.46	1.20
124	89-105-11	GENO133	118.90	132.86	129.08	126.65	126.87	-0.56
125	NAUTILUS	GENO134	136.72	121.63	113.97	132.32	126.16	1.41
126	157-103-11	GENO136	252.17	185.27	207.54	173.26	204.56	2.42
127	133-112-11	GENO137	138.21	171.41	135.65	156.94	150.55	0.48
128	944-208-10	GENO138	96.77	95.56	91.47	105.69	97.37	0.35
129	PRIVELIGE	GENO139	239.63	226.27	237.53	135.68	209.78	0.02
130	966-203-10	GENO140	88.21	138.28	79.21	144.69	112.60	1.07

131	904-212-10	GENO141	113.13	78.00	99.34	99.65	97.53	0.61
132	BETTINA	GENO142	155.81	157.41	155.43	160.85	157.37	0.04
133	125-104-11	GENO143	100.94	159.81	102.98	116.87	120.15	0.40
134	SWING	GENO144	92.76	NA	NA	NA	92.76	5.45
135	758-109-09	GENO145	103.13	98.69	100.44	157.56	114.95	0.14
136	735-102-09	GENO146	124.90	90.50	124.43	143.65	120.87	-0.28
137	99-102-11	GENO147	111.80	111.41	105.43	119.56	112.05	0.43
138	TERRANA	GENO148	253.99	178.00	115.00	124.87	167.97	8.75
139	104-103-11	GENO149	204.17	162.54	162.15	181.28	177.53	2.47
140	SFHIT	GENO150	77.30	77.09	93.78	85.65	83.46	-1.12
141	KIWI	GENO151	94.58	112.54	94.20	107.42	102.18	0.19
142	KIEBITZ	GENO152	101.31	87.18	83.84	106.76	94.77	1.06
143	BONUS	GENO153	102.35	117.78	103.44	128.68	113.06	0.07
144	509-104-09	GENO154	145.08	99.22	106.46	90.65	110.35	2.20
145	43-118-11	GENO155	125.99	121.63	120.43	110.54	119.65	0.34
146	BEO	GENO156	164.36	151.72	139.63	148.62	151.08	1.57
147	BALTICCREAM	GENO157	75.31	85.59	59.21	72.18	73.07	1.19
148	868-201-10	GENO158	80.41	98.99	127.67	127.69	108.69	-3.04
149	860-201-10	GENO159	85.99	91.04	105.21	90.65	93.22	-1.26
150	DUKATA	GENO160	123.99	66.27	136.75	119.67	111.67	-1.40
151	84-107-11	GENO161	124.40	117.17	116.46	135.67	123.43	0.47
152	128-105-11	GENO162	69.63	83.45	66.47	93.56	78.28	0.34
153	140-107-11	GENO163	134.40	145.96	131.46	152.18	141.00	0.31
154	PELIKAN	GENO164	165.48	151.95	135.87	144.76	149.52	1.89
155	KOLIBRI	GENO165	75.31	NA	83.73	NA	79.52	5.20
156	82-119-11	GENO167	79.50	114.45	114.21	105.65	103.45	-2.04
157	WENDY	GENO168	136.22	147.41	126.84	132.76	135.81	0.74
158	ROMANZE	GENO169	261.85	224.68	204.10	245.65	234.07	3.59
159	PRESTIGE	GENO170	160.41	158.31	151.77	178.77	162.31	0.57
160	MAXI	GENO171	160.76	139.60	122.64	136.41	139.85	2.40
161	FASAN	GENO172	137.13	154.14	138.84	131.88	140.50	0.04
162	Madaleine	GENO173	227.13	228.00	216.51	192.31	215.99	0.73
163	POMQUEEN	GENO174	121.80	125.59	128.53	124.42	125.09	-0.42
164	MUNGO	GENO175	78.72	83.23	94.87	83.87	85.17	-1.06
165	ALBATROS	GENO176	121.67	128.91	126.46	128.15	126.30	-0.26
166	FIDELIA	GENO177	279.98	217.09	264.62	177.88	234.89	0.47
167	TACOMA	GENO178	260.54	235.36	213.54	231.41	235.21	2.96
168	BONZA	GENO179	195.81	138.99	181.54	186.56	175.73	0.45
169	ADRETTA	GENO180	152.76	124.36	141.46	130.65	137.31	0.51
170	POWER	GENO181	133.49	140.10	125.10	121.68	130.09	0.63
171	GOLDMARIE	GENO182	131.44	88.28	128.87	103.13	112.93	-0.22
172	RITA	GENO183	94.40	89.19	104.09	98.69	96.59	-0.71
173	SUMMERGOLD	GENO184	71.85	116.87	101.54	79.66	92.48	-1.60
174	DIPLOMAT	GENO185	55.31	75.36	67.62	94.99	73.32	-0.65
175	CASCADA	GENO186	153.13	122.63	131.65	145.98	138.35	1.18
176	SOLIST	GENO187	106.72	144.68	110.53	170.42	133.09	0.09

177	LOLITA	GENO188	45.99	98.99	92.75	89.41	81.79	-2.69
178	KARATOP	GENO189	240.54	226.18	148.06	125.41	185.05	6.16
179	INARA	GENO190	95.86	105.56	79.84	NA	93.75	1.18
180	ACAPELLA	GENO191	133.13	110.10	118.47	140.54	125.56	0.78
181	ALLORA	GENO192	118.16	129.22	121.46	249.61	154.61	-0.12
182	ARKULA	GENO193	61.27	106.46	NA	73.65	80.46	-0.43
183	TOKIO	GENO194	127.63	116.46	115.91	152.89	128.22	0.69
184	BIRTE	GENO195	101.27	128.31	121.67	132.18	120.86	-1.14
185	900-205-10	GENO196	92.58	74.68	86.46	84.65	84.59	0.25
186	MAXILLA	GENO197	86.90	82.54	76.56	99.46	86.37	0.66
187	TUCAN	GENO198	159.63	162.54	147.78	163.31	158.32	0.83
188	946-202-10	GENO199	124.04	137.09	110.37	124.87	124.09	1.05
189	KORMORAN	GENO200	141.67	97.18	141.78	112.42	123.26	-0.42
190	JUMBO	GENO202	95.31	86.27	95.53	101.32	94.61	-0.10
191	LOGO	GENO203	81.67	72.54	94.87	80.42	82.38	-0.98
192	102-102-11	GENO204	220.41	197.17	180.83	214.57	203.24	2.48
		Mean	146.83	144.18	135.86	141.53	141.92	

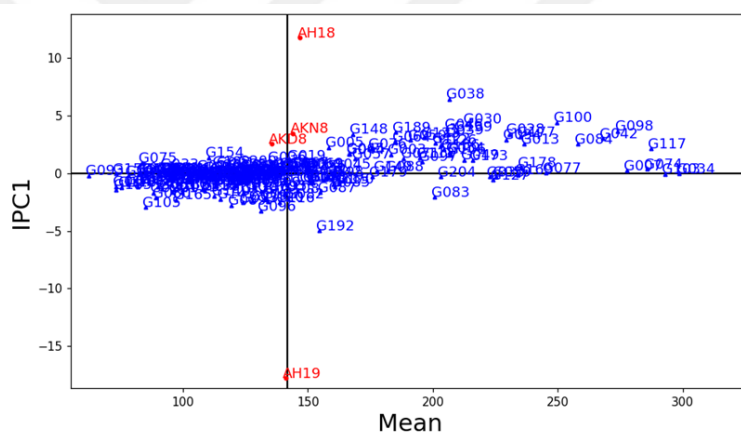


Fig.S9. Ammi biplot for mean of total phenolic contents of 192 genotypes across four environments (AH18, AKN18, AKD18, AH19) plotted against IPC1 (Interactive principal component).

APPENDIX-J Phenotypic data of tuber flesh colour L* coordinate (FCL) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S. No.	Genotype Names	Codes	FCL H18	FCL KN18	FCL KD18	FCL H19	Mean FCL	b_i
1	JELLY	GENO2	66.19	65.59	67.55	NA	66.44	1.66
2	RUMBA	GENO3	65.09	64.20	68.57	NA	65.95	1.12
3	HERMES	GENO4	66.26	67.70	70.36	NA	68.11	4.54
4	ALEGRIA	GENO5	65.18	62.70	69.48	NA	65.78	9.03
5	ROYAL	GENO6	70.65	67.32	70.65	68.59	69.30	3.56
6	ELECTRA	GENO7	62.67	62.93	66.39	64.31	64.07	5.24
7	DT14003.01	GENO9	73.07	65.99	68.69	68.62	69.09	1.08
8	DT14038.01	GENO10	65.97	66.47	64.71	66.65	65.95	-2.40
9	DT14010.18	GENO11	70.94	62.44	65.85	69.10	67.08	1.55
10	DT14004.17	GENO12	65.33	65.27	70.34	64.61	66.38	7.50
11	DT14010.14	GENO13	63.33	64.54	67.23	67.44	65.64	4.49
12	DT14085.03	GENO14	69.55	70.24	71.66	68.12	69.89	2.39
13	DT14013.15	GENO16	68.10	NA	NA	69.02	68.56	-102.01
14	DT14018.32	GENO18	67.01	66.89	66.15	68.03	67.02	-1.15
15	DT14042.27	GENO19	65.27	66.35	68.76	67.56	66.99	4.02
16	DT14005.09	GENO20	66.59	64.50	71.38	74.02	69.12	9.34
17	DT14030.11	GENO21	65.92	66.03	66.42	67.84	66.55	0.62
18	DT14057.37	GENO22	66.61	70.01	69.13	66.80	68.14	0.10
19	DT14065.01	GENO23	65.67	70.12	64.65	NA	66.81	-6.28
20	DT14016.01	GENO24	65.60	67.82	68.76	66.79	67.24	2.31
21	DT14016.34	GENO25	66.56	66.62	66.48	68.13	66.95	-0.18
22	DT14078.03	GENO26	67.01	66.73	70.29	70.03	68.52	5.17
23	DT14028.03	GENO27	68.02	63.69	69.69	69.41	67.70	7.11
24	DT14054.11	GENO28	63.04	63.10	68.75	67.37	65.56	8.41
25	DT14037.18	GENO29	66.29	65.35	69.80	71.92	68.34	6.21
26	DT14091.04	GENO30	62.54	65.05	69.70	70.76	67.01	7.93
27	DT14083.28	GENO31	73.53	73.00	71.94	NA	72.82	-1.79
28	DT14015.22	GENO32	65.60	68.80	69.67	67.11	67.79	2.61
29	DT14051.15	GENO33	69.03	67.48	67.19	72.28	68.99	-1.07
30	DT14047.38	GENO34	61.44	60.26	64.67	62.25	62.16	6.05
31	DT14026.04	GENO35	63.81	65.36	65.53	66.81	65.38	0.89
32	DT14068.07	GENO36	65.95	63.82	70.25	68.26	67.07	8.66
33	DT14063.12	GENO37	66.71	67.50	73.60	67.22	68.76	9.38
34	DT14036.01	GENO38	63.90	NA	NA	NA	63.90	-26.38
35	DT14055.25	GENO39	63.71	NA	NA	67.57	65.64	-98.64
36	LadyOlympia	GENO41	64.81	69.12	66.32	65.21	66.36	-2.37
37	BANBA	GENO42	61.89	64.42	68.96	68.52	65.95	7.78
38	VanGOGH	GENO43	65.14	66.63	71.73	70.57	68.52	8.18

39	DT14049.10	GENO44	64.11	68.54	71.76	68.05	68.12	6.61
40	DT14061.23	GENO45	64.78	66.28	67.98	67.44	66.62	3.14
41	DT14006.07	GENO46	64.24	64.55	66.91	71.24	66.73	3.63
42	DT14046.19	GENO47	65.61	66.01	67.12	68.33	66.77	1.81
43	DT14014.27	GENO48	64.80	66.29	70.18	67.89	67.29	6.39
44	DT14011.18	GENO49	63.76	69.67	67.68	66.45	66.89	-0.51
45	DT14069.13	GENO50	63.78	64.30	66.76	67.04	65.47	3.86
46	DT14026.21	GENO52	64.86	66.27	69.35	69.31	67.45	5.15
47	DT14042.24	GENO53	67.74	64.56	67.40	65.66	66.34	2.90
48	DT14090.11	GENO54	64.45	66.51	68.40	69.84	67.30	3.65
49	DT14071.19	GENO55	71.59	64.04	70.60	69.44	68.92	6.61
50	DT14027.08	GENO56	68.99	66.20	71.50	69.36	69.01	6.71
51	DT14034.03	GENO57	64.93	66.83	70.99	70.62	68.34	6.96
52	DT14057.36	GENO58	65.95	69.38	70.54	68.51	68.59	3.14
53	DT14062.08	GENO59	63.86	71.03	72.72	NA	69.20	5.47
54	DT14079.02	GENO60	70.07	69.30	74.54	70.47	71.10	7.46
55	DT14053.03	GENO61	67.28	NA	NA	NA	67.28	-27.78
56	DT13088.03	GENO63	66.06	65.24	69.17	68.99	67.36	5.49
57	DT14051.66	GENO64	63.21	67.68	68.56	69.39	67.21	3.15
58	DT13100.02	GENO65	64.61	69.83	70.57	71.20	69.06	3.25
59	DT13162.15	GENO66	68.29	69.07	72.57	67.40	69.33	5.51
60	DT13162.12	GENO67	65.32	70.18	70.19	70.38	69.02	2.02
61	DT11107.01	GENO68	75.23	73.29	71.83	74.13	73.62	-2.97
62	ZIRVE	GENO69	64.70	NA	70.20	69.37	68.09	1.04
63	DT12012.02	GENO70	71.33	67.12	70.17	69.73	69.59	2.79
64	DT13136.22	GENO71	63.80	68.52	68.40	68.43	67.29	1.77
65	DT13045.74	GENO72	66.56	71.71	70.49	70.47	69.81	0.32
66	DT13124.21	GENO73	66.57	67.80	66.49	68.19	67.26	-1.44
67	BORWINA	GENO74	61.92	65.99	71.15	64.38	65.86	9.34
68	BROOKE	GENO75	76.88	70.31	73.40	73.04	73.41	1.87
69	TESSA	GENO76	62.96	63.56	66.42	70.08	65.76	4.49
70	DT13143.49	GENO77	63.89	66.71	74.83	66.25	67.92	13.21
71	DT13130.48	GENO78	67.58	68.69	70.29	70.55	69.28	2.83
72	DT13143.54	GENO79	70.82	66.94	67.89	66.71	68.09	-0.19
73	DT13007.03	GENO80	68.86	71.35	72.01	69.47	70.42	2.01
74	KUTUP	GENO81	65.63	68.63	70.32	69.91	68.62	3.75
75	DT13028.01	GENO82	65.78	68.80	67.86	64.25	66.67	-0.15
76	DT13093.92	GENO83	64.74	64.16	66.87	66.89	65.66	3.78
77	DT13051.10	GENO84	62.21	65.75	68.84	67.04	65.96	6.05
78	DT13143.58	GENO85	64.84	65.19	67.35	NA	65.79	3.35
79	DT13026.10	GENO86	67.94	71.86	67.01	70.57	69.34	-5.58
80	DT13049.50	GENO87	65.90	71.69	70.27	65.23	68.27	0.28
81	DT13072.19	GENO88	66.51	68.24	69.99	69.51	68.56	3.31
82	DT13083.01	GENO89	67.53	67.14	71.04	65.86	67.89	5.62
83	LadyRosetta	GENO90	65.62	NA	71.72	NA	68.67	-103.87
84	DT11007.01	GENO91	67.37	68.22	70.92	67.82	68.58	4.36

85	DT11108.02	GENO92	68.85	68.26	75.57	70.14	70.71	10.60
86	DORUK	GENO93	69.82	71.52	74.48	72.58	72.10	5.09
87	DT13085.01	GENO94	62.66	67.64	72.42	68.52	67.81	9.15
88	DT12068.21	GENO95	65.47	68.48	68.34	69.25	67.88	1.04
89	DT11088.01	GENO96	67.04	70.61	69.49	64.87	68.00	-0.19
90	DT13045.42	GENO97	63.31	66.65	70.82	68.94	67.43	7.57
91	DT13147.17	GENO98	60.50	63.46	63.98	67.16	63.78	1.99
92	DT13048.10	GENO99	66.28	68.24	68.11	68.89	67.88	0.62
93	DT13052.23	GENO100	58.16	67.06	68.08	69.07	65.59	5.19
94	DT13037.31	GENO101	67.90	71.43	74.54	67.02	70.22	6.07
95	DT13045.103	GENO102	68.43	69.54	72.32	69.01	69.82	4.58
96	DT13037.35	GENO103	57.74	66.19	70.48	64.71	64.78	9.85
97	DT13047.08	GENO104	74.16	65.66	69.62	72.09	70.38	2.36
98	DT13162.16	GENO105	74.47	71.55	69.99	65.45	70.37	-3.52
99	DT13067.03	GENO106	64.15	68.44	72.88	66.62	68.02	8.36
100	SORAYA	GENO107	65.42	67.41	67.62	68.74	67.30	1.13
101	LAURA	GENO108	68.10	66.01	66.28	64.93	66.33	-0.46
102	SHEPODY	GENO109	67.37	75.73	74.74	73.54	72.84	1.98
103	43-111-11	GENO110	75.89	68.37	71.35	69.39	71.25	1.32
104	KARLENA	GENO111	65.64	68.56	71.47	68.56	68.56	5.52
105	139-101-11	GENO112	64.77	67.05	68.70	69.49	67.50	3.39
106	84-105-11	GENO113	67.29	69.14	71.38	69.18	69.25	4.09
107	NANDU	GENO114	68.90	69.62	71.54	NA	70.02	3.15
108	882-202-10	GENO115	68.29	66.64	72.80	66.77	68.63	8.46
109	TALENT	GENO116	65.68	64.70	69.38	63.73	65.87	6.54
110	57-104-11	GENO117	62.03	64.10	65.89	67.06	64.77	3.51
111	878-202-10	GENO118	66.27	67.39	67.76	67.85	67.32	1.01
112	146-103-11	GENO120	66.89	65.24	65.01	64.91	65.51	-1.02
113	SALUTE	GENO121	65.74	66.48	70.49	71.44	68.54	6.25
114	68-105-11	GENO122	63.16	66.13	72.08	70.55	67.98	10.05
115	63-113-11	GENO123	63.57	66.29	69.80	71.44	67.78	6.33
116	106-105-11	GENO124	66.56	NA	68.10	68.63	67.76	1.42
117	939-201-10	GENO125	65.03	68.51	73.47	67.73	68.69	8.79
118	NIXE	GENO126	62.06	67.52	70.88	67.68	67.03	7.24
119	51-109-11	GENO127	64.37	67.08	68.16	67.60	66.80	2.72
120	ETIKETSIZNORIK	GENO128	66.73	70.65	68.31	64.05	67.43	-1.85
121	40-103-11	GENO130	65.09	64.99	68.90	68.49	66.87	5.76
122	99-115-11	GENO131	66.36	67.53	68.74	68.86	67.87	2.28
123	141-104-11	GENO132	67.86	68.46	67.66	67.87	67.96	-0.94
124	89-105-11	GENO133	67.05	65.91	68.68	69.55	67.80	3.64
125	NAUTILUS	GENO134	66.87	71.32	70.16	67.11	68.86	0.12
126	157-103-11	GENO136	63.12	66.65	71.25	67.61	67.16	8.28
127	133-112-11	GENO137	68.55	64.36	65.02	66.65	66.14	-0.75
128	944-208-10	GENO138	68.48	71.03	70.79	67.31	69.40	0.70
129	PRIVELIGE	GENO139	63.24	66.32	71.05	69.90	67.63	8.29
130	966-203-10	GENO140	69.75	67.77	75.62	66.90	70.01	10.83

131	904-212-10	GENO141	71.85	70.29	71.90	70.49	71.13	1.74
132	BETTINA	GENO142	64.78	63.31	68.08	68.53	66.17	6.47
133	125-104-11	GENO143	68.14	70.01	70.90	69.37	69.61	2.09
134	SWING	GENO144	67.19	NA	NA	NA	67.19	-27.74
135	758-109-09	GENO145	69.00	68.55	72.96	66.97	69.37	6.36
136	735-102-09	GENO146	65.97	66.50	68.32	65.77	66.64	2.92
137	99-102-11	GENO147	67.11	66.13	67.52	68.94	67.43	1.66
138	TERRANA	GENO148	63.43	68.74	72.29	66.26	67.68	7.46
139	104-103-11	GENO149	62.34	72.06	68.14	69.84	68.10	-1.80
140	SFHIT	GENO150	69.64	69.51	70.68	70.26	70.02	1.68
141	KIWI	GENO151	67.56	69.48	71.23	67.71	69.00	3.39
142	KIEBITZ	GENO152	67.05	71.23	73.69	70.75	70.68	5.38
143	BONUS	GENO153	66.50	65.29	69.63	67.19	67.15	5.94
144	509-104-09	GENO154	64.81	66.25	68.54	70.27	67.47	3.99
145	43-118-11	GENO155	66.55	67.17	67.65	70.77	68.03	0.97
146	BEO	GENO156	66.11	66.65	65.96	68.37	66.77	-0.80
147	BALTICCREAM	GENO157	68.65	65.58	72.38	67.88	68.62	8.82
148	868-201-10	GENO158	69.52	66.44	68.12	69.78	68.47	1.22
149	860-201-10	GENO159	71.08	69.22	71.24	71.60	70.79	2.23
150	DUKATA	GENO160	66.77	72.59	67.87	70.19	69.35	-4.60
151	84-107-11	GENO161	65.11	67.21	70.60	66.50	67.35	5.90
152	128-105-11	GENO162	75.11	64.36	73.83	69.28	70.64	9.61
153	140-107-11	GENO163	64.79	67.89	67.44	67.33	66.86	0.61
154	PELIKAN	GENO164	65.71	64.95	70.40	68.30	67.34	7.77
155	KOLIBRI	GENO165	65.73	NA	67.13	NA	66.43	-99.01
156	82-119-11	GENO167	69.23	64.89	70.18	70.87	68.79	6.06
157	WENDY	GENO168	65.47	69.66	72.24	66.99	68.59	5.56
158	ROMANZE	GENO169	62.73	70.61	68.01	65.68	66.76	-0.60
159	PRESTIGE	GENO170	65.90	54.56	66.21	64.76	62.86	12.60
160	MAXI	GENO171	65.77	68.20	73.01	68.60	68.90	8.14
161	FASAN	GENO172	68.09	63.39	71.40	67.84	67.68	9.94
162	Madaleine	GENO173	59.95	65.66	69.39	66.38	65.34	7.89
163	POMQUEEN	GENO174	65.39	73.80	71.85	68.72	69.94	0.58
164	MUNGO	GENO175	71.05	76.01	74.43	69.27	72.69	-0.30
165	ALBATROS	GENO176	65.41	65.71	70.46	68.82	67.60	7.17
166	FIDELIA	GENO177	63.03	65.97	66.03	67.56	65.65	1.30
167	TACOMA	GENO178	63.93	65.02	65.18	65.20	64.83	0.69
168	BONZA	GENO179	64.74	69.74	68.28	69.89	68.16	-0.10
169	ADRETTA	GENO180	65.12	69.92	69.89	69.73	68.67	1.94
170	POWER	GENO181	70.88	69.14	69.11	72.71	70.46	-0.76
171	GOLDMARIE	GENO182	65.49	68.34	70.49	69.06	68.34	4.37
172	RITA	GENO183	68.10	69.15	68.54	70.23	69.00	-0.47
173	SUMMERGOLD	GENO184	68.75	66.92	70.66	71.43	69.44	4.79
174	DIPLOMAT	GENO185	68.79	68.11	74.54	71.31	70.69	9.26
175	CASCADA	GENO186	64.85	66.12	67.93	69.05	66.99	3.21
176	SOLIST	GENO187	67.20	63.75	69.31	65.73	66.50	6.82

177	LOLITA	GENO188	66.02	69.32	66.19	66.77	67.08	-3.28
178	KARATOP	GENO189	64.01	66.32	69.92	68.69	67.24	6.29
179	INARA	GENO190	73.48	65.71	67.95	NA	69.05	0.11
180	ACAPELLA	GENO191	67.17	69.71	72.57	66.40	68.96	5.29
181	ALLORA	GENO192	68.65	65.40	67.95	62.25	66.06	2.44
182	ARKULA	GENO193	76.28	68.03	NA	70.71	71.67	0.57
183	TOKIO	GENO194	68.07	71.20	70.53	66.90	69.17	0.30
184	BIRTE	GENO195	73.36	67.06	69.42	67.85	69.42	0.90
185	900-205-10	GENO196	68.43	68.88	70.44	72.31	70.02	2.50
186	MAXILLA	GENO197	74.19	63.17	74.42	67.13	69.73	12.14
187	TUCAN	GENO198	64.79	64.07	68.80	64.42	65.52	6.72
188	946-202-10	GENO199	68.76	67.10	69.58	67.60	68.26	2.99
189	KORMORAN	GENO200	66.77	71.19	72.13	69.23	69.83	3.22
190	JUMBO	GENO202	71.08	71.62	68.79	67.31	69.70	-3.98
191	LOGO	GENO203	68.90	69.54	72.04	68.88	69.84	3.97
192	102-102-11	GENO204	63.99	65.63	67.67	68.44	66.43	3.70
		Mean	66.60	67.42	69.67	68.37	67.97	

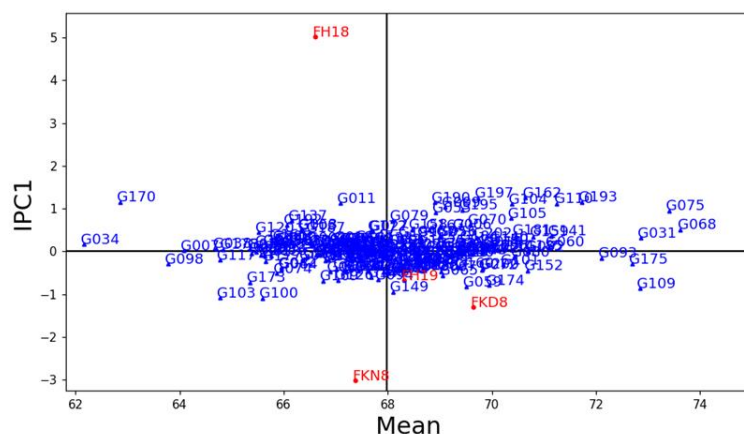


Fig.S10. Ammi biplot for mean of tuber flesh colour L* of 192 genotypes across four environments (FH18, FKN18, FKN19, FKN20) plotted against IPC1 (Interactive principal component)

APPENDIX-K Phenotypic data of tuber flesh colour b^* coordinate (FCb) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). b_i corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S.No.	Genotype Names	Codes	FCb H18	FCb KN18	FCb KD18	FCb H19	Mean FCb	b_i
1	JELLY	GENO2	19.07	26.43	26.92	NA	24.14	1.51
2	RUMBA	GENO3	18.57	25.45	25.24	NA	23.09	1.24
3	HERMES	GENO4	17.88	25.73	26.70	NA	23.44	1.30
4	ALEGRIA	GENO5	14.71	23.00	23.56	NA	20.42	1.70
5	ROYAL	GENO6	25.43	23.62	24.73	22.90	24.17	-0.23
6	ELECTRA	GENO7	15.86	20.54	20.95	19.87	19.30	0.97
7	DT14003.01	GENO9	8.69	22.97	25.52	24.24	20.36	3.10
8	DT14038.01	GENO10	16.45	19.12	19.36	19.55	18.62	0.55
9	DT14010.18	GENO11	17.92	19.65	22.82	24.39	21.20	0.69
10	DT14004.17	GENO12	17.81	22.89	27.58	24.42	23.17	1.53
11	DT14010.14	GENO13	17.55	20.20	23.47	21.76	20.75	0.89
12	DT14085.03	GENO14	26.39	30.87	30.37	29.27	29.22	0.83
13	DT14013.15	GENO16	18.69	NA	NA	24.12	21.41	-1.61
14	DT14018.32	GENO18	3.23	17.33	21.94	24.39	16.72	3.30
15	DT14042.27	GENO19	18.34	23.88	23.59	25.39	22.80	1.06
16	DT14005.09	GENO20	17.65	21.38	24.82	23.17	21.75	1.12
17	DT14030.11	GENO21	23.50	26.12	24.66	25.67	24.99	0.36
18	DT14057.37	GENO22	19.34	24.36	24.22	20.85	22.19	0.98
19	DT14065.01	GENO23	16.63	23.39	21.27	NA	20.43	1.10
20	DT14016.01	GENO24	17.23	21.91	22.38	22.45	20.99	0.98
21	DT14016.34	GENO25	21.00	21.93	22.63	22.44	22.00	0.26
22	DT14078.03	GENO26	23.66	25.08	27.63	25.87	25.56	0.56
23	DT14028.03	GENO27	19.89	19.63	25.05	20.90	21.37	0.55
24	DT14054.11	GENO28	16.64	19.76	21.98	21.31	19.92	0.86
25	DT14037.18	GENO29	15.57	19.73	21.39	20.20	19.22	1.01
26	DT14091.04	GENO30	15.30	19.58	19.54	19.43	18.46	0.84
27	DT14083.28	GENO31	14.99	31.81	33.06	NA	26.62	3.46
28	DT14015.22	GENO32	15.85	25.39	24.64	24.35	22.56	1.80
29	DT14051.15	GENO33	18.54	23.36	22.85	27.27	23.01	0.90
30	DT14047.38	GENO34	17.43	17.37	21.29	19.09	18.80	0.42
31	DT14026.04	GENO35	19.76	20.72	23.23	24.82	22.13	0.47
32	DT14068.07	GENO36	17.05	22.03	25.25	23.29	21.91	1.34
33	DT14063.12	GENO37	19.56	23.16	28.50	23.04	23.57	1.31
34	DT14036.01	GENO38	20.07	NA	NA	NA	20.07	-3.96
35	DT14055.25	GENO39	17.46	NA	NA	21.17	19.32	-1.62
36	LadyOlympia	GENO41	21.56	23.18	25.84	22.04	23.16	0.62
37	BANBA	GENO42	17.68	19.09	24.72	21.86	20.84	0.90

38	VanGOGH	GENO43	19.30	25.21	27.06	25.27	24.21	1.37
39	DT14049.10	GENO44	16.93	22.32	24.25	23.09	21.65	1.28
40	DT14061.23	GENO45	21.29	26.79	28.06	30.72	26.72	1.23
41	DT14006.07	GENO46	17.29	21.25	21.08	26.49	21.53	0.76
42	DT14046.19	GENO47	20.67	25.16	25.13	23.60	23.64	0.88
43	DT14014.27	GENO48	19.49	25.79	23.65	21.74	22.67	1.01
44	DT14011.18	GENO49	22.25	29.46	29.84	29.44	27.75	1.47
45	DT14069.13	GENO50	22.56	24.28	24.45	24.79	24.02	0.36
46	DT14026.21	GENO52	15.86	22.07	25.49	21.72	21.29	1.61
47	DT14042.24	GENO53	19.84	21.70	23.05	23.05	21.91	0.52
48	DT14090.11	GENO54	16.83	18.02	18.08	17.28	17.55	0.24
49	DT14071.19	GENO55	5.75	23.48	26.70	25.84	20.44	3.86
50	DT14027.08	GENO56	22.80	25.20	28.06	27.96	26.00	0.79
51	DT14034.03	GENO57	16.52	22.75	24.64	26.52	22.61	1.44
52	DT14057.36	GENO58	20.28	23.52	24.42	22.84	22.77	0.74
53	DT14062.08	GENO59	10.45	14.38	15.88	NA	13.57	0.94
54	DT14079.02	GENO60	22.71	28.48	31.35	26.40	27.23	1.46
55	DT14053.03	GENO61	19.30	NA	NA	NA	19.30	-3.81
56	DT13088.03	GENO63	18.84	19.22	25.13	19.68	20.72	0.73
57	DT14051.66	GENO64	17.22	19.05	18.75	18.66	18.42	0.33
58	DT13100.02	GENO65	18.59	21.44	24.19	24.87	22.27	0.87
59	DT13162.15	GENO66	20.05	25.60	25.38	25.49	24.13	1.07
60	DT13162.12	GENO67	21.02	26.63	24.72	25.78	24.54	0.90
61	DT11107.01	GENO68	6.24	20.65	22.75	19.71	17.34	3.08
62	ZIRVE	GENO69	16.92	NA	23.75	18.16	19.61	0.73
63	DT12012.02	GENO70	5.73	22.37	20.54	20.56	17.30	3.08
64	DT13136.22	GENO71	15.31	22.16	23.33	18.94	19.93	1.48
65	DT13045.74	GENO72	21.50	21.94	23.26	25.10	22.95	0.23
66	DT13124.21	GENO73	18.69	22.19	21.98	21.84	21.18	0.67
67	BORWINA	GENO74	18.65	22.46	26.06	21.18	22.09	1.15
68	BROOKE	GENO75	7.40	21.79	23.85	25.49	19.63	3.07
69	TESSA	GENO76	19.45	22.71	22.34	21.72	21.56	0.60
70	DT13143.49	GENO77	20.58	28.24	29.65	25.03	25.88	1.67
71	DT13130.48	GENO78	19.01	27.19	21.85	23.63	22.92	1.02
72	DT13143.54	GENO79	5.91	27.57	27.67	20.78	20.48	4.29
73	DT13007.03	GENO80	19.60	25.11	24.30	23.64	23.16	1.00
74	KUTUP	GENO81	20.13	28.17	26.32	23.10	24.43	1.38
75	DT13028.01	GENO82	20.59	27.74	24.96	29.73	25.76	1.10
76	DT13093.92	GENO83	21.65	23.35	22.52	26.93	23.61	0.24
77	DT13051.10	GENO84	14.30	19.94	22.09	25.16	20.37	1.35
78	DT13143.58	GENO85	21.64	22.71	22.05	NA	22.13	0.14
79	DT13026.10	GENO86	15.97	23.62	18.05	21.39	19.76	0.89
80	DT13049.50	GENO87	22.15	22.34	22.97	20.80	22.07	0.11
81	DT13072.19	GENO88	21.59	19.61	29.02	24.54	23.69	0.66
82	DT13083.01	GENO89	21.39	23.01	26.41	22.61	23.36	0.70

83	LadyRosetta	GENO90	18.49	NA	25.19	NA	21.84	-1.48
84	DT11007.01	GENO91	17.84	18.75	18.56	18.01	18.29	0.16
85	DT11108.02	GENO92	20.07	23.47	21.83	23.07	22.11	0.49
86	DORUK	GENO93	21.67	27.90	26.08	27.06	25.68	1.03
87	DT13085.01	GENO94	16.91	24.77	29.04	22.69	23.35	2.03
88	DT12068.21	GENO95	19.18	24.83	23.95	26.61	23.64	1.02
89	DT11088.01	GENO96	19.44	29.94	24.89	21.76	24.01	1.51
90	DT13045.42	GENO97	15.82	24.59	27.38	25.59	23.35	2.04
91	DT13147.17	GENO98	16.47	21.87	22.16	21.37	20.47	1.10
92	DT13048.10	GENO99	18.25	22.84	26.57	26.03	23.42	1.32
93	DT13052.23	GENO100	20.08	25.02	23.61	22.92	22.91	0.82
94	DT13037.31	GENO101	17.38	26.71	28.22	25.40	24.43	2.01
95	DT13045.103	GENO102	17.17	16.45	20.99	17.93	18.13	0.36
96	DT13037.35	GENO103	16.74	23.50	26.97	21.73	22.23	1.72
97	DT13047.08	GENO104	8.62	24.85	25.54	25.82	21.21	3.28
98	DT13162.16	GENO105	8.38	27.86	24.51	25.82	21.64	3.48
99	DT13067.03	GENO106	20.78	23.33	21.07	19.96	21.29	0.25
100	SORAYA	GENO107	22.75	27.77	26.81	27.56	26.22	0.88
101	LAURA	GENO108	29.50	29.49	31.36	24.80	28.79	0.21
102	SHEPODY	GENO109	15.85	14.81	17.69	16.79	16.29	0.11
103	43-111-11	GENO110	6.45	21.40	19.81	20.31	16.99	2.78
104	KARLENA	GENO111	19.95	24.15	27.22	28.73	25.01	1.17
105	139-101-11	GENO112	19.32	26.01	24.89	26.19	24.10	1.20
106	84-105-11	GENO113	24.08	30.60	31.67	29.96	29.08	1.41
107	NANDU	GENO114	20.60	28.28	28.21	NA	25.70	1.51
108	882-202-10	GENO115	12.92	14.74	17.34	16.74	15.43	0.65
109	TALENT	GENO116	23.82	28.26	25.01	26.88	25.99	0.52
110	57-104-11	GENO117	18.00	23.97	22.70	21.39	21.51	1.04
111	878-202-10	GENO118	21.43	21.37	22.93	24.55	22.57	0.16
112	146-103-11	GENO120	7.17	23.14	23.71	21.38	18.85	3.22
113	SALUTE	GENO121	21.64	28.31	29.75	27.99	26.92	1.48
114	68-105-11	GENO122	20.90	24.69	29.12	28.01	25.68	1.24
115	63-113-11	GENO123	20.19	23.13	24.24	22.84	22.60	0.70
116	106-105-11	GENO124	24.35	NA	26.35	26.61	25.77	0.42
117	939-201-10	GENO125	22.35	23.75	28.99	27.05	25.53	0.86
118	NIXE	GENO126	23.86	31.33	31.78	27.06	28.51	1.53
119	51-109-11	GENO127	20.52	24.55	23.49	22.08	22.66	0.68
120	ETIKETSIZNORIKA	GENO128	23.29	27.52	22.89	25.99	24.92	0.32
121	40-103-11	GENO130	14.65	22.12	24.12	23.42	21.08	1.70
122	99-115-11	GENO131	21.28	22.34	25.84	23.68	23.28	0.60
123	141-104-11	GENO132	22.98	23.01	21.62	24.08	22.92	-0.15
124	89-105-11	GENO133	20.87	27.95	28.36	29.33	26.63	1.44
125	NAUTILUS	GENO134	22.55	27.51	23.75	22.69	24.12	0.56
126	157-103-11	GENO136	20.21	24.71	28.20	24.08	24.30	1.28
127	133-112-11	GENO137	18.45	19.30	22.01	20.30	20.01	0.47

128	944-208-10	GENO138	19.53	24.14	28.43	25.01	24.28	1.39
129	PRIVELIGE	GENO139	20.13	23.97	27.10	21.85	23.26	1.11
130	966-203-10	GENO140	17.89	21.49	23.86	23.13	21.59	0.97
131	904-212-10	GENO141	15.51	22.79	21.15	18.91	19.59	1.26
132	BETTINA	GENO142	20.49	24.22	26.39	26.43	24.38	0.98
133	125-104-11	GENO143	24.95	31.79	34.04	27.30	29.52	1.60
134	SWING	GENO144	22.69	NA	NA	NA	22.69	-4.48
135	758-109-09	GENO145	15.13	19.36	19.17	18.33	18.00	0.81
136	735-102-09	GENO146	27.28	28.00	26.61	29.69	27.89	-0.01
137	99-102-11	GENO147	29.21	20.54	20.63	22.74	23.28	-1.70
138	TERRANA	GENO148	14.10	18.78	22.06	19.27	18.55	1.29
139	104-103-11	GENO149	20.93	25.47	25.55	25.82	24.44	0.91
140	SFHIT	GENO150	21.31	23.31	24.08	23.66	23.09	0.48
141	KIWI	GENO151	22.58	28.15	27.07	26.17	25.99	0.98
142	KIEBITZ	GENO152	20.44	28.22	26.54	26.85	25.51	1.35
143	BONUS	GENO153	25.92	23.98	21.89	21.94	23.43	-0.62
144	509-104-09	GENO154	14.48	14.34	17.28	17.26	15.84	0.30
145	43-118-11	GENO155	21.07	19.82	21.26	19.09	20.31	-0.09
146	BEO	GENO156	20.28	25.27	23.39	24.44	23.34	0.78
147	BALTICCREAM	GENO157	14.30	16.13	20.27	18.36	17.26	0.82
148	868-201-10	GENO158	17.04	20.33	18.24	18.52	18.53	0.42
149	860-201-10	GENO159	16.87	20.66	23.14	19.92	20.15	1.02
150	DUKATA	GENO160	23.38	23.17	23.38	22.85	23.20	-0.02
151	84-107-11	GENO161	22.22	28.50	30.46	26.20	26.85	1.46
152	128-105-11	GENO162	7.16	23.74	24.82	24.62	20.09	3.40
153	140-107-11	GENO163	19.06	22.56	22.65	22.08	21.59	0.70
154	PELIKAN	GENO164	19.41	24.26	28.57	23.27	23.88	1.44
155	KOLIBRI	GENO165	20.55	NA	24.97	NA	22.76	-1.90
156	82-119-11	GENO167	22.04	24.70	25.27	27.21	24.81	0.59
157	WENDY	GENO168	22.93	27.81	29.36	28.12	27.05	1.14
158	ROMANZE	GENO169	21.16	24.94	25.05	26.76	24.48	0.76
159	PRESTIGE	GENO170	14.87	20.84	23.13	20.16	19.75	1.43
160	MAXI	GENO171	20.30	22.84	25.65	21.60	22.60	0.81
161	FASAN	GENO172	19.73	23.01	25.87	24.06	23.17	0.97
162	Madaleine	GENO173	17.52	22.78	27.27	24.50	23.02	1.54
163	POMQUEEN	GENO174	23.40	31.85	29.81	26.78	27.96	1.44
164	MUNGO	GENO175	16.49	18.29	20.22	19.11	18.53	0.57
165	ALBATROS	GENO176	18.51	23.27	22.81	24.63	22.31	0.89
166	FIDELIA	GENO177	19.89	26.46	27.07	30.46	25.97	1.37
167	TACOMA	GENO178	19.43	26.28	24.98	23.47	23.54	1.21
168	BONZA	GENO179	25.07	28.69	26.79	28.57	27.28	0.50
169	ADRETTA	GENO180	19.05	23.35	24.18	28.64	23.80	0.94
170	POWER	GENO181	19.15	23.44	22.63	22.81	22.01	0.76
171	GOLDMARIE	GENO182	20.34	28.82	30.82	29.46	27.36	1.90
172	RITA	GENO183	23.41	29.22	24.94	25.98	25.89	0.67

173	SUMMERGOLD	GENO184	19.29	22.85	24.93	22.74	22.45	0.93
174	DIPLOMAT	GENO185	24.13	29.29	30.32	29.11	28.21	1.13
175	CASCADA	GENO186	22.88	28.32	31.80	28.95	27.99	1.46
176	SOLIST	GENO187	25.28	23.79	27.63	24.78	25.37	0.13
177	LOLITA	GENO188	21.41	27.73	28.16	26.17	25.87	1.30
178	KARATOP	GENO189	22.15	22.50	24.78	23.34	23.19	0.32
179	INARA	GENO190	8.43	25.34	26.86	NA	20.21	3.51
180	ACAPELLA	GENO191	21.58	24.38	27.55	27.62	25.28	0.91
181	ALLORA	GENO192	7.61	20.51	23.34	21.01	18.12	2.86
182	ARKULA	GENO193	8.22	24.16	NA	24.37	18.92	3.17
183	TOKIO	GENO194	24.85	32.33	27.57	27.07	27.95	0.95
184	BIRTE	GENO195	17.17	28.79	30.98	21.92	24.72	2.54
185	900-205-10	GENO196	20.32	23.01	23.03	22.35	22.18	0.53
186	MAXILLA	GENO197	6.34	23.26	28.27	20.22	19.52	3.90
187	TUCAN	GENO198	17.09	17.61	19.68	21.64	19.00	0.33
188	946-202-10	GENO199	23.16	25.47	24.28	26.05	24.74	0.32
189	KORMORAN	GENO200	18.83	21.81	26.08	17.15	20.97	1.06
190	JUMBO	GENO202	14.75	24.81	25.98	26.03	22.89	2.12
191	LOGO	GENO203	20.92	29.45	27.15	29.51	26.76	1.43
192	102-102-11	GENO204	21.82	27.28	31.88	29.67	27.66	1.59
		Mean	18.65	23.83	24.83	23.78	22.67	

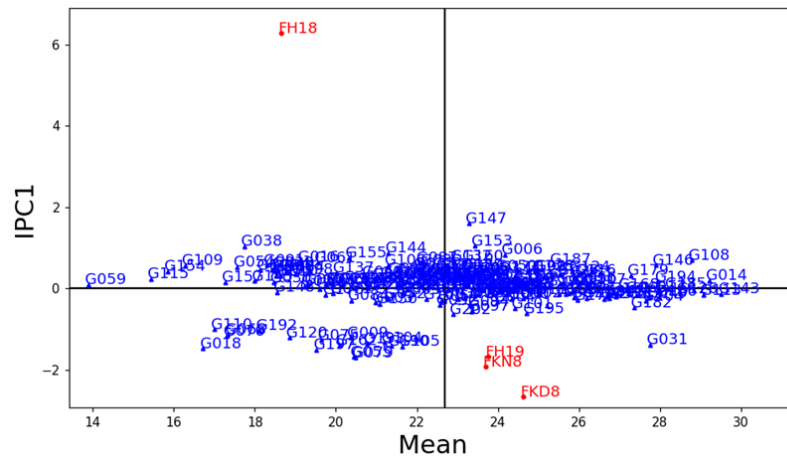


Fig.S11. Ammi biplot for mean of tuber flesh colour b^* of 192 genotypes across four environments (FH18, FKN18, FKD18, FH19) plotted against IPC1 (Interactive principal component)

APPENDIX-L Phenotypic data of tuber flesh colour a* coordinate (FCa) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S.No.	Genotype Names	Codes	Fca_H18	Fca_KN18	Fca_KD18	Fca_H19	Mean FCa	b_i
1	JELLY	GENO2	1.76	2.45	2.64	NA	2.28	2.33
2	RUMBA	GENO3	1.54	1.51	1.67	NA	1.58	0.74
3	HERMES	GENO4	1.13	1.60	1.95	NA	1.56	2.04
4	ALEGRIA	GENO5	0.81	0.96	1.19	NA	0.99	0.89
5	ROYAL	GENO6	1.88	2.66	2.43	1.47	2.11	1.73
6	ELECTRA	GENO7	1.31	0.84	1.58	1.09	1.21	0.18
7	DT14003.01	GENO9	-1.23	0.23	1.41	1.20	0.40	6.52
8	DT14038.01	GENO10	1.03	0.67	1.36	1.11	1.04	0.39
9	DT14010.18	GENO11	0.39	1.52	1.62	0.41	0.98	3.39
10	DT14004.17	GENO12	0.75	2.23	2.29	1.58	1.71	4.29
11	DT14010.14	GENO13	1.16	0.52	1.30	0.66	0.91	-0.22
12	DT14085.03	GENO14	1.98	2.80	2.16	2.06	2.25	1.01
13	DT14013.15	GENO16	1.06	NA	NA	0.92	0.99	-2.27
14	DT14018.32	GENO18	-1.05	0.39	0.89	0.67	0.22	5.08
15	DT14042.27	GENO19	1.94	2.81	1.74	1.33	1.95	0.27
16	DT14005.09	GENO20	0.61	1.43	1.49	0.49	1.01	2.43
17	DT14030.11	GENO21	1.49	1.92	2.04	1.32	1.69	1.46
18	DT14057.37	GENO22	0.96	1.68	3.13	1.06	1.71	4.98
19	DT14065.01	GENO23	0.67	0.66	1.60	NA	0.98	1.89
20	DT14016.01	GENO24	1.28	0.93	0.84	0.46	0.88	-1.17
21	DT14016.34	GENO25	1.30	0.86	1.44	1.44	1.26	-0.06
22	DT14078.03	GENO26	2.17	2.55	2.86	1.45	2.25	1.70
23	DT14028.03	GENO27	1.07	0.93	1.14	0.82	0.99	0.03
24	DT14054.11	GENO28	0.09	0.64	0.42	0.44	0.40	1.10
25	DT14037.18	GENO29	0.65	1.22	1.02	0.63	0.88	1.20
26	DT14091.04	GENO30	1.43	0.58	0.35	0.69	0.76	-2.86
27	DT14083.28	GENO31	-0.74	1.96	3.12	NA	1.45	9.97
28	DT14015.22	GENO32	0.72	2.67	1.70	1.40	1.62	3.52
29	DT14051.15	GENO33	0.73	1.27	1.24	1.03	1.07	1.46
30	DT14047.38	GENO34	0.74	0.79	1.47	0.81	0.95	1.53
31	DT14026.04	GENO35	2.42	1.09	1.60	1.62	1.68	-2.71
32	DT14068.07	GENO36	0.75	1.03	1.85	1.90	1.38	2.46
33	DT14063.12	GENO37	1.68	1.31	1.17	0.69	1.21	-1.33
34	DT14036.01	GENO38	1.65	NA	NA	NA	1.65	-4.65
35	DT14055.25	GENO39	1.65	NA	NA	1.28	1.47	-3.65
36	LadyOlympia	GENO41	1.43	1.56	3.50	1.56	2.01	4.32
37	BANBA	GENO42	1.93	1.73	1.90	1.04	1.65	-0.22
38	VanGOGH	GENO43	1.92	3.03	2.15	1.23	2.08	1.34

39	DT14049.10	GENO44	1.46	1.46	1.49	1.13	1.38	0.06
40	DT14061.23	GENO45	0.67	1.56	1.55	1.37	1.29	2.49
41	DT14006.07	GENO46	1.06	0.74	0.53	0.44	0.69	-1.33
42	DT14046.19	GENO47	1.57	1.44	1.53	1.31	1.46	-0.18
43	DT14014.27	GENO48	1.53	3.63	1.01	0.96	1.78	0.58
44	DT14011.18	GENO49	1.32	3.55	2.86	2.00	2.43	4.88
45	DT14069.13	GENO50	1.39	0.82	1.21	1.73	1.29	-0.81
46	DT14026.21	GENO52	0.96	1.95	1.65	1.53	1.52	2.18
47	DT14042.24	GENO53	1.47	1.31	1.52	1.64	1.49	-0.02
48	DT14090.11	GENO54	0.80	0.51	0.62	0.80	0.68	-0.59
49	DT14071.19	GENO55	-0.07	1.08	1.48	0.68	0.79	4.05
50	DT14027.08	GENO56	1.18	1.84	1.88	1.35	1.56	1.94
51	DT14034.03	GENO57	1.30	1.74	1.69	1.33	1.51	1.14
52	DT14057.36	GENO58	1.72	1.20	1.09	1.67	1.42	-1.69
53	DT14062.08	GENO59	0.97	0.22	0.52	NA	0.57	-1.50
54	DT14079.02	GENO60	0.80	2.22	1.65	1.11	1.44	2.84
55	DT14053.03	GENO61	0.80	NA	NA	NA	0.80	-2.25
56	DT13088.03	GENO63	1.27	1.10	1.50	0.87	1.19	0.34
57	DT14051.66	GENO64	1.10	0.97	0.84	1.05	0.99	-0.63
58	DT13100.02	GENO65	1.29	1.10	1.27	0.78	1.11	-0.19
59	DT13162.15	GENO66	0.84	1.21	0.89	1.42	1.09	0.39
60	DT13162.12	GENO67	1.15	0.14	1.59	5.79	2.17	0.11
61	DT11107.01	GENO68	-0.62	1.06	1.31	0.63	0.59	5.24
62	ZIRVE	GENO69	1.24	NA	0.88	0.49	0.87	-1.81
63	DT12012.02	GENO70	-0.53	0.61	0.56	0.54	0.30	3.11
64	DT13136.22	GENO71	0.77	0.77	1.19	0.42	0.79	0.86
65	DT13045.74	GENO72	1.28	0.64	1.00	0.74	0.91	-1.07
66	DT13124.21	GENO73	0.62	0.60	1.29	0.85	0.84	1.35
67	BORWINA	GENO74	2.48	1.65	2.19	1.14	1.86	-1.24
68	BROOKE	GENO75	-1.06	0.81	0.83	1.10	0.42	5.31
69	TESSA	GENO76	1.56	1.54	1.22	0.53	1.21	-0.71
70	DT13143.49	GENO77	1.21	0.90	1.20	1.03	1.08	-0.26
71	DT13130.48	GENO78	0.39	1.39	0.48	0.39	0.66	0.96
72	DT13143.54	GENO79	-0.90	1.14	0.80	1.26	0.58	5.06
73	DT13007.03	GENO80	1.13	0.92	0.55	0.89	0.87	-1.35
74	KUTUP	GENO81	1.51	0.79	1.82	0.69	1.20	0.07
75	DT13028.01	GENO82	1.43	1.59	1.79	1.61	1.61	0.86
76	DT13093.92	GENO83	1.41	0.91	0.55	1.65	1.13	-2.14
77	DT13051.10	GENO84	0.59	1.03	1.47	1.32	1.10	2.14
78	DT13143.58	GENO85	0.60	0.31	0.82	NA	0.58	0.22
79	DT13026.10	GENO86	0.44	0.41	0.65	0.63	0.53	0.40
80	DT13049.50	GENO87	2.12	0.35	1.33	1.16	1.24	-2.99
81	DT13072.19	GENO88	1.84	2.01	3.23	1.94	2.25	2.96
82	DT13083.01	GENO89	0.45	0.37	0.72	1.30	0.71	0.49
83	LadyRosetta	GENO90	1.73	NA	1.78	NA	1.76	-3.48

84	DT11007.01	GENO91	0.53	0.80	0.75	1.08	0.79	0.66
85	DT11108.02	GENO92	0.90	1.92	0.41	0.71	0.98	-0.20
86	DORUK	GENO93	1.66	1.44	1.27	0.93	1.33	-0.97
87	DT13085.01	GENO94	1.28	1.49	0.95	1.00	1.18	-0.51
88	DT12068.21	GENO95	1.13	1.29	1.30	1.39	1.28	0.47
89	DT11088.01	GENO96	1.17	1.73	1.14	1.51	1.39	0.38
90	DT13045.42	GENO97	0.68	2.29	2.08	0.86	1.47	4.11
91	DT13147.17	GENO98	1.32	1.23	1.24	1.39	1.29	-0.23
92	DT13048.10	GENO99	1.10	1.16	2.11	1.89	1.57	2.10
93	DT13052.23	GENO100	1.48	1.47	1.20	1.12	1.32	-0.58
94	DT13037.31	GENO101	0.71	0.18	0.95	1.41	0.81	0.07
95	DT13045.103	GENO102	0.69	1.09	1.14	1.23	1.04	1.23
96	DT13037.35	GENO103	2.71	2.34	0.86	1.16	1.77	-4.06
97	DT13047.08	GENO104	-0.77	1.28	1.92	1.14	0.89	7.08
98	DT13162.16	GENO105	-1.42	0.44	1.31	1.14	0.37	7.01
99	DT13067.03	GENO106	1.82	1.80	1.40	1.49	1.63	-0.87
100	SORAYA	GENO107	1.08	1.45	1.95	1.20	1.42	2.06
101	LAURA	GENO108	1.96	2.16	6.91	1.42	3.11	10.24
102	SHEPODY	GENO109	1.12	0.60	0.84	0.77	0.83	-0.98
103	43-111-11	GENO110	-1.52	1.38	0.92	0.51	0.32	7.24
104	KARLENA	GENO111	1.08	0.74	1.18	1.06	1.02	-0.06
105	139-101-11	GENO112	1.16	1.85	1.43	1.44	1.47	1.09
106	84-105-11	GENO113	1.60	1.70	2.32	1.49	1.78	1.54
107	NANDU	GENO114	0.90	1.49	2.80	NA	1.73	4.33
108	882-202-10	GENO115	1.52	1.48	0.71	1.49	1.30	-1.68
109	TALENT	GENO116	1.75	2.90	1.63	2.37	2.16	0.65
110	57-104-11	GENO117	1.80	0.71	0.67	0.95	1.03	-3.15
111	878-202-10	GENO118	0.96	1.17	1.52	1.04	1.17	1.30
112	146-103-11	GENO120	0.06	1.12	1.47	1.53	1.04	3.70
113	SALUTE	GENO121	2.28	1.53	1.22	1.15	1.54	-2.74
114	68-105-11	GENO122	2.40	1.99	2.12	1.02	1.88	-0.89
115	63-113-11	GENO123	1.78	0.96	1.72	0.76	1.31	-0.76
116	106-105-11	GENO124	2.05	NA	2.51	1.02	1.86	-1.74
117	939-201-10	GENO125	2.24	1.08	1.65	1.15	1.53	-2.11
118	NIXE	GENO126	1.90	1.88	2.15	1.58	1.88	0.49
119	51-109-11	GENO127	2.69	0.84	0.73	0.57	1.21	-5.44
120	ETIKETSIZNORIK	GENO128	0.32	0.71	0.93	1.55	0.88	1.55
121	40-103-11	GENO130	0.74	1.36	1.39	0.80	1.07	1.81
122	99-115-11	GENO131	1.11	0.97	1.77	0.93	1.19	1.23
123	141-104-11	GENO132	0.29	2.12	2.04	2.02	1.62	4.99
124	89-105-11	GENO133	1.23	1.98	1.78	0.96	1.49	1.71
125	NAUTILUS	GENO134	0.89	0.42	0.92	0.96	0.80	-0.31
126	157-103-11	GENO136	1.59	1.47	1.24	1.94	1.56	-0.81
127	133-112-11	GENO137	1.43	0.52	2.73	1.51	1.55	1.94
128	944-208-10	GENO138	1.18	0.60	1.79	2.12	1.42	0.79

129	PRIVELIGE	GENO139	0.58	1.38	1.68	0.56	1.05	2.87
130	966-203-10	GENO140	0.79	1.93	0.77	1.97	1.37	0.85
131	904-212-10	GENO141	1.04	0.52	1.22	1.39	1.04	-0.04
132	BETTINA	GENO142	2.09	3.62	2.23	0.64	2.15	1.48
133	125-104-11	GENO143	1.08	1.50	2.13	1.56	1.57	2.47
134	SWING	GENO144	1.60	NA	NA	NA	1.60	-4.51
135	758-109-09	GENO145	2.14	2.10	1.10	1.48	1.71	-2.15
136	735-102-09	GENO146	1.94	1.28	1.11	1.55	1.47	-2.21
137	99-102-11	GENO147	0.65	0.53	0.76	0.52	0.61	0.13
138	TERRANA	GENO148	1.72	0.63	1.17	1.09	1.15	-1.97
139	104-103-11	GENO149	0.94	0.94	1.66	1.00	1.14	1.47
140	SFHIT	GENO150	0.60	1.81	1.21	0.94	1.14	2.19
141	KIWI	GENO151	0.95	1.11	1.24	0.96	1.06	0.72
142	KIEBITZ	GENO152	2.59	2.65	2.24	2.18	2.41	-0.67
143	BONUS	GENO153	1.72	2.63	0.76	1.56	1.67	-1.24
144	509-104-09	GENO154	1.02	1.17	2.63	1.05	1.47	3.40
145	43-118-11	GENO155	0.90	1.15	0.99	1.37	1.10	0.38
146	BEO	GENO156	0.87	1.35	2.57	1.35	1.53	3.84
147	BALTICCREAM	GENO157	1.10	1.53	0.71	1.27	1.15	-0.46
148	868-201-10	GENO158	0.37	1.14	0.90	0.95	0.84	1.68
149	860-201-10	GENO159	0.71	1.62	1.59	1.45	1.34	2.50
150	DUKATA	GENO160	1.96	0.89	1.25	0.63	1.18	-2.28
151	84-107-11	GENO161	1.91	1.75	2.29	1.47	1.86	0.65
152	128-105-11	GENO162	-1.47	4.51	0.69	0.96	1.18	9.07
153	140-107-11	GENO163	0.79	0.57	1.47	1.13	0.99	1.21
154	PELIKAN	GENO164	0.69	1.91	2.18	1.59	1.59	3.99
155	KOLIBRI	GENO165	1.42	NA	2.24	NA	1.83	-2.25
156	82-119-11	GENO167	1.47	2.85	1.64	1.42	1.85	1.42
157	WENDY	GENO168	1.46	1.01	1.77	1.29	1.38	0.27
158	ROMANZE	GENO169	1.15	0.69	1.30	1.80	1.23	-0.05
159	PRESTIGE	GENO170	0.51	1.92	2.26	1.87	1.64	4.67
160	MAXI	GENO171	1.66	1.18	0.91	1.01	1.19	-1.90
161	FASAN	GENO172	1.52	1.52	1.27	1.13	1.36	-0.51
162	Madaleine	GENO173	2.26	1.31	1.14	0.62	1.33	-3.02
163	POMQUEEN	GENO174	2.81	2.12	2.52	1.84	2.32	-1.13
164	MUNGO	GENO175	1.00	0.50	1.24	2.05	1.20	0.10
165	ALBATROS	GENO176	1.36	1.95	0.63	1.90	1.46	-1.03
166	FIDELIA	GENO177	0.97	1.03	1.04	2.58	1.40	0.19
167	TACOMA	GENO178	2.00	2.35	2.32	1.82	2.12	0.93
168	BONZA	GENO179	3.04	1.26	1.47	1.40	1.80	-4.59
169	ADRETTA	GENO180	0.21	0.69	1.33	0.71	0.74	2.66
170	POWER	GENO181	0.82	1.74	2.03	0.99	1.40	3.18
171	GOLDMARIE	GENO182	1.67	0.77	1.76	1.59	1.45	-0.52
172	RITA	GENO183	1.92	0.80	1.94	1.30	1.49	-0.83
173	SUMMERGOLD	GENO184	1.24	1.70	1.47	0.94	1.33	0.83

174	DIPLOMAT	GENO185	2.03	2.14	2.32	2.21	2.18	0.68
175	CASCADA	GENO186	2.40	2.26	4.81	2.43	2.97	4.80
176	SOLIST	GENO187	0.74	1.43	2.00	1.20	1.34	3.10
177	LOLITA	GENO188	1.95	1.64	2.36	1.05	1.75	0.59
178	KARATOP	GENO189	0.84	0.98	1.05	1.07	0.98	0.54
179	INARA	GENO190	-1.38	1.49	1.87	NA	0.66	8.86
180	ACAPELLA	GENO191	0.61	0.56	0.79	0.44	0.60	0.33
181	ALLORA	GENO192	-1.69	0.91	1.15	0.90	0.32	7.82
182	ARKULA	GENO193	-1.51	0.64	NA	1.25	0.13	7.30
183	TOKIO	GENO194	1.04	0.55	1.16	1.50	1.06	-0.14
184	BIRTE	GENO195	-0.98	1.05	1.35	1.56	0.75	6.30
185	900-205-10	GENO196	1.27	1.54	2.00	1.09	1.47	1.70
186	MAXILLA	GENO197	-1.31	1.92	0.00	0.76	0.34	5.19
187	TUCAN	GENO198	0.43	1.13	0.84	1.01	0.85	1.38
188	946-202-10	GENO199	0.77	1.71	1.60	1.45	1.38	2.42
189	KORMORAN	GENO200	1.02	1.09	1.09	0.89	1.02	0.20
190	JUMBO	GENO202	1.72	0.83	2.63	2.08	1.82	1.16
191	LOGO	GENO203	1.04	2.13	1.16	2.03	1.59	1.10
192	102-102-11	GENO204	1.15	1.30	1.51	1.39	1.34	0.85
		Mean	1.07	1.37	1.53	1.24	1.30	

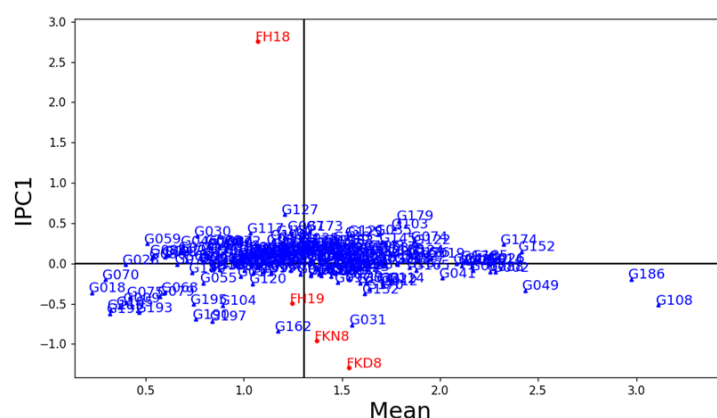


Fig.S12. Amami biplot for mean of tuber flesh colour a* of 192 genotypes across four environments (FH18, FKN18, FKD18, FH19) plotted against IPC1 (Interactive principal component).

APPENDIX-M Phenotypic data of tuber skin colour L* coordinate (SCL) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S.No.	Genotype Names	Codes	SCL_ H18	SCL_ KN18	SCL_ KD18	SCL_ H19	Mean SCL	b_i
1	JELLY	GENO2	59.56	62.87	59.38	NA	60.60	-0.42
2	RUMBA	GENO3	60.29	59.85	60.31	NA	60.15	0.06
3	HERMES	GENO4	59.21	60.26	61.41	NA	60.29	0.90
4	ALEGRIA	GENO5	58.98	58.06	58.66	NA	58.57	0.24
5	ROYAL	GENO6	58.85	60.26	62.35	63.46	61.23	-1.40
6	ELECTRA	GENO7	57.79	60.74	62.21	61.84	60.64	-1.93
7	DT14003.01	GENO9	66.10	63.51	58.28	62.97	62.71	3.04
8	DT14038.01	GENO10	59.11	57.99	62.74	61.18	60.25	-1.08
9	DT14010.18	GENO11	59.60	58.12	58.86	63.65	60.06	0.47
10	DT14004.17	GENO12	54.25	56.11	49.65	49.54	52.39	1.30
11	DT14010.14	GENO13	60.02	59.94	60.53	61.85	60.58	-0.16
12	DT14085.03	GENO14	60.17	60.36	60.59	64.35	61.37	-0.17
13	DT14013.15	GENO16	61.68	NA	NA	60.30	60.99	21.23
14	DT14018.32	GENO18	66.84	59.96	61.77	69.93	64.62	2.73
15	DT14042.27	GENO19	61.28	61.06	59.97	63.91	61.55	0.48
16	DT14005.09	GENO20	63.86	64.84	65.79	70.33	66.20	-0.80
17	DT14030.11	GENO21	62.42	60.78	61.51	62.91	61.91	0.55
18	DT14057.37	GENO22	62.44	59.60	62.03	63.71	61.94	0.55
19	DT14065.01	GENO23	60.58	61.46	59.34	NA	60.46	0.30
20	DT14016.01	GENO24	58.51	59.71	62.88	63.62	61.18	-1.66
21	DT14016.34	GENO25	64.60	62.88	63.12	64.87	63.87	0.75
22	DT14078.03	GENO26	61.27	64.82	61.17	64.85	63.03	-0.48
23	DT14028.03	GENO27	63.02	62.19	63.84	65.39	63.61	-0.16
24	DT14054.11	GENO28	63.38	64.26	63.73	65.17	64.13	-0.25
25	DT14037.18	GENO29	53.88	54.67	54.44	54.74	54.43	-0.31
26	DT14091.04	GENO30	56.17	64.71	65.33	66.88	63.27	-4.36
27	DT14083.28	GENO31	68.97	60.43	51.13	NA	60.18	7.32
28	DT14015.22	GENO32	61.69	60.25	61.34	63.00	61.57	0.33
29	DT14051.15	GENO33	61.85	62.47	60.85	64.99	62.54	0.25
30	DT14047.38	GENO34	60.17	59.05	60.79	64.38	61.10	-0.05
31	DT14026.04	GENO35	63.52	64.30	60.54	65.16	63.38	0.90
32	DT14068.07	GENO36	63.31	60.31	62.51	65.80	62.98	0.71
33	DT14063.12	GENO37	62.91	63.89	62.48	66.14	63.85	0.00
34	DT14036.01	GENO38	58.38	NA	NA	NA	58.38	28.36
35	DT14055.25	GENO39	59.72	NA	NA	60.86	60.29	20.20
36	LadyOlympia	GENO41	61.73	61.97	64.25	67.58	63.88	-0.89
37	BANBA	GENO42	57.74	55.57	59.80	64.65	59.44	-0.39
38	VanGOGH	GENO43	57.75	57.03	57.17	64.15	59.03	0.30

39	DT14049.10	GENO44	58.01	61.93	62.01	59.65	60.40	-1.93
40	DT14061.23	GENO45	62.76	61.72	55.19	62.10	60.44	2.73
41	DT14006.07	GENO46	56.80	59.30	56.01	62.10	58.55	-0.09
42	DT14046.19	GENO47	59.80	61.45	59.81	62.52	60.90	-0.24
43	DT14014.27	GENO48	59.82	61.16	63.49	60.12	61.15	-1.45
44	DT14011.18	GENO49	57.60	61.60	62.69	64.95	61.71	-2.31
45	DT14069.13	GENO50	57.61	56.79	62.01	60.51	59.23	-1.38
46	DT14026.21	GENO52	63.18	61.51	63.44	66.73	63.72	0.15
47	DT14042.24	GENO53	58.41	59.80	59.49	61.23	59.73	-0.57
48	DT14090.11	GENO54	60.50	61.16	60.35	60.12	60.53	-0.04
49	DT14071.19	GENO55	66.59	60.04	61.95	60.50	62.27	2.53
50	DT14027.08	GENO56	64.97	64.04	63.93	66.53	64.87	0.49
51	DT14034.03	GENO57	61.06	61.20	58.05	69.28	62.40	1.01
52	DT14057.36	GENO58	62.31	62.61	62.57	65.62	63.28	-0.13
53	DT14062.08	GENO59	66.98	64.13	65.63	NA	65.58	0.87
54	DT14079.02	GENO60	64.04	61.15	61.35	63.88	62.61	1.34
55	DT14053.03	GENO61	65.29	NA	NA	NA	65.29	31.72
56	DT13088.03	GENO63	57.91	62.66	61.77	65.33	61.92	-2.00
57	DT14051.66	GENO64	61.51	61.56	59.05	66.21	62.08	0.83
58	DT13100.02	GENO65	62.11	61.70	62.12	65.75	62.92	0.06
59	DT13162.15	GENO66	62.23	51.36	62.74	64.88	60.30	1.40
60	DT13162.12	GENO67	59.72	60.99	69.57	62.98	63.31	-3.54
61	DT11107.01	GENO68	69.43	59.52	61.57	67.69	64.55	4.12
62	ZIRVE	GENO69	57.95	NA	59.71	61.46	59.71	-1.45
63	DT12012.02	GENO70	67.67	60.31	58.40	64.79	62.79	4.23
64	DT13136.22	GENO71	61.24	59.84	61.07	63.80	61.49	0.26
65	DT13045.74	GENO72	60.20	61.01	60.96	64.57	61.68	-0.38
66	DT13124.21	GENO73	60.81	57.04	58.19	66.50	60.64	1.44
67	BORWINA	GENO74	62.62	60.67	58.91	63.75	61.49	1.55
68	BROOKE	GENO75	69.84	60.42	59.36	67.22	64.21	4.94
69	TESSA	GENO76	55.86	60.98	54.86	66.77	59.62	-0.40
70	DT13143.49	GENO77	60.03	62.15	63.77	61.52	61.87	-1.58
71	DT13130.48	GENO78	60.28	53.21	62.61	65.23	60.33	0.23
72	DT13143.54	GENO79	66.03	57.25	54.56	59.23	59.27	5.18
73	DT13007.03	GENO80	58.39	64.63	61.91	63.02	61.99	-2.10
74	KUTUP	GENO81	57.52	57.27	59.14	60.30	58.56	-0.52
75	DT13028.01	GENO82	51.59	57.75	59.67	52.55	55.39	-3.65
76	DT13093.92	GENO83	59.20	63.13	60.04	64.35	61.68	-0.86
77	DT13051.10	GENO84	63.14	61.18	62.82	62.47	62.40	0.39
78	DT13143.58	GENO85	60.84	62.86	63.41	NA	62.37	-1.17
79	DT13026.10	GENO86	58.33	56.62	61.18	60.23	59.09	-0.72
80	DT13049.50	GENO87	61.18	61.65	56.48	64.00	60.83	1.53
81	DT13072.19	GENO88	46.52	51.35	48.53	42.98	47.34	-1.38
82	DT13083.01	GENO89	63.70	57.91	63.63	60.42	61.41	0.86
83	LadyRosetta	GENO90	51.04	NA	53.51	NA	52.28	17.04
84	DT11007.01	GENO91	59.67	55.57	57.41	62.43	58.77	1.36

85	DT11108.02	GENO92	59.91	62.34	62.04	64.03	62.08	-1.08
86	DORUK	GENO93	57.90	57.82	57.99	60.69	58.60	-0.02
87	DT13085.01	GENO94	58.11	63.80	60.34	64.47	61.68	-1.58
88	DT12068.21	GENO95	58.99	58.56	63.37	66.52	61.86	-1.43
89	DT11088.01	GENO96	58.48	54.43	60.72	55.85	57.37	-0.18
90	DT13045.42	GENO97	63.33	63.01	64.60	66.89	64.46	-0.39
91	DT13147.17	GENO98	58.49	63.79	62.37	64.68	62.33	-2.09
92	DT13048.10	GENO99	60.97	62.33	62.13	61.12	61.64	-0.59
93	DT13052.23	GENO100	58.15	59.72	62.10	60.77	60.18	-1.57
94	DT13037.31	GENO101	62.43	63.64	62.28	64.67	63.25	-0.12
95	DT13045.103	GENO102	61.06	66.43	62.18	63.23	63.22	-1.16
96	DT13037.35	GENO103	61.55	64.38	65.25	62.84	63.51	-1.67
97	DT13047.08	GENO104	69.56	60.99	56.42	62.95	62.48	5.72
98	DT13162.16	GENO105	65.78	61.81	63.71	61.10	63.10	1.28
99	DT13067.03	GENO106	57.89	60.27	60.87	63.34	60.59	-1.36
100	SORAYA	GENO107	64.70	57.94	57.42	65.53	61.40	3.46
101	LAURA	GENO108	51.78	49.83	51.73	63.10	54.11	0.30
102	SHEPODY	GENO109	60.33	56.23	61.72	65.95	61.06	0.12
103	43-111-11	GENO110	68.58	59.28	59.51	64.16	62.88	4.44
104	KARLENA	GENO111	57.95	59.84	58.61	59.11	58.88	-0.50
105	139-101-11	GENO112	58.65	56.35	59.61	64.56	59.79	0.01
106	84-105-11	GENO113	57.83	62.52	60.78	62.63	60.94	-1.69
107	NANDU	GENO114	62.85	52.77	61.41	NA	59.01	1.95
108	882-202-10	GENO115	55.63	61.91	58.12	62.58	59.56	-1.76
109	TALENT	GENO116	61.02	59.71	58.24	61.31	60.07	1.14
110	57-104-11	GENO117	59.34	58.14	58.90	64.28	60.17	0.32
111	878-202-10	GENO118	57.15	60.86	59.81	62.73	60.14	-1.44
112	146-103-11	GENO120	63.55	55.32	54.45	63.29	59.15	4.29
113	SALUTE	GENO121	59.15	57.02	59.54	65.38	60.27	0.18
114	68-105-11	GENO122	55.21	61.16	58.32	62.15	59.21	-1.92
115	63-113-11	GENO123	57.43	60.53	56.89	64.74	59.90	-0.26
116	106-105-11	GENO124	55.45	NA	58.06	59.61	57.71	-1.80
117	939-201-10	GENO125	58.62	58.44	62.24	59.35	59.66	-1.21
118	NIXE	GENO126	56.82	61.34	59.34	63.87	60.34	-1.51
119	51-109-11	GENO127	62.48	62.96	58.97	63.42	61.96	1.13
120	ETIKETSIZNORIK	GENO128	61.79	57.93	61.66	64.18	61.39	0.60
121	40-103-11	GENO130	63.55	56.35	61.49	63.15	61.14	1.75
122	99-115-11	GENO131	60.93	63.64	59.89	65.83	62.57	-0.04
123	141-104-11	GENO132	55.32	58.25	61.76	65.47	60.20	-2.62
124	89-105-11	GENO133	59.84	60.52	56.10	62.39	59.71	1.18
125	NAUTILUS	GENO134	60.29	58.49	62.44	63.64	61.21	-0.47
126	157-103-11	GENO136	59.68	60.04	60.99	65.36	61.52	-0.50
127	133-112-11	GENO137	59.22	55.84	53.11	59.98	57.04	2.57
128	944-208-10	GENO138	59.89	57.32	58.15	62.45	59.45	0.97
129	PRIVELIGE	GENO139	62.86	57.90	59.89	67.37	62.00	1.73
130	966-203-10	GENO140	61.27	60.51	63.97	65.00	62.69	-0.81

131	904-212-10	GENO141	64.57	58.69	61.34	65.38	62.50	1.95
132	BETTINA	GENO142	55.86	61.67	61.43	65.79	61.19	-2.74
133	125-104-11	GENO143	57.85	56.55	61.66	62.87	59.73	-1.11
134	SWING	GENO144	57.62	NA	NA	NA	57.62	27.99
135	758-109-09	GENO145	56.48	60.13	59.00	66.47	60.52	-1.39
136	735-102-09	GENO146	58.30	57.88	53.48	59.82	57.37	1.70
137	99-102-11	GENO147	60.24	58.65	58.18	58.00	58.77	0.93
138	TERRANA	GENO148	55.61	58.06	57.51	63.36	58.64	-1.00
139	104-103-11	GENO149	54.60	53.26	59.42	64.49	57.94	-1.45
140	SFHIT	GENO150	62.78	60.39	64.10	65.57	63.21	-0.10
141	KIWI	GENO151	63.72	60.77	62.97	63.04	62.63	0.68
142	KIEBITZ	GENO152	58.37	56.33	62.77	61.15	59.65	-1.20
143	BONUS	GENO153	59.85	59.48	62.05	61.26	60.66	-0.70
144	509-104-09	GENO154	55.33	58.96	64.25	61.30	59.96	-3.57
145	43-118-11	GENO155	61.95	60.73	65.29	67.36	63.83	-0.96
146	BEO	GENO156	56.03	58.09	53.91	60.54	57.14	0.42
147	BALTICCREAM	GENO157	60.70	60.74	61.69	66.09	62.31	-0.34
148	868-201-10	GENO158	57.82	53.71	56.92	63.24	57.92	0.90
149	860-201-10	GENO159	59.75	61.62	60.59	68.20	62.54	-0.56
150	DUKATA	GENO160	57.91	55.15	61.50	63.63	59.55	-0.82
151	84-107-11	GENO161	62.78	61.27	62.69	64.40	62.79	0.25
152	128-105-11	GENO162	66.78	63.14	61.58	65.39	64.22	2.30
153	140-107-11	GENO163	56.39	55.98	60.03	61.81	58.55	-1.18
154	PELIKAN	GENO164	59.13	56.46	59.64	63.79	59.76	0.21
155	KOLIBRI	GENO165	57.34	NA	61.15	NA	59.25	19.00
156	82-119-11	GENO167	57.61	59.36	56.95	62.80	59.18	-0.03
157	WENDY	GENO168	58.06	59.62	64.14	65.48	61.83	-2.30
158	ROMANZE	GENO169	46.89	48.88	49.45	44.91	47.53	-1.16
159	PRESTIGE	GENO170	59.93	56.61	59.57	63.92	60.01	0.60
160	MAXI	GENO171	59.28	61.95	63.50	65.61	62.59	-1.83
161	FASAN	GENO172	59.56	58.73	57.75	62.95	59.75	0.74
162	Madaleine	GENO173	63.87	61.23	62.59	63.33	62.76	0.82
163	POMQUEEN	GENO174	60.68	58.83	62.78	67.91	62.55	-0.45
164	MUNGO	GENO175	59.21	54.94	57.43	62.41	58.50	1.23
165	ALBATROS	GENO176	57.27	58.91	61.44	63.11	60.18	-1.66
166	FIDELIA	GENO177	62.78	60.21	60.33	51.29	58.65	1.21
167	TACOMA	GENO178	61.60	62.17	62.40	64.22	62.60	-0.36
168	BONZA	GENO179	58.11	56.56	60.14	60.80	58.90	-0.47
169	ADRETTA	GENO180	61.23	59.57	59.35	55.15	58.83	0.88
170	POWER	GENO181	60.27	58.96	56.96	63.89	60.02	1.32
171	GOLDMARIE	GENO182	59.01	59.45	63.21	63.37	61.26	-1.50
172	RITA	GENO183	60.91	55.60	59.88	64.00	60.10	1.12
173	SUMMERGOLD	GENO184	61.62	60.71	57.46	67.32	61.78	1.55
174	DIPLOMAT	GENO185	58.68	58.70	63.71	60.29	60.34	-1.72
175	CASCADA	GENO186	58.74	57.21	60.09	62.54	59.65	-0.24
176	SOLIST	GENO187	62.79	59.38	58.30	60.80	60.31	2.02

177	LOLITA	GENO188	60.78	55.72	62.65	60.23	59.84	0.10
178	KARATOP	GENO189	58.55	58.71	59.17	63.77	60.05	-0.23
179	INARA	GENO190	66.64	57.28	57.48	NA	60.46	4.48
180	ACAPELLA	GENO191	58.57	60.10	62.04	62.41	60.78	-1.40
181	ALLORA	GENO192	70.82	61.73	64.23	65.01	65.45	3.56
182	ARKULA	GENO193	67.90	63.29	NA	64.32	65.17	1.89
183	TOKIO	GENO194	63.25	59.63	64.97	65.00	63.21	-0.06
184	BIRTE	GENO195	67.34	61.52	62.39	63.91	63.79	2.53
185	900-205-10	GENO196	58.41	60.93	59.34	65.80	61.12	-0.68
186	MAXILLA	GENO197	69.50	61.66	61.70	59.63	63.13	3.80
187	TUCAN	GENO198	62.13	60.52	61.84	63.99	62.12	0.33
188	946-202-10	GENO199	60.63	56.87	62.16	65.67	61.33	0.02
189	KORMORAN	GENO200	58.71	57.86	58.13	63.28	59.50	0.32
190	JUMBO	GENO202	57.86	59.42	60.76	66.16	61.05	-1.21
191	LOGO	GENO203	63.06	58.99	54.96	60.33	59.33	3.35
192	102-102-11	GENO204	58.16	59.56	58.00	62.48	59.55	-0.15
		Mean	60.38	59.65	60.30	63.08	60.79	

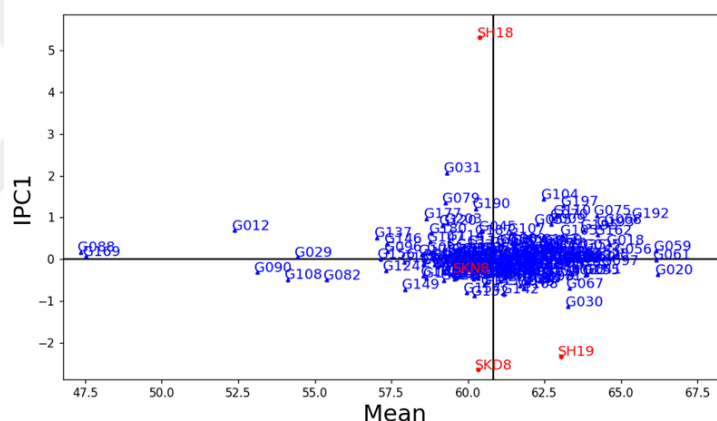


Fig. S13. Ammi biplot for mean of tuber skin colour L* of 192 genotypes across four environments (SH18, SKN18, SKD18, SH19) plotted against IPC1 (Interactive principal component).

APPENDIX-N Phenotypic data of tuber skin colour b^* coordinate (SCb) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). b_i corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S.No.	Genotype Names	Codes	SCb H18	SCb KN18	SCb KD18	SCb H19	Mean SCb	b_i
1	JELLY	GENO2	25.13	25.05	26.05	NA	25.41	0.69
2	RUMBA	GENO3	24.96	23.41	26.03	NA	24.80	1.23
3	HERMES	GENO4	22.65	24.40	24.94	NA	23.99	0.84
4	ALEGRIA	GENO5	24.87	23.68	26.00	NA	24.85	1.61
5	ROYAL	GENO6	26.00	22.72	27.46	30.54	26.68	3.31
6	ELECTRA	GENO7	20.63	25.56	21.08	29.56	24.20	-3.16
7	DT14003.01	GENO9	14.91	24.96	20.93	31.65	23.12	-2.95
8	DT14038.01	GENO10	20.99	25.96	19.09	30.21	24.06	-4.80
9	DT14010.18	GENO11	25.25	18.99	22.75	29.15	24.03	2.70
10	DT14004.17	GENO12	14.26	16.59	17.91	19.73	17.12	0.86
11	DT14010.14	GENO13	24.24	25.32	28.49	30.39	27.11	2.15
12	DT14085.03	GENO14	27.60	28.01	24.96	33.00	28.39	-2.10
13	DT14013.15	GENO16	22.52	NA	NA	28.89	25.71	-19.94
14	DT14018.32	GENO18	11.61	19.51	29.63	29.06	22.45	6.79
15	DT14042.27	GENO19	23.08	23.03	26.81	27.56	25.12	2.59
16	DT14005.09	GENO20	24.76	25.46	29.77	33.67	28.41	2.94
17	DT14030.11	GENO21	27.70	23.73	27.55	31.19	27.54	2.69
18	DT14057.37	GENO22	27.33	25.11	23.11	30.96	26.63	-1.33
19	DT14065.01	GENO23	21.27	27.31	25.59	NA	24.72	-1.29
20	DT14016.01	GENO24	21.12	25.09	27.15	28.84	25.55	1.34
21	DT14016.34	GENO25	27.06	25.20	27.83	29.86	27.49	1.84
22	DT14078.03	GENO26	27.95	28.61	25.65	32.30	28.63	-2.04
23	DT14028.03	GENO27	27.35	27.31	30.06	33.25	29.49	1.89
24	DT14054.11	GENO28	25.28	26.59	77.71	30.18	39.94	35.04
25	DT14037.18	GENO29	14.35	16.39	15.42	15.74	15.47	-0.70
26	DT14091.04	GENO30	25.02	28.65	30.02	33.09	29.20	0.87
27	DT14083.28	GENO31	16.93	28.95	30.61	NA	25.50	0.91
28	DT14015.22	GENO32	22.74	24.89	27.31	28.08	25.75	1.62
29	DT14051.15	GENO33	20.63	27.14	24.96	30.56	25.82	-1.62
30	DT14047.38	GENO34	26.86	23.36	26.06	30.18	26.61	1.92
31	DT14026.04	GENO35	24.31	27.81	26.42	30.34	27.22	-1.02
32	DT14068.07	GENO36	27.57	26.21	25.42	31.35	27.64	-0.52
33	DT14063.12	GENO37	25.33	28.68	31.14	29.13	28.57	1.63
34	DT14036.01	GENO38	21.81	NA	NA	NA	21.81	0.41
35	DT14055.25	GENO39	18.77	NA	NA	29.90	24.34	-20.72
36	LadyOlympia	GENO41	27.81	20.97	22.74	28.85	25.09	1.34
37	BANBA	GENO42	20.51	22.45	21.08	30.58	23.65	-0.98
38	VanGOGH	GENO43	22.65	20.89	20.78	29.23	23.39	-0.04
39	DT14049.10	GENO44	25.72	24.78	23.65	29.50	25.91	-0.76

40	DT14061.23	GENO45	26.01	18.45	23.89	32.48	25.21	3.87
41	DT14006.07	GENO46	21.54	24.95	21.38	30.13	24.50	-2.51
42	DT14046.19	GENO47	24.01	19.57	27.47	29.21	25.06	5.50
43	DT14014.27	GENO48	21.16	19.31	26.42	30.69	24.39	4.91
44	DT14011.18	GENO49	23.36	28.08	22.54	32.76	26.69	-3.89
45	DT14069.13	GENO50	24.67	23.74	27.97	28.64	26.26	2.92
46	DT14026.21	GENO52	24.64	26.48	26.87	33.64	27.91	0.23
47	DT14042.24	GENO53	24.55	25.64	25.55	31.64	26.85	-0.08
48	DT14090.11	GENO54	26.14	24.66	24.48	28.68	25.99	-0.10
49	DT14071.19	GENO55	9.33	18.47	25.09	30.26	20.79	4.37
50	DT14027.08	GENO56	26.35	28.16	29.75	31.72	28.99	1.06
51	DT14034.03	GENO57	24.63	23.51	27.30	32.59	27.01	2.62
52	DT14057.36	GENO58	21.68	27.62	26.29	31.56	26.79	-1.02
53	DT14062.08	GENO59	23.71	21.69	25.03	NA	23.48	2.33
54	DT14079.02	GENO60	23.48	28.06	25.23	33.11	27.47	-2.03
55	DT14053.03	GENO61	29.45	NA	NA	NA	29.45	0.55
56	DT13088.03	GENO63	25.07	18.07	28.02	31.58	25.68	6.96
57	DT14051.66	GENO64	26.90	20.66	20.82	31.23	24.90	0.23
58	DT13100.02	GENO65	25.32	25.47	27.45	32.21	27.61	1.36
59	DT13162.15	GENO66	24.10	25.58	20.76	33.25	25.92	-3.33
60	DT13162.12	GENO67	21.60	24.40	24.36	28.93	24.82	-0.08
61	DT11107.01	GENO68	14.19	19.78	28.20	29.92	23.02	5.67
62	ZIRVE	GENO69	23.88	NA	26.30	30.39	26.86	2.76
63	DT12012.02	GENO70	11.73	19.25	25.10	30.62	21.67	3.87
64	DT13136.22	GENO71	23.66	25.26	26.34	27.52	25.70	0.71
65	DT13045.74	GENO72	23.68	22.89	27.62	33.43	26.90	3.26
66	DT13124.21	GENO73	25.13	23.29	23.52	30.40	25.58	0.19
67	BORWINA	GENO74	26.40	22.66	22.56	29.63	25.31	0.00
68	BROOKE	GENO75	18.26	21.26	28.17	32.57	25.06	4.68
69	TESSA	GENO76	22.20	21.79	23.02	33.70	25.18	0.85
70	DT13143.49	GENO77	28.85	21.48	24.43	29.28	26.01	2.16
71	DT13130.48	GENO78	30.52	20.75	21.12	31.93	26.08	0.44
72	DT13143.54	GENO79	14.91	23.38	22.37	29.41	22.51	-0.85
73	DT13007.03	GENO80	21.09	20.76	19.72	32.17	23.44	-0.71
74	KUTUP	GENO81	19.85	24.61	25.79	28.84	24.77	0.72
75	DT13028.01	GENO82	16.59	19.40	16.32	21.16	18.37	-2.17
76	DT13093.92	GENO83	21.59	28.21	23.95	32.36	26.53	-3.05
77	DT13051.10	GENO84	24.14	26.45	27.54	29.73	26.97	0.70
78	DT13143.58	GENO85	24.12	22.01	21.29	NA	22.48	-0.45
79	DT13026.10	GENO86	16.38	24.36	18.86	29.82	22.35	-3.92
80	DT13049.50	GENO87	28.56	22.91	25.68	28.57	26.43	2.01
81	DT13072.19	GENO88	8.40	17.54	13.96	11.30	12.80	-2.63
82	DT13083.01	GENO89	22.32	24.60	22.62	28.48	24.51	-1.40
83	LadyRosetta	GENO90	13.60	NA	18.44	NA	16.02	-12.74
84	DT11007.01	GENO91	21.73	25.82	23.79	30.24	25.40	-1.47
85	DT11108.02	GENO92	23.96	15.74	21.19	28.62	22.38	3.89

86	DORUK	GENO93	25.13	26.06	26.25	32.94	27.59	0.11
87	DT13085.01	GENO94	17.22	22.09	28.03	30.80	24.54	3.98
88	DT12068.21	GENO95	29.87	26.30	22.97	34.03	28.29	-2.22
89	DT11088.01	GENO96	21.48	22.30	19.12	26.66	22.39	-2.20
90	DT13045.42	GENO97	22.98	25.51	26.85	31.97	26.83	0.87
91	DT13147.17	GENO98	22.27	18.78	26.04	29.69	24.19	5.04
92	DT13048.10	GENO99	23.04	20.87	21.29	28.96	23.54	0.33
93	DT13052.23	GENO100	23.40	17.07	19.02	31.72	22.80	1.46
94	DT13037.31	GENO101	22.08	20.65	25.45	29.15	24.33	3.32
95	DT13045.103	GENO102	25.01	21.59	26.94	26.83	25.09	3.73
96	DT13037.35	GENO103	26.64	21.62	20.60	28.81	24.42	-0.61
97	DT13047.08	GENO104	12.96	23.88	21.51	30.22	22.14	-1.83
98	DT13162.16	GENO105	15.08	21.81	21.21	30.60	22.17	-0.54
99	DT13067.03	GENO106	24.77	25.76	25.66	29.71	26.47	-0.09
100	SORAYA	GENO107	26.67	18.21	25.09	31.64	25.40	4.88
101	LAURA	GENO108	14.75	14.79	15.48	30.23	18.81	0.47
102	SHEPODY	GENO109	25.68	24.00	28.16	28.67	26.63	2.88
103	43-111-11	GENO110	17.54	21.39	28.94	35.46	25.83	5.11
104	KARLENA	GENO111	22.18	19.08	25.39	29.04	23.92	4.39
105	139-101-11	GENO112	22.90	23.48	22.30	31.52	25.05	-0.82
106	84-105-11	GENO113	21.72	20.61	26.39	30.67	24.85	3.99
107	NANDU	GENO114	30.46	22.22	25.15	NA	25.94	2.16
108	882-202-10	GENO115	19.59	19.46	25.08	28.47	23.15	3.86
109	TALENT	GENO116	25.63	18.71	25.88	31.69	25.48	5.05
110	57-104-11	GENO117	22.87	23.47	22.36	32.28	25.25	-0.77
111	878-202-10	GENO118	24.17	22.64	21.83	30.25	24.72	-0.53
112	146-103-11	GENO120	16.08	18.66	25.53	33.83	23.53	4.66
113	SALUTE	GENO121	23.44	25.57	28.60	32.19	27.45	2.04
114	68-105-11	GENO122	20.69	18.33	21.79	32.43	23.31	2.42
115	63-113-11	GENO123	23.88	21.20	25.49	31.21	25.44	2.99
116	106-105-11	GENO124	23.44	NA	24.63	30.85	26.31	4.24
117	939-201-10	GENO125	25.49	23.83	22.04	29.69	25.26	-1.20
118	NIXE	GENO126	27.43	21.59	28.03	34.55	27.90	4.53
119	51-109-11	GENO127	20.19	22.43	22.58	31.36	24.14	0.06
120	ETIKETSIZNORIK	GENO128	27.18	24.47	27.87	30.69	27.55	2.38
121	40-103-11	GENO130	21.57	21.87	22.61	29.82	23.97	0.50
122	99-115-11	GENO131	25.61	22.33	22.62	32.22	25.70	0.26
123	141-104-11	GENO132	27.63	25.02	28.15	31.06	27.96	2.20
124	89-105-11	GENO133	22.64	20.53	22.40	30.72	24.07	1.32
125	NAUTILUS	GENO134	29.48	26.42	21.58	31.76	27.31	-3.26
126	157-103-11	GENO136	24.78	20.80	29.68	31.77	26.75	6.17
127	133-112-11	GENO137	25.02	23.23	17.80	31.47	24.38	-3.69
128	944-208-10	GENO138	24.17	18.49	22.90	31.48	24.26	3.13
129	PRIVELIGE	GENO139	27.33	23.42	24.69	30.40	26.46	0.94
130	966-203-10	GENO140	22.89	25.68	28.12	33.33	27.51	1.62
131	904-212-10	GENO141	26.83	26.41	27.91	31.05	28.05	1.04

132	BETTINA	GENO142	22.95	19.64	24.01	34.01	25.15	3.06
133	125-104-11	GENO143	26.30	25.63	24.51	34.74	27.79	-0.76
134	SWING	GENO144	23.14	NA	NA	NA	23.14	0.43
135	758-109-09	GENO145	20.00	18.72	24.55	30.03	23.32	4.02
136	735-102-09	GENO146	27.03	21.73	23.44	32.74	26.23	1.27
137	99-102-11	GENO147	22.70	22.67	22.98	28.48	24.21	0.21
138	TERRANA	GENO148	22.26	19.72	23.80	29.61	23.85	2.85
139	104-103-11	GENO149	25.49	21.44	25.31	30.93	25.79	2.73
140	SFHIT	GENO150	75.94	24.22	21.40	30.31	37.97	-0.97
141	KIWI	GENO151	29.85	23.81	29.86	33.07	29.14	4.26
142	KIEBITZ	GENO152	21.78	22.41	24.40	32.40	25.25	1.35
143	BONUS	GENO153	30.98	18.74	20.68	32.24	25.66	1.56
144	509-104-09	GENO154	23.71	20.92	23.29	29.31	24.30	1.68
145	43-118-11	GENO155	29.89	21.84	28.64	34.14	28.63	4.81
146	BEO	GENO156	20.52	22.49	21.61	27.18	22.95	-0.64
147	BALTICCREAM	GENO157	22.11	19.66	26.20	26.67	23.66	4.53
148	868-201-10	GENO158	25.89	21.39	20.57	33.01	25.21	-0.48
149	860-201-10	GENO159	25.92	26.66	25.67	31.70	27.49	-0.69
150	DUKATA	GENO160	27.11	22.85	18.77	32.40	25.28	-2.72
151	84-107-11	GENO161	25.22	20.11	26.72	32.46	26.13	4.63
152	128-105-11	GENO162	18.48	21.08	30.40	33.46	25.85	6.34
153	140-107-11	GENO163	25.99	26.15	20.63	30.97	25.94	-3.79
154	PELIKAN	GENO164	20.59	22.27	29.02	32.60	26.12	4.60
155	KOLIBRI	GENO165	22.53	NA	20.46	NA	21.50	-14.00
156	82-119-11	GENO167	25.11	20.62	21.31	30.11	24.29	0.56
157	WENDY	GENO168	22.37	34.01	28.76	31.71	29.21	-3.82
158	ROMANZE	GENO169	13.11	13.13	13.20	12.39	12.96	0.05
159	PRESTIGE	GENO170	21.73	23.39	21.07	29.21	23.85	-1.62
160	MAXI	GENO171	24.44	20.15	31.95	30.55	26.77	8.17
161	FASAN	GENO172	24.11	19.87	20.18	31.31	23.87	0.29
162	Madaleine	GENO173	24.69	25.47	27.49	30.97	27.16	1.37
163	POMQUEEN	GENO174	22.56	23.70	28.40	33.45	27.03	3.20
164	MUNGO	GENO175	27.25	23.28	24.98	33.48	27.25	1.24
165	ALBATROS	GENO176	24.53	20.86	28.47	32.69	26.64	5.29
166	FIDELIA	GENO177	21.13	26.49	26.49	16.18	22.57	-0.10
167	TACOMA	GENO178	25.26	26.10	22.52	33.32	26.80	-2.47
168	BONZA	GENO179	26.79	24.94	22.65	33.27	26.91	-1.54
169	ADRETTA	GENO180	22.98	20.46	21.21	26.88	22.88	0.56
170	POWER	GENO181	26.37	24.08	23.74	31.49	26.42	-0.19
171	GOLDMARIE	GENO182	25.81	26.21	29.95	33.29	28.82	2.56
172	RITA	GENO183	25.48	23.14	21.30	32.06	25.49	-1.22
173	SUMMERGOLD	GENO184	24.47	18.32	26.44	31.00	25.06	5.68
174	DIPLOMAT	GENO185	24.51	23.40	30.86	31.80	27.64	5.14
175	CASCADA	GENO186	26.83	25.49	26.42	29.74	27.12	0.66
176	SOLIST	GENO187	28.56	19.55	21.19	29.88	24.79	1.29

177	LOLITA	GENO188	26.52	21.85	28.23	29.11	26.43	4.46
178	KARATOP	GENO189	25.37	20.68	23.40	31.84	25.32	1.95
179	INARA	GENO190	14.38	24.86	21.71	NA	20.32	-2.36
180	ACAPELLA	GENO191	22.70	20.80	23.16	31.41	24.52	1.65
181	ALLORA	GENO192	12.72	22.71	27.51	28.43	22.85	3.11
182	ARKULA	GENO193	8.95	22.68	NA	31.34	20.99	5.68
183	TOKIO	GENO194	27.38	24.52	25.21	31.29	27.10	0.53
184	BIRTE	GENO195	17.75	19.37	24.32	30.48	22.98	3.37
185	900-205-10	GENO196	23.86	25.78	25.46	30.18	26.32	-0.26
186	MAXILLA	GENO197	11.06	20.99	25.72	29.04	21.70	3.06
187	TUCAN	GENO198	28.13	21.62	27.54	30.52	26.95	4.18
188	946-202-10	GENO199	26.25	24.52	22.17	30.20	25.78	-1.58
189	KORMORAN	GENO200	24.26	18.64	24.73	31.24	24.71	4.28
190	JUMBO	GENO202	23.50	26.73	22.02	32.21	26.12	-3.29
191	LOGO	GENO203	26.50	20.56	24.46	27.50	24.75	2.79
192	102-102-11	GENO204	21.87	23.04	24.33	30.61	24.96	0.86
		Mean	23.34	22.89	24.79	30.38	25.22	

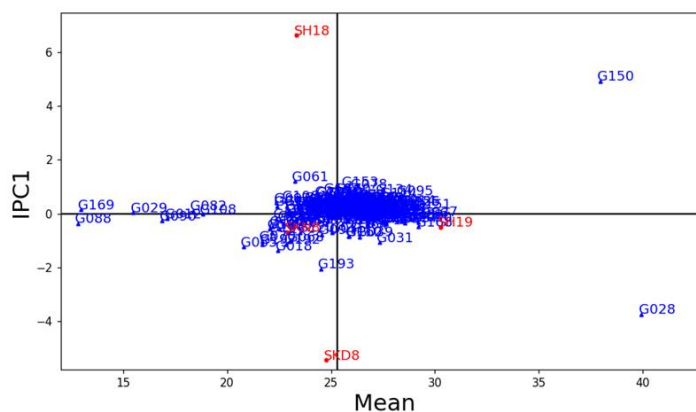


Fig.S14. Ammi biplot for mean of tuber skin colour b* of 192 genotypes across four environments (SH18, SKN18, SKD18, SH19) plotted against IPC1 (Interactive principal component).

APPENDIX-O Phenotypic data of tuber skin colour a* coordinate (Sca) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *bi* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability ($b_i=1$, not significantly different from one at $P<0.05$).

S.No.	Genotype Names	Codes	Sca_H18	Sca_KN18	Sca_KD18	Sca_H19	Mean SCa	<i>b_i</i>
1	JELLY	GENO2	8.39	7.65	8.00	NA	8.01	0.82
2	RUMBA	GENO3	7.55	6.51	7.54	NA	7.20	0.95
3	HERMES	GENO4	7.04	6.21	6.18	NA	6.47	1.07
4	ALEGRIA	GENO5	7.81	6.69	7.54	NA	7.35	1.12
5	ROYAL	GENO6	8.46	6.12	7.18	7.40	7.29	2.60
6	ELECTRA	GENO7	7.10	5.90	6.82	6.99	6.70	1.19
7	DT14003.01	GENO9	5.32	4.48	6.63	7.47	5.97	0.28
8	DT14038.01	GENO10	6.82	6.36	5.90	7.23	6.58	0.76
9	DT14010.18	GENO11	8.22	7.03	7.54	7.15	7.48	1.33
10	DT14004.17	GENO12	10.39	7.13	13.65	14.03	11.30	1.75
11	DT14010.14	GENO13	7.78	6.30	7.16	7.32	7.14	1.58
12	DT14085.03	GENO14	8.80	7.79	7.23	7.66	7.87	1.50
13	DT14013.15	GENO16	6.80	NA	NA	8.06	7.43	1.39
14	DT14018.32	GENO18	5.62	6.37	6.96	3.85	5.70	-1.18
15	DT14042.27	GENO19	6.78	6.46	7.20	6.55	6.75	0.13
16	DT14005.09	GENO20	6.42	4.88	5.92	5.07	5.57	1.59
17	DT14030.11	GENO21	6.17	5.93	6.06	7.00	6.29	0.26
18	DT14057.37	GENO22	7.29	7.03	6.24	6.94	6.88	0.63
19	DT14065.01	GENO23	6.30	6.18	6.11	NA	6.20	0.18
20	DT14016.01	GENO24	8.57	6.42	5.51	6.76	6.81	3.09
21	DT14016.34	GENO25	6.63	5.50	6.24	6.39	6.19	1.17
22	DT14078.03	GENO26	7.25	5.68	7.75	6.82	6.87	1.24
23	DT14028.03	GENO27	7.30	6.45	6.67	6.79	6.80	1.01
24	DT14054.11	GENO28	4.96	4.73	5.62	5.87	5.30	-0.04
25	DT14037.18	GENO29	13.45	7.71	9.77	14.85	11.45	6.59
26	DT14091.04	GENO30	9.38	5.79	6.50	5.79	6.87	4.33
27	DT14083.28	GENO31	4.70	6.68	7.88	NA	6.42	-2.98
28	DT14015.22	GENO32	6.73	6.77	6.64	5.91	6.51	0.00
29	DT14051.15	GENO33	5.35	5.61	5.77	6.19	5.73	-0.39
30	DT14047.38	GENO34	6.41	5.39	6.48	5.37	5.91	0.90
31	DT14026.04	GENO35	6.80	18.18	6.41	6.04	9.36	-10.20
32	DT14068.07	GENO36	6.30	5.07	7.08	5.90	6.09	0.83
33	DT14063.12	GENO37	7.14	5.52	8.45	4.65	6.44	0.98
34	DT14036.01	GENO38	8.18	NA	NA	NA	8.18	10.48
35	DT14055.25	GENO39	6.85	NA	NA	6.93	6.89	2.48
36	LadyOlympia	GENO41	6.20	6.17	6.16	4.17	5.68	0.04
37	BANBA	GENO42	6.00	7.63	6.82	6.33	6.70	-1.79

38	VanGOGH	GENO43	8.77	7.17	8.86	6.54	7.84	1.42
39	DT14049.10	GENO44	7.68	6.23	7.02	11.41	8.09	1.56
40	DT14061.23	GENO45	7.18	6.21	6.75	7.12	6.81	1.04
41	DT14006.07	GENO46	8.52	6.39	6.94	7.00	7.21	2.52
42	DT14046.19	GENO47	7.88	6.42	7.96	7.16	7.35	1.30
43	DT14014.27	GENO48	6.74	6.37	5.96	8.63	6.93	0.63
44	DT14011.18	GENO49	8.27	6.01	5.54	6.71	6.63	3.07
45	DT14069.13	GENO50	8.26	5.88	7.31	7.87	7.33	2.52
46	DT14026.21	GENO52	6.12	5.00	5.86	6.36	5.83	1.11
47	DT14042.24	GENO53	7.63	6.02	7.86	8.59	7.53	1.38
48	DT14090.11	GENO54	7.73	5.45	5.66	8.03	6.72	2.84
49	DT14071.19	GENO55	6.14	5.72	7.01	9.32	7.05	0.06
50	DT14027.08	GENO56	6.68	6.35	6.64	5.82	6.37	0.31
51	DT14034.03	GENO57	8.32	7.48	8.44	4.98	7.30	0.72
52	DT14057.36	GENO58	7.25	6.29	6.59	7.26	6.85	1.12
53	DT14062.08	GENO59	5.00	5.68	5.24	NA	5.31	-0.71
54	DT14079.02	GENO60	7.10	7.59	7.28	7.74	7.43	-0.51
55	DT14053.03	GENO61	5.98	NA	NA	NA	5.98	7.66
56	DT13088.03	GENO63	9.35	5.77	6.35	6.19	6.91	4.37
57	DT14051.66	GENO64	6.90	6.31	5.85	5.89	6.24	0.93
58	DT13100.02	GENO65	6.78	6.65	6.81	6.33	6.64	0.11
59	DT13162.15	GENO66	7.01	7.45	6.66	6.35	6.87	-0.27
60	DT13162.12	GENO67	7.31	5.78	1.12	7.93	5.54	3.69
61	DT11107.01	GENO68	5.23	6.12	7.48	5.41	6.06	-1.65
62	ZIRVE	GENO69	8.37	NA	8.16	7.32	7.95	0.58
63	DT12012.02	GENO70	4.83	6.11	6.94	5.89	5.94	-1.95
64	DT13136.22	GENO71	6.37	7.15	6.55	5.15	6.30	-0.78
65	DT13045.74	GENO72	8.93	7.18	6.66	7.55	7.58	2.44
66	DT13124.21	GENO73	5.66	7.53	5.90	5.63	6.18	-1.79
67	BORWINA	GENO74	6.48	6.18	7.49	6.24	6.60	-0.10
68	BROOKE	GENO75	4.55	6.87	7.60	5.36	6.10	-3.24
69	TESSA	GENO76	10.23	5.79	7.93	5.79	7.44	4.89
70	DT13143.49	GENO77	8.07	6.37	7.38	7.74	7.39	1.80
71	DT13130.48	GENO78	5.51	7.14	5.93	5.64	6.06	-1.64
72	DT13143.54	GENO79	5.34	7.25	7.54	8.86	7.25	-2.55
73	DT13007.03	GENO80	6.96	5.82	6.53	6.85	6.54	1.20
74	KUTUP	GENO81	6.75	7.05	8.23	7.88	7.48	-0.82
75	DT13028.01	GENO82	10.98	7.20	6.86	12.20	9.31	4.97
76	DT13093.92	GENO83	8.04	4.59	6.32	7.54	6.62	3.78
77	DT13051.10	GENO84	6.83	6.41	6.68	6.70	6.66	0.44
78	DT13143.58	GENO85	5.77	5.59	5.94	NA	5.77	0.10
79	DT13026.10	GENO86	7.51	8.24	5.48	8.36	7.40	0.09
80	DT13049.50	GENO87	7.80	6.77	8.60	6.43	7.40	0.64
81	DT13072.19	GENO88	3.51	5.33	4.01	5.44	4.57	-1.84
82	DT13083.01	GENO89	4.92	7.05	6.17	6.52	6.16	-2.40

83	LadyRosetta	GENO90	10.52	NA	9.90	NA	10.21	4.48
84	DT11007.01	GENO91	7.47	7.26	7.54	7.17	7.36	0.16
85	DT11108.02	GENO92	8.11	5.94	6.97	6.06	6.77	2.40
86	DORUK	GENO93	9.57	8.57	8.80	9.15	9.02	1.20
87	DT13085.01	GENO94	6.26	5.07	6.79	5.39	5.88	0.88
88	DT12068.21	GENO95	8.14	7.25	6.49	6.33	7.05	1.42
89	DT11088.01	GENO96	8.19	7.51	6.35	9.78	7.96	1.30
90	DT13045.42	GENO97	5.18	6.04	6.11	5.22	5.64	-1.13
91	DT13147.17	GENO98	6.76	5.03	5.44	5.03	5.57	2.06
92	DT13048.10	GENO99	7.42	6.92	6.83	8.51	7.42	0.67
93	DT13052.23	GENO100	8.12	5.80	6.68	7.63	7.06	2.64
94	DT13037.31	GENO101	6.24	5.78	6.70	8.02	6.69	0.25
95	DT13045.103	GENO102	6.29	3.93	6.27	6.17	5.66	2.15
96	DT13037.35	GENO103	6.78	6.47	5.91	6.97	6.53	0.61
97	DT13047.08	GENO104	4.63	5.73	6.12	7.63	6.03	-1.55
98	DT13162.16	GENO105	5.81	6.33	6.75	8.60	6.87	-0.82
99	DT13067.03	GENO106	7.91	6.42	7.21	7.14	7.17	1.61
100	SORAYA	GENO107	7.20	6.00	8.11	6.82	7.03	0.75
101	LAURA	GENO108	15.56	9.51	12.09	5.92	10.77	6.79
102	SHEPODY	GENO109	8.74	7.02	7.56	5.99	7.33	2.00
103	43-111-11	GENO110	3.55	6.13	7.25	5.30	5.56	-3.72
104	KARLENA	GENO111	4.99	6.15	7.58	7.48	6.55	-2.02
105	139-101-11	GENO112	8.10	8.02	7.20	6.33	7.41	0.41
106	84-105-11	GENO113	9.06	6.71	8.03	7.66	7.86	2.52
107	NANDU	GENO114	6.17	8.06	7.23	NA	7.15	-2.11
108	882-202-10	GENO115	10.33	6.60	8.72	6.74	8.10	3.99
109	TALENT	GENO116	7.23	6.41	7.61	7.56	7.20	0.60
110	57-104-11	GENO117	5.96	4.67	5.54	5.65	5.45	1.33
111	878-202-10	GENO118	7.78	6.39	7.62	6.79	7.14	1.32
112	146-103-11	GENO120	6.87	5.05	7.13	6.90	6.49	1.56
113	SALUTE	GENO121	8.88	6.75	7.54	7.59	7.69	2.43
114	68-105-11	GENO122	9.42	6.15	6.83	7.37	7.44	3.94
115	63-113-11	GENO123	8.24	6.37	7.79	5.67	7.02	1.87
116	106-105-11	GENO124	9.24	NA	7.10	8.52	8.29	2.21
117	939-201-10	GENO125	8.03	6.23	6.89	6.93	7.02	2.06
118	NIXE	GENO126	6.40	5.92	6.27	7.37	6.49	0.48
119	51-109-11	GENO127	3.29	6.11	6.58	5.08	5.27	-3.79
120	ETIKETSIZNORIKA	GENO128	6.29	5.86	6.86	6.89	6.48	0.18
121	40-103-11	GENO130	5.15	6.51	5.86	6.12	5.91	-1.50
122	99-115-11	GENO131	8.53	5.87	5.96	6.17	6.63	3.37
123	141-104-11	GENO132	11.03	5.76	6.71	5.30	7.20	6.40
124	89-105-11	GENO133	7.43	6.48	7.80	7.42	7.28	0.73
125	NAUTILUS	GENO134	7.97	6.52	6.80	7.98	7.32	1.75
126	157-103-11	GENO136	7.85	6.41	6.72	5.28	6.57	1.73
127	133-112-11	GENO137	8.42	6.82	4.57	7.16	6.74	2.89

128	944-208-10	GENO138	8.02	6.46	8.06	7.48	7.50	1.40
129	PRIVELIGE	GENO139	6.93	7.17	7.60	4.14	6.46	-0.47
130	966-203-10	GENO140	6.78	6.55	6.43	6.57	6.58	0.34
131	904-212-10	GENO141	6.55	7.01	7.50	8.15	7.30	-0.77
132	BETTINA	GENO142	9.70	6.46	5.83	5.75	6.93	4.39
133	125-104-11	GENO143	8.05	8.04	7.22	8.54	7.96	0.32
134	SWING	GENO144	8.35	NA	NA	NA	8.35	10.70
135	758-109-09	GENO145	9.73	6.29	7.05	5.57	7.16	4.12
136	735-102-09	GENO146	9.00	4.89	9.00	7.97	7.72	3.74
137	99-102-11	GENO147	6.32	7.33	7.11	8.71	7.37	-1.21
138	TERRANA	GENO148	9.33	6.43	8.04	7.45	7.82	3.12
139	104-103-11	GENO149	8.09	8.15	7.49	6.24	7.49	0.17
140	SFHIT	GENO150	7.74	6.87	6.10	5.55	6.57	1.40
141	KIWI	GENO151	7.00	6.67	6.80	7.21	6.92	0.37
142	KIEBITZ	GENO152	7.67	7.12	6.78	9.21	7.69	0.83
143	BONUS	GENO153	7.70	6.51	6.96	7.64	7.20	1.36
144	509-104-09	GENO154	8.68	7.15	5.85	6.65	7.08	2.44
145	43-118-11	GENO155	7.12	6.67	5.10	5.50	6.10	1.16
146	BEO	GENO156	6.83	6.37	7.55	7.21	6.99	0.15
147	BALTICCREAM	GENO157	6.31	6.39	6.41	5.53	6.16	-0.11
148	868-201-10	GENO158	7.88	6.20	6.78	6.80	6.92	1.94
149	860-201-10	GENO159	5.92	8.05	8.49	6.94	7.35	-2.89
150	DUKATA	GENO160	8.85	7.64	6.29	6.10	7.22	2.05
151	84-107-11	GENO161	8.28	6.79	7.63	6.87	7.39	1.60
152	128-105-11	GENO162	4.83	6.49	7.58	5.96	6.21	-2.53
153	140-107-11	GENO163	6.22	7.67	7.30	6.81	7.00	-1.72
154	PELIKAN	GENO164	7.40	7.63	7.91	7.89	7.71	-0.40
155	KOLIBRI	GENO165	8.01	NA	6.69	NA	7.35	4.18
156	82-119-11	GENO167	8.98	6.64	6.79	7.99	7.60	2.94
157	WENDY	GENO168	7.19	6.27	6.53	5.68	6.42	1.08
158	ROMANZE	GENO169	11.71	10.74	10.22	15.43	12.03	1.44
159	PRESTIGE	GENO170	5.78	7.10	6.18	4.97	6.00	-1.35
160	MAXI	GENO171	7.65	6.44	6.82	6.20	6.78	1.41
161	FASAN	GENO172	7.64	6.95	7.11	7.22	7.23	0.82
162	Madaleine	GENO173	5.28	5.76	6.69	6.40	6.03	-0.96
163	POMQUEEN	GENO174	9.31	7.36	7.57	6.08	7.58	2.42
164	MUNGO	GENO175	8.07	7.08	8.25	6.72	7.53	0.83
165	ALBATROS	GENO176	9.10	6.01	5.73	6.74	6.89	4.06
166	FIDELIA	GENO177	5.64	4.22	4.25	16.50	7.65	1.81
167	TACOMA	GENO178	7.35	6.17	6.62	7.15	6.82	1.34
168	BONZA	GENO179	9.49	7.47	7.19	8.69	8.21	2.69
169	ADRETTA	GENO180	5.35	5.62	6.86	9.95	6.94	-0.81
170	POWER	GENO181	7.80	7.41	8.31	7.19	7.68	0.16
171	GOLDMARIE	GENO182	8.25	5.68	6.80	6.90	6.91	2.88
172	RITA	GENO183	7.80	8.06	7.39	5.92	7.29	-0.08

173	SUMMERGOLD	GENO184	6.38	5.62	7.16	4.77	5.98	0.40
174	DIPLOMAT	GENO185	8.43	6.18	7.68	10.31	8.15	2.32
175	CASCADA	GENO186	7.66	7.13	7.55	7.91	7.56	0.52
176	SOLIST	GENO187	7.38	6.59	6.87	6.91	6.94	0.91
177	LOLITA	GENO188	7.81	6.79	6.22	8.10	7.23	1.52
178	KARATOP	GENO189	6.80	6.14	7.31	6.44	6.67	0.41
179	INARA	GENO190	4.75	7.68	7.33	NA	6.59	-3.62
180	ACAPELLA	GENO191	5.93	6.85	6.51	5.15	6.11	-1.05
181	ALLORA	GENO192	2.22	5.85	4.82	4.37	4.32	-4.27
182	ARKULA	GENO193	6.59	5.70	NA	7.13	6.47	0.61
183	TOKIO	GENO194	6.63	7.30	5.78	5.83	6.39	-0.29
184	BIRTE	GENO195	6.22	6.38	7.04	6.99	6.66	-0.45
185	900-205-10	GENO196	9.12	7.15	7.87	5.94	7.52	2.26
186	MAXILLA	GENO197	5.59	6.82	6.05	9.08	6.89	-1.29
187	TUCAN	GENO198	6.42	6.24	6.97	5.73	6.34	-0.04
188	946-202-10	GENO199	7.27	7.95	6.79	5.90	6.98	-0.44
189	KORMORAN	GENO200	7.92	6.20	8.03	6.06	7.05	1.52
190	JUMBO	GENO202	10.20	5.59	6.67	5.53	7.00	5.50
191	LOGO	GENO203	7.33	7.11	8.37	7.84	7.66	-0.19
192	102-102-11	GENO204	6.26	5.93	6.86	6.37	6.36	0.08
		Mean	7.33	6.56	6.96	7.01	6.99	

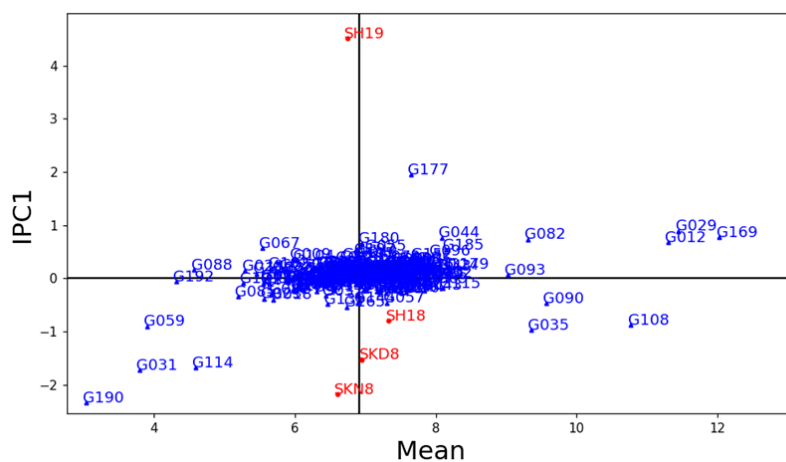


Fig.S15. Ammi biplot for mean of tuber skin colour a* of 192 genotypes across four environments (SH18, SKN18, SKD18, SH19) plotted against IPC1 (Interactive principal component)

APPENDIX-P Phenotypic data of skin (periderm) thickness (mm) showing the estimated values measured in four different environmental conditions (Hatay-2018; Konya standard water application-2018; Konya drought conditions-2018; Hatay-2019). *b_i* corresponds to regression coefficient according to Finlay and Wilkinson stability and adaptability (1963) model. Bold values correspond to average stability (*b_i*=1, not significantly different from one at *P*<0.05).

S.No.	Genotype Names	Codes	PT_ H18	PT_ KN18	PT_ KD18	PT_ H19	Mean PT	<i>b_i</i>
1	JELLY	GENO2	0.065	0.063	0.076	NA	0.068	2.58
2	RUMBA	GENO3	0.085	0.085	0.091	NA	0.087	1.10
3	HERMES	GENO4	0.084	0.081	0.088	NA	0.084	1.07
4	ALEGRIA	GENO5	0.080	0.078	0.071	NA	0.076	-1.09
5	ROYAL	GENO6	0.080	0.079	0.079	0.076	0.078	0.10
6	ELECTRA	GENO7	0.066	0.054	0.074	0.053	0.062	4.81
7	DT14003.01	GENO9	0.042	0.048	0.049	0.041	0.045	-0.39
8	DT14038.01	GENO10	0.064	0.068	0.060	0.064	0.064	-1.85
9	DT14010.18	GENO11	0.044	0.049	0.036	0.037	0.042	-2.86
10	DT14004.17	GENO12	0.111	0.105	0.115	0.122	0.113	2.41
11	DT14010.14	GENO13	0.097	0.091	0.095	0.099	0.095	1.30
12	DT14085.03	GENO14	0.049	0.048	0.056	0.058	0.053	1.56
13	DT14013.15	GENO16	0.066	NA	NA	0.059	0.063	-10.17
14	DT14018.32	GENO18	0.066	0.072	0.064	0.069	0.068	-2.04
15	DT14042.27	GENO19	0.077	0.076	0.080	0.076	0.077	0.83
16	DT14005.09	GENO20	0.064	0.059	0.069	0.066	0.065	2.31
17	DT14030.11	GENO21	0.056	0.061	0.055	0.052	0.056	-1.58
18	DT14057.37	GENO22	0.047	0.046	0.058	0.078	0.057	2.30
19	DT14065.01	GENO23	0.090	0.092	0.080	NA	0.087	-2.39
20	DT14016.01	GENO24	0.053	0.052	0.055	0.054	0.053	0.65
21	DT14016.34	GENO25	0.062	0.067	0.063	0.062	0.064	-1.21
22	DT14078.03	GENO26	0.060	0.059	0.058	0.049	0.057	-0.09
23	DT14028.03	GENO27	0.076	0.070	0.089	0.085	0.080	4.06
24	DT14054.11	GENO28	0.085	0.083	0.081	0.085	0.083	-0.18
25	DT14037.18	GENO29	0.044	0.049	0.044	0.045	0.045	-1.39
26	DT14091.04	GENO30	0.066	0.060	0.061	0.078	0.066	0.75
27	DT14083.28	GENO31	0.062	0.059	0.087	NA	0.069	5.43
28	DT14015.22	GENO32	0.068	0.068	0.067	0.067	0.068	-0.18
29	DT14051.15	GENO33	0.039	0.073	0.042	0.070	0.056	-8.93
30	DT14047.38	GENO34	0.064	0.071	0.060	0.060	0.064	-2.69
31	DT14026.04	GENO35	0.084	0.075	0.092	0.091	0.085	3.98
32	DT14068.07	GENO36	0.066	0.070	0.060	0.061	0.064	-2.22
33	DT14063.12	GENO37	0.050	0.049	0.052	0.049	0.050	0.65
34	DT14036.01	GENO38	0.037	NA	NA	NA	0.037	3.52
35	DT14055.25	GENO39	0.063	NA	NA	0.068	0.066	-12.96
36	LadyOlympia	GENO41	0.068	0.051	0.070	0.090	0.070	5.11
37	BANBA	GENO42	0.048	0.038	0.044	0.042	0.043	2.05
38	VanGOGH	GENO43	0.065	0.065	0.065	0.070	0.066	0.00
39	DT14049.10	GENO44	0.080	0.075	0.085	NA	0.080	2.31

40	DT14061.23	GENO45	0.048	0.056	0.052	0.047	0.051	-1.50
41	DT14006.07	GENO46	0.064	0.061	0.069	0.062	0.064	1.75
42	DT14046.19	GENO47	0.069	0.065	0.078	0.061	0.068	2.77
43	DT14014.27	GENO48	0.047	0.038	0.056	0.047	0.047	4.16
44	DT14011.18	GENO49	0.060	0.062	0.058	0.066	0.061	-0.92
45	DT14069.13	GENO50	0.089	0.081	0.079	0.084	0.083	0.39
46	DT14026.21	GENO52	0.061	0.066	0.065	0.062	0.064	-0.66
47	DT14042.24	GENO53	0.055	0.053	0.053	0.057	0.055	0.19
48	DT14090.11	GENO54	0.063	0.060	0.069	0.072	0.066	1.94
49	DT14071.19	GENO55	0.051	0.052	0.055	0.043	0.050	0.46
50	DT14027.08	GENO56	0.070	0.061	0.078	0.061	0.068	3.98
51	DT14034.03	GENO57	0.057	0.055	0.056	0.057	0.057	0.37
52	DT14057.36	GENO58	0.081	0.079	0.074	0.083	0.079	-0.73
53	DT14062.08	GENO59	0.050	0.064	0.082	NA	0.065	1.97
54	DT14079.02	GENO60	0.065	0.065	0.067	0.064	0.065	0.37
55	DT14053.03	GENO61	0.060	NA	NA	NA	0.060	5.71
56	DT13088.03	GENO63	0.100	0.081	0.099	0.085	0.091	5.11
57	DT14051.66	GENO64	0.077	0.040	0.070	0.032	0.055	9.03
58	DT13100.02	GENO65	0.063	0.068	0.060	0.059	0.063	-1.94
59	DT13162.15	GENO66	0.040	0.044	0.047	0.039	0.043	0.17
60	DT13162.12	GENO67	0.060	0.064	0.065	0.056	0.061	-0.20
61	DT11107.01	GENO68	0.069	0.068	0.066	0.064	0.067	-0.27
62	ZIRVE	GENO69	0.059	NA	NA	0.054	0.057	-9.44
63	DT12012.02	GENO70	0.065	0.065	0.064	0.069	0.066	-0.18
64	DT13136.22	GENO71	0.072	0.080	0.077	0.076	0.076	-1.31
65	DT13045.74	GENO72	0.062	0.063	0.056	0.064	0.061	-1.38
66	DT13124.21	GENO73	0.048	0.047	0.050	0.056	0.050	0.65
67	BORWINA	GENO74	0.068	0.063	0.077	0.069	0.069	3.05
68	BROOKE	GENO75	0.079	0.078	0.097	0.094	0.087	3.58
69	TESSA	GENO76	0.062	0.063	0.067	0.065	0.064	0.64
70	DT13143.49	GENO77	0.050	0.049	0.058	0.053	0.053	1.75
71	DT13130.48	GENO78	0.071	0.064	0.064	0.069	0.067	0.71
72	DT13143.54	GENO79	0.083	0.077	0.075	0.081	0.079	0.20
73	DT13007.03	GENO80	0.075	0.071	0.070	0.083	0.075	0.20
74	KUTUP	GENO81	0.042	0.044	0.049	0.044	0.045	0.73
75	DT13028.01	GENO82	0.085	0.083	0.095	0.096	0.090	2.39
76	DT13093.92	GENO83	0.055	0.057	0.059	0.060	0.058	0.18
77	DT13051.10	GENO84	0.044	0.043	0.044	0.041	0.043	0.28
78	DT13143.58	GENO85	0.058	0.065	0.060	0.062	0.061	-1.58
79	DT13026.10	GENO86	0.056	0.058	0.059	0.059	0.058	-0.01
80	DT13049.50	GENO87	0.066	0.059	0.069	0.066	0.065	2.50
81	DT13072.19	GENO88	0.099	0.097	0.119	0.123	0.110	4.23
82	DT13083.01	GENO89	0.066	0.068	0.075	0.070	0.070	1.09
83	LadyRosetta	GENO90	0.051	NA	NA	NA	0.051	4.85
84	DT11007.01	GENO91	0.066	0.067	0.076	0.073	0.070	1.56
85	DT11108.02	GENO92	0.064	0.065	0.054	0.067	0.062	-2.11

86	DORUK	GENO93	0.050	0.044	0.044	0.049	0.047	0.57
87	DT13085.01	GENO94	0.081	0.086	0.082	0.068	0.079	-1.21
88	DT12068.21	GENO95	0.062	0.069	0.070	0.069	0.068	-0.48
89	DT11088.01	GENO96	0.048	0.045	0.051	0.050	0.048	1.39
90	DT13045.42	GENO97	0.038	0.044	0.040	0.038	0.040	-1.31
91	DT13147.17	GENO98	0.082	0.065	0.069	0.067	0.071	2.35
92	DT13048.10	GENO99	0.076	0.060	0.066	0.073	0.069	2.62
93	DT13052.23	GENO100	0.051	0.050	0.055	0.046	0.051	1.01
94	DT13037.31	GENO101	0.053	0.052	0.058	0.053	0.054	1.20
95	DT13045.103	GENO102	0.062	0.061	0.058	0.063	0.061	-0.46
96	DT13037.35	GENO103	0.081	0.071	0.086	0.088	0.082	3.71
97	DT13047.08	GENO104	0.075	0.075	0.066	0.073	0.072	-1.65
98	DT13162.16	GENO105	0.067	0.062	0.073	0.065	0.067	2.50
99	DT13067.03	GENO106	0.049	0.043	0.049	0.046	0.047	1.67
100	SORAYA	GENO107	0.066	0.058	0.065	0.054	0.061	2.05
101	LAURA	GENO108	0.062	0.063	0.059	0.059	0.061	-0.83
102	SHEPODY	GENO109	0.079	0.078	0.078	0.074	0.077	0.10
103	43-111-11	GENO110	0.059	0.062	0.066	0.063	0.063	0.45
104	KARLENA	GENO111	0.138	0.111	0.124	0.106	0.120	4.96
105	139-101-11	GENO112	0.070	0.065	0.071	0.069	0.069	1.58
106	84-105-11	GENO113	0.076	0.075	0.085	0.076	0.078	1.93
107	NANDU	GENO114	0.073	0.071	0.077	NA	0.074	1.29
108	882-202-10	GENO115	0.079	0.073	0.085	0.073	0.077	2.77
109	TALENT	GENO116	0.054	0.059	0.054	0.053	0.055	-1.39
110	57-104-11	GENO117	0.052	0.057	0.059	0.051	0.055	-0.11
111	878-202-10	GENO118	0.078	0.073	0.077	0.076	0.076	1.21
112	146-103-11	GENO120	0.043	0.049	0.042	0.046	0.045	-1.86
113	SALUTE	GENO121	0.041	0.042	0.045	0.034	0.041	0.46
114	68-105-11	GENO122	0.077	0.078	0.082	0.072	0.077	0.64
115	63-113-11	GENO123	0.073	0.068	0.078	0.065	0.071	2.31
116	106-105-11	GENO124	0.067	0.068	0.078	0.065	0.069	1.74
117	939-201-10	GENO125	0.067	0.064	0.064	0.069	0.066	0.29
118	NIXE	GENO126	0.083	0.058	0.086	0.075	0.075	7.52
119	51-109-11	GENO127	0.074	0.076	0.069	0.066	0.071	-1.48
120	ETIKETSIZNORIK	GENO128	0.054	0.054	0.062	0.057	0.057	1.47
121	40-103-11	GENO130	0.061	0.060	0.062	0.053	0.059	0.46
122	99-115-11	GENO131	0.067	0.061	0.079	0.071	0.070	3.88
123	141-104-11	GENO132	0.060	0.060	0.074	0.068	0.066	2.57
124	89-105-11	GENO133	0.065	0.061	0.066	0.065	0.064	1.30
125	NAUTILUS	GENO134	0.073	0.069	0.077	0.081	0.075	1.85
126	157-103-11	GENO136	0.063	0.045	0.060	0.058	0.056	4.47
127	133-112-11	GENO137	0.042	0.041	0.054	0.049	0.046	2.48
128	944-208-10	GENO138	0.064	0.062	0.075	0.069	0.068	2.58
129	PRIVELIGE	GENO139	0.065	0.061	0.078	0.069	0.068	3.50
130	966-203-10	GENO140	0.052	0.052	0.050	0.049	0.051	-0.37
131	904-212-10	GENO141	0.063	0.066	0.062	0.052	0.061	-1.02

132	BETTINA	GENO142	0.069	0.063	0.072	0.060	0.066	2.22
133	125-104-11	GENO143	0.092	0.091	0.106	0.099	0.097	2.85
134	SWING	GENO144	0.061	NA	NA	NA	0.061	5.80
135	758-109-09	GENO145	0.053	0.060	0.054	0.054	0.055	-1.77
136	735-102-09	GENO146	0.082	0.060	0.082	0.083	0.077	6.13
137	99-102-11	GENO147	0.075	0.072	0.088	0.090	0.081	3.22
138	TERRANA	GENO148	0.068	0.066	0.074	0.068	0.069	1.66
139	104-103-11	GENO149	0.060	0.053	0.068	0.062	0.061	3.42
140	SFHIT	GENO150	0.065	0.067	0.066	0.053	0.063	-0.37
141	KIWI	GENO151	0.058	0.059	0.060	0.055	0.058	0.09
142	KIEBITZ	GENO152	0.054	0.056	0.060	0.053	0.056	0.54
143	BONUS	GENO153	0.065	0.060	0.079	0.072	0.069	3.96
144	509-104-09	GENO154	0.060	0.047	0.060	0.068	0.059	3.62
145	43-118-11	GENO155	0.071	0.069	0.064	0.073	0.069	-0.73
146	BEO	GENO156	0.043	0.038	0.044	0.038	0.041	1.58
147	BALTICCREAM	GENO157	0.046	0.046	0.058	0.033	0.046	2.20
148	868-201-10	GENO158	0.063	0.063	0.081	0.075	0.071	3.30
149	860-201-10	GENO159	0.042	0.035	0.039	0.039	0.039	1.40
150	DUKATA	GENO160	0.083	0.078	0.075	0.078	0.079	-0.08
151	84-107-11	GENO161	0.051	0.058	0.059	0.059	0.057	-0.48
152	128-105-11	GENO162	0.065	0.062	0.075	0.073	0.069	2.67
153	140-107-11	GENO163	0.054	0.056	0.063	0.049	0.056	1.09
154	PELIKAN	GENO164	0.095	0.092	0.101	0.090	0.095	1.94
155	KOLIBRI	GENO165	0.043	NA	NA	NA	0.043	4.09
156	82-119-11	GENO167	0.040	0.044	0.066	0.068	0.055	3.66
157	WENDY	GENO168	0.070	0.067	0.074	0.067	0.070	1.57
158	ROMANZE	GENO169	0.098	0.107	0.105	0.101	0.102	-1.22
159	PRESTIGE	GENO170	0.054	0.048	0.064	0.052	0.055	3.51
160	MAXI	GENO171	0.076	0.078	0.076	0.072	0.076	-0.56
161	FASAN	GENO172	0.043	0.038	0.051	0.039	0.043	2.86
162	Madaleine	GENO173	0.063	0.075	0.087	0.057	0.071	1.06
163	POMQUEEN	GENO174	0.057	0.049	0.065	0.046	0.054	3.70
164	MUNGO	GENO175	0.079	0.079	0.089	0.087	0.084	1.84
165	ALBATROS	GENO176	0.054	0.059	0.059	0.048	0.055	-0.48
166	FIDELIA	GENO177	0.097	0.096	0.103	0.093	0.097	1.38
167	TACOMA	GENO178	0.072	0.072	0.066	0.076	0.072	-1.10
168	BONZA	GENO179	0.063	0.060	0.062	0.061	0.062	0.65
169	ADRETTA	GENO180	0.053	0.052	0.064	0.065	0.058	2.30
170	POWER	GENO181	0.060	0.052	0.070	0.058	0.060	4.07
171	GOLDMARIE	GENO182	0.072	0.076	0.078	0.070	0.074	-0.01
172	RITA	GENO183	0.054	0.072	0.092	0.061	0.070	1.96
173	SUMMERGOLD	GENO184	0.054	0.059	0.054	0.060	0.057	-1.39
174	DIPLOMAT	GENO185	0.044	0.048	0.048	0.047	0.047	-0.38
175	CASCADA	GENO186	0.088	0.084	0.085	0.086	0.086	0.56
176	SOLIST	GENO187	0.075	0.077	0.069	0.069	0.072	-1.66
177	LOLITA	GENO188	0.056	0.054	0.061	0.057	0.057	1.48

178	KARATOP	GENO189	0.045	0.045	0.046	0.050	0.047	0.18
179	INARA	GENO190	0.060	0.055	0.064	NA	0.060	2.13
180	ACAPELLA	GENO191	0.045	0.045	0.042	0.038	0.043	-0.55
181	ALLORA	GENO192	0.057	0.051	0.058	0.055	0.055	1.86
182	ARKULA	GENO193	0.056	0.049	0.044	0.046	0.049	-0.25
183	TOKIO	GENO194	0.059	0.060	0.054	0.051	0.056	-1.20
184	BIRTE	GENO195	0.070	0.059	0.063	0.065	0.064	1.78
185	900-205-10	GENO196	0.054	0.048	0.065	0.059	0.057	3.69
186	MAXILLA	GENO197	0.066	0.065	0.068	0.062	0.065	0.65
187	TUCAN	GENO198	0.073	0.069	0.078	0.077	0.074	2.03
188	946-202-10	GENO199	0.063	0.064	0.063	0.070	0.065	-0.28
189	KORMORAN	GENO200	0.074	0.075	0.074	0.070	0.073	-0.28
190	JUMBO	GENO202	0.063	0.056	0.064	0.050	0.058	2.13
191	LOGO	GENO203	0.086	0.075	0.088	0.074	0.081	3.43
192	102-102-11	GENO204	0.073	0.062	0.078	0.071	0.071	3.98
		Mean	0.065	0.063	0.068	0.065	0.065	

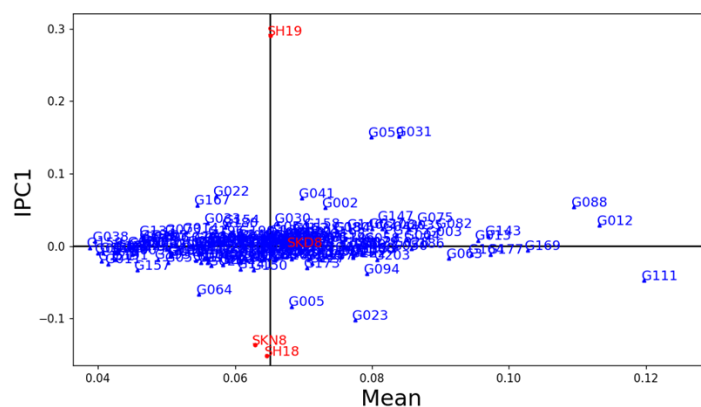


Fig.S16. Ammi biplot for mean of tuber skin (periderm) thickness of 192 genotypes across four environments (SH18, SKN18, SKD18, SH19) plotted against IPC1 (Interactive principal component)

APPENDIX Q: ANOVA TABLES FOR AUGMENTED DESIGN ANALYSIS

APPENDIX Q1: Analysis of Variance (ANOVA) based on Augmented Design for Dry matter content (DMC) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	DMC_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	1430.104	6.976118	6.2	<.0001
Block	7	165.4162	23.63088	20.99	<.0001
Among checks (Entryc)	5	50.60096	10.12019	8.99	<.0001
Among test genotypes	193	1214.087	6.290606	5.59	<.0001
Error	28	31.5283	1.126011		
Corrected Total	233	1461.632			
	DMC_KN18				
Model (checks vs tests vs blocks)	192	1220.531	6.356933	7.77	<.0001
Block	4	55.27793	13.81948	16.9	<.0001
Among checks (Entryc)	5	62.35744	12.47149	15.25	<.0001
Among test genotypes	183	1102.896	6.026753	7.37	<.0001
Error	14	11.44962	0.81783		
Corrected Total	206	1231.981			
	DMC_KD18				
Model (checks vs tests vs blocks)	192	1353.844	7.05127	7.05	0.0009
Block	4	40.73903	10.18476	10.18	0.0015
Among checks (Entryc)	5	75.88319	15.17664	15.17	0.0002
Among test genotypes	183	1237.222	6.760774	6.76	0.0011
Error	10	10.00689	1.000689		
Corrected Total	202	1363.851			
	DMC_H19				
Model (checks vs tests vs blocks)	197	892.1372	4.528615	4.29	<.0001
Block	15	144.497	9.633135	9.12	<.0001
Among checks (Entryc)	5	114.1419	22.82838	21.6	<.0001
Among test genotypes	177	633.4983	3.579087	3.39	<.0001
Error	60	63.409	1.056817		
Corrected Total	257	955.5462			

Acronyms: *DF: Degree of freedom; SS: Sum of square; MS: Mean square*

APPENDIX Q2: Analysis of Variance (ANOVA) based on Augmented Design for Specific gravity (SG) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	SG_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	0.032269	0.000157	6.23	<.0001
Block	7	0.004136	0.000591	23.37	<.0001
Among checks (Entryc)	5	0.001126	0.000225	8.9	<.0001
Among test genotypes	193	0.027007	0.00014	5.54	<.0001
Error	28	0.000708	2.53E-05		
Corrected Total	233	0.032977			
	SG_KN18				
Model (checks vs tests vs blocks)	189	0.026411	0.00014	8.39	<.0001
Block	4	0.001527	0.000382	22.91	<.0001
Among checks (Entryc)	5	0.001353	0.000271	16.24	<.0001
Among test genotypes	180	0.023531	0.000131	7.84	<.0001
Error	14	0.000233	1.67E-05		
Corrected Total	203	0.026645			
	SG_KD18				
Model (checks vs tests vs blocks)	191	0.069378	0.000363	0.08	1.000
Block	4	0.001254	0.000314	0.07	0.9902
Among checks (Entryc)	5	0.021113	0.004223	0.92	0.5081
Among test genotypes	182	0.047011	0.000258	0.06	1.0000
Error	10	0.046058	0.004606		
Corrected Total	201	0.115436			
	SG_H19				
Model (checks vs tests vs blocks)	197	0.020002	0.000102	4.35	<.0001
Block	15	0.003075	0.000205	8.78	<.0001
Among checks (Entryc)	5	0.002562	0.000512	21.93	<.0001
Among test genotypes	177	0.014365	8.12E-05	3.47	<.0001
Error	60	0.001402	2.34E-05		
Corrected Total	257	0.021404			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q3: Analysis of Variance (ANOVA) based on Augmented Design for reducing sugars “RSS” (g/100g DW) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	RSS_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	1.547333	0.007548	9.49	<.0001
Block	7	0.034513	0.00493	6.2	0.0002
Among checks (Entryc)	5	0.010514	0.002103	2.64	0.0444
Among test genotypes	193	1.502306	0.007784	9.78	<.0001
Error	28	0.022275	0.000796		
Corrected Total	233	1.569608			
	RSS_KN18				
Model (checks vs tests vs blocks)	189	0.998445	0.005283	4.59	0.0012
Block	4	0.038315	0.009579	8.32	0.0012
Among checks (Entryc)	5	0.00445	0.00089	0.77	0.5847
Among test genotypes	180	0.95568	0.005309	4.61	0.0011
Error	14	0.016115	0.001151		
Corrected Total	203	1.01456			
	RSS_KD18				
Model (checks vs tests vs blocks)	191	0.366968	0.001921	1.17	0.4223
Block	4	0.008133	0.002033	1.24	0.3548
Among checks (Entryc)	5	0.006797	0.001359	0.83	0.5573
Among test genotypes	182	0.352038	0.001934	1.18	0.4169
Error	10	0.016403	0.00164		
Corrected Total	201	0.383371			
	RSS_H19				
Model (checks vs tests vs blocks)	197	2.048093	0.010396	15.68	<.0001
Block	15	0.208542	0.013903	20.97	<.0001
Among checks (Entryc)	5	0.166905	0.033381	50.35	<.0001
Among test genotypes	177	1.672646	0.00945	14.25	<.0001
Error	60	0.039782	0.000663		
Corrected Total	257	2.087874			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q4: Analysis of Variance (ANOVA) based on Augmented Design for sucrose “SUC” (g/100g DW) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	SUC_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	0.630493	0.003076	7.07	<.0001
Block	7	0.023563	0.003366	7.74	<.0001
Among checks (Entryc)	5	0.014336	0.002867	6.59	0.0004
Among test genotypes	193	0.592593	0.00307	7.06	<.0001
Error	28	0.012185	0.000435		
Corrected Total	233	0.642678			
	SUC_KN18				
Model (checks vs tests vs blocks)	189	0.736265	0.003896	20.53	<.0001
Block	4	0.011528	0.002882	15.19	<.0001
Among checks (Entryc)	5	0.051125	0.010225	53.89	<.0001
Among test genotypes	180	0.673612	0.003742	19.72	<.0001
Error	14	0.002656	0.00019		
Corrected Total	203	0.738921			
	SUC_KD18				
Model (checks vs tests vs blocks)	191	1.222301	0.006399	32.88	<.0001
Block	4	0.011299	0.002825	14.51	0.0004
Among checks (Entryc)	5	0.008845	0.001769	9.09	0.0018
Among test genotypes	182	1.202158	0.006605	33.94	<.0001
Error	10	0.001946	0.000195		
Corrected Total	201	1.224247			
	SUC_H19				
Model (checks vs tests vs blocks)	197	0.677289	0.003438	9.78	<.0001
Block	15	0.047347	0.003156	8.98	<.0001
Among checks (Entryc)	5	0.057512	0.011502	32.72	<.0001
Among test genotypes	177	0.57243	0.003234	9.2	<.0001
Error	60	0.02109	0.000352		
Corrected Total	257	0.698379			

Acronyms: *DF: Degree of freedom; SS: Sum of square; MS: Mean square*

APPENDIX Q5: Analysis of Variance (ANOVA) based on Augmented Design for Free asparagine “ASP” (g/100g DW) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	ASP_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	204	0.173059	0.000848	2.43	0.0034
Block	7	0.014438	0.002063	5.91	0.0003
Among checks (Entryc)	5	0.009834	0.001967	5.63	0.001
Among test genotypes	192	0.148786	0.000775	2.22	0.0072
Error	28	0.009774	0.000349		
Corrected Total	232	0.182833			
	ASP_KN18				
Model (checks vs tests vs blocks)	189	0.17561	0.000929	3.85	0.003
Block	4	0.000415	0.000104	0.43	0.7846
Among checks (Entryc)	5	0.010077	0.002015	8.36	0.0008
Among test genotypes	180	0.165119	0.000917	3.8	0.0033
Error	14	0.003375	0.000241		
Corrected Total	203	0.178986			
	ASP_KD18				
Model (checks vs tests vs blocks)	192	0.332076	0.00173	8.08	0.0005
Block	4	0.004628	0.001157	5.41	0.014
Among checks (Entryc)	5	0.007264	0.001453	6.79	0.0052
Among test genotypes	183	0.320184	0.00175	8.18	0.0005
Error	10	0.00214	0.000214		
Corrected Total	202	0.334216			
	ASP_H19				
Model (checks vs tests vs blocks)	197	0.171806	0.000872	2.73	<.0001
Block	15	0.007259	0.000484	1.51	0.1294
Among checks (Entryc)	5	0.026195	0.005239	16.38	<.0001
Among test genotypes	177	0.138352	0.000782	2.44	<.0001
Error	60	0.019188	0.00032		
Corrected Total	257	0.190993			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q6: Analysis of Variance (ANOVA) based on Augmented Design for Starch “ST” (%) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	ST_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	6283.287	30.65018	5.83	<.0001
Block	7	140.2822	20.04031	3.81	0.005
Among checks (Entryc)	5	427.2134	85.44268	16.26	<.0001
Among test genotypes	193	5715.792	29.6155	5.64	<.0001
Error	28	147.1541	5.255504		
Corrected Total	233	6430.441			
	ST_KN18				
Model (checks vs tests vs blocks)	190	3305.051	17.395	3.55	0.0047
Block	4	40.97189	10.24297	2.09	0.1364
Among checks (Entryc)	5	173.5482	34.70964	7.08	0.0017
Among test genotypes	181	3090.531	17.07475	3.48	0.0052
Error	14	68.59723	4.899802		
Corrected Total	204	3373.648			
	ST_KD18				
Model (checks vs tests vs blocks)	191	2897.664	15.17102	3.57	0.015
Block	4	10.77727	2.694319	0.63	0.6497
Among checks (Entryc)	5	109.8603	21.97205	5.17	0.0133
Among test genotypes	182	2777.027	15.25839	3.59	0.0147
Error	10	42.49543	4.249542		
Corrected Total	201	2940.16			
	ST_H19				
Model (checks vs tests vs blocks)	197	4169.673	21.16585	3.46	<.0001
Block	15	439.9351	29.32901	4.79	<.0001
Among checks (Entryc)	5	721.3212	144.2642	23.56	<.0001
Among test genotypes	177	3008.417	16.99671	2.78	<.0001
Error	60	367.4466	6.12411		
Corrected Total	257	4537.12			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q7: Analysis of Variance (ANOVA) based on Augmented Design for Beta carotene “BCRT” (ug/g DW) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	BCRT_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	6079.062	29.65396	6.06	<.0001
Block	7	317.8685	45.40979	9.28	<.0001
Among checks (Entryc)	5	572.9225	114.5845	23.41	<.0001
Among test genotypes	193	5188.271	26.88223	5.49	<.0001
Error	28	137.0387	4.894241		
Corrected Total	233	6216.101			
	BCRT_KN18				
Model (checks vs tests vs blocks)	189	3811.794	20.16822	7.24	<.0001
Block	4	48.64756	12.16189	4.37	0.0168
Among checks (Entryc)	5	121.2239	24.24477	8.71	0.0006
Among test genotypes	180	3641.922	20.2329	7.27	<.0001
Error	14	38.97799	2.784142		
Corrected Total	203	3850.772			
	BCRT_KD18				
Model (checks vs tests vs blocks)	191	3656.438	19.14366	7.95	0.0005
Block	4	146.4655	36.61637	15.2	0.0003
Among checks (Entryc)	5	98.96774	19.79355	8.22	0.0026
Among test genotypes	182	3411.005	18.74179	7.78	0.0006
Error	10	24.08794	2.408794		
Corrected Total	201	3680.526			
	BCRT_H19				
Model (checks vs tests vs blocks)	196	5264.599	26.8602	7.21	<.0001
Block	15	166.2913	11.08609	2.98	0.0014
Among checks (Entryc)	5	1023.379	204.6758	54.95	<.0001
Among test genotypes	176	4074.928	23.153	6.22	<.0001
Error	60	223.4982	3.72497		
Corrected Total	256	5488.097			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q8: Analysis of Variance (ANOVA) based on Augmented Design for Total antioxidant activity “TAA” (mg AAE/100g DW) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	TAA_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	4911.014	23.95617	3.25	0.0002
Block	7	49.09229	7.013185	0.95	0.4843
Among checks (Entryc)	5	683.4264	136.6853	18.54	<.0001
Among test genotypes	193	4178.495	21.65023	2.94	0.0006
Error	28	206.3935	7.371195		
Corrected Total	233	5117.407			
	TAA_KN18				
Model (checks vs tests vs blocks)	189	3427.234	18.13351	7.61	<.0001
Block	4	81.01437	20.25359	8.5	0.0011
Among checks (Entryc)	5	155.774	31.1548	13.08	<.0001
Among test genotypes	180	3190.445	17.7247	7.44	<.0001
Error	14	33.34901	2.382072		
Corrected Total	203	3460.583			
	TAA_KD18				
Model (checks vs tests vs blocks)	191	1261.381	6.604089	2.57	0.0494
Block	4	24.29555	6.073887	2.37	0.1228
Among checks (Entryc)	5	29.0483	5.809661	2.26	0.1272
Among test genotypes	182	1208.037	6.637566	2.59	0.0487
Error	10	25.66746	2.566746		
Corrected Total	201	1287.048			
	TAA_H19				
Model (checks vs tests vs blocks)	197	5158.73	26.18645	3.81	<.0001
Block	15	208.1998	13.87999	2.02	0.0287
Among checks (Entryc)	5	1434.175	286.835	41.69	<.0001
Among test genotypes	177	3516.355	19.86641	2.89	<.0001
Error	60	412.7869	6.879782		
Corrected Total	257	5571.517			

Acronyms: *DF: Degree of freedom; SS: Sum of square; MS: Mean square*

APPENDIX Q9: Analysis of Variance (ANOVA) based on Augmented Design for Total phenolic contents “TPC” (mg FAE/100g DW) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	TPC_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	973012	4746.4	2.52	0.0025
Block	7	47800.64	6828.662	3.62	0.0066
Among checks (Entryc)	5	60370.03	12074.01	6.41	0.0004
Among test genotypes	193	864841.4	4481.043	2.38	0.0041
Error	28	52761.69	1884.346		
Corrected Total	233	1025774			
	TPC_KN18				
Model (checks vs tests vs blocks)	189	617679.3	3268.144	9.43	<.0001
Block	4	6865.618	1716.405	4.95	0.0107
Among checks (Entryc)	5	25582.33	5116.466	14.76	<.0001
Among test genotypes	180	585231.3	3251.285	9.38	<.0001
Error	14	4853.15	346.6536		
Corrected Total	203	622532.4			
	TPC_KD18				
Model (checks vs tests vs blocks)	191	515513	2699.021	11.15	0.0002
Block	4	22285.64	5571.409	23.02	<.0001
Among checks (Entryc)	5	14944.88	2988.976	12.35	0.0008
Among test genotypes	182	478282.4	2627.926	10.86	0.0003
Error	9	2178.312	242.0346		
Corrected Total	200	517691.3			
	TPC_H19				
Model (checks vs tests vs blocks)	196	489314.3	2496.501	14.73	<.0001
Block	15	16123.63	1074.909	6.34	<.0001
Among checks (Entryc)	5	123807.4	24761.48	146.07	<.0001
Among test genotypes	176	349383.3	1985.132	11.71	<.0001
Error	60	10170.85	169.5142		
Corrected Total	256	499485.1			

Acronyms: *DF: Degree of freedom; SS: Sum of square; MS: Mean square*

APPENDIX Q10: Analysis of Variance (ANOVA) based on Augmented Design for Tuber flesh colour L*coordinate “FCL” in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	FCL_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	2064.668	10.07155	4.77	<.0001
Block	7	44.20993	6.315704	2.99	0.0178
Among checks (Entryc)	5	38.12245	7.62449	3.61	0.012
Among test genotypes	193	1982.336	10.27117	4.87	<.0001
Error	28	59.11334	2.111191		
Corrected Total	233	2123.782			
	FCL_KN18				
Model (checks vs tests vs blocks)	189	1558.075	8.243783	3.41	0.0058
Block	4	8.784604	2.196151	0.91	0.4857
Among checks (Entryc)	5	172.8036	34.56073	14.29	<.0001
Among test genotypes	180	1376.487	7.647148	3.16	0.0085
Error	14	33.84917	2.417798		
Corrected Total	203	1591.924			
	FCL_KD18				
Model (checks vs tests vs blocks)	191	1155.232	6.048336	6.36	0.0014
Block	4	55.19773	13.79943	14.5	0.0004
Among checks (Entryc)	5	58.6321	11.72642	12.32	0.0005
Among test genotypes	182	1041.402	5.721991	6.01	0.0018
Error	10	9.516435	0.951643		
Corrected Total	201	1164.749			
	FCL_H19				
Model (checks vs tests vs blocks)	197	1235.828	6.273237	3.53	<.0001
Block	15	48.69111	3.246074	1.82	0.0519
Among checks (Entryc)	5	380.9647	76.19294	42.81	<.0001
Among test genotypes	177	806.1719	4.554644	2.56	<.0001
Error	60	106.776	1.7796		
Corrected Total	257	1342.604			

Acronyms: *DF: Degree of freedom; SS: Sum of square; MS: Mean square*

APPENDIX Q11: Analysis of Variance (ANOVA) based on Augmented Design for Tuber flesh colour b*coordinate “FCb” in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	FCb_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	4143.824	20.21378	7.64	<.0001
Block	7	68.67768	9.811097	3.71	0.0059
Among checks (Entryc)	5	123.8534	24.77068	9.36	<.0001
Among test genotypes	193	3951.293	20.47302	7.73	<.0001
Error	28	74.12526	2.647331		
Corrected Total	233	4217.949			
	FCb_KN18				
Model (checks vs tests vs blocks)	189	2468.418	13.06041	4.43	0.0014
Block	4	31.89538	7.973845	2.7	0.0736
Among checks (Entryc)	5	82.79908	16.55982	5.62	0.0048
Among test genotypes	180	2353.724	13.07624	4.44	0.0014
Error	14	41.27242	2.94803		
Corrected Total	203	2509.691			
	FCb_KD18				
Model (checks vs tests vs blocks)	191	2162.141	11.32011	5.98	0.0018
Block	4	39.32874	9.832184	5.2	0.0158
Among checks (Entryc)	5	93.1427	18.62854	9.85	0.0013
Among test genotypes	182	2029.67	11.15203	5.89	0.002
Error	10	18.91879	1.891879		
Corrected Total	201	2181.06			
	FCb_H19				
Model (checks vs tests vs blocks)	197	4012.446	20.36775	8.24	<.0001
Block	15	136.8237	9.121577	3.69	0.0001
Among checks (Entryc)	5	2160.069	432.0138	174.84	<.0001
Among test genotypes	177	1715.553	9.692391	3.92	<.0001
Error	60	148.2505	2.470842		
Corrected Total	257	4160.696			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q12: Analysis of Variance (ANOVA) based on Augmented Design for Tuber flesh colour a*coordinate “FCa” in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	FCa_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	159.9925	0.780451	5.22	<.0001
Block	7	3.853212	0.550459	3.68	0.0061
Among checks (Entryc)	5	8.015493	1.603099	10.71	<.0001
Among test genotypes	193	148.1238	0.767481	5.13	<.0001
Error	28	4.189397	0.149621		
Corrected Total	233	164.1819			
	FCa_KN18				
Model (checks vs tests vs blocks)	189	98.15522	0.51934	4.41	0.0014
Block	4	2.224124	0.556031	4.72	0.0127
Among checks (Entryc)	5	7.152088	1.430418	12.15	0.0001
Among test genotypes	180	88.779	0.493217	4.19	0.0019
Error	14	1.647806	0.1177		
Corrected Total	203	99.80302			
	FCa_KD18				
Model (checks vs tests vs blocks)	191	119.649	0.626434	2.7	0.0419
Block	4	4.829548	1.207387	5.2	0.0158
Among checks (Entryc)	5	7.277857	1.455571	6.27	0.0069
Among test genotypes	182	107.5416	0.590888	2.55	0.0513
Error	10	2.320384	0.232038		
Corrected Total	201	121.9694			
	FCa_H19				
Model (checks vs tests vs blocks)	197	69.8523	0.35458	2.54	<.0001
Block	15	5.404078	0.360272	2.58	0.0049
Among checks (Entryc)	5	8.82212	1.764424	12.63	<.0001
Among test genotypes	177	55.6261	0.314272	2.25	0.0002
Error	60	8.378793	0.139647		
Corrected Total	257	78.23109			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q13: Analysis of Variance (ANOVA) based on Augmented Design for Tuber skin colour L*coordinate “SCL” in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	SCL_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	2867.95	13.99	1.93	0.0204
Block	7	113.0241	16.1463	2.23	0.0621
Among checks (Entryc)	5	31.24393	6.248785	0.86	0.5184
Among test genotypes	193	2723.682	14.11234	1.95	0.0194
Error	28	202.8955	7.246269		
Corrected Total	233	3070.846			
	SCL_KN18				
Model (checks vs tests vs blocks)	189	1656.118	8.762532	2.58	0.0229
Block	4	70.29782	17.57446	5.17	0.0091
Among checks (Entryc)	5	69.33484	13.86697	4.08	0.0171
Among test genotypes	180	1516.486	8.424921	2.48	0.0276
Error	14	47.6165	3.401178		
Corrected Total	203	1703.735			
	SCL_KD18				
Model (checks vs tests vs blocks)	191	1923.583	10.07112	3.19	0.0229
Block	4	35.13103	8.782756	2.78	0.0862
Among checks (Entryc)	5	28.5381	5.70762	1.81	0.1988
Among test genotypes	182	1859.914	10.21931	3.24	0.0218
Error	10	31.55741	3.155741		
Corrected Total	201	1955.141			
	SCL_H19				
Model (checks vs tests vs blocks)	197	3011.024	15.28438	1.84	0.0033
Block	15	233.7484	15.58323	1.88	0.0444
Among checks (Entryc)	5	677.6252	135.525	16.31	<.0001
Among test genotypes	177	2099.65	11.86243	1.43	0.0453
Error	60	498.5393	8.308989		
Corrected Total	257	3509.563			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q14: Analysis of Variance (ANOVA) based on Augmented Design for Tuber skin colour b*coordinate “SCb” in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	SCb_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	6561.691	32.00825	5.12	<.0001
Block	7	246.4704	35.21006	5.63	0.0004
Among checks (Entryc)	5	233.957	46.7914	7.48	0.0001
Among test genotypes	193	6081.263	31.50914	5.04	<.0001
Error	28	175.1848	6.256601		
Corrected Total	233	6736.875			
	SCb_KN18				
Model (checks vs tests vs blocks)	189	1846.135	9.767909	6.01	0.0002
Block	4	9.514303	2.378576	1.46	0.2659
Among checks (Entryc)	5	39.91007	7.982014	4.91	0.0084
Among test genotypes	180	1796.71	9.981725	6.14	0.0002
Error	14	22.76771	1.626265		
Corrected Total	203	1868.903			
	SCb_KD18				
Model (checks vs tests vs blocks)	191	5011.474	26.23809	7.51	0.0007
Block	4	12.41403	3.103508	0.89	0.5052
Among checks (Entryc)	5	24.11872	4.823745	1.38	0.3098
Among test genotypes	182	4974.942	27.33484	7.83	0.0006
Error	10	34.92831	3.492831		
Corrected Total	201	5046.403			
	SCb_H19				
Model (checks vs tests vs blocks)	197	5664.306	28.75282	4.92	<.0001
Block	15	345.5937	23.03958	3.95	<.0001
Among checks (Entryc)	5	3683.933	736.7866	126.17	<.0001
Among test genotypes	177	1634.78	9.236043	1.58	0.0204
Error	60	350.3697	5.839495		
Corrected Total	257	6014.676			

Acronyms: *DF: Degree of freedom; SS: Sum of square; MS: Mean square*

APPENDIX Q15: Analysis of Variance (ANOVA) based on Augmented Design for Tuber skin colour a*coordinate “SCa” in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	SCa_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	595.6583	2.90565	1.8	0.0328
Block	7	45.70274	6.528963	4.05	0.0035
Among checks (Entryc)	5	25.87174	5.174347	3.21	0.0205
Among test genotypes	193	524.0838	2.71546	1.68	0.0514
Error	28	45.13873	1.612098		
Corrected Total	233	640.797			
	SCa_KN18				
Model (checks vs tests vs blocks)	189	291.2869	1.541201	3.62	0.0042
Block	4	12.82261	3.205652	7.53	0.0019
Among checks (Entryc)	5	6.703545	1.340709	3.15	0.0412
Among test genotypes	180	271.7608	1.509782	3.55	0.0047
Error	14	5.959864	0.425705		
Corrected Total	203	297.2468			
	SCa_KD18				
Model (checks vs tests vs blocks)	191	279.6684	1.464232	9.48	0.0002
Block	4	3.658196	0.914549	5.92	0.0104
Among checks (Entryc)	5	11.31009	2.262019	14.64	0.0003
Among test genotypes	182	264.7001	1.454396	9.41	0.0002
Error	10	1.544828	0.154483		
Corrected Total	201	281.2132			
	SCa_H19				
Model (checks vs tests vs blocks)	197	657.1155	3.335612	2.22	0.0002
Block	15	50.91034	3.394023	2.26	0.0136
Among checks (Entryc)	5	73.05201	14.6104	9.71	<.0001
Among test genotypes	177	533.1531	3.012164	2	0.0012
Error	60	90.27747	1.504624		
Corrected Total	257	747.3929			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

APPENDIX Q16: Analysis of Variance (ANOVA) based on Augmented Design for Tuber skin (periderm) thickness “PT” (mm) in four environments (H18: Hatay-2018; KN18: Konya standard water conditions-2018; KD18: Konya drought-2018; H19: Hatay-2019).

	PT_H18				
Source	DF	SS	MS	F value	P value
Model (checks vs tests vs blocks)	205	0.049815	0.000243	8.02	<.0001
Block	7	0.000833	0.000119	3.93	0.0042
Among checks (Entryc)	5	0.007867	0.001573	51.9	<.0001
Among test genotypes	193	0.041115	0.000213	7.03	<.0001
Error	28	0.000849	3.03E-05		
Corrected Total	233	0.050664			
	PT_KN18				
Model (checks vs tests vs blocks)	190	0.038439	0.000202	6.62	0.0001
Block	4	0.000663	0.000166	5.43	0.0075
Among checks (Entryc)	5	0.004403	0.000881	28.82	<.0001
Among test genotypes	181	0.033373	0.000184	6.03	0.0002
Error	14	0.000428	3.06E-05		
Corrected Total	204	0.038867			
	PT_KD18				
Model (checks vs tests vs blocks)	189	0.190523	0.001008	8.85	0.0003
Block	4	0.002736	0.000684	6	0.01
Among checks (Entryc)	5	0.00391	0.000782	6.86	0.005
Among test genotypes	180	0.183877	0.001022	8.97	0.0003
Error	10	0.001139	0.000114		
Corrected Total	199	0.191662			
	PT_H19				
Model (checks vs tests vs blocks)	197	0.059846	0.000304	10.17	<.0001
Block	15	0.003948	0.000263	8.81	<.0001
Among checks (Entryc)	5	0.013643	0.002729	91.35	<.0001
Among test genotypes	177	0.042255	0.000239	7.99	<.0001
Error	60	0.001792	2.99E-05		
Corrected Total	257	0.061638			

Acronyms: DF: Degree of freedom; SS: Sum of square; MS: Mean square

CURRICULUM VITAE

Muhammad Naeem was born on in Multan, Pakistan. He completed his higher education from Fazaia Degree College MRF PAC Kamra District Attock in 2008. Later, he joined Bahauddin Zakariya University, Multan for his undergraduate studies. He completed his B.Sc. (Hons.) Agriculture with Agronomy as a major subject from the Department of Agronomy, BZU, Multan in 2012. He did his masters in the subject of Agriculture (Agronomy) in 2014 from the Department of Agronomy, University of Agriculture, Faisalabad. He enrolled in Graduate School of Natural and Applied Sciences, Department of Agricultural Genetic Engineering at Niğde Ömer Halisdemir University to pursue his Ph.D. education under the supervision of Prof. Dr. Mehmet Emin ÇALIŞKAN in 2016. During his Ph.D. thesis he worked on the association mapping of quality traits in potato (*Solanum tuberosum* L.). He successfully completed his Ph.D. in February 2021.

PUBLICATIONS PRODUCED DURING THESIS WORK

Naeem, M. and Çalışkan, M.E., “Comparison of methods for dry matter content determination in potato using multi-environments field data and stability statistics”, *Turkish Journal of Field Crops* 25, 197-207, 2020.

International Conferences/Congress

Naeem, M., Yousaf, M.F., Yavuz, C., Yagiz, A.K., Naawe, E.K., Demirel, U., Çalışkan, S. and Çalışkan, M.E., “A comparative method study to measure dry matter content of potato genotypes under different environmental conditions”, In: *International Turkic World Congress on Science and Engineering*, Niğde Omer Halisdemir University, Niğde, Turkey, 17-18 June, 2019.

Caliskan, M.E., Demirel, U., Naeem, M., Bulbul, M.K. and Caliskan, S., “Effects of drought stress on yield and quality of potato genotypes”, In: *Proceedings of First International Biological, Agricultural and Life Science Congress*, Lviv, Ukraine, 7-8 November, 2019.