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

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

MUHAMMAD FARHAN YOUSAF

May 2021

M. F. YOUSAF, 2021

DOCTOR OF PHILOSOPHY THESIS

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Doctoral Thesis

Supervisor

Prof. Dr. Mehmet Emin ÇALIŞKAN

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The study entitled **“ASSOCIATION MAPPING OF UNDERGROUND TRAITS IN POTATO (*Solanum tuberosum* L.)”** and presented by Muhammad Farhan YOUSAF under the supervision of Prof. Dr. Mehmet Emin ÇALIŞKAN 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 ÇALIŞKAN 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. Nejdet KANDEMIR, Tokat Gaziosmanpaşa Ü. Ziraat Fak. Tarla Bitkileri Böl.

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

Member: Ass. Dr. Emre AKSOY 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

As an author I affirm that the thesis is written in the best of my knowledge and belief. All material and information presented as part of this thesis is in accordance with scientific and academic rules. Whatever help I have received in the preparation of the thesis, and the use of all means, has been accredited in the thesis.

MUHAMMAD FARHAN YOUSAF

SUMMARY

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

YOUSAF, Muhammad Farhan
Niğde Ömer Halisdemir University
Graduate School of Natural and Applied Sciences
Department of Agricultural Genetic Engineering

Supervisor : Prof. Dr. Mehmet Emin ÇALIŞKAN

2021, 218 pages

Tuber crops have measurable biological variation in root, stolon and tuber phenotyping, and these variations may be utilized to identify the genomic regions controlling these traits. This is the first comprehensive association mapping study related to potato underground traits. A diverse panel of 192 tetraploid potato (*Solanum tuberosum* L.) genotypes were grown in aeroponics and pots to reveal a biologically significant variation. High-throughput phenotyping was performed for root traits by WinRHIZO, and manual phenotyping was done for stolon and tuber traits, while SolCAP 25K potato array was used for SNP genotyping. Significant variation was observed among the potato genotypes for underground traits along with high heritabilities. For marker-trait associations, Q+K linear mixed model was implemented and 174 novel genomic regions were detected using additive gene action model. Structure and PCA analysis grouped genotypes into four sub-populations disclosing population genetic diversity. LD decay was observed at 2.316 Mbps (r^2=0.29) in the population. The identified SNPs had a putative gene function. The findings of our study will be employed in the future potato breeding programs for the improvements in potato production.

Keywords: Aeroponic, association mapping, pot, potato, SolCAP array, underground traits

ÖZET

PATATESTE (*Solanum tuberosum* L.) TOPRAK ALTI ÖZELLIKLERININ ILIŞKILENDIRME HARITALAMASI

YOUSAF, Muhammad Farhan
Niğde Ömer Halisdemir University
Fen Bilimleri Enstitüsü
Tarımsal Genetik Mühendisliği Anabilim Dali

Danışman :Prof. Dr. Mehmet Emin ÇALIŞKAN

2021, 218 sayfa

Yumru bitkileri, kök, gövde ve yumru fenotiplemesinde ölçülebilir biyolojik varyasyona sahiptir ve bu varyasyonlar, bu özellikleri kontrol eden genomik bölgeleri tanımlamak için kullanılabilir. Bu çalışma, bu konuda yapılan ilk kapsamlı ilişkilendirme haritalaması çalışmasıdır. Biyolojik olarak önemli bir varyasyonu ortaya çıkarmak için genetik varyasyonu yüksek olan 192 tetraploid patates (*Solanum tuberosum* L.) genotipinden oluşan paneldeki bitkiler aeroponik ve saksılarda büyütülmüştür. Kök özellikleri için fenotipleme WinRHIZO programıyla yapılırken stolon ve yumru özellikleri için manuel fenotipleme yapılmıştır. SNP genotiplemesi için SolCAP 25K patates dizisi kullanılmıştır. Kök özellikleri bakımından patates genotipleri arasında yüksek kalıtsallık ile önemli istatistiksel farklılıklar gözlemlenmiştir. Markör-özellik ilişkileri için, Q + K doğrusal karma model uygulanmış ve 174 yeni genomik bölge tespit edilmiştir. STRUCTURE ve PCA analizi, genotipleri dört alt popülasyonda gruplandırırken 2.316 Mbps'de ($r^2 = 0.29$) LD bozunması belirlenmiştir. Tanımlanan SNP'ler varsayılan bir gen fonksiyonlarına sahiptir. Elde edilen bulgular, patates üretimindeki iyileştirmeler için ilerideki patates ıslah programlarında kullanılabilecektir.

Anahtar Sözcükler: Aeroponik, ilişkilendirme haritalama, saksı, solcap dizisi, toprak altı, patates

ACKNOWLEDGEMENTS

Above all, it is **ALLAH Subhanahu wa Ta'ala** who is the Merciful, the Compassionate, and Whose Virtue and Blessings nurtured my thoughts, and strengthened my intentions to promote my modest efforts in the form of this thesis. My humblest tributes to the **HOLY PROPHET HAZRAT MUHAMMAD** (Peace Be upon Him) who is the reason for the creation of the universe and only the perfect human being ever, enlightened our conscience with the essence of faith in Allah Almighty.

Now I want to take some time to pay special thanks to those personalities who travelled with me during this journey. Even though it’s just my name on the cover, but many people contributed by their own way. I sincerely thank and extend my heartfelt commendation to my supervisor, mentor, great researcher and an actual soul of this project, **Prof. Dr. Mehmet Emin ÇALIŞKAN** for his continuous encouragement and giving me a confidence during my PhD studies and research. I am so grateful for their kind support, smart and effective supervision, that helped me significantly in research and writing this thesis as well. Additionally, I also highly thankful to **Assoc. Prof. Dr. Ufuk DEMIREL** who is very humble personality with a great scientific knowledge regarding this field. His valuable suggestions and technical guidance, due to which this research work has found its way to successful completion. I would also like to thank the thesis jury members, **Prof. Dr. Mehmet ARSLAN, Prof. Dr. Nejdet KANDEMIR** and **Ass. Prof. Dr. Emre AKSOY** whose knowledge, worthy comments and scholarly advice were critical to this effort. I am also highly indebted to **Prof. Dr. Sevgi ÇALIŞKAN** for their kind behavior, valuable suggestions and technical guidance. I am immensely grateful to **Ass. Prof. Dr. Allah BAKHSH** who always proved a symbol of kindness and affection for me.

This acknowledgment would not be complete without thanking my Parents, wife, siblings, and cousins who believed in me more than I did in myself. I feel myself helpless in searching proper words to pay back, and in fact no one could ever be able to do the same for their family.

They have been extremely patient through all my highs and lows and provided me great encouragement. They always encouraged my dreams and will always be my strength. Thank you for all the little success I have till now and all that to come in the future is all because of you.

I also want to say thanks to my Pakistani friends. I want to acknowledge Dr. Ali Saeed and Dr. Usman Khalid Chaudhry who was with me to guide and help whenever I needed.

I am highly obliged my research colleagues Dr. Muhammad Naeem, Eric, Arslan Asim, Yahya, Acar, Sani Ibrahim, and Ali Onaran, 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, Nigde Omer Halisdemir University for their gentle support.

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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
GWASpoly	Genome Wide Association Studies in Autopolyploids (R package)

CHAPTER I

INTRODUCTION

The potato crop (*Solanum tuberosum* L.) is of great economic value, and it stands as the 3rd largest food crop around the world after wheat and rice (FAOSTAT, 2020). It is grown in many countries throughout Asia, Australia, Africa, Europe, North, and South America except Antarctica (USDA-ARS 2014). Potato cultivation mainly began with the domestication of a single *Solanum bukasovii* in the southern part of Peru (Spooner et al., 2005). Initially, it was cultivated as an ornamental plant in gardens due to its splendid flowers in Europe but by the end of 1577, it was cultivated as a food crop. (Oliemans, 1988). According to FAOSTAT (2020), the total area and production worldwide were estimated at 19,302,642 ha and 388,190,674 tonnes, respectively. Potato contributes significantly to the economy of the Turkey and many other countries as well (Caliskan et al., 2010). It contributes about 3.1% in Turkey's Gross National Agricultural Production and about 3% in 27 countries of Europe. In Turkey, it is grown on an area of 143,000 ha with a total production of 4.8 Mt (million tonnes) in 2019-20 (TUİK 2020). 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. Likewise, in Pakistan, it is cultivated on an area of 193,992 ha with an annual production of 4.59 Mt (million tonnes) (FAOSTAT, 2020).

At the start, potato was considered as a food for poor people (Oliemans, 1988), but later it gained a significant value in human diets around the globe. The underground part of the potato, namely the tuber is highly nutritious (Çalışkan et al., 2010) and contains carbohydrates (75%), vitamins (B6-29%, B1-16%, and folate-16%). It also provides minerals such as Fe, Mg, and K. It is a rich source of antioxidants such as polyphenols, ascorbic acid, carotenoids, tocopherols, and flavonoids It also contains reducing sugars i.e., monosaccharides (glucose and fructose) and non-reducing disaccharide i.e., sucrose (Lachman and Hamouz, 2005; Bors and Saran, 1987). The protein content in potato ranges from 1.7 to 2.1 g per 100 g (Lutaladio and Castaldi, 2009). Besides its nutritional value, it also provides income and employment to the peoples as a cash crop (Scott et al., 2000).

Although the importance of the upper-ground parts of the plants cannot be ignored, in tuber crops such as potato, the underground traits (i.e., tubers, roots, and stolons) are of great importance. Roots participate in the absorption of nutrient ions and water from the soil, attach the plants to the soil, and interact with beneficial organisms as well as pathogenic in the rhizosphere (Paez-Garcia et al., 2015). They are also involved in the synthesis, storage, and reproduction of growth-regulators (Bradeen et al., 2011). The potato root system is considered as adventitious and is classified as basal roots (i.e., stem origin) or stolon roots (i.e., underground stems) (Khan et al., 2016). Preceding studies showed that the root-system not only a significantly important in the development of the plant but as well improves the absorption capacity of nutrients and water, which offers greater tolerance against different abiotic and biotic stress factors (Fita et al, 2006). The plants having large root soil interfaces (i.e., longer roots with more surface-area) are considered to be efficient at capturing certain resources as compared with shorter surface areas. Mostly the commercial potatoes have shallow root architecture, that reduces the ability to infiltrate in the compacted soils, (Porter et al. 1999, Gregory and Symonds, 1992) and poor utilization of phosphorus (P) and nitrogen (N). Zeberth et al., 2004; Hammond and White, 2011). According to one estimate, potato roots retrieve <70% broadcast nitrogen and <10% broadcast phosphorous fertilizers (White and Chaubey, 2005). It requires regular supply of a disproportionate amount of irrigation (Levy et al., 2013), P (Bélanger et al., 2001) phosphorous and nitrogen to maintain the production and quality of tubers (Porter et al., 1999; Tolessa et al., 2009). Therefore, a larger and deeper root system helps to improve the nutrient and water use efficiency which ultimately increases crop yields (White and Chaubey, 2005). In addition to the root system, another under-ground trait of economic value are stolons that play an important role in the storage of carbohydrates necessary for the plant to survive under different biotic and abiotic stress conditions (Schiavon et al., 2016). Tuber is usually a swollen form of stolon (Ewing and Wareing, 1978). Potato stolons are the lateral shoots from the most basal nodes usually at the under-ground level. The formation of tubers on stolons has an indeterminate nature with simultaneous development of stolons and tubers. After the swelling of stolons, it undergoes different stages such as tuber formation, tuber growth, and tuber maturation. Stolon development and formation may be considered as fingerprint of specific variety due to presence of biological variation and thus needs careful assessment under managed systems.

The morphological characteristics of the potato tuber, i.e., the regularity of the shape, size, and weight of the tuber are considered important in the breeding, processing industry, and also in the fresh market. Previous studies on the inheritance of the tuber trait have shown conflicting results. While some suggest that this is a monogenic feature (Okwuagwu, 1982; Taylor, 1978; van Eck et al., 1994; Masson, 1985), and some studies have identified many loci on various chromosomes responsible for the variation of this trait (Sørensen, 2006; Śliwka et al., 2008; Prashar et al., 2014; Björn et al., 2014).

Potato is considered to be one of the most passionately stable crops in the world to reduce human hunger and poverty, and sustainable production practices and techniques for food security and social stability are needed in the future. The climate change scenario calls for higher crop yields to cope with the population explosion. There are now 7.25 billion people exist on the planet and this number is expected to increase to 9.2 billion by 2050. To tackle the drastic increase in population and hunger, potato breeders are working effectively to increase the production to tackle the scenario ahead. Traditionally, breeding programs have focused on the aerial parts of the plant for food and fibre production. However, in tuber crops such as potato, breeding efforts should focus on the under-ground characteristics of the potato, as these traits allow a plant to use water and nutrients more efficiently in different environments and ultimately increase the yield of the crop. These characteristics (i.e., tubers, roots, and stolons) are not easily observed due to their underground existence, making this ideotype difficult to choose. Strategies require for the identification of plants that have excellent underground characteristics which make a plant more efficient in different environments. Under field conditions, these traits can be greatly affected by uncontrolled environmental factors, and traits can change due to a lack of uniformity in the environment (Eshel and Waisel, 2012). Many studies studied the relationship between these traits and crop productivity under fluctuating environments. The selection of the trait of interest by utilizing markers that are tightly linked to the genes, controlling these traits is one of the ways. Efficient phenotyping protocols are required to find robust markers (Trachsel et al., 2013). However, the lack of effective and accurate phenotyping of large mapping populations has been a major obstacle to the widespread use of root-related genetic information in breeding programs (De Dorlodot et al., 2007; Chen et al., 2011a). Presently, several new methods have been developed for better assessment of under-ground traits in a field, like “Shovelomics.” However, some obstacles remain such as the long data collection time, the high cost of non-invasive imaging, and limited detailed data of the underground traits (de Dorlodot et al., 2007; Smith and Smet, 2012; Trachsel et al., 2011). Furthermore, roots and stolons are very sensitive and prone to damage during excavating from the soil. For this scenario it is necessary to use a fast, capable and user-friendly system for estimating of underground features. As an alternative to field studies, several indoor growing systems have been developed that allows a low-cost, rapid, and reliable analysis of these traits. In the controlled environment, various non-destructive and destructive approaches of the subterranean portion of the plant are available. By destructive sampling, removal the entire root system from containers filled with soil for example, “pots” were used in phenotyping studies (Chen et al., 2015). This method offers an environment for crop growth that may somewhat mimic that in the field. In recent years, non-destructive approaches have been developed for phenotypic modelling of under-ground characteristics such as “aeroponics” (Chen et al., 2015). It increases the availability and high-throughput phenotyping of these critical under-ground characteristics in potato. Aeroponics is a soil-less growing system in which the under-ground portion is kept in a dark environment in which aerosol nutrients are dissolved (Christie and Nichols, 2003). The roots can be grown under optimal conditions and appear to be disease or pest free. Additionally, it reduces sampling errors (Eshel and Waisel, 2012). Aeroponic and pot experiments provides a relatively sophisticated platform for studying underground features as an alternative to the field. After that, an efficient imaging technique is required to achieve the best phenotyping results. These imaging techniques includes Neutron radiography (Oswald et al., 2008), Stereoscopy (Wulfsohn et al., 1999), Ground-penetrating radar (Stover et al., 2007), X-ray computed tomography (CT), and Magnetic resonance imaging (MRI) (Rascher et al., 2011). New imaging approach such as X-ray CT-based offers good images with a ‘deep-phenotyping’ to the plant breeders (Mooney et al., 2012; Flavel et al., 2012). For the investigation of images from imaging techniques, more than thirty different software tools are available, (e.g., RootScan, DART, RootNav, GiARoots, RootReade, RootSystemAnalyzer, RootReader3D, RooTracker, Root View, MR-RIPL, WinRhizoTRON, IJ_Rhizo, and ImageJ, etc.) (French et al., 2009). Among them, WinRHIZO is the most flexible and reliable program to perform many specialized tasks (Pierret et al., 2013). Combined with recent developments in structure-function simulation modellings, these advanced approaches will increase understanding of the association between root structure, function, complexity, and its interaction with soil, leading to improved crop production and yield.

Potato is a highly heterozygous and tetraploid crop. Generation of a new variety with desirable characteristics can take eight to ten years in the classical breeding approach (Flavel et al., 2012). Phenotypic variations in the under-ground traits (tubers, roots, and stolons) are influenced by many factors such as QTLs, genotypes and growing cultures. The presence of natural changes in the DNA sequences among the individuals results in the development of molecular marker techniques (Gebhardt, 2004). These molecular markers are used for the visualization of the variations in DNA sequence among the individuals. Some of these molecular markers are restriction enzyme-based and some are PCR based. Recent advances in next-generation sequencing (NGS) are enabling the rapid development of genome-wide markers (SNPs) that allow exploring the relationship, with the resolution previously unattainable between genetic and phenotypic diversity. Therefore, a new generation breeding approach like Association mapping (AM) is required for potato breeding aiming to improve underground characteristics. The discovery of new SNP markers related to underground features in potatoes through AM has the potential not only to reduce the breeding cycle to four to six years but also to increase tuber yield (Spindel et al., 2015). AM helps to identify specific functional variants (i.e., alleles) associated with phenotypic differences in a trait (Oraguzie and Wilcox, 2007). It is also recognized as Linkage disequilibrium mapping. AM has advantages over QTL mapping, as more variations can be observed in AM as there is no need to develop a segregating population and generally, the mapping resolution is better or higher as compared with the populations obtained from controlled biparental crosses (Gupta et al., 2005; Myles et al., 2009); SNP variants of potato varieties with biological variations of underground can be identified in diverse populations using the NGS platform combined with AM for QTL identification.

Several research articles have been published on AM in different crops such as wheat (Breseghello and Sorrells, 2006), Arabidopsis thaliana (Hagenblad and Nordborg, 2002), sugarbeet (Kraft et al., 2000), barley (Kraakman et al., 2006), sugarcane (Jannoo et al., 1999), and soybean (Zhu et al., 2003). In potato crop many different studies related to AM have already been conducted (Simko et al., 2004; Li et al., 2005; Malosetti et al., 2007 and Gebhardt et al., 2004; Zia et al., 2020). Although the architecture of the root system is complex and controlled by several genes of minor effects (Dorlodot et al., 2007), there is an evidence of stable differences among cultivars, breeding lines and wild relatives (Iwama, 2008; Bradshaw et al. 2006). These traits are polygenic, so association mapping based on SNP markers is a powerful tool to dissect these complex traits and to identify novel markers and QTLs to select the genotype of interest with the desired traits and ultimately aids in marker-assisted selection (MAS).

The response of root growth and development under different growing conditions provides different results and opportunities to explore natural diversity and identify beneficial root traits to increase plant productivity in agricultural systems (Paez-García et al., 2015). Comparison of the performance of these subterranean traits across different cultural systems can better understand the genetic basis of these traits and ultimately establish stable SNPs for future map-based cloning and markers assisted selection.

So far, very little or limited work has been done to study the links between the underground characteristics of potatoes. However, to our knowledge, there is no study to discover genomic regions associated with underground traits of the potato. The current study hypothesized that tuber crops have measurable biological variation in root, stolon and tuber phenotyping and thus may be utilized to identify genomic regions associated with these variations. A diverse panel of 192 tetraploid potato (*Solanum tuberosum* L.) genotypes were grown in aeroponics and pots with the objectives of revealing the biologically significant variation and detecting the genomic regions linked with the root, stolon and tuber traits by association mapping.

CHAPTER II

REVIEW OF LITERATURE

2.1 Importance of Potato

According to FAOSTAT, 2020; Grossi et. al., (2020) the potato (*Solanum tuberosum* L.) crop ranked at 3rd position in terms of production (17.34 million ha) among food crop in the world, followed by wheat (*Triticum aesitvum* L. and *T. durum*) and rice (*Oryza sativa* L.). Because of his great economic worth, it is grown in many countries throughout Europe, Africa, Australia, Asia, North and South America, except Antarctica (USDA-ARS 2014; FAOSTAT, 2020; Rowe and Powelson, 2002). Potatoes are considered as a staple crop that has the potential to alleviate human hunger and poverty in the world. Many nutrients are present in potato that are essential for the human diet such as vitamins (16%, 29%, B1, and B6 respectively), 75% carbohydrates, 16% folate, iron (Fe), potassium (K) and magnesium (mg) as well (Çalışkan et al., 2010). Moreover, a good quantity of antioxidants like ascorbic acid (8 to 54mg/100g), polyphenols (123 to 140mg/100g), carotenoids (up to 0.4mg/100g), flavonoids and tocopherols (up to 0.3 mg/100g) are also in potato (Bors and Saran, 1987; Lachman and Hamouz, 2005). Reducing sugars such as monosaccharide (glucose 0.15 to 1.5% and fructose 0.15 to 1.5%), non-reducing sugar like disaccharide (sucrose 0.4 to 6.6%) and protein content 1.7-2.1g/100g available in potato (Lutaladio and Castaldi, 2009). In addition to its nutritional values, it also provides employment and income to the peoples as a cash crop (Scott et al., 2000). Tuber shape is very important for processing industry and it attracts the fresh market as well. It can be utilized for many industrial purposes such as the production of glucose, starch, dextrin, and alcohol. Many textile factories used potato starch (i.e., farina) and it also used in laundry purposes.

2.2 Origin and Domestication of Potato

Potato cultivation began primarily in the southern region of Peru by the domestication of single *Solanum bukasovii* (Spooner et al., 2005). The domestication of potato was started between 8000 and 5000 BC (Haris and Hillman, 2014). It was authenticated by the earliest archaeological that the potato tuber was found in central Peru (the coastal site of Ancon) date from 2500-BC (Harris and hillman, 2014; Martins-Farias, 1976). The most cultivated potato specie of Chiloe Archipelago peoples were (*Solanum tuberosum*) before Spanish conquest, because it was an indigenous cultivar of the native peoples (Miller, 2008; Solano et al., 2007). As per normal estimation, the potato was accountable for 1/4 of the world population growth and urbanization during 17's and 19's (Nunn and Qian, 2011). In the Altiplano region, the potato was the main source of energy for the Inca nation and the pre- and post -Spanish settlers. The potato was shifted from Inca empire to Europe in the 2nd half of the 16th century by the Colombian stock exchange program subsequently the Spanish conquest. Afterward, it was transported from European Marines to other territories and ports all over the world. Beginning times, it was cultivated as a decorative or an ornamental plant due to having good-looking flowers. Gradually, the European farmers started to adopt and it was considered a food just for only the deprived peoples (Oliemans, 1988) but finally in the nineteenth century, it became an important food which gained a significant value in the diet of the whole world, and currently they are cultivating from 65N - 50S latitude and altitudes ranging from the sea level to 4000 meters (Hijmans, 2001). Adaptation of potato varies in the tropical and subtropical summers; long summer days in the temperate regions and to the short winter days in the subtropical lowlands and subtropical. Potato can also be grown in the areas that are neither too cold and nor too hot, but plenty of water available either by irrigation or rain.

2.3 Potato Breeding and Genetics

As early as 1850, the selection was made based on seedlings. Seedlings are often grown from berries, that is come after the pollination between two crossing parents. The fundamental characteristics that were most talked during this period were the day length adapted to the crop, yield, size and shape of the tuber. Over time and in the 19th century, the introduction of well documented germplasm to expand the gene-pool from Latin American was wiped out due to the rise of *Phytophthora infestans* (late blight disease). "Rough Purple Chili" is an example representing the ancestry of the potato in both US and Europe (EU), which has a notable variety list in their pedigree (van Berloo et al., 2007; Plaisted and Hoopes, 1989; Glendinning, 1983). Ortiz (1998) disclosed that Rough Purple Chili was from the US gene pool obtained from the open-pollinated seedling variety known as Garnet chili. It was later revealed that Garnet Chili was the parent of Early Rose, along with the descendants of Russet Burbank, and is among the cultivars grown only in the USA. After 1850, most breeders were started to cross the potato cultivars. Increasing the resistance to pathogens in potatoes with the aid of frequent back-crossings in the germplasm of wild species took place in the twentieth (20^{th}) century. Although present day potato varieties generally belong to wild-relatives and older ancestors, just because of the selection of about 80% of the genes that they had are the outcome of a very few number of cultivars that were being cultivated early in 20th century (Glendinning, 1983).

Due to their narrow genetic basis and the absence of sexual generations in the beginning most up-to-date commercial potato genotypes are highly inter-connected, (Love, 1999). Moreover, the rate of recombination is limited to atleast one crossover per chromosome, saving 50% of all available chromatids that are not recombined (Van Os et al., 2006). Therefore, it is normal for the LD (linkage disequilibrium) to be stretched more in the potato-genome compared to other outbreeding-crops such as corn. This means that fine mapping may seem like the best for potatoes where mapping resolution can be increased by utilizing the genetically diverse population as compared with the full-sib-category mapping population used in quantitative trait loci (QTL) research.

Traditional potato breeding is tough due to tetra ploidy nature of the cultivated potato with tetrasomic inheritance and it encompasses highly heterozygous individuals that suffer inbreeding depression upon selfing (Bradshaw, 2006; Bradshaw and Mackay, 1994). By introducing modern techniques such as embryo rescue and protoplast fusion it has become possible to obtain desirable results (Bradshaw and Mackay, 1994; Ortiz, 1998). It is very difficult to obtain a homozygous potato genotype mainly due to the immense inbreeding depression, which leads to loss of vigor and fertility, and many attempts to make the potato truly homozygous through consecutive self-fertilization were unsuccessful (Douches et al., 1996). Effectively implemented method is a “mutation breeding” in ornamental plants that propagate asexually, and consequently, it is doubtful that it is a direct substitute for common practices in potato breeding, since mutations will be disguised by the action of other alleles in tetratomic inheritance, although there are some cases of success that have been reported in terms of yield, resistance to late-blight and starch properties (Kowalski and Cassells, 1999; Muth et al., 2008; Jacobsen et al., 1989). With the advent of linkage maps and molecular markers, MAS (marker assisted selection) has become a useful driver for breeding programs for plants and animals. Undoubtedly, the marker-assisted selection is beneficial for potato breeding.

2.4 Potato Genome and Molecular Mapping

After the rediscovery of Mendel's law, the researchers have been started to determine the pattern of inheritance of agronomic traits, and Potato was the first plant species to be studied in this regard. Over the next 60 years, potato genetic analysis was mainly limited to a single dominant trait (Cockerham, 1970). The morphological features were used to develop the classical linkage maps, but due to tetraploidy and tetrasomic inheritance in potato makes these maps not practical, as well as make the linkage detection difficult and prevents the recovery of recessive phenotypes (Rick and Fobes, 1975). Over the past 15 years two technical advancements helped in the development of detailed genetic mapping in potatoes (a) Reduction in the ploidy such as tetra-ploid to diploid and (b) Introduction of the DNA markers. Diploid plants can be obtained from *2n* gametes or by pollinating the certain genotypes of *Solanum phureja* with tetraploid plants. These are highly heterozygous and self-incompatible. Progenies belongs to the diploid potato shows same phenomenon of linkage analysis as in human genetics. Parents of heterozygous nature have the ability to produce segregating F1 progeny that permit the construction of linkage maps in F1 generation on the basis of female and male parent recombination's (Reuters et al., 1990).

Natural DNA variations have led to DNA-based markers in populations of the same species. Molecular-based variations include, insertion or deletion (InDels), point mutation like single nucleotide polymorphisms (SNPs) and DNA fragment inversions. In contrast to these induced mutations that have a devastating effect on phenotypes, since evolutionary times these DNA polymorphisms have existed and have not impaired the viability and competitiveness of the individual carrying them. Around in last 23 years, several tools have been developed by molecular genetics to unfold the natural variations of DNA or genetic mutations, that was initiated by Botstein et al., (1980), with the introduction of Restriction Fragment Length Polymorphism (RFLP) that works on the basis of hybridization and then ending with single nucleotide polymorphism (SNP) a PCR based technique to detect SNPs by using competitive allele sequencing (Reiter, 2001 review)

A linkage map was developed by the aid of DNA based molecular markers using a backcross population of 67 diploid potato plants (Jacobs et al., 1995). The parents who cross for the development of mapping populations mostly included *Solanum tuberosum* and other closely related species that are easy to cross with *Solanum*. Linkage map has been constructed by the use of AFLP markers, covering forty-eight tetraploid potato linkage groups. Genetic and molecular mapping coupled with DNA-markers are the backbone in potato genetic analysis (Vos et al., 1995; Meyer et al., 1998) needs to remove

2.5 Molecular Markers Evolution.

Molecular markers have been developed during the last two to three decades when sequencing of DNA was tough or just about to impossible. These markers helped to find the variations present among the diverse population.

2.5.1 Allozymes

Allozyme was the first molecular marker. It works on the basis of protein variants present in enzymes that can be recognised by gel-electrophoresis. This marker was initially used in humans and drosophila (flies). The number of loci that detected by allozymes used for further mapping studies was very small (Hillis et al., 1996). In addition, the neutral evolution of some markers has often been challenged (Berry and Krietman, 1993; Krieger and Ross, 2002). Allozymes indirectly detect differences in DNA and this is a very strict method. DNA-based markers have a benefit over allozymes. This allows them to calculate the number of mutations between different alleles.

2.5.2 DNA-based markers

2.5.2.1 RFLP - Restriction fragment length polymorphism

The pioneering DNA marker “Restriction fragment length polymorphism (RFLP)” was discovered in the 1960s by utilizing the restricted enzymes at the recognition sites to identify the differences in the DNA sequences. By the aid of RFLP markers the first DNA based genetic map was constructed (Kerem et al., 1989). It requires the appropriate hybridization probe to find the polymorphism and the need for huge amount of good quality DNA that is the obstacle and leads to prevent further exploitation. Barone et al., (1990) used RFLP markers for the linkage map against numerous pathotypes of the root cyst nematode *Globodera rostochiensis* in potato.

2.5.2.2 Minisatellites

Digestion of genomic DNA is the pre-requisite for minisatellite analysis. These consist of tandem-repeats (Jeffreys et al., 1999). Minisatellites were used very rarely for mapping purposes due to their non-random distribution throughout the genome. Despite of their high polymorphism and the success of forensic and paternity testing, Minisatellites were not widely used in genetic mapping and population genetics due to their complex banding patterns and non-random distributions Single-locus mini-satellite were later developed, but they were technically difficult (Armour et al., 1990).

2.5.3 PCR-based molecular markers

Currently several studies depend on PCR based markers. PCR machine/Thermal cycle invention in the area of molecular genetics, allows us to amplify any genomic region and analyse without the condition of cloning or isolating a large amount of ultra-pure DNA.

2.5.3.1 Microsatellites

Since the invention of the PCR machine, simple sequence repeats (SSR) or microsatellite was beginning in the year 1989 (Weber and May, 1989; Tautz, 1989; Litt and Luty, 1989). They are similar to minisatellites but their repeat sequence is shorter than minisatellites. They are 1-6 base pairs repeats and mostly present in nuclear and organelle DNA (Cregan and Quigley, 1997). These are co-dominant and highly polymorphic markers, and they are evenly distributed all over the genome. These characteristics make it the most popular genetic marker for mapping studies, Bell and Ecker (1994) used these markers in *Arabidopsis thaliana* and soybean. Hereafter, these were used in several genetic studies, such as association mapping (AM), genetic mapping, comparative mapping, and quantitative trait loci (QTL) mapping and functional genetics (Varshney et al., 2005). Despite their advantages, of reproducibility and codominance, they have some disadvantages, such as complex mutation patterns, which makes complications for population genetics analyses. Moreover, some glitches such as the PCR (stutter band) artifact complicate automated microsatellite allele scoring. The density of the informative microsatellite loci might be too low for some mapping applications in the eukaryotic genome despite the high number of microsatellite loci (Tóth et al., 2000; Dieringer and Schlötterer, 2003). Provan et al., (1996) and Kawchuk et al., (1996) were the first time to formulate the microsatellites in potato. Milbourne et al., (1998) formulated 112 pairs of SSR primers with a small set of 6 potato clones that showed polymorphically. An experiment was carried out at the International Potato Center (CIP) Peru, where they tested 70 already known SSR loci in a samples of potato cultivars that came from 9 taxonomic groups (Ghislain et al., 1999). Later, 61 ESTs emerged as SSRs along with about 100 already present SSRs that were designed for potato (Feingold et al., 2005). SSR mapping is readily available in diploid species; However, they do not yet understand in tetraploid species (Landergott et al., 2006; Esselink et al., 2004).

2.5.3.2 AFLP - Amplified Fragment Length Polymorphism.

This technique was invented by Vos et al., (1995) based on the PCR reaction. In this technique, cleaved genomic DNA is used without any prior-sequence information as a template and resulting multi-locus DNA markers are generated (Saiki et al., 1988).

2.5.3.3 SNPs - Single nucleotide polymorphism

The markers discussed till date, need some tactics to detect the variations in the genome. Advances in the field of genomics or marker studies have led to an effective and efficient way to find point mutations, which includes a sequence of amplicons obtained from the same primer pair from DNA templates of different diploid and tetraploid potato genotypes. In tetraploid-potato genotypes, a high-quality trace file can allow estimation of allele dosage based on the proportion of 2 nucleotide peaks migrating together. Trace files can also help to find the Insertion/deletion polymorphisms. The comparative sequencing of seventy-eight amplicons was used to explore the frequency of SNPs and indels in potato genome. This sequencing technique was initially used by Rickert et al., (2003) in a panel of 11 diploids and 17 tetraploid potato genotypes and unfold that SNP every 21 base pairs and indel every 243 base pairs shows a variation of the natural DNA sequence present in potato (Gebhardt et al., 1998). SNPs scoring can be done by many techniques, such as SNuPE (single-nucleotide primer extension) or pyrosequencing (Rickert et al., 2002). In the future, new technologies such as array technology will be available for parallel scoring of many SNPs on a single chip (Rasheed et al., 2017). Studies concluded that the SNPs are the best marker choice for comprehensive population genetics studies, linkage disequilibrium studies, and also for breeding applications. Agronomic traits/characteristics linked to SNPs can be converted into easy-to-use allele specific PCR assays (Sattarzadeh et al., 2006; Niewöhner et al., 1995).

2.6 QTL Mapping and Potato

A QTL is a part of a DNA that deals with a variation in the phenotype of an organism population, to find that specific region or part that involves in the mutation or variation is known as QTL mapping by the aid of molecular markers (Paterson et al., 1988). This technique necessitates mapping populations such as RILs (Recombinant inbred lines), F2 generation, Backcross and DH (Double haploids) (Kearsey and Farquhar, 1998; Kearsey, 1998; Collard et al., 2005). According to statistical point of view it considered better to use of diploid population of potato for QTL mapping. Several QTL studies have been performed successfully in diploid species to find the loci responsible for different biotic stress resistance such as (insect, disease, nematode and thrips resistance) Bonierbale et al., 1994; Visker et al., 2003; Bradshaw et al., 2006; Costanzo et al., 2005; Collins et al., 1999; Park et al., 2005; Leonards-Schippers et al., 1994; Trognitz et al., 2002; Rouppe van der Voort et al., 1998, 2000; Bryan et al., 2002; Kreike et al., 1993; Galvez et al., 2005). Many studies also indicated that the different QTLs have been discovered related to morphological/agronomic and quality characteristics in potato such as tuber shape (Sliwka et al., 2008; Van Eck et al., 1994a,b), aging (Malosetti et al., 2006), specific gravity, dormancy of crop (Freyer and douches, 1994; Ewing et al., 2004; Freyer et al., 1994), chlorosis (Simko et al., 2008), tuberization of specific crop cultivar (Fernandez-Del-Carmen et al., 2007), chip colour (Douches and Freyer, 1994), enzymatic activities causes discoloration (Werij et al., 2007), glycoalkaloid contents (Sorenson et al., 2008; Yencho et al., 1998), starch contents and yield (Schafer-Pregl et al., 1998).

Few researchers have used tetraploid mapping populations for QTL analysis. Tetraploid mapping population (i.e., 12601ab1 x Stirling) was grown at the Institute of Scottish Crop

Research. According to some reports, the use of a tetraploid mapping population for mapping studies showed limited linkages with the trait's that are based on major QTL or either on a single gene. In addition to all this QTL studies have some disadvantages like low-resolution, need of preparing mapping population, and detection of limited genetic diversity due to segregating population.

2.7 Potato SNP Platform (Introduction to Infinium SolCAP SNP array)

In potato, SolCAP - array has been established in the near past (Felcher et al., 2012). The introduction of this array makes SNP genotyping more efficient and cheaper in potato germplasm and further led to the identification of 69,011 highly reliable SNPs (Hamilton et al., 2011). Additionally, Vos et al., (2015) developed a 20K Infinium SNP array which facilitated the understanding of the history of potato breeding. In the development of the SolCAP SNP array, a sequence of five North American potato cultivars (Premier Russet, Kennebec, Atlantic, Shepody, and Snowden) and one European variety (Bintje) was used (Hamilton et al., 2011). Population structure (Q) can be analysed by using SNP-genotyping platforms (i.e., Illumina) with the utilization of various available random SNP markers. The information from "Q" and historical recombination can be used efficiently in association mapping studies while finding the relationship between marker and trait (Ortiz, 2020). The first application of SolCAP SNP array, was implemented as a pilot study to determine the population structure and linkage disequilibrium on European potato germplasm consisting of thirty-six different tetraploid potato cultivars and 8 diploid clones (Stich et al., 2013), The customized array is used for the analysis of large amounts of SNPs per genotype (Hamilton et al., 2011). The marker loci for the array were designed in such a way that 36% of the markers are in candidate gene of interest and 6% are from the previously marked markers. An additional number of markers that count 57% in the coding region were selected so that maximum coverage to the potato genome can be given (Felcher et al., 2012). In 2012, Felcher et al. elaborated on the design of the array as well as explained the incorporation of two linkage maps of diploid species with the potato genome sequence. Also, with SolCAP SNP potato array tetraploid bi-parental mapping population was genotyped (Hackett et al., 2013).

2.8 Association Mapping; A Technique

Recent advances in DNA sequencing make genotypic data acquisition cheap and consistent. Many ways are there to recognize the plant species consisting of large root length as well as surface area. The relationship of root morphology with DNA sequence information permits the identification of the genetic regions that shape up root characteristics, e.g., Quantitative trait loci (QTL) analysis or association mapping (AM) approach. As potato root traits are polygenic in nature and controlled by minor genes so AM considers a best tool to dissect these traits with high resolution (de Dorlodot et al., 2007; Cai et al., 2012). Basically, occurrence of distinction among the genotypes serves as the genetic material for association mapping studies. With the robust statistical analysis approaches in research programs, association mapping is one of the attractive and inexpensive techniques to discover the variations. By the examination of marker trait associations among the diversified genotype collection it identifies quantitative trait loci on the chromosomes. Since its start in plant species its importance has enormously increased. Very promising results were achieved in human beings with association mapping approach and also found some novel loci that were never thought to be achieved before (The Wellcome Trust Case Control Consortium, 2007). Same method is now being implemented in plant species. Association mapping gives more functional variation in a broader germplasm context at relatively low cost as compared with previous linkages mapping studies in plants. Phenotypic variations in the plants are influenced by QTLs, environment, interaction among each other as well as with environment. To deal with such kind of complex traits two approaches namely linkage analysis and association mapping is used. These two approaches are mostly influenced by co-inheritance of functional DNA variations. To study the marker trait association, linkage analysis approach by utilizing F2 mapping population provides low resolution as compared to association mapping due to less chance of recombination among the family that is restricted to 10-20 cM interval. There are hundreds of linkage analysis that have been performed by different scientists (Holland, 2007; Kearsey & Farquhar, 1998), but regardless of many studies only a restricted number of identified QTLs have been cloned till date (Price, 2006).

Association mapping offers three major advantages over linkage analysis, which include (i) Unlimited mapping population (ii) increased number of alleles found (iii) detection time is shortened (Yu and Buckler, 2006). Due to high-throughput genomic technologies, development in statistical methods, and identification of elite novel alleles AM has gained more favour in genetic research since its introduction to plants (Thornsberry et al., 2001). As per the aim of study, Association mapping is divided into two major classes (i) Candidate gene approach, uses the selected genes that control phenotypic variation among specific traits under study. Information of the genes involved in the regulation and biochemical pathways are mainly required. Candidate gene sequences for several complex traits are now available for further association analysis and fortunately, the presence of annotated genome sequences from several model species and different genomic technologies that include gene expression profiling, genotyping, sequencing, comparative genomics, linkage analysis, bioinformatics, mutagenesis, and biochemistry are almost the complete (ii) Genome-wide association studies also termed as genome scan, have the capability to scan the entire genome, as well as the variations among the complex traits are also detected (Risch and Merikangas, 1996).

Association mapping allows for analysing marker-trait associations. D’hoop et al., 2008 used AM for the first time, but the number of markers he used was low. Another example of AM with low genotypic panel came from Uitdewilligen et al., 2013. Association mapping is quite approachable as well as covers a large number of SNPs as compared with the candidate gene approach. Many researchers are moving towards this approach due to the analysis of complex traits. *Arabidopsis* HapMap, for an example have provided an enormous number of genetic markers of around 1 million SNPs (i.e., on average one SNP after every 166 bp) (Clark et al., 2007), this is the proportion almost 11 times higher than human population (Hinds et al., 2005). It was found to be very difficult to perform linkage analysis with few hundred molecular markers and the cost of genotyping.

Then at this point, a question arose that many researchers are facing: "How one can benefit and take advantage from these high throughput genomic techniques??? Association mapping with the ultimate goal of connecting functional polymorphism to the complex traits respond in a decent manner to the emerging new technologies. To find out the variations of complex traits to single genes or individual nucleotides natural diversity is exploited through association mapping. On the other hand, traditional linkage approaches use bi-parental populations from the same or genetically related populations. To modify traits and germplasm scrutiny, breeding lines, landraces as well as the samples from the natural population display inordinate possibility and also possess a massive capacity to map QTLs.

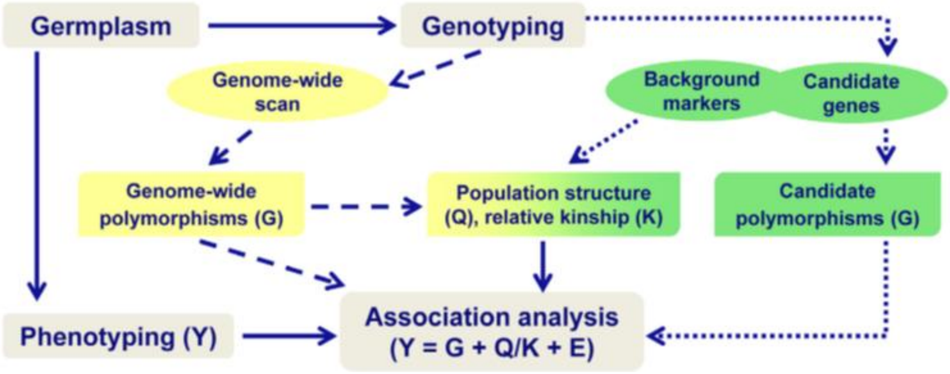


Figure 2.1. Figure illustrating candidate gene approach and genome-wide association mapping (GWAS). The presence of Q (population structure), K (relative kinship), or both in association analysis depends on the genetic linkage of the association mapping panel and the deviation of the trait under study. While E stands for the residual variance

2.9 Development of Methodology in Association Mapping

Traditional linkage analysis contains (a) analysis of single marker, (b) Interlude mapping or Interval mapping, (c) mapping on multiple-interval, and (d) Bayesian interval mapping. All these kind of conservative mapping approaches are well established and authenticated as well (Doerge, 2002; Zeng, 2005). Association mapping requires less struggle to develop a robust method as compared to the linkage mapping. The only drawback of association mapping is the detection of false positives among the population however they can be handled properly to get rid of these (Zhao et al., 2007). therefore, it is difficult to reproduce to get some substantial results in independent sort of studies. Both the population structure and family relationship are exploited during association mapping studies (Yu and Buckler, 2006). For instance, potato genotypes being grown now a days are truly a group of the individuals that are related with each other (Gebhardt et al., 2005). Several statistical methods have been anticipated to comprehend the population structure and the family relationship, and that include mixed model approach (Yu et al., 2006), structured association (SA) (Falush et al., 2003; Pritchard and Rosenberg, 1999; Pritchard et al., 2000a), principal components analysis (Price et al., 2006) and genomic control (GC) (Devlin and Roeder, 1999). All these approaches use genotypic information of molecular markers throughout the genome to find out familial relatedness and population structure among mapping population. There is a possibility of sleuthing a significant association based on genetic relationship among the genotypes under study however marker cannot always be associated with QTL (Pritchard et al., 2000). Based on genetic markers there are several ways to detect population structure in potato crop. Principal coordinate analysis (PCoA) and principal component analysis (PCA) have emerged from factor analysis approach (Urbany et al., 2011; D'hoop et al., 2010; Pajerowska-Mukhtar et al., 2009), in which after the knowhow of genotyping molecular data is analysed. By putting molecular data in “Structure” software, it is accessed through Bayesian clustering approach (Pritchard et al., 2000). AMOVA (Analysis of Molecular Variance) as well as Hierarchical clustering can also be practiced to retrieve the population structure. (D’hoop et al., 2010). Many studies in potato have been reported by using these techniques (Pajerowska-Mukhtar et al., 2009; Simko et al., 2006; Simko, 2004; D’hoop et al., 2010; Li et al., 2008).

2.10 Recent Scenario About Association Mapping (AM)

Till date several researchers have focused and worked on association mapping. Several crops including soybean (*Glycine max* (L.) Merr.), tomato (*Lycopersicon esculentum* Mill.), maize (*Zea mays,* L.), wheat (*Triticum aestivum* L.), sorghum (*Sorghum bicolor* (L.) Moench), barley (*Hordeum vulgare* L.), potato (Solanum *tuberosum* L.), as well as many trees like loblolly pine (*Pinus taeda* L.), aspen (*Populus tremula* L.) have undergone association mapping.

Table 2.1. Few examples of association mapping studies in various crop species

Crops	Traits	References
Maize	✓ Flowering time ✓ Composition of kernel ✓ Color of kernel ✓ Sweet-taste ✓ Oleic-acid contents ✓ Carotenoid contents ✓ Water-logging tolerance ✓ Association mapping of roots that response to temperature extremes ✓ Root system architecture ✓ QTLs of seedling root development	Thornsberry et al. (2001); Wilson et al. (2004); Palaisa et al. (2004); Tracy et al. (2006); Belo et al. (2008); Harjes et al. (2008); Zhang et al. (2013); Reimer et al. (2013); Zurek et al. (2015); Pace et al. (2015)

Wheat	✓ kernel size and milling quality were mapped with AM ✓ Root system architecture ✓ Root length for water stress resistance ✓ Root and shoot traits	Breseghello and Sorells (2006); Cane et al. (2014); Ayalew et al. (2017); Li et al. (2019)
Rice	✓ Glutinous Phenotype ✓ Starch quality ✓ Yield components ✓ Salinity tolerance ✓ Metal tolerance ✓ Root traits ✓ Nitrogen use efficiency trait	Olsen and Purugganan (2002); Bao et al. (2006); Agrama et al. (2007); Kumar et al. (2015); Zheng et al. (2015); Phung et al. (2016); Liu et al. (2016)
Arabidopsis Thaliana	✓ Flowering time ✓ Disease resistance ✓ Shoot branching ✓ Metals tolerance of roots ✓ Root development ✓ Root-knot nematode	Olsen et al. (2004); Aranzana et al. (2005); Ehrenreich et al. (2007); Tazib et al., 2009 Meijón et al. (2014); Warmerdam et al. (2018)
Barley	✓ Agronomical and morphological traits (Days to heading, leaf rust, Yellow dwarf virus) ✓ Root characteristics ✓ Salt tolerance and ion homeostasis ✓ Root and shoot variation in barley	Kraakman et al. (2006); Ataei et al. (2013); Long et al. (2013); Reinert et al. (2016)
Sorghum	✓ Nodal root angle ✓ Root and yield traits ✓ Brace root traits	Mace et al. (2012); Fakrudin et al. (2013); Li et al. (2014)
Sugarcane	✓ Disease resistance	McIntyre et al. (2005); Wei et al. (2006); Gouy et al. (2015)
Sugar beet	✓ Amplified Fragment Length Polymorphism in Sugar beet	Kraft et al. (2000)
Soyabean	✓ Redistributing of SNPs in Soybean	Zhu et al. (2003)

2.11 Comparison of Association Mapping with Linkage Mapping

Association mapping (AM) offers three benefits as compared to linkage mapping (Flint-Garcia et al., 2003). Firstly, no mapping population is required for association mapping and hence it offers higher mapping resolution with the utilization of diverse breeding lines, clones and varieties. Higher number of meiotic recombination events was observed in association mapping as compared to single meiotic event in linkage mapping (Gebhardt, 2007). This diversity in population structure is important for the mining of favourable alleles in clonal propagated crops such as potato (Gebhardt et al., 2004)

Secondly, the allele numbers were increased in AM. In a mapping population involving segregating parents, the allele number at a locus is four in case of diploid linkage mapping, but in tetraploid it is eight. AM involving 200 tetraploid genotypes consists of 800 alleles theoretically at a single locus. Due to decreased statistical competence, marker-trait associations cannot reveal the infrequent allele. For that reason; AM is considered more reliable to find the typical variations.

Lastly, the diagnostic markers identified represents a reliable polymorphism originating from diverse group of individuals holding linkage disequilibrium that can be used effectively in any breeding program after validation. (Stich and Melchinger, 2010).

2.12 Association Mapping in Potato

Till now, AM in potato has been focussed for disease resistance (Kasai et al., 2000; Gebhardt et al., 2001; Gebhardt et al., 2004; Simko et al., 2004; Flis et al., 2005; Song et al., 2005; Sattarzadeh et al., 2006; Malosetti et al., 2007; Pajerowska-Mukhtar et al., 2009) and quality traits of tubers (Li et al., 2005, 2008; D'hoop et al., 2008). Mapping studies identified genes related to PVY and *Globodera Pallida* cyst nematode in a diverse population. Later the cultivars with known phenotypes such as disease and abiotic resistance/tolerance have been tested to find the marker-trait association (Kasai et al., 2000; Song et al., 2005; Flis et al., 2005; Witek et al., 2006; Sattarzadeh et al., 2006). Simko et al. (2004) assessed 137 North American tetraploid population and advance breeding lines to detect the genomic regions associated with Verticillium wilt (*Verticillium dahlia*) disease resistance. Comparative genomics study was used to recognize the orthologous locus *StVe* on chr 9 in potato similar to resistance gene *Ve* mapped on tomato genome. (Kawchuk et al., 2001). Resistance to *Verticillium dahlia* was observed in the SSR allele directly related to St_{Ve} with a position of 1.5 cM on chr 9 (Simko et al., 2004). Malosetti et al. (2007) discovered quantitative resistance against late blight by utilizing 123 different potato varieties. R genes were found to be associated with resistance to late blight (*Phytophthora infestans*) (Gebhardt and Valkonen, 2001; Simko et al., 2007).

In association mapping studies, the candidate gene approach was extended to detect DNA variations associated with late plant maturity and resistance to late blight disease (Pajerowska-Mukhtar et al., 2009). A study was carried out by cultivating 192 tetraploid breeding potato clones genotyped for 230 SNPs in 24 different candidate loci to verify the resistance of late blight in field and plant maturity. 9 SNPs were found to be linked with resistance to late blight in potato explaining a genetic variance of 50%. Malosetti (2007) performed an association mapping of 204 tetraploid cultivars for profiling of nucleotide-binding site (NBS). Association tests have been performed with phenotypic data available for late blight showing 2 and 30 trait marker associations according to the model applied for the association. An unidentified map position of two NBS markers was steadily linked with late blight resistance. In tuber phenotypic characters, common alleles and polygenic inheritance may cause genotypic changes (van Eck, 2007). Furthermore, carbohydrate linked traits have been identified by the aid of candidate gene approach and several QTLs have been detected on nearly all chromosomes associated with reducing sugars, sucrose and starch contents of tuber. These QTLs enable us to understand the biosynthetic pathways involved for carbohydrate metabolism (Hofius and Bornke, 2007).

Ongoing, breeders are mainly focused on some characteristics of the tuber or upper ground portion of the plant but underground part specially roots and stolons traits received little to no attention.

2.13 Underground Traits of Potato

2.13.1 Significance of root system

The roots absorb minerals and water from the soil and make them available for other important functions in the plant. Plant root system or root architecture plays a significant role in the efficient uptake of nutrients and growth of the plant (i.e., root to shoot ratio, root dimension, root branching pattern (topological properties) and roots distribution in the soil) (Joshi et al., 2016; Tinker & Nye 2000). It is indicated by some researchers that, 30% and 10% of the TRL (total root length) are activated during the absorption of water and nutrients, respectively (Opena et al., 1999; Hodge et al., 2009). The development of the roots varies from one species to another. Normally, the roots are classified in two types: (a) primary and seminal roots in corn developed from the embryo, primary or tap root in beans (Hochholdinger, 2009; Lynch and Brown, 2012), (b) adventitious roots formed post-embryo.

The roots of the potato are adventitious and sensitive to drought stress as well as less efficient to utilize nitrogen (N) and phosphorus (P) to maintain tuber quality and yield. It requires more fertilization rate and high number of irrigation (Iwama, 2008; Ahmadi et al., 2011; Joshi and Ginzberg, 2020). The absorption of water and nutrients uptake in diverse and extreme situations can be improved by exploiting the potato root system. The penetration of the potato roots in the soil are week (i.e., grow horizontally with not more than 20cm depth) due to shallow root system (Stalham et al., 2007; Iwama, 2008; Weaver, 1926; Cutter 1992). The root growth is accelerated by 1 to 2cm d^{-1} after 3-5 weeks of emergence, followed by a slower <1 cm d^{-1} and cease at the end of the season. (Stalham and Allen, 2001). When the total root length (TRL) is close to its maximum position, then 50% to 60% of the roots are spread in 0 to 30 cm soil under non-irrigated and irrigated situations (Svoboda et al., 2020; Joshi and Ginzberg, 2020; Boguszewska-Mańkowska et al., 2020). Moreover, it varies from soil conditions and genotypes to genotypes and generally it reaches maximum as 140cm (Stalham and Allen, 2001; Svoboda et al., 2020). During favourable conditions the late growing cultivars depict larger root mass as compared to earlier growing cultivars. The cultivars having large roots are more resistant to drought conditions as compared to smaller roots (Deguchi et al., 2010; Wishart et al., 2014). The positive relationship was revealed by a study between tuber yield and root mass (Iwama, 2008; Wishart et al., 2013).

2.13.2 Importance of stolon in tuber growth

In potato research, the aspects involved in the formation of tubers are always important. (Pelacho and Mingo-Castel, 1991; Struik et al., 1989; Helder et al., 1993; Brown, 2007; Wurr et al., 1997; Chang et al., 2012) and the tubers are derived from the swelling stolons. Underground feature such as "stolon" is very important aside from RSA. Carbohydrates are stored in the stolon which is necessary for plant growth during different biotic and abiotic stress situations (Di Paola and Beard, 1992). The potato plant rhizomes also called stolons, which are lateral shoots, originate from the most basal nodes of the subterranean level. Naturally, they are Diageo-tropic shoots with long internodes hooked at the tips. (Struik, 2007). Stolon formation usually begins in the lower nodes and progresses acropetally (Cutter, 1992). Normally tuber is a swollen form of stolon and stolon can undergo different phases for tuber formation, development and maturation (Ewing and Wareing, 1978).

It was observed that the average length of stolon can vary between the cultivars, but no significant difference among the years (Kratzke et al., 1992). An experiment was conducted by Wurr on 3 varieties (Maris Piper, Desiree and Pentland Crown) and observed that the tuber formation pattern and the degree of tuber growth differed greatly among the tested varieties. Other experiment conducted by Engels and Marschner (1986c) by using 3 weeks old tubers and revealed a significant positive correlation between tuber volume and stolon length, stolon diameter and stolon volume, this might be due to increase in stolon-given carbohydrate sinks. It can also be due to more stolon roots and their longer size can get more water and nutrients.

Stolon initiation and growth are stimulated by long photoperiod and high temperature, whereas a short period and low temperature lead to tuberization and tuber expansion (Struik et al., 1989; Ewing and Wareing, 1978; Brown, 2007; Pelacho and Mingo-Castel, 1991).

2.14 Molecular mapping and Root System

Generally, two types of variability are present in the root system architecture (such as phenotypic plasticity and genotypic variability) because of 2 different developmental-pathways 1- genetic determinants pathway and 2- environmentally triggered responsive pathway (Malamy, 2005). The 3D root structure is formed as a combination of these two pathways, which is influenced by genetics and heterogeneous soil-environment (Baddeley et al., 2007). Though, tuberous crops like potatoes, cassava, sweet potatoes and yams may have more potential to provide food security in upcoming days. Knowing the root system means paying attention to the comestible part. Genotyping techniques; high-throughput phenotyping; data analysis pathways and robust databases for root characteristics modelling can offer a valued foundation for a truly "green revolution" Genetic bottleneck and historical migration patterns (Brown, 1990), in potato, make a genetic variation in commercial varieties of *Solanum tuberosum* L for economically important traits, including rooting characteristics (Hawkes, 1979; Simmonds, 1962). According to the previous discussion, potatoes are prone to various abiotic stresses, cultivars with improved overall root length and area is need to be developed to improve their ability to forage nitrogen and water. As human population is increasing and they also require different resources to survive such as fresh water, in that scenario the development of such varieties which have the ability to survive in a diverse condition, required low fertilizers, reduced competition for limited fresh-water resources. More recently, agronomists and breeders have begun to identify different types of potatoes that have a better root system structure to deal with different stresses. (Fita et al., 2006). The roots are tangled and grow in a heterogenous and opaque soil and influenced by uncontrollable environmental factors. For the improvement of RSA, a complete information or understanding of the RSA on the genetic basis is pre-requisite.

In many crops, root traits were manipulated by the aid of molecular markers. Many genes associated with RSA have been identified in different ways such as QTL analysis. The QTL mapping was considered a foremost approach to investigating the genetics of maize root because the root traits are genetically controlled by several loci with little effect (Cai et al., 2012; de Dorlodot et al., 2007). There are significant differences in RSA between maize genotypes, giving enough genetic material to map QTLs (Tuberosa et al., 2003; Jenison et al., 1981; Kumar et al., 2012; Chun et al., 2005). For the validation of the QTLs constancy by using different mapping population, different studies have been performed with different growth conditions at different growth stages but still more studies are required (Hund et al., 2011).

A molecular marker named (QTL; qWT_Gm03) is associated with the number of adventitious roots in soybean crop, was validated for waterlogging tolerant breeding in multiple environments by using near-isogenic mapping population (Ye et al., 2018). Similarly, overexpression of *DRO1* in rice crops aids deep rooting and eventually making the crop drought tolerant (Uga et al., 2013). The total surface area was increased by the overexpression of *PSTOL1* which ultimately helps to obtain the phosphorous from the phosphorous deficit soils (Gamuyao et al., 2012). QTLs have been cloned in rice and maize which are involved in the uptake of nutrients and water (Uga et al., 2013; Gamuyao et al., 2012; Hanzawa et al., 2013; Lebreton et al. 1995; Liu et al., 2008; Hund et al., (2004, 2011); Zhu et al., (2005a, b, 2006).

2.15 Phenotyping for Genetic Studies; prerequisite for GWAS

Quantitative genetic studies required efficient phenotyping protocols (Trachsel et al., 2013). Contrarily with other crop species, potato crop has different growth patterns with roots, tubers and stolons features hidden under-ground that make it difficult to track the development of these features. In potatoes, a special attention is required to dissect the genetic regulations of these underground features (i.e., roots, tubers and stolons). Multiple QTLs are responsible for the phenotypic variation in underground features, that are controlled by minor effect loci. These traits are difficult to assess in the field; This is because the roots and stolons are sensitive and chance of damage when removed from the soil. In addition, in the field situation, the non-invasive imaging of under-ground traits is not a cost-effective approach. (de Dorlodot et al., 2007; Trachsel et al., 2011; Smith and De smith, 2012). This situation demands the use of a easy to use, fast, capable, and user friendly system for the assessment of under-ground traits. Besides, effective-phenotyping is necessary for quantitative genetic studies (Trachsel et al., 2013). However, the inability of effective phenotyping of large mapping populations has been a key obstacle to the large-scale use of genetic information regarding roots in breeding (Chen et al., 2011a; De Dorlodot et al., 2007). Therefore, effective and accurate phenotyping of root-related traits is one of the most important in breeding.

2.15.1 Systems for phenotyping

2.15.2 Destructive method – Shovelomics

Currently multifarious conventional methods are in practice to evaluate the root characteristics of the plants. From all of the existing methods the most common one is “core sampling” or “shoveling”. These methods are employed for the collection of root samples to measure root traits at different depths (Smit et al., 2000; Iwama, 2008). Samples can be taken by digging trenches along the row in sequenced crops, then root washing, root sampling, scanning, and lengths can be calculated with the help of software.

2.15.3 Plexiglass tubes/Minirhizotron

There is another method known as minirhizotrons in which Plexiglass tubes are used that are placed vertically along with the cameras in ground to record/observe the growth of roots (Rewald & Ephrath, 2013). There is a limitation for this method as it is expensive, additionally it might disrupt the growth of roots while digging.

2.15.4 Controlled environments

It is difficult or nearly impossible to measure the roots and stolon traits of potato under field conditions due the sensitivity of these traits to be damaged while uprooting the plants from field. In order to overcome this problem, indoor growing systems are better instead of the field for precise and accurate analysis of under-ground traits. Moreover, in controlled environment/systems several approaches are available to observe phenotypic performance which includes destructive and non-destructive methods. Furthermore, controlled systems have advantage as they provide information of the soil and the distribution of water around individual roots. Among all the aeroponics growing system is the best choice to observe underground traits of the potato. Pot studies are also beneficial to mimic natural growth conditions for potato.

2.15.5 Pots filled with soil

Soil filled pots are used in numerous studies to quantify various root traits, that includes number of roots, length of root, diameter of root, surface area of the root, and mass of root that can measured from different soil depths (Araki and Iijima, 1998). Contrarily it is time-consuming that needs thorough washing of the roots. Likewise, during sample collection, it also might result in damaging of roots, stolon, and tubers of potato. However, pot studies have advantage over this for easy collection of root samples for studying root characteristics. Additionally, this is a friendly approach for plants with minimal damage to roots and pretend field conditions (Chen et al., 2015).

2.15.6 Soil-less culture “aeroponics”

Currently aeroponics is a newly introduced system for growing plants under controlled conditions and in this method, nutrients are directly sprayed onto the plant roots or underground parts of plants such as potato tubers/stolon’s (Barak et al., 1996). Its basic principle is growth of crops under controlled/semi-controlled conditions. The roots of the plants are directly exposed to air and they can absorb readily available nutrients in the form of mist that assist in development of new structure and grow. In this system special type of table is used that has holes at the top for the anchorage of plants with the help of foam plugs or cotton plugs that gently hold the stems and allow roots to grow downward in the aeroponic system. As it is a controlled growth system that makes it possible to easily control plants at each growth stage from existing field diseases/insects’ infestations. In this way it provides an extra benefit of least damage to crops. Additionally, it discourages the use of pesticides and no need to apply herbicides as it is soil-less medium for plant growth. Plant growth without soil medium was firstly introduced in 1920s. Firstly this system was adopted to analyse the structure and growth of roots. Later In 1940s it was used for research purpose to evaluate root physiological changes in plants (Barker, 1922). The very first study was done by Carter (1942), in which it was revealed that it is promising tool to observe root characteristics in detail. Later after fifteen years this system was named as “aeroponic” by Went (1957). With the passage of time this system became a promising tool for several ornamental and horticultural crops (Biddinger et al., 1998). In case of potato, it drastically increased the production of minituber with the introduction of aeroponic system (Ritter et al., 2001). Moreover, it was reported to maintain perennial crops under this system (Peterson and Krueger, 1988). Root’s response to varying environmental conditions such as drought stress, nutrient stress, and salinity stress etc and root growth in response varying oxygen concentration can mimicked in this system to observe the response of cultivars (Hung and Sylvia, 1988; Khan and Sinclair, 1992; Sylvia and Jarstfer, 1992; Wagner and Wilkinson, 1992; Mavoungou et al., 1982; Hubick et al., 1986; Robertson et al., 1990a, b; Shtrausberg and Rakitina, 1970; Soffer and Burger, 1988). This system also offers the precise high-throughput phenotyping of critical under-ground traits of potato. It can be used for the optimization of root aeration compared with the hydroponic system and other techniques that are in practice (Soffer and Burger, 1988). It has another advantage to cope with the continuously decreasing water resources as it uses very less water compared to field production of potatoes.

In aeroponics water continuously circulates that helps in maintaining the pH. It provides equal availability of nutrients for plants with the least fungal infestation and free from soil-borne diseases. Moreover, it requires less space and results in higher yield and there is no need of crop-rotation as compared to field-grown crops. The mini tubers can be collected at any stage depending upon the requirement ranging from 5 g to 30 g solely under this system. Some of the researchers highlighted that the efficacy of this system is more effective than traditional methods (Muthoni et al. 2010; CIP 2010)

In potato there is still research gaps regarding the study of genes/QTLs effect on their phenotype and performance of plants to the different environmental conditions. That is the reason, under field conditions RSA responds differently due to soil conditions. Kitomi et al., (2015) revealed that genotypes might have different rooting angles despite having the same functional alleles of (*DROI*). Small effect of QTLs is thought to be the part of minor QTLs. For this kind of cases, analysis of data and its integration into controlled conditions as well as further validations under field studies are essential for the establishment of targeted gene of interest for future studies. Contrarily large QTLs effect yielded promising results due to its stability across varying environmental conditions. In one of the study multi-genic as well as multi-environment effectiveness of *qDTY12:1* was confirmed with the identification of large-effect QTL on chromosome12 of the rice genome (Dixit et al., 2015).

Table 2.2. Some examples of aeroponic platforms used for different crops

Crops	Purposes	References
Pineapple	Plant root studies Investigate resistance to *P. cinnamomic* and develop molecular markers.	Carter (1942); Sanewski et al. (2017)
Citrus and Avocado	Root studies	Klotz (1944)
Wheat	To determine the effect of barley yellow dwarf on root and shoot Analysis of root system architecture at the genetics level	Hoffman and Kolb (1977); Thaon (2018)
Tomato	Quantification of sugar and organic acid contents	Osvald et al. (2001); Leoni et al. (2008)

	Production of quality tomato	
Potato	Mini tuber production; Investigate the effect of plant density and harvesting intervals Mini tuber productions	Farran and Mingo-castel (2006); Mbiyu et al. (2012) Chang et al. (2012)
Lettuce	Study root, shoot, and photosynthetic response Nitrate uptake	He and Le (1998); Johnstone et al. (2011)
Cranberry	Measuring nutrient uptake	Barak et al. (1996)
Medicinal plants	Best for the growth of root-based plants.	Kamies et al. (2010)

2.16 Imaging-Analysis Platforms

Root phenotypic characteristics needs to be characterized by using best imaging techniques. Numerous techniques can be used for this purpose, some of them are neutron radiography (Oswald et al., 2008), stereoscopic (Wulfsohn et al., 1999), ground-penetrating radar (e.g., Stover et al., 2007), X-ray computed tomography (CT) and (MRI) magnetic resonance imaging (Rascher et al., 2011) (Flavel et al., 2012). One of the newly used X-ray CT-based imaging approach resulted in good images with a ‘deep phenotyping’ to the breeders (Flavel et al., 2012; Mooney et al., 2012). However, the use of imaging technique can also vary with the proposed aim, for example, architectural features are correlated with water and nutrient absorption, so underground plant system can be studied with high resolution and 3D. Currently more than 30 software’s are available for analysing underground traits of plants which includes RootScan, RootView, GiARoots, DART RootReade, RootReader3D, RootSystemAnalyzer, RootNav, MR-RIPL, RooTracker, RooTracker, RooTracker, IJ_Rhizo, ImageJ, and WinRhizoTRON, etc. (French et al., 2009). Among all of them WinRhizo is the most commonly used one because it is reliable and flexible software that can perform several tasks as compared to other available software’s (Pierret et al., 2013). Recent advancement in structure simulation models, modern approaches will be helpful to enhance our understanding of root architecture and functions, likewise the interaction of root with the soil.

Carrot primary root growth was studied by X-ray CT (computed tomography) (Rosenfeld et al., 2002). General traits that need to be measured for root growth are total root length, density of root, diameter of root, root dry weight, and maximum root depth (Stalham & Allen, 2001). In case of carrots root system, root length and other root characteristics per plant is the preferred for measurement rather than soil surface area. Furthermore, total surface area is preferred for fibrous roots per unit weight of the plant (cm^2 g^{-1} dry root) is commonly used (Pietola & Smucker, 1998).

Table 2.3. Some examples of WinRHIZO software used in different crop species

Crops	Traits	References
Pea	Taproot length, root surface area, and root diameter	Desgroux et al. (2018)
Wheat	Total root length, surface area, root average diameter, and root tips Total root length	Liu et al. (2019); Li et al. (2019)
Arabidopsis	Root length and root tips	Warmerdam et al. (2018)
Maize	Length of axial roots Total root length Root traits	Reimer et al. (2013); Morosini et al. (2017); Ma et al. (2020)
Rapeseed	Root volume	He et al. (2019)
Potato	Total root length Total root length, surface area, and average diameter	Wishart et al. (2013); Zarzyńska et al. (2017)
Rice	Root length and root diameter Total root length, surface area, average diameter, and root volume	Kato et al. (2010); Chen et al. (2011)
Sweet potato	Root length, surface area, root diameter	Van Nguyen et al. (2020)

CHAPTER III

MATERIALS AND METHODS

3.1 Plant Materials

The research was carried out using an association mapping panel of 192 tetraploid potato genotypes. All the genotypes used in this study belong to *Solanum tuberosum* L. 91 (47.3%) genotypes were selected from the German breeding company (Norika GmbH) including 37 breeding lines and 54 commercial varieties, 86 (44.7%) genotypes were obtained from the Turkish breeding company (Doğa seeds) consisting of 83 breeding lines and 3 commercial varieties, while 15 (7.81%) common genotypes grown in both countries were also included. Most of the varieties and breeding lines were developed for processing quality traits. This panel was chosen because it represents a range of genotypes commercially grown in both countries and were evaluated for their potential underground traits. Detailed information of these genotypes is provided in the Table 3.1.

Table 3.1. List of genotypes under studied with their origins, clusters and pedigrees information

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
33	37	DT14063.12	Cluster1	TR breeding line	Lady Olympia x CIP 397039.51
34	38	DT14036.01	Cluster1	TR breeding line	CIP 397077.16 x Lindita
35	39	DT14055.25	Cluster2	TR breeding line	Jelly x Lindita
36	41	LadyOlympia	Cluster1	Common genotypes in both DE and TR	Agria x KW 78-34-470
37	42	BANBA	Cluster1	DE variety	Slaney x Estima
38	43	VanGOGH	Admixed	Common genotypes in both DE and TR	ZPC 69 C 239 x Gloria
39	44	DT14049.10	Cluster1	TR breeding line	Innavator x Alegria
40	45	DT14061.23	Cluster1	TR breeding line	Lady Olympia x Lindita
41	46	DT14006.07	Cluster1	TR breeding line	Atlantic x Soleia
42	47	DT14046.19	Cluster2	TR breeding line	(Fasan x Hermes) x Jelly
43	48	DT14014.27	Cluster1	TR breeding line	Bettina x Lindita
44	49	DT14011.18	Cluster1	TR breeding line	Banba x Lindita
45	50	DT14069.13	Cluster1	TR breeding line	Madeleine x CIP 397039.51
46	52	DT14026.21	Cluster2	TR breeding line	CIP 396286.6 x Jelly
47	53	DT14042.24	Cluster3	TR breeding line	Fasan x Jelly
48	54	DT14090.11	Cluster3	TR breeding line	(Tucan x Challenger) 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
80	87	DT13049.50	Cluster1	TR breeding line	Isla of Jura x Maris Bard
81	88	DT13072.19	Cluster1	TR breeding line	Lady Olympia x Romanze
82	89	DT13083.01	Cluster1	TR breeding line	Marabel x Melody

83	90	LadyRosetta	Cluster1	Common genotypes in both DE and TR	Cardinal x SVP 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
90	97	DT13045.42	Cluster2	TR breeding line	Isla of Jura x Challanger
91	98	DT13147.17	Cluster3	TR breeding line	Spunta x Alegria
92	99	DT13048.10	Cluster2	TR breeding line	Isla of Jura x Jelly
93	100	DT13052.23	Cluster3	TR breeding line	Innara x Alegria
94	101	DT13037.31	Cluster1	TR breeding line	Horizon x Alegria
95	102	DT13045.103	Cluster1	TR breeding line	Isla of Jura x Challanger
96	103	DT13037.35	Cluster3	TR breeding line	Horizon x Alegria
97	104	DT13047.08	Cluster1	TR breeding line	Isla of Jura x Gala
98	105	DT13162.16	Cluster3	TR breeding line	Van Gogh x Alegria
99	106	DT13067.03	Cluster2	TR breeding line	Lady Claire x Challanger
100	107	SORAYA	Cluster2	Common genotypes in both DE and TR	Marabel x 1.307 120-93
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
104	111	KARLENA	Cluster4	DE variety	Adretta x 3-69.121/55
105	112	139-101-11	Cluster4	DE breeding line	668 106-03 x Kiwi
106	113	84-105-11	Admixed	DE breeding line	Margit x 821 208-04
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
111	118	878-202-10	Cluster1	DE breeding line	320 206-02 x Innovator

112	120	146-103-11	Cluster4	DE breeding line	668 106-03 x 617 107-03
113	121	SALUTE	Cluster4	DE variety	1.230 101-93 x 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
116	124	106-105-11	Cluster2	DE breeding line	AR 00-0799 x Delikat
117	125	939-201-10	Cluster1	DE breeding line	Kiebitz x W 2133-1
118	126	NIXE	Admixed	DE variety	852 105-99 x 916 218-00
119	127	51-109-11	Cluster4	DE breeding line	Dukata x Tessa
120	128	ETIKETSIZNORIKA	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
123	132	141-104-11	Cluster4	DE breeding line	668 106-03 x 630 104-03
124	133	89-105-11	Cluster4	DE breeding line	Margit x Delikat
125	134	NAUTILUS	Cluster1	DE variety	Innovator x 107 204-96
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 107 204-96
130	140	966-203-10	Cluster4	DE breeding line	Jumbo x 1133 203-00
131	141	904-212-10	Cluster2	DE breeding line	581 115-03 x 600 111-03
132	142	BETTINA	Cluster2	DE variety	Franzi x 795 / 883
133	143	125-104-11	Cluster4	DE breeding line	Kea x Omega
134	144	SWING	Cluster2	DE variety	Talent x Topas
135	145	758-109-09	Cluster4	DE breeding line	Opal x 999 211-00
136	146	735-102-09	Cluster4	DE breeding line	Kiwi x Clarina
137	147	99-102-11	Cluster1	DE breeding line	Naviga x Nautilus
138	148	TERRANA	Cluster4	DE variety	1.195 311-70 x 51.4212 158-83
139	149	104-103-11	Cluster1	DE breeding line	AR 00-0799 x Fontane
140	150	SFHIT	Cluster4	DE variety	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
144	154	509-104-09	Cluster4	DE breeding line	AR 98-0452 x 947 204-00
145	155	43-118-11	Cluster4	DE breeding line	581 115-03 x Tessa
146	156	BEO	Cluster4	DE variety	Pirol x Kiwi
147	157	BALTICCREAM	Cluster4	DE variety	Diana x Jupiter
148	158	868-201-10	Cluster3	DE breeding line	Carmona x 581 115-03
149	159	860-201-10	Cluster2	DE breeding line	Jelly x Topas
150	160	DUKATA	Cluster4	DE variety	1.833 103-95 x Talent
151	161	84-107-11	Admixed	DE breeding line	Margit x 821 208-04
152	162	128-105-11	Cluster4	DE breeding line	Kea x 668 106-03
153	163	140-107-11	Cluster4	DE breeding line	668 106-03 x Pelikan
154	164	PELIKAN	Cluster2	DE variety	1. 97 201-92 x 1. 87 204-92
155	165	KOLIBRI	Cluster4	DE variety	61.107 018-80 x 1.328 001-73
156	167	82-119-11	Cluster4	DE breeding line	1077 201-00 x 320 206-02
157	168	WENDY	Admixed	DE variety	1.742 102-95 x Gala
158	169	ROMANZE	Cluster4	DE variety	3. 14 104-90 x Rasant
159	170	PRESTIGE	Cluster1	DE variety	Sjamero x Panda
160	171	MAXI	Cluster4	DE variety	Sibu x W2899/9b
161	172	FASAN	Cluster4	Common genotypes in both DE and TR	6.915 2023-77 x 1.299 103-77
162	173	Madaleine	Admixed	Common genotypes in both DE and TR	Leyla x KO 85-1002
163	174	POMQUEEN	Cluster1	Common genotypes in both DE and TR	Agria x Disco
164	175	MUNGO	Cluster4	DE variety	Bonza x W2899/9b
165	176	ALBATROS	Cluster4	DE variety	1.293 112-77 x 1.3014 102-81
166	177	FIDELIA	Admixed	Common genotypes in both DE and TR	1.742 102-95 x Filea
167	178	TACOMA	Cluster2	DE variety	Marabel x Borwina
168	179	BONZA	Cluster4	DE variety	Petra x Maxilla
169	180	ADRETTA	Cluster4	DE variety	LU. 59.884/3 x Axilia

170	181	POWER	Cluster4	DE variety	Indira x Bonanza
171	182	GOLDMARIE	Admixed	DE variety	Andante x Agila
172	183	RITA	Admixed	DE variety	W978/334 x W7224/308
173	184	SUMMERGOLD	Cluster4	DE variety	Indira x Eleisa
174	185	DIPLOMAT	Cluster4	DE variety	Marabel x Melina
175	186	CASCADA	Cluster3	DE variety	Solara x Gala
176	187	SOLIST	Cluster2	DE variety	Karlena x Karatop
177	188	LOLITA	Admixed	DE variety	Exquisa x Ditta
178	189	KARATOP	Admixed	DE variety	2-73.4312 x Karat
179	190	INARA	Cluster1	DE variety	Marabel x 1.236 103-93
180	191	ACAPELLA	Cluster4	DE variety	33. 36 020-79 x Karlena
181	192	ALLORA	Cluster4	DE variety	Apart x Borwina
182	193	ARKULA	Cluster1	DE variety	Axilia x (Saskia x Schwalbe)
183	194	TOKIO	Admixed	DE variety	Inara x Amanda
184	195	BIRTE	Cluster2	DE variety	Marabel x 1.572 101-90
185	196	900-205-10	Admixed	DE breeding line	581 115-03 x Innovator
186	197	MAXILLA	Cluster4	DE variety	MA. 62.34/21 x LU. 62.356/11
187	198	TUCAN	Cluster4	DE variety	Albatros x Pazifik
188	199	946-202-10	Cluster4	DE breeding line	332 201-02 x Troja
189	200	KORMORAN	Cluster4	DE variety	3.608 001-85 x 51.4212 158-83
190	202	JUMBO	Cluster4	DE variety	Assia x W2754/8b
191	203	LOGO	Cluster4	DE variety	Ekra x (Panda x W610/33)
192	204	102-102-11	Admixed	DE breeding line	AR 01-0978 x 596 120-03

[a]*DE= Deutschland (Germany),* [b]*TR= Turkish (Turkey),* [c]*DT= Doğa Tohumculuk,* [d]*Clusters= Corresponds to clustering in Fig 4.1 and 4.2., Clusters in Fig. 4.2 followed the sequence of serial no. of genotypes.*
,[e]*Admixed=Clutsers having Q values (i.e., population structure covariates) less than 0.40*

3.2 Phenotyping Experiments in Two Growing Systems

Phenotyping data of underground traits (roots, stolons and tubers) were evaluated in two growing systems i.e., aeroponics-2019, aeroponics-2020 and pot experiment-2020.

3.2.1 Aeroponic experiments

The aeroponic culture experiments were conducted to obtain the phenotyping data for the underground traits (tubers, roots and stolons) during the year summer 2019, and winter 2020, in an automated semi-controlled greenhouse system located at the Faculty of Agricultural Sciences and Technology (FAST), Niğde Omer Halisdemir University Niğde, Turkey (37°56´32”N, 34°37´25”E, 1229 m elevation). The aeroponic system was electronically controlled and constructed with a 10 mm thick polycarbonate sheet, mounted on a galvanized metal frame and covered with black polyethylene inside, and a Styrofoam (5 cm thick) was used on the top as a production bed. The dimension of each aeroponics production unit was 1000 x 100 x 80 cm (length x width x depth).

Potato sprouts were used as an explant after breaking dormancy (Fig. 3.2 and Fig. 3.3). The sprouts of 192 genotypes were transplanted on the aeroponic production beds following a completely randomized design (CRD) with 20 cm and 10 cm distance between the rows and plants, respectively. Seven sprouts of each genotype were planted in each row (Fig. 3.4 and Fig. 3.5). The range of relative humidity in the greenhouse was 55-60% and 25-45% in the year 2019 and 2020, respectively. Minimum, maximum, and mean temperatures (°C) during the experiment is given in Figure 3.1. In the summer season, fans and cooling pads were used along with a shade cloth that provides a cooling effect with an automatically controlled greenhouse roof. In the winter season, a moderate heating system was used to avoid chilling effects or injury to plants, controlled from a central automatic operating system. Plant roots were misted for 20 sec at every 6 minutes with an improved and modified solution mentioned in Table 3.1. The pH and EC of the solution were maintained at 6.2 to 6.8 and 2.0 mS cm^{-1}, respectively. The nutrient solution was changed on weekly basis. Standard potato production practices were followed during the growing period (Fig. 3.6 and Fig. 3.7). Lahlou and Ledent (2005) reported that potato roots have attained maximum depth after 80 days of planting. Therefore, a standard 85 days of the growing period was opted for the harvesting and excavation of roots, stolons and tubers in both years (Fig. 3.8a and b)

Table 3.2. Nutrient solution used in aeroponic system

Nutrient	Per liter	Percentage
NPK	0.540 g	18 + 18 + 18
KNO_3	0.122 g	13.5% K + 45.5% K
K_2SO_4	0.205 g	51% K + 18% S
$Ca(NO_3)_2$	0.487 g	26.3% Ca + 15.5% N
$MgSO_4$	0.281 g	9.1% Mg + 14% S

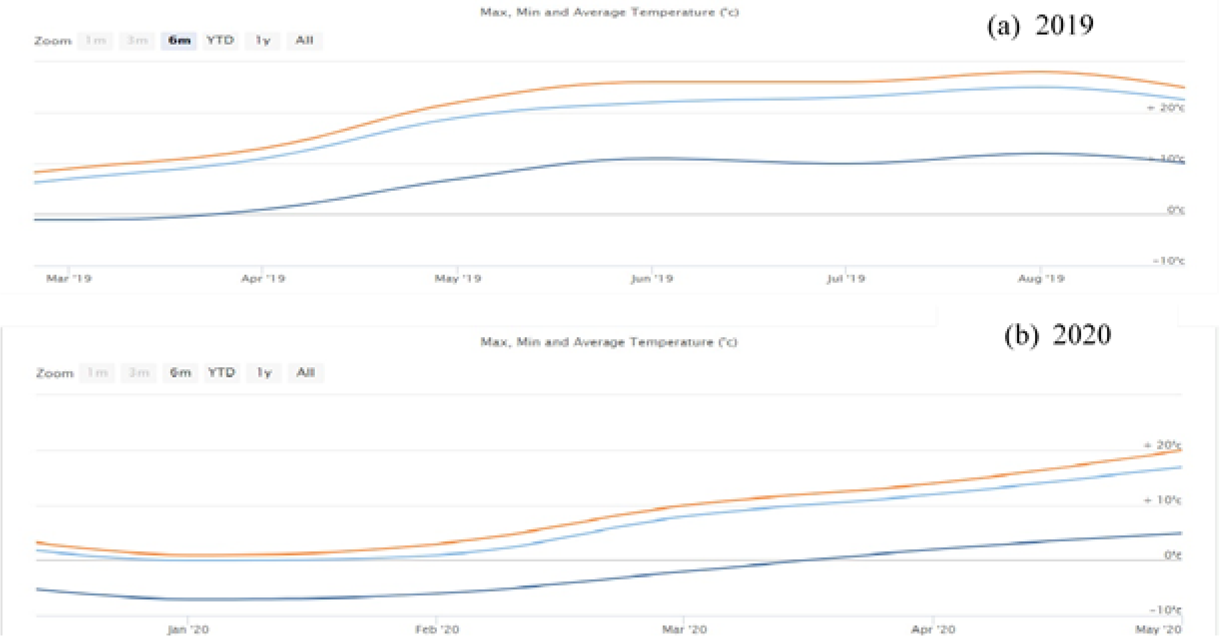


Figure 3.1. Minimum, maximum and mean temperatures (°C) during the years 2019 (a) and 2020 (b) under aeroponic experimentation

Figure 3.2. Dormancy break before experimental setup in aeroponics 2019

Figure 3.3. Dormancy break before experimental setup in aeroponics 2020

Figure 3.4. Tuber sprouts are ready for transplanting during the years 2019 (a) and 2020 (b)

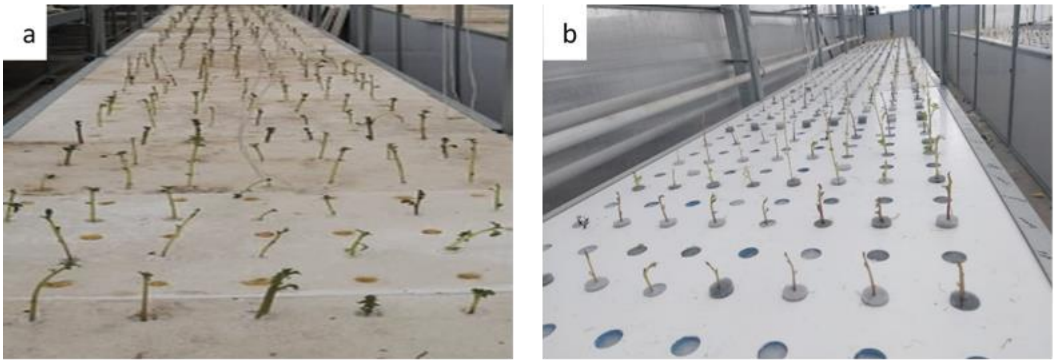


Figure 3.5. Tuber sprouts transferred to the aeroponic production bed in 2019 (a) and 2020 (b)

Figure 3.6. Potato growth under aeroponics during the 2019 summer

Figure 3.7. Potato growth under aeroponics during the winter 2020

Figure 3.8. Root, stolon and tuber phenotyping under aeroponics - 2019 (a), 2020 (b) and pot experiment 2020 (c)

3.2.2 Pot experiment

The pot experiment was conducted in the screenhouse (37°56′32”N, 34°37′25”E, 1229 m elevation) at the Faculty of Agricultural Sciences and Technology (FAST), Niğde Omer Halisdemir University Niğde, Turkey. Specially constructed cylindrical pots (5 L with dimensions of 22.5 cm top diameter, 16.5 cm bottom diameter, and 18 cm depth) were used to derive the phenotyping data of under-ground traits in pot experiment. Before planting tubers, pots were filled with peat and perlite mixture at 2:1 v/v. Plants were grown during the period from June to September, 2020, in a completely randomized design (CRD) with three replications. Plants were watered regularly until the harvesting and fertilized with N-P-K (18%-18%-18%) twice during the growing period. The temperature during the experiment is presented in Figure 3.9. Standard potato production practices were applied during the growing period. A pictorial summary of pot experiment is shown in Figure 3.10.

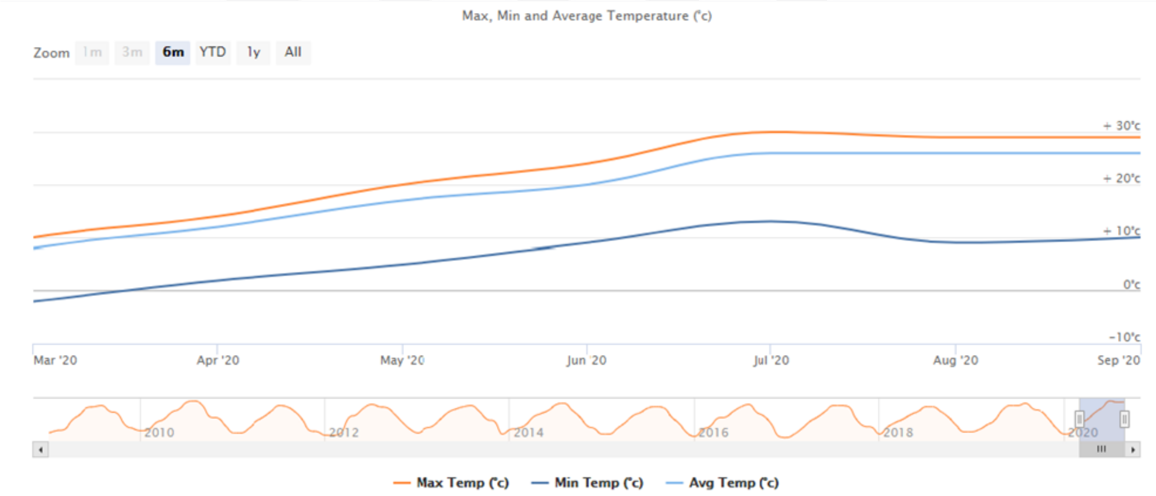


Figure 3.9. Minimum, maximum and mean temperatures (°C) during the year 2020 under pot experiment

Figure 3.10. Potato growth in pot experiment during the year 2020

3.3 Phenotyping Data Acquisition

The variables investigated in the current study includes; **Root Traits** such as total root length (TRL), root volume (RV), root surface area (RSA), root diameter (RD), root branching pattern (RBP), root fresh weight (RFW), and root dry weight (RDW); **Stolon Traits** such as stolon length (SL), stolon diameter (SD), total number of stolons (TNS), branching of stolons (BS), stolon fresh weight (SFW), and stolon dry weight (SDW); **Tuber Traits** including the total number of tubers per plant (TNT), tuber shape (TS), average tuber weight (ATW), and average tuber yield (ATY). In an aeroponic system, five samples per genotype were taken for the examination of roots, stolons and tuber traits, whereas in pot experiment three samples per genotype were taken for the acquisition of phenotypic data. The phenotyping descriptors of the aforementioned traits are discussed below.

3.3.1 Root traits

The root system (3.3.1.1 to 3.3.1.4) was scanned by using scanner XL-11000 and analysed by using WinRHIZO software (Arsenault et al., 1995) (Fig. 3.11)

3.3.1.1 Total root length (TRL)

with the help of WinRHIZO software, the cumulative length of all roots was measured in centimetres (cm).

3.3.1.2 Root surface area (RSA)

with the help of WinRHIZO software, the cumulative surface area of entire root system was measured in square centimeters (cm^2).

3.3.1.3 Root diameter (RD)

with the help of WinRHIZO software, the cumulative root volume of all roots was measured in milli-meter (mm).

3.3.1.4 Root volume (RV)

with the help of WinRHIZO software, the cumulative root volume of all roots was measured in cubic centimetre (cm^3).

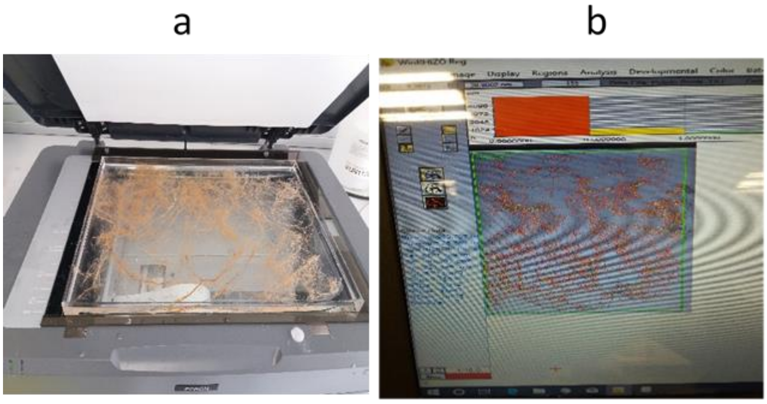


Figure 3.11. Root spread on the scanner by transparent tray for image acquisition (a) and Root traits analysis by WinRHIZO software (b)

3.3.1.5 Root fresh weight (RFW)

Root fresh weight was taken immediately after the harvesting by calibrated precision weighing balance.

3.3.1.6 Root dry weight (RDW)

The roots were dried in an oven at 70 °C until constant mass was achieved (24 hours) and then samples were weighed using a calibrated precision weighing balance.

3.3.1.7 Root branching pattern (RBP)

After measuring the previous parameters, the branching pattern of potato root architecture were recorded by the method proposed by Yen (1987). According to his classification (Fig. 3.12), the branching pattern of root architecture can be categorized as:
1- H-type, 2- R-type, 3- VH-type, 4- V-type, 5- M-type, 6- W-type.

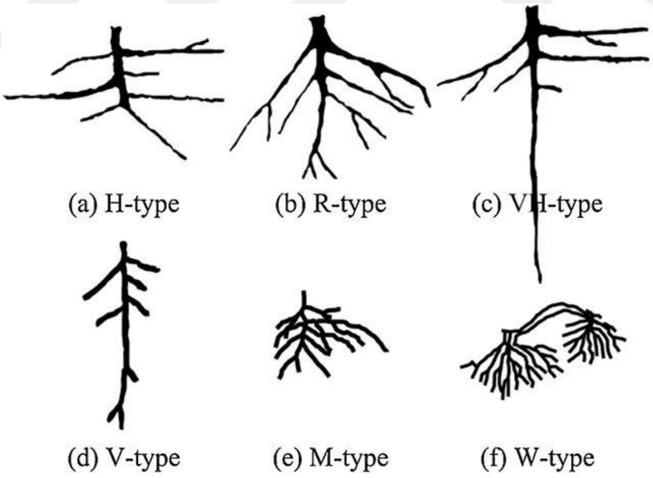

(a) H-type
(b) R-type
(c) VH-type
(d) V-type
(e) M-type
(f) W-type

Figure 3.12. Root branching pattern as suggested by Yen (1987)

3.3.2 Stolon traits

3.3.2.1 Stolon length (SL)

With the aid of measuring tape an entire stolon length (excluding BS) was measured in centimetres (cm) from the base of plant to the end point of stolon.

3.3.2.2 Stolon diameter (SD)

Stolon diameter was measured in millimetres (mm) with the help of vernier calliper from five different points on the stolon and then averaged (Fig. 3.13).

Figure 3.13. Measurement of stolon diameter by vernier calliper

3.3.2.3 Total number of stolons (TNS)

The total number of stolons were counted manually at the base of shoot excluding the BS.

3.3.2.4 Branching of Stolons (BS)

It is collection of all nodes on stolon representing the branching at axillary buds.

3.3.2.5 Stolon fresh weight (SFW)

Stolon fresh weight was taken by a calibrated precision weighing balance immediately after harvesting.

3.3.2.6 Stolon dry weight (SDW)

The stolons were oven dried at 70 °C until constant mass was reached after 24 hours and then the samples were weighed using a calibrated precision weighing balance.

3.3.3 Tuber Traits

3.3.3.1 Total number of tubers per plant (TNT)

Total number of tubers per plant were counted and averaged.

3.3.3.2 Tuber shape (TS)

The shape of tuber was measured according to the potato descriptors (Fig.3.14) (Potato Guidelines by International Union for Protection of New Varieties of Plants in GENEVA). As per descriptor, tuber shape was classified in six different classes i.e., Round-1, Short Oval-2, Oval-3, Long Oval-4, Long-5, Very Long-6.

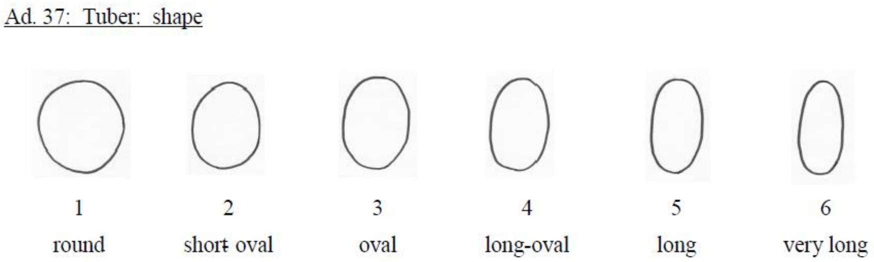


Figure 3.14. Descriptors/classes of tuber shape

3.3.3.3 Average tuber weight (ATW)

Average tuber weight was calculated by following formula:

$$\text{Average tuber weight} = \frac{\text{Total wt.of tubers/plant}}{\text{Total no.of tubers/ plant}}$$

3.3.3.4 Average tuber yield (ATY)

Average tuber yield was calculated by using following formula:

$$\text{Average tuber yield} = \frac{\text{Total wt.of tubers}}{\text{Total no.ofreplications}}$$

3.4 Statistical Analysis

Statistix 8.1 software was implemented to perform the analysis of variance (ANOVA) for a completely randomized design (CRD) pertaining to the data of aeroponics 2019 and 2020, as well as pot experiment 2020. The best linear unbiased prediction (BLUP) was estimated using *lme4* package in R software.

$$yi = \mu + fi + ei + \mathcal{E}i \qquad 3.1$$

where; yi = BLUP value of individual i, μ = mean of all environments, fi and ei are the genetic and environment effects, respectively and $\mathcal{E}i$ is the random error. μ was considered a constant/fixed effect while fi and ei were random effects.

Marker-trait association was calculated by using the BLUP values of all traits through *GWASpoly* R package. By using the *SPSS* software platform, Pearson correlations (*r*) were performed among the traits under study, while analysis of correlation scatter matrix was done through R package "*psych*". The broad-sense heritability (H^2) for each trait was estimated by using following equation;

$$H^2 = V_G/V_P \qquad 3.2$$

Where; V_G and V_P are genotypic and phenotypic variance components, respectively (Bahmankar et al., 2014; Ogunniyan and Olakojo, 2014).

3.5 Genotyping

The Gene JET Plant Genomic DNA Purification mini kit (Thermo Scientific) was used to performed the extraction of genomics DNA according to suppliers' directions. Electrophoresis on 1.2% agarose gel was used to determine the quality and concentration of DNA (Figure 3.15) and further confirmed by using the BioSpec-nano (Shimadzu) spectrophotometry. Before it was sent for the SNP genotyping, a total of 500 ng of high-quality DNA were dried. 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.

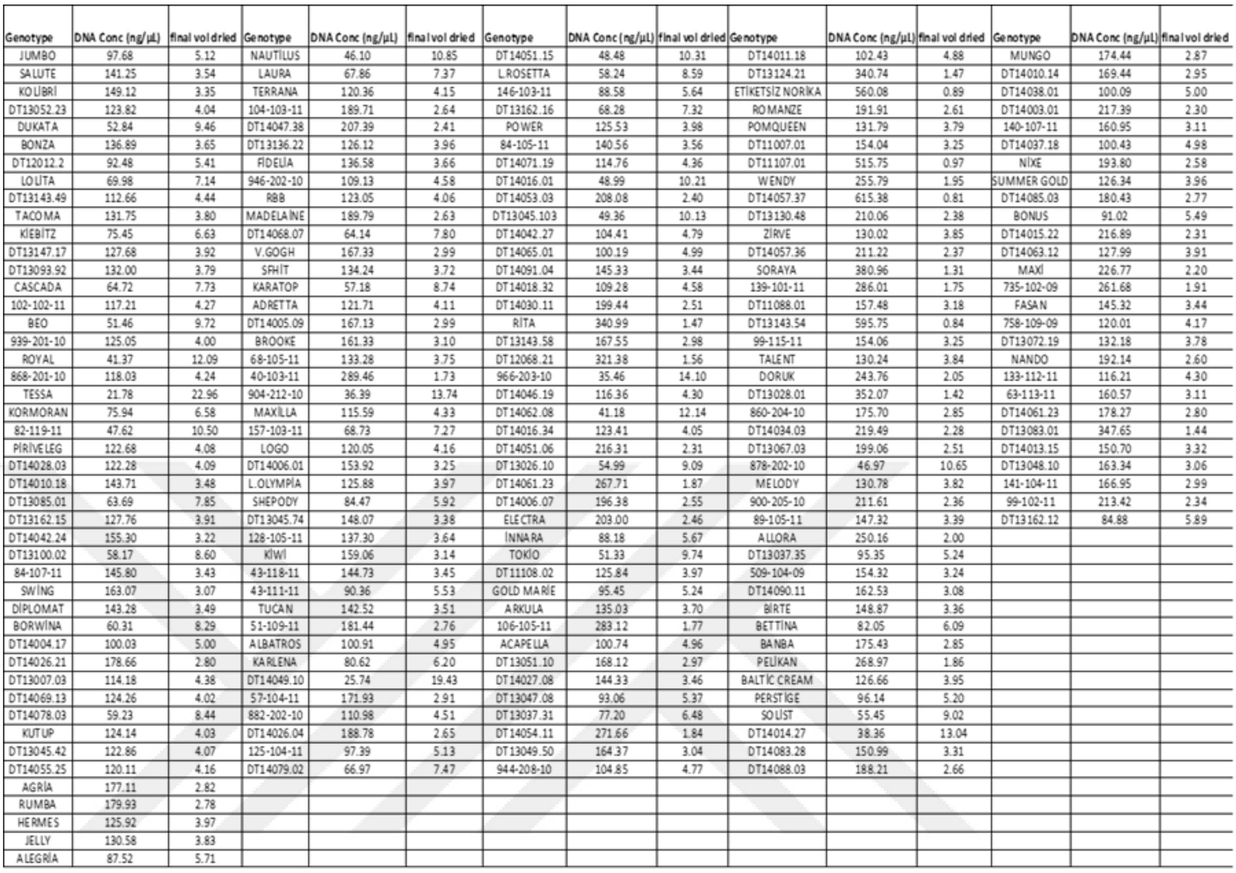
SNP genotyping was done for 192 genotypes by using SolCAP 25K potato array, which includes tetraploid SNPs and utilizes ILMN’S (Illumina) new Genome Studio tetraploid calling (Hamilton et al., 2011; Uitdewilligen et al., 2013). SNP genotyping was done by NEOGEN GeneSeek Laboratory, Lincoln Nebraska (NE), USA. Illumina HiScan SQ system was used to read the array. For the assignment of genotypes to each locus a software named “Genome Studio” was used. After SolCAP 25K array, a tetraploid allelic combination from nulliplex - quadriplex, with a total of diverse 21226 markers were obtained.

3.6 Population Structure (Q) and Principal Component Analyses

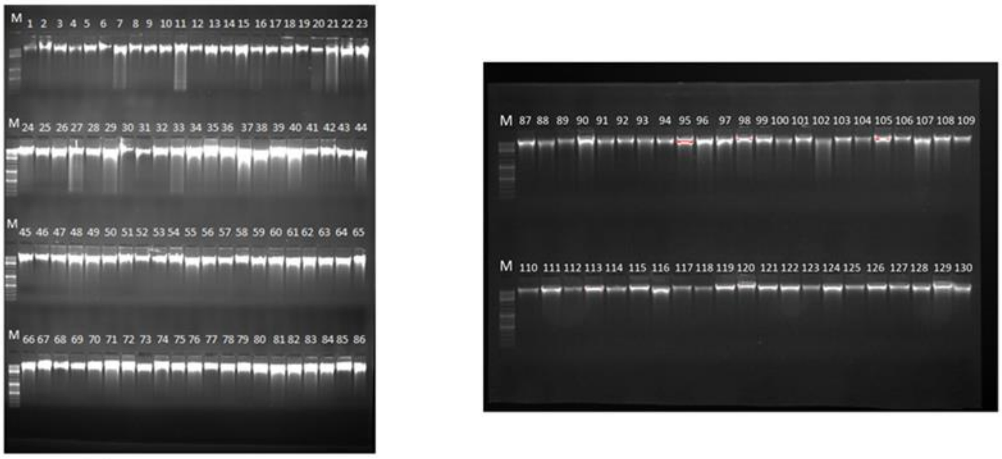
For an association mapping studies the population structure is considered as a main pillar. STRUCTURE software was used to analyze the population structure on the basis of Bayesian clustering approach (Pritchard et al., 2000). For the analysis of population structure the numeric file was made as per following format. For example; SNP T/C: TTTT=AAAA=0; TTTC=AAAB=1; TTCC=AABB=2; TCCC=ABBB=3; CCCC=BBBB=4. Once the numeric file was made, the markers were filtered using criteria such as P and Q frequency calculation; minor-allele frequency (MAF) and missing percentage (%) of SNPs. While searching for polymorphic SNPs, SNPs were tested based on MAF> 0.05, whereas only SNPs with missing percentage of less than and equal to “≤” 10% (sample call rate = 0.9) were selected. After filtering, 13606 (64.10%) polymorphic SNP markers were obtained. 35.90% SNP markers were removed as being monomorphic in nature. Selected polymorphic markers had to explain the “Q” population structure and the “K” kinship of our population.

The STRUCTURE v.2.3.4 was implemented with admixture-based clustering model (Pritchard et al., 2000). Adjust the simulation alike 100000 burn-in and 100000 iterations. 10 independent runs were done with 5 replications ranging from 1 to 10 for each K value. The sub-population (K) was chosen based on Evanno et al. (2005) using STRUCTURE HARVESTER (Earl, 2012). A bar plot based on Q sorting with an optimum ΔK value was used to visualize the population structure. To visualize the genotype clustering on the basis of sub-population a principal component analysis (PCA) was performed with *Prcomp* package in R v. 3.6.3. The *ggplot2* function in R was used to design the first two principal components (PCs).

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



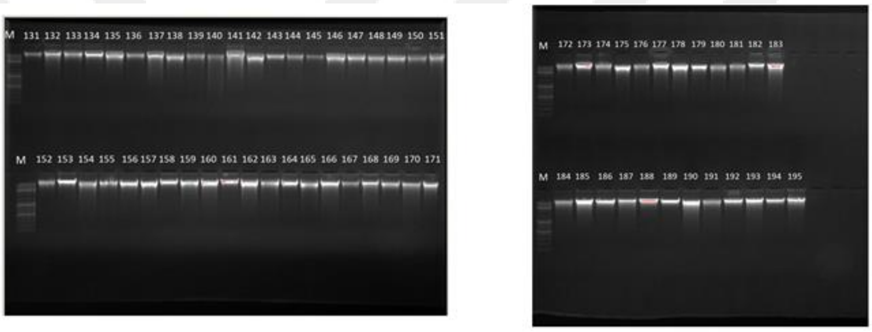
Genotype	DNA Conc (ng/µL)	final vol dried	Genotype	DNA Conc (ng/µL)	final vol dried	Genotype	DNA Conc (ng/µL)	final vol dried	Genotype	DNA Conc (ng/µL)	final vol dried	Genotype	DNA Conc (ng/µL)	final vol dried
JUMBO	97.68	5.12	NAUTİLUS	46.10	10.85	DT14051.15	48.48	10.31	DT14011.18	102.43	4.88	MUNGO	174.44	2.87
SALUTE	141.25	3.54	LAURA	67.86	7.37	L.ROSETTA	58.24	8.59	DT13124.21	340.74	1.47	DT14010.14	169.44	2.95
KOLİBRİ	149.12	3.35	TERRANA	120.36	4.15	146-103-11	88.58	5.64	ETİKETSİZ NORİKA	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	FİDELİA	136.58	3.66	DT14071.19	114.76	4.36	DT11107.01	515.75	0.97	NİXE	193.80	2.58
LOLİTA	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	MADELAİNE	189.79	2.63	DT13045.103	49.36	10.13	DT13130.48	210.06	2.38	BONUS	91.02	5.49
KİEBİTZ	75.45	6.63	DT14068.07	64.14	7.80	DT14042.27	104.41	4.79	ZİRVE	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	SFHİT	134.24	3.72	DT14091.04	145.33	3.44	SORAYA	380.96	1.31	MAXİ	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	RİTA	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	MAXİLLA	115.59	4.33	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
PİRİVELEG	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.OLYMPİA	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	İNNARA	88.18	5.67	ALLORA	250.16	2.00			
DT13100.02	58.17	8.60	KİWİ	159.06	3.14	TOKİO	51.33	9.74	DT13037.35	95.35	5.24			
84-107-11	145.80	3.43	43-118-11	144.73	3.45	DT11108.02	125.84	3.97	509-104-09	154.32	3.24			
SWİNG	163.07	3.07	43-111-11	90.36	5.53	GOLD MARİE	95.45	5.24	DT14090.11	162.53	3.08			
DİPLOMAT	143.28	3.49	TUCAN	142.52	3.51	ARKULA	135.03	3.70	BİRTE	148.87	3.36			
BORWİNA	60.31	8.29	51-109-11	181.44	2.76	106-105-11	283.12	1.77	BETTİNA	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	PELİKAN	268.97	1.86			
DT13007.03	114.18	4.38	DT14049.10	25.74	19.43	DT14027.08	144.33	3.46	BALTİC CREAM	126.66	3.95			
DT14069.13	124.26	4.02	57-104-11	171.93	2.91	DT13047.08	93.06	5.37	PERSTİGE	96.14	5.20			
DT14078.03	59.23	8.44	882-202-10	110.98	4.51	DT13037.31	77.20	6.48	SOLİST	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			
AGRİA	177.11	2.82												
RUMBA	179.93	2.78												
HERMES	125.92	3.97												
JELLY	130.58	3.83												
ALEGRİA	87.52	5.71												



1. JUMBO; 2. SALUTE; 3.KALİBRİ; 4.DT13052.23; 5.DUKATA; 6.BONZA; 7. DT12012.2; 8. LOLITA 9. DT13143.49; 10.TACOMA; 11. KİEBİTZ; 12.DT13147.17; 13.DT13093.92; 14.CASCADA; 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.PİRİVELEG; 24. DT14028.03; 25. DT14010.18; 26.DT13085.01; 27.DT13162.15; 28.DT14042.24; 29.DT13100.02; 30.84-107-11; 31. SWİNG; 32.DİPLOMAT; 33.BORWİNA; 34.DT14004.17; 35.DT14026.21; 36.DT13007.03; 37.DT14069.13; 38.DT14078.03; 39.KUTUP; 40.DT13045.42; 41.DT14055.25; 42.AGRİA; 43.RUMBA; 44. HERMES; 45.JELLY; 46.NAUTİLUS; 47.LAURA; 48.ALEGRİA; 49.TERRANA; 50.104-103-11; 51.DT14047.38; 52.DT13136.22; 53.FİDELİA; 54.946-202-10; 55.RBB; 56.MADELAINE; 57.DT14068.07; 58.V.GOGH; 59. SFHİT; 60.KARATOP; 61.ADRETTA; 62.DT14005.09; 63.BROOKE; 64. 68-105-11; 65.40-103-11; 66. 904-212-10; 67.MAXİLLA; 68.157-103-11; 69.LOGO; 70.DT14006.01; 71.L.OLYMPİA; 72.SHEPODY; 73.DT13045.74; 74.128-105-11; 75.KİWİ; 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.DT14026.04; 85.125-104-11; 86.DT14079.02

M: Gene Ruler Mix Marker;

87. PRESTIGE; 88. SOLIST; 89. DT14014.27; 90. 735-102-09; 91. 758-109-09; 92. DT13072.19; 93. NANDO; 94.133-112-11; 95. 63-113-11; 96. DT14061.23; 97.DT13083.01; 98. DT14013.15; 99. DT13048.10; 100. 141-104-11; 101. 99-102-11; 102. DT13162.12; 103. DT14051.15; 104. L.ROSETTA; 105. 146-103-11; 106. DT13162.16; 107. POWER; 108. 84-105-11; 109. DT14071.19; 110. DT14016.01; 111. DT14053.03; 112. DT13045.103; 113.DT14042.27; 114.DT14065.01; 115.DT14091.04; 116.14018.32; 117.DT14030.11; 118.RITA; 119.DT13143.58; 120. DT12068.21; 121. 966-203-10; 122. DT14046.19; 123. DT14062.08; 124. DT14016.34; 125. DT13026.10; 126. DT14051.06; 127.DT14061.23; 128. 14006.07; 129. ELECTRA; 130. INNARA



M: Gene Ruler Mix Marker;

131. TOKIO; 132. DT11108.02; 133. GOLD MARIE; 134. ARKULA; 135. 106-105-11; 136. ACAPELLA; 137. DT13051.10; 138. DT14027.08; 139. DT13047.08; 140. DT13037.31; 141. DT14054.11; 142. DT13049.50; 143. 944-208-10; 144. DT14011.18; 145. DT13124.21; 146. ETIKETSIZ NORIKA; 147. ROMANZE; 148. POMQUEEN 149. DT11007.01; 150. DT11107.01; 151. WENDY; 152. DT14057.37; 153. DT13130.48; 154. ZIRVE; 155. DT14057.36; 156. SORAYA; 157. DT139101.11; 158. DT11088.01; 159. DT13143.54; 160. 99-115-11; 161. TALENT; 162. DORUK; 163. DT13028.01; 164. 860-204-10; 165. DT14034.03; 166. DT14067.03; 167. 878-202-10; 168. MELODY; 169. 900-205-10; 170. 89-105-11; 171. ALLORA

M: Gene Ruler Mix Marker;

172. DT13037.35; 173. 509-104-09; 174. DT14090.11; 175. BIRTE; 176. BETTINA; 177. BANBA; 178. PELIKAN; 179. BALTIC CREAM; 180. DT14083.28; 181. DT14088.03; 182. MUNGO; 183. DT14010.14; 184. DT14038.01; 185. DT14003.01; 186. 140-107-11; 187. DT14037.18; 188. NIXE; 189. SUMMER GOLD; 190. DT14085.03; 191. BONUS; 192. DT14015.22; 193. DT14063.12; 194. MAXI; 195. 735-102-09

Figure 3.15. Agarose gel electrophoresis of Genomic DNA samples; (Labelled from Left to Right)

3.7 Assessment of Linkage Disequilibrium (LD)

TASSEL was used to determine the LD between marker pairs based on D’ and r^2 (Hill and Robertson 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

Association mapping were done by using the GWASpoly R package, using the “Q+K” linear mixed model approach for auto-polyploids (Rosyara et al., 2016). GWASpoly has its unique features; i.e., it can analyse the diverse panel of tetraploids and work on the basis of 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. rrBLUP is required for the accurate and proper functioning of GWASpoly package. It was also used for the construction of Quantile-Quantile (Q-Q) plots. Q-Q plots showed the normal distribution of the data. Q-Q plots further illustrate the false positives, family structure, and population stratification by a scale of -log10(P) between observed and expected *p* values. The null hypothesis was accepted as true, if there was a uniform distribution (1:1 straight line without tailing on either side between expected and observed -log10 (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). False positives were appropriately controlled by the additive model in the study as depicted by sharp deviation of observed vs expected *p* values in the tail area. A detailed explanation of Q-Q plots for each studied trait is further illustrated in each section.

An association mapping analysis was performed for 17 different roots, stolons and tuber traits of potato using diverse 13606 tetra-allelic polymorphic SNPs in 192 genotypes. Best linear unbiased predictions (BLUPs) estimated from 2019 and 2020 aeroponics and 2020 pot experiment were calculated for each trait and used to detect the 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 2019 and 2020 aeroponics and 2020 pot experiment were performed by REML (Restricted Maximum Likelihood) using *lme4* R package (R Core Team, 2014).

Manhattan plots were obtained by using linear mixed model approach in *GWASpoly* R package with additive gene action, showing the significance threshold for each locus along with the location of SNPs corresponding to each phenotypic trait. Additive gene action was used with an assumption that the SNP effect is proportional to the minor allele dosage. Bonferroni correction method was used to calculate a threshold of -log10(P)=5.4 following a formula “α/m”; where “α” refers to *P* value=0.05 and ‘”m” relates to number of markers = 13606) (Cockram et al., 2015). False negative associations may arise due to this strict threshold value, thus an arbitrary corrected significant threshold of -log10(P) was adjusted at 3.23, as observed in preceding association mapping studies (Riaz et al 2018; Phan et al 2018). GWASpoly R package was used to visualize the Manhattan plots. Association analysis revealing significant SNPs to each trait was taken with a *P*-value ≤ 0.00059 following Bonferroni correction. The dotted line in blue colour showed -log10(P) threshold of ≥ 3.23, which allows for significant SNP identification. A research gap exists for marker-trait association linked to roots, stolons, and tuber traits in potato. Therefore, the current study is novel in this aspect. The chromosome number and position of the identified SNPs were determined from the *GWASpoly* R and re-confirmed from “potato genome assembly” and found to be the same.

3.9 Physical map of chromosomes

A physical chromosomal map of SNP markers linked with studied root, stolon and tuber traits along with the corresponding physical distance in base pairs (bp) were designed to detect the localization of SNP markers at specific regions on the chromosome using R package “*LinkageMapView*”. It helps in understanding and identification of the recombination points and possible QTLs associated with the studied traits.

3.10 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 descriptive statistics and ANOVA showed substantial variation and highly significant ($P < 0.01$) results for all underground traits (i.e., roots, stolons and tubers) (Table 4.1). The range of mean data for the year 2019 (aeroponic experiment) and 2020 (aeroponics and pot experiments) for the variables total root length, root surface area, root average diameter, root volume, root fresh weight, root dry weight, root branching pattern, stolon fresh weight, stolon dry weight, total number of stolons, stolon length, stolon diameter, branching of stolon, total number of tubers, average tuber weight, and average tuber yield was 3743.77 to 24619.00 cm, 679.56 to 5563.10 cm^2, 0.51 to 1.33 mm, 10.24 to 126.46 cm^3, 7.50 to 74.28 g, 0.81 to 7.31 g, 1 to 5, 0.61 to 89.54 g, 0.03 to 6.06 g, 1 to 9.75, 7 to 323.60 cm, 0.82 to 4.87 mm, 2.56 to 103.67, 1 to 13.67, 2.62 to 36.64 g, and 5.2 to 342.67 g, respectively (Table 4.2). Heritability was calculated for the data set of aeroponic experiments done in 2019 and 2020, and pot experiment performed in 2020. The broad sense heritability (H^2) observed in our experiment ranged from 0.64 to 0.99 (aeroponic 2019), 0.70 to 0.98 (aeroponic 2020), and 0.55 to 0.99 (pot experiment 2020) (Table 4.3). H^2 values in our experiment showed the genetic contribution to the observed variability in the measured root, stolon, and tuber traits and suggested that these were a stable trait under the different growth conditions. (Rodrigues et al., 2003; Phung et al., 2016; Liu et al., 2017). However, the environment may also contribute to the biological variation among the phenotypic traits due to range of heritability (low to high).

Data illustrated in Table 4.2 showed that all root traits (TRL, RSA, RV, RAD, RFW, RDW, RBP) were higher in potato plants grown under aeroponics during the year 2019 as compared to same growing conditions in 2020. The average temperature in 2019 was relatively higher as compared to 2020, which may influence these polygenic traits (Boguszewska-Mańkowskaet al., 2020). In aeroponic (soil-less environment) conditions, an average temperature of 24-26°C/18-20°C (day/night) resulted in higher values of root traits in 2019 as compared to lower average temperature 18-20°C /12-14°C (day/night) encountered during 2020. Saha et al. (1974) found that raising night temperatures increases root length. Furthermore, Sattelmacher et al. (1990) reported that potato plants depicted reduced root size, root diameter and root surface area, if the temperature dropped to less than 20°C. In pot experiment (edaphic environment), although the root length was small, higher average root diameter and root fresh weight was observed compare to aeroponics. It could be due to the effects of edaphic environment. Constant uptake of mineral nutrients and water in an edaphic environment causes the division of meristematic cells and may cause thick root diameter (Gu et al., 2014) (Table 4.2 and Fig. 3.8).

Regarding the stolon traits under aeroponic conditions, stolon length, and diameter were less in 2020 as compared to 2019. This could be due to genotypic variation and also attributed to environmental differences such as temperature between the years. Moorby and Milthorpe (1975) and Struik et al. (1989) reported that high temperatures stimulate stolon length, thick stolons and favours stolon branching. Interestingly, branching of stolons were observed to be the same but the total number of stolons were more in aeroponics 2020 as compared to 2019. This scenario dictates that average lower temperatures in aeroponics 2020 (18-20°C /12-14°C) may results in the formation of more number of stolons. Another possibility could be better moisture retention and nutrient availability within the aeroponic compartment that favours higher stolon numbers in aeroponics 2020. A study conducted by Midmore (1984) showed that stolon length was increased because of the delay in tuber initiation, it might be due to high temperatures (as observed in aeroponics 2019), thus allowing more time and providing more assimilates for further stolon formation. This result was in accordance with less number of tubers obtained in aeroponics 2019 due to more mobilization of assimilates towards long stolon formation. In pot experiment, total number of stolons were higher than aeroponics of both years, but branching of stolon were noted to be the same. However, the stolon diameter was less than aeroponics 2019 and higher than aeroponics 2020. Both, stolon fresh weight and stolon length were lower in pots as compared to both years of aeroponics. Stolons formation depends upon the darkness and the extent of stolon branching is positively correlated to moisture (Lahlou and Ledent, 2005). Since, aeroponic atmosphere allows the continuous supply of water as mist, thus long stolons were observed in aeroponics. In pots, instead of an increment in stolon length, diameter and stolon fresh weight, the number of stolons were increased. It might be due to less accumulation of assimilates in stolons under pot conditions and higher mobilization of these assimilates towards tuber initiation and formation (Table 4.2 and Fig. 3.8).

Photoperiod plays an important role in the induction and initiation of tuber formation in the potato plant (Wheeler, 2006). Higher temperatures delay or inhibit tuber initiation as compared to lower temperatures. (Jackson, 1999). In the aeroponics, the number of tubers, average tuber weight and average tuber yield were higher in the year 2020 as compared to the year 2019, due to temperature difference as explained above. Kooman et al. (1996) reported that temperatures around 22°C shortens the duration of the developmental phase in potato plants, from emergence to tuber initiation. At temperatures above 22°C, the development is slower, and tuber initiation is delayed (Ewing and Struik, 1992). The tuber yield of potato is very sensitive to temperature, showing a decreasing trend as the average temperature increased above 27°C (Yandel et al., 1988). Lafta and Lorenzen (1995) also observed that high temperatures caused the formation of fewer number of tubers. In pot experiment 2020, all tuber attributes (i.e., TNT, ATW and ATY) were higher as compared to both years of aeroponics. Better moisture retention and slow release of nutrients under soil conditions might attributed to the increase in tuber traits under pot experiment. Contrarily, increase in the number of tubers per plant can be attributed to the longer growing season and multiple harvests in the aeroponics system (Caliskan et al., 2020). In our experiment, only single harvesting was done that may also contribute to lower number of tubers.

In summary, roots and stolons were long and thick under aeroponics, while average tuber weight and yield was higher under pot experiment. Svoboda et al., (2020) conducted a research and came with the result that the total root length increased significantly with drip irrigation in potato. The switch from stolons to tubers is critical and influenced by planting depth, planting density, moisture availability, photoperiod and temperature. High temperature favours stolon initiation and growth while low temperatures favour tuber initiation and expansion (Gao et al., 2014). This is in accordance with the results of our study.

4.2 Correlation Analysis

Pearson correlation (*r*) analysis was done among all traits to identify the relationship among them. A highly significant correlation was found among the studied underground traits. BLUP values were used for the correlation analysis of root, stolon, and tuber traits. A significantly strong correlation was found between TRL and RSA (*r* = 0.906**), RSA with RV (*r* = 0.91**), RFW (*r* = 0.83**) and RDW (*r* = 0.86**). SFW was strongly correlated with SDW (*r* = 0.98**), SL (*r* = 0.82**), SD (*r* = 0.72**), and BS (*r* = 0.63**). SL was also highly correlated to BS (*r* = 0.86**). TNT also showed strong relationship with ATY (*r* = 0.61**), while ATW was correlated with ATY (*r* = 0.64**) (Table 4.4). Previous studies also showed highly significant correlation among root traits in the potato genotypes (Wishart et al., 2013; Zarzyńska et al., 2017). Furthermore, Kratzke and Palta, (1992) were found a significant correlation between branching of stolons with stolon length (*r* = 0.74** to 0.92**) that is in accordance with our findings (*r* = 0.856**) and according to Bisognin et al., (2012) tuber shape is correlated with average tuber weight.Similarly, Khayatnezhad et al., (2011) found a highly significantly correlation between average tuber weight and average tuber yield (*r* = 0.992**).

Table 4.1. Summary of ANOVA following a completely randomized design for the roots, stolons, and tuber traits of potato in the year 2019 (aeroponics) and 2020 (aeroponics and pot). (**) shows highly significant results at P < 0.01

Traits	**SOV**	**F value**		
		Aero-2019	**Aero-2020**	**Pot-2020**
Total root length	Genotypes	36.9**	8.26**	5.29**
Root surface area	Genotypes	19.9**	7.86**	5.43**
Root diameter	Genotypes	6.42**	4.11**	3.86**
Root volume	Genotypes	17.3**	6.62**	3.69**
Root fresh weight	Genotypes	20.5**	9.67**	4.69**
Root dry weight	Genotypes	2.02**	9.99**	4.22**
Stolon fresh weight	Genotypes	74.9**	7.52**	3.79**
Stolon dry weight	Genotypes	49.1**	5.61**	1.57**
Total no. of stolon	Genotypes	3.49**	5.33**	4.24**
Stolon length	Genotypes	68.9**	10.1**	5.06**
Stolon diameter	Genotypes	10.3**	3.46**	4.88**
Branches of stolon	Genotypes	28.0**	8.11**	6.40**
Total no. of tubers/plant	Genotypes	3.11**	4.34**	2.76**
Tuber shape	Genotypes	11.8**	7.41**	74.8**
Average tuber weight	Genotypes	5.93**	2.73**	3.22**
Average tuber yield	Genotypes	5.76**	2.54**	5.21**

SOV= Source of variation; Aero= Aeroponics

Table 4.2. Descriptive statistics for data of aeroponic experiments 2019, 2020, and pot experiment 2020

Traits	Aero-19 ± SE	Aero-20 ± SE	Pot-20 ± SE	Mean ± SE	Min	Max
TRL (cm)	10028.51 ± 431.06	8230.92 ± 246.23	3963.78 ± 113.15	7476.72 ± 190.95	3743.77	24619.00
RSA (cm^2)	2973.84 ± 128.16	1989.17 ± 63.15	1112.1 ± 36.26	2033.88 ± 52.80	679.56	5563.10
RAD (mm)	0.95 ± 0.02	0.76 ± 0.01	0.89 ± 0.02	0.87 ± 0.01	0.51	1.33
RV (cm^3)	75.37 ± 3.78	40.1 ± 1.52	26.53 ± 1.15	47.31 ± 1.48	10.24	126.46
RFW (g)	31.45 ± 1.62	27.61 ± 1.1	32.06 ± 1.27	30.35 ± 0.83	7.50	74.28
RDW (g)	3.92 ± 0.19	2.26 ± 0.09	2.78 ± 0.11	2.99 ± 0.09	0.81	7.31
RBP	3.06 ± 0.12	2.43 ± 0.12	2 ± 0.09	2.52 ± 0.07	1.00	5.00
SFW (g)	26.55 ± 2.57	8.53 ± 0.76	6.43 ± 0.49	14.09 ± 1.07	0.61	89.54
SDW (g)	1.63 ± 0.15	0.54 ± 0.04	0.49 ± 0.04	0.91 ± 0.07	0.03	6.06
TNS	2.59 ± 0.12	4.08 ± 0.17	6.77 ± 0.29	4.46 ± 0.12	1.00	9.75
SL (cm)	103.03 ± 7.92	71.55 ± 5.87	58.18 ± 4.22	78.21 ± 4.37	7.00	323.60
SD (mm)	3.13 ± 0.14	2.04 ± 0.06	2.33 ± 0.08	2.52 ± 0.06	0.82	4.87
BS	24.75 ± 1.51	24.91 ± 2.46	25 ± 1.98	24.89 ± 1.29	2.56	103.67
TNT (g)	2.01 ± 0.14	4.11 ± 0.18	5.96 ± 0.24	4.00 ± 0.13	1.00	13.67
TS	2.19 ± 0.12	3 ± 0.12	2.66 ± 0.09	2.61 ± 0.08	1.00	5.00
ATW (g)	8.85 ± 0.75	16 ± 0.79	21.32 ± 1.12	15.26 ± 0.53	2.62	36.64
ATY (g)	25.08 ± 2.24	62.44 ± 3.27	126.79 ± 7.88	71.00 ± 3.33	5.20	342.67

Aero=Aeroponics; SE= Standard error; Min= Minimum; Max=Maximum

TRL (Total root length); RSA (Root surface area); RAD (Average Root diameter); RV (Root volume); RFW (Root fresh weight); RDW (Root dry weight); RBP (Root branching pattern); SFW (Stolon fresh weight); SDW (Stolon dry weight); TNS (Total number of stolons); SL (Stolon length); SD (Stolon diameter); BS (Branches of stolon); TNT (Total number of tubers per plant); TS (Tuber shape); ATW (Average tuber weight); ATY (Average tuber yield).

Stolons; Aero Aeroponics

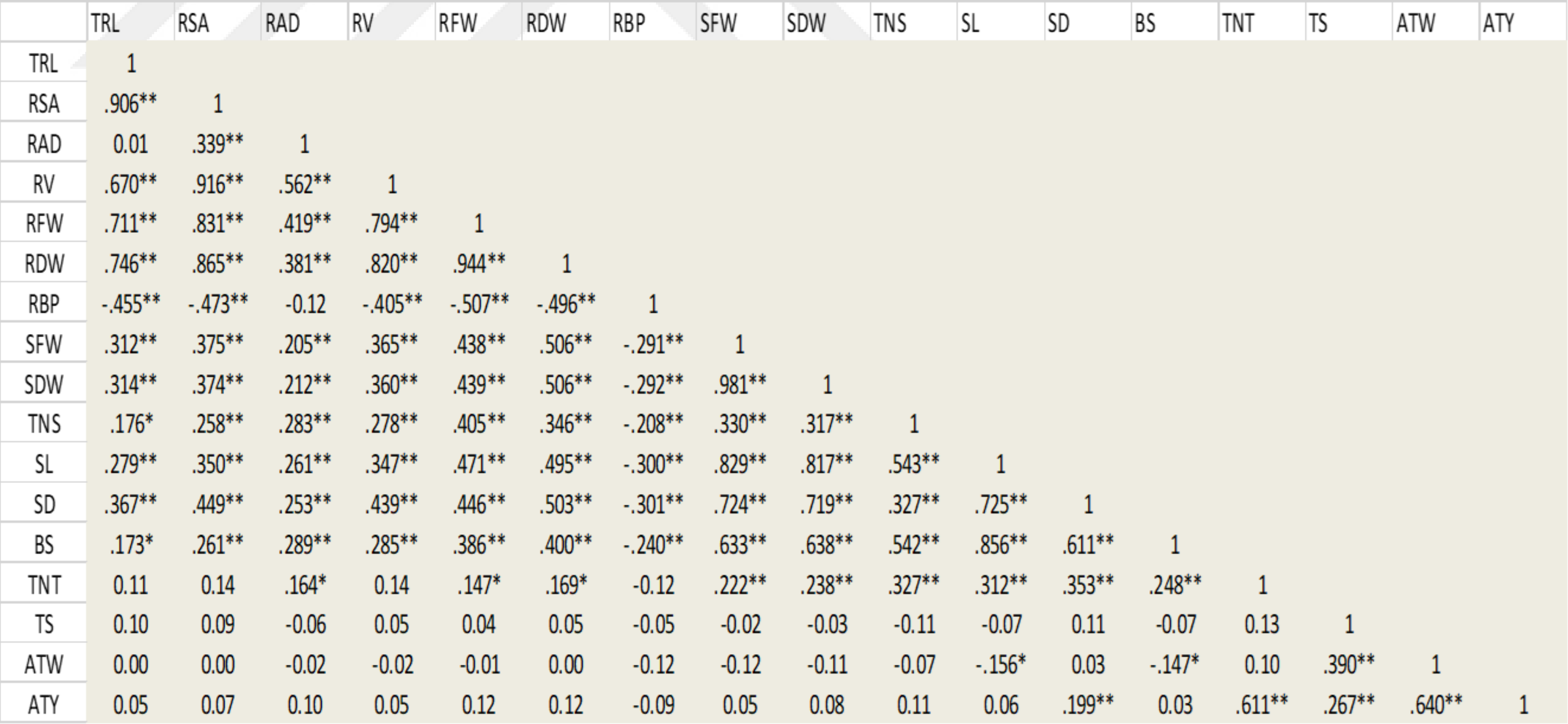
Table 4.3. Broad sense heritability (H^2) for data of aeroponic experiments 2019, 2020, and pot experiment 2020

	Genotypic variance				**Phenotypic variance**				**Heritability (H^2)**			
Traits	**Aero-19**	**Aero-20**	**Pot-20**	**Mean**	**Aero-19**	**Aero-20**	**Pot-20**	**Mean**	**Aero-19**	**Aero-20**	**Pot-20**	**Mean**
TRL	74551429.50	20044706.00	2352590.33	32316242.00	76585711.50	22545882.00	2826964.33	33986186.00	0.97	0.89	0.83	0.90
RSA	6785837.25	1448828.25	314952.00	2849873.00	7131824.25	1639203.25	376779.00	3049269.00	0.95	0.88	0.84	0.89
RAD	0.13	0.05	0.12	0.10	0.15	0.06	0.15	0.12	0.86	0.79	0.78	0.81
RV	6301.90	982.99	430.67	2571.85	6671.81	1137.28	558.98	2789.36	0.94	0.86	0.77	0.86
RFW	1209.16	546.41	508.20	754.59	1268.79	604.39	624.88	832.69	0.95	0.90	0.81	0.89
RDW	20158.33	4.00	3.93	6722.09	31571.03	4.41	4.94	10526.79	0.64	0.91	0.80	0.78
RBP	7.00	4.97	2.83	4.94	7.01	5.10	3.35	5.15	0.99	0.98	0.84	0.94
SFW	3057.00	323.09	99.85	1159.98	3097.97	367.55	128.73	1198.08	0.99	0.88	0.78	0.88
SDW	11.09	1.21	0.95	4.42	11.32	1.44	1.71	4.83	0.98	0.84	0.55	0.79
TNS	6.54	13.14	29.58	16.42	8.56	15.73	37.16	20.48	0.76	0.84	0.80	0.80
SL	29968.25	16943.45	7701.54	18204.41	30404.85	18662.05	9332.05	19466.32	0.99	0.91	0.83	0.91
SD	9.27	1.31	1.96	4.18	10.20	1.72	2.38	4.77	0.91	0.76	0.82	0.83
BS	1094.73	2333.41	1771.42	1733.18	1134.13	2630.43	2063.18	1942.58	0.97	0.89	0.86	0.90
TNT	9.41	14.56	18.14	14.04	12.70	18.11	25.64	18.82	0.74	0.80	0.71	0.75
TS	6.85	4.87	2.49	4.74	7.44	5.36	2.53	5.11	0.92	0.91	0.99	0.94
ATW	310.37	266.71	450.88	342.65	365.04	374.09	606.99	448.70	0.85	0.71	0.74	0.77
ATY	3163.24	4632.29	23156.17	10317.23	3736.85	6654.41	27908.87	12766.71	0.85	0.70	0.83	0.79

TRL (Total root length); RSA (Root surface area); RAD (Average Root diameter); RV (Root volume); RFW (Root fresh weight); RDW (Root dry weight); SFW (Stolon fresh weight); SDW (Stolon dry weight); TNS (Total number of); SL (Stolon length); SD (Stolon diameter); BS (Branches of stolon); TNT (Total number of tubers per plant); TS (Tuber shape); ATW (Average tuber weight); ATY (Average tuber yield).

Table 4.4. Pearson correlation coefficients (r) of all roots, stolons and tuber variables of potato

Pearson correlation coefficients, N = 192
Prob > |*r*| under H_0: ρ =0



	TRL	RSA	RAD	RV	RFW	RDW	RBP	SFW	SDW	TNS	SL	SD	BS	TNT	TS	ATW	ATY
TRL	1																
RSA	.906**	1															
RAD	0.01	.339**	1														
RV	.670**	.916**	.562**	1													
RFW	.711**	.831**	.419**	.794**	1												
RDW	.746**	.865**	.381**	.820**	.944**	1											
RBP	-.455**	-.473**	-0.12	-.405**	-.507**	-.496**	1										
SFW	.312**	.375**	.205**	.365**	.438**	.506**	-.291**	1									
SDW	.314**	.374**	.212**	.360**	.439**	.506**	-.292**	.981**	1								
TNS	.176*	.258**	.283**	.278**	.405**	.346**	-.208**	.330**	.317**	1							
SL	.279**	.350**	.261**	.347**	.471**	.495**	-.300**	.829**	.817**	.543**	1						
SD	.367**	.449**	.253**	.439**	.446**	.503**	-.301**	.724**	.719**	.327**	.725**	1					
BS	.173*	.261**	.289**	.285**	.386**	.400**	-.240**	.633**	.638**	.542**	.856**	.611**	1				
TNT	0.11	0.14	.164*	0.14	.147*	.169*	-0.12	.222**	.238**	.327**	.312**	.353**	.248**	1			
TS	0.10	0.09	-0.06	0.05	0.04	0.05	-0.05	-0.02	-0.03	-0.11	-0.07	0.11	-0.07	0.13	1		
ATW	0.00	0.00	-0.02	-0.02	-0.01	0.00	-0.12	-0.12	-0.11	-0.07	-.156*	0.03	-.147*	0.10	.390**	1	
ATY	0.05	0.07	0.10	0.05	0.12	0.12	-0.09	0.05	0.08	0.11	0.06	.199**	0.03	.611**	.267**	.640**	1

TRL (Total root length); RSA (Root surface area); RAD (Average Root diameter); RV (Root volume); RFW (Root fresh weight); RDW (Root dry weight); SFW (Stolon fresh weight); SDW (Stolon dry weight); TNS (Total number of stolons); SL (Stolon length); SD (Stolon diameter); BS (Branches of stolon); TNT (Total number of tubers per plant); TS (Tuber shape); ATW (Average tuber weight); ATY (Average tuber yield).

4.3. Population Structure and Clustering

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. 4.1a). In order to assess the genetic variation in potato genotypes, PCA analysis was done by using SNP Hapmap numeric matrix with tetra-allelic SNP dosage. PCA results clearly grouped the genotypes into 4 clusters, which authenticates the results of structure analysis (Fig. 4.1b). 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 Figure 4.1b). Individuals having Q values ≥ 0.40 grouped in the same cluster, while those depicting Q values < 0.40 grouped as admixed (Fig. 4.2 and Table 4.5).

Among the 192 genotypes, 1 and 4 clusters contain 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%). Twenty (10.41%) genotypes were classified as admixed ($Q < 0.40$). Cluster 1 and 4 were assigned with more than 50% genotypes. Mostly Turkish breeding lines falls in clusters 1, 2 and 3 with a relative percentage of 64.29%, 60.61% and 80.77%, respectively. Maximum proportion of German verities (52.63%) were found in cluster 4 and German breeding lines (38.60%). Some varieties fall as admixed group/cluster that includes, German varieties (40%), German breeding lines (30%), Turkish breeding lines (15%), and some common varieties grown in both Germany and Turkey (15%). Compared to others, Turkish breeding lines are more distinct and different, possibly due to CIP lines from the International Potato Center in Peru as a parent (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). After structure analysis the Delta K values were obtained and drawn against the number of runs (say 10) to obtain the value of K. Population structure matrix “Q” of the designated K value was used for association mapping analysis as covariates. For example, 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 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 (Klaassen 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 4.5.

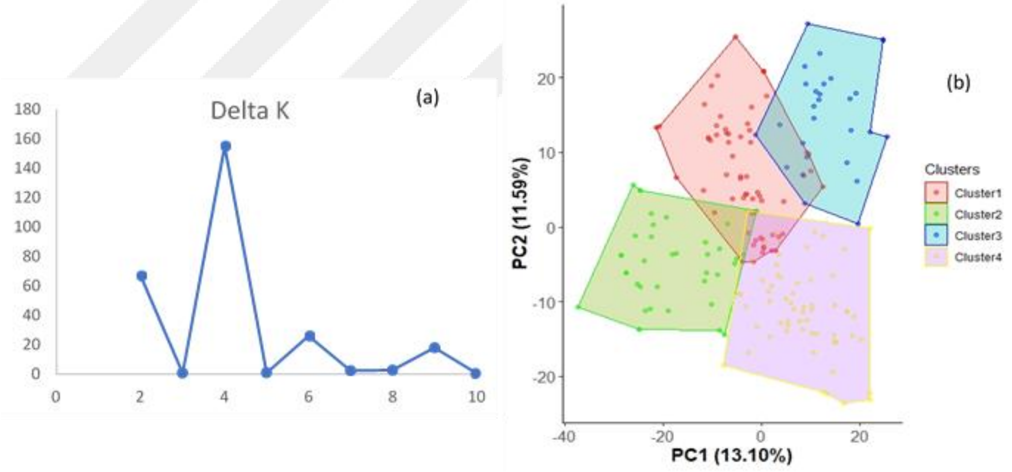


Figure 4.1. Delta K values over 10 runs (ΔK=4) (a), PCA scatter plot of the first two principal components (PC1 and PC2) depicting the clustering of genotypes into 4 clusters as indicated by delta K results from STRUCTURE (b)

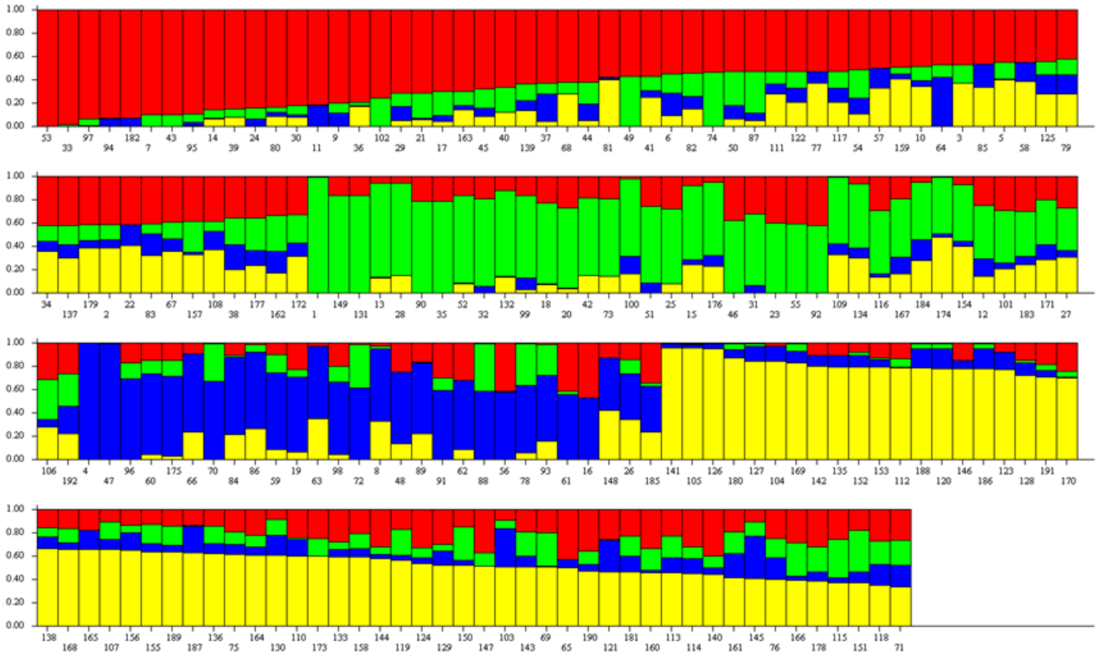


Figure 4.2. Bar plot displaying population sub-structure of 192 genotypes at a population size delta K=4. Sub-population clusters 1, 2, 3 and 4 were represented by colours red, green, blue and yellow, respectively according to the Q values (estimated membership covariates). X axis represents serial no. of genotypes corresponding to each individual bar plot as mentioned in Table S1, whereas y axis symbolizes Q values obtained from structure software

Table 4.5. (a) 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 ($Q \geq 0.40$) (a), Clustering of genotypes in percentage (b)

(a)

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

(b)

Clusters	Common	DE_BL	DE_Var	TR_BL	TR_Var
Admixed	15.00	30.00	40.00	15.00	0.00
1	12.50	8.93	12.50	64.29	1.79
2	9.09	9.09	21.21	60.61	0.00
3	0.00	3.85	7.69	80.77	7.69
4	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

Linkage Disequilibrium (LD) is the non-random association between two different loci and is a pairwise measurement between the polymorphic loci. LD among markers has got a vital role in association mapping studies because it provides information related to the resolution and strength of mapping (Flint-Garcia et al 2005). LD decay is an outcome of genetic distance. LD can decay both short and long-distances, depending on the population, species studied, and the chromosome region studied.

After filtering the monomorphic markers from a total set of 21226 SNPs, 13606 polymorphic markers were obtained and further used to perform LD and association mapping. LD was found for 13386 SNP markers which were mapped on the potato genome. LD was calculated for each chromosome separately as shown in Table 4.6 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 (Mbps). A proposed marker data set showed LD decay at around 2.31 Mbps to an r^2 value of 0.29. (Fig. 4.3).

Extent of LD appears to be between two groups; r^2 at 0.85 Mbp was 0.53 and declined to 0.05 at physical distance of 4.95 Mbp. 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). In this study 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).

221 tetraploid potato genotypes were genotyped with AFLP markers and an LD decay of 5 cM was observed with an r^2 threshold of 0.1 (D'hoop et al 2008), while 10 cM LD decay was reported by Simko et al. (2006). This distance is equal to the 2 and 4 Mbp genetic distance (Vos et al 2017). In this study LD (2.316 Mbp) was within the stipulated range as mentioned in previous studies. Some studies, however, reported slow LD decay at 275 bp Stich et al (2013), but it depends upon the non-linear regression trendline in combination with the choice of r^2 threshold. The LD estimation is proportional to the frequency of large haplotype blocks in the population (Björn et al 2010). In GWAS, LD patterns and haplotype blocks, thus affect the identification of actual SNP variants. Up till now, very few studies attempted to estimate LD in potato using various numbers of genotypes. Zia et al. (2020) obtained significant LD of 47.4% in a diverse panel of 237 potato genotypes, showing an LD decay of 1.22 Mbp against an r^2 value of 0.2. The most important factor that affects LD is the mating system of the species (Nordborg et al 2002). These findings imply the presence of abundant genetic variation suitable to find marker-trait associations.

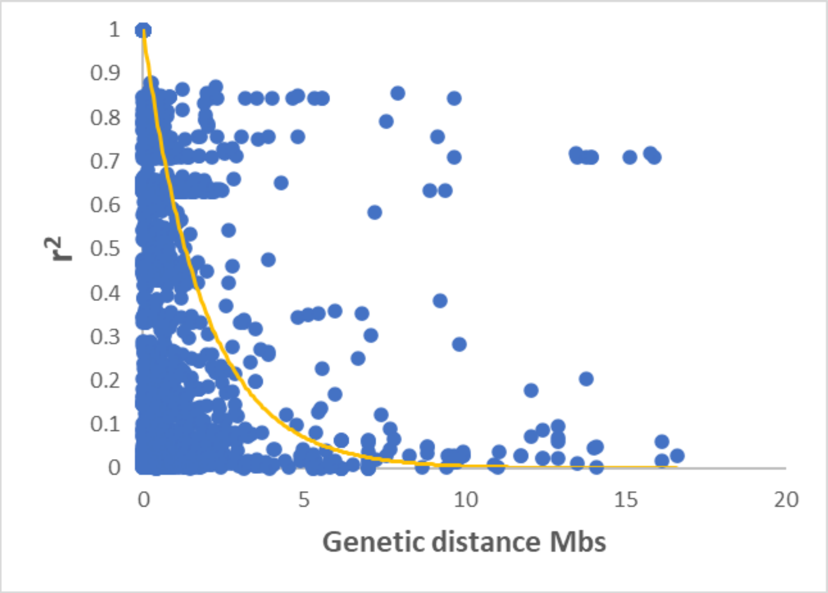


Figure 4.3. Estimated LD (Linkage disequilibrium) decay plotted between r^2 and genetic distance (Mbps) with non-linear trend line. Mean estimated r^2 value is 0.29 with LD decay at 2.31 Mbps calculated from each chromosome as mentioned in Table 4.6

Table 4.6. 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

4.5.1 Root Traits

The potato has shallow adventitious roots (AR) that originate at the base of a sprout once it emerges from the mother tuber. Understanding the origin and nature of AR systems in important crops will contribute to increased production and improve global food security (Joshi and Ginzberg, 2020).

4.5.1.1 Total root length (TRL)

Total root length is an important trait for every crop especially crops having shallow-roots like potato. It is more closely related to water and nutrient uptake than other root variables. The normal distribution of the data was analysed through quantile-quantile plots (Q-Q plots) and revealed normal distribution. Q-Q plots further illustrate the false positives, family structure, and population stratification by a scale of -log10(P) between observed and expected p values. Q-Q plot by additive model showing normal distribution between the observed and expected *p* values (Fig. 4.4).

Manhattan plot was obtained by using additive model in the *GWASpoly* R, showing the significance threshold at -log10(P) ≥ 3.23 (P ≤ 0.00059) for each locus along with the location of SNPs corresponding to each phenotypic trait. We found five SNP markers associated with TRL on chromosomes 2, 7, and 12 (Table 4.7). These SNPs were present in the genes with a putative gene function as protein dehydration-induced, sucrose synthase, phosphoinositide phosphate SAC3, indole-3-acetic acid-amido synthetase and one SNP was found to be uncharacterized.

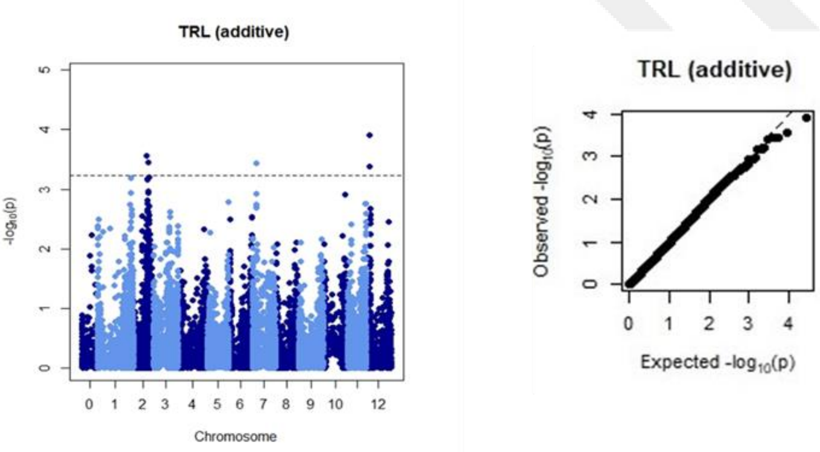


Figure 4.4. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) and Q-Q plot (right) for total root length (TRL) of potato using BLUPs

Table 4.7. SNP markers along with chromosome number and position (bp) found by additive model using BLUPs data set for total root length with sequence ID and its annotation (threshold: -log10(P) ≥ 3.23; P ≤ 0.00059)

SNP Markers	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
solcap_snp_c2_51985	2	33352128	A/G	XM_006364229.2	Protein dehydration-induced 19
PotVar0046554	2	36941161	A/C	PGSC0003DMG400016730	Sucrose synthase
solcap_snp_c1_10842	7	9755448	C/T	XM_006344505.2	Phosphoinositide phosphate SAC3
solcap_snp_c2_34762	12	8063612	A/G	XM_006363449.2	indole-3-acetic acid-amido synthetase
solcap_snp_c2_53918	12	8593980	A/G	XM_006367473.2	uncharacterized

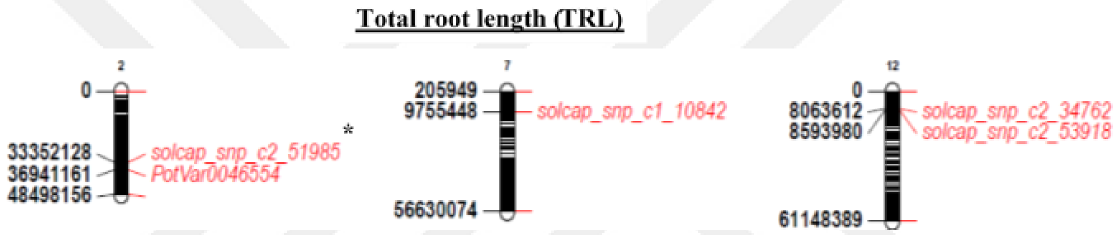


Figure 4.5. Physical chromosomal map exhibiting the localization of significant SNPs linked with TRL along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated with *

A physical map based on chromosome number and physical base pair distance between the SNPs associated with TRL is shown in Figure 4.5. A narrow region of 0.53 Mbp on chr 12 was found to be associated with TRL. Both SNP markers on chr 12 appeared to be closely linked with each other and thus could be possible QTL controlling total root length. Furthermore, gene annotation of the SNP (solcap_snp_c2_34762) located on chr 12 showed a putative gene function of indole-3-acetic acid-amido synthetase. An increase in lateral root length and elongated hypocotyl was observed in *Arabidopsis thaliana* exposed to IAA (Indole acetic acid) (Aoi et al., 2020). According to literature Loudet et al., (2005) identified 13 QTLs associated with traits like root growth and architecture in *Arabidopsis thaliana*. Likewise, Gupta et al., (2020) found a total of 36 QTLs for 15 traits and the number of QTLs ranged from one (root length, root dry biomass, cauline leaf width, number of internodes and internode distance) to seven (for bolting days). So, based on evidence from Arabidopsis, increase in root length can be attributed to the function of indole-3-acetic acid-amido synthetase in potatoes.

4.4.1.2 Root surface area (RSA)

A strong correlation exists between total root length and root surface area. Q-Q plots revealed the normal distribution of the data as the observed vs expected *p* values were uniformly distributed as a straight-line till -log10(P)=3.5. Soon after 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). Furthermore, it illustrates that the model is controlling population stratification (Fig. 4.6).

Manhattan plots were created through MLM in GWASpoly R with additive model using BLUPs. Ten SNPs markers were found to be associated with root surface area through additive model at a threshold of $-\log10(P) \geq 3.23$ ($P \leq 0.00059$). These SNPs were located on chromosomes 2, 10 and 11 (Fig. 4.6 and Table 4.8). Physical map of chromosomes is presented in Figure 4.7. Eight SNPs were present on chr 11 within a narrow region of 1.6 Mbp (43.87 to 45.42 Mbp) and exhibited the presence of a possible QTL on chr 11 linked to RSA. The SNPs on chr 11 were located in the genes with a putative function as protein kinase. Protein kinases are group of proteins that are involved in the development of root hairs and root tip growth in Arabidopsis (Wei and Li, 2018). Root hairs greatly enhances the surface area of the root, thus the SNPs with a plausible gene function as protein kinases in our study could potentially be tagged as a major QTL controlling RSA in potato. RSA was associated with SNP named solcap_snp_c1_10252 located on chr 11 with a putative gene function of calcium transporting ATPase. Ca^{+2}-ATPase plays an important role in the transport and uptake of calcium ions in plant root cells (Hong-Quang and Yu-Ling, 2005). Thus, genomic regions found on chromosome 11 were considered as potential QTL associated with RSA. No any QTLs associated with the studied traits of root i.e., RSA, RV, RFW, RDW were found in potato and closely related species to the best of our knowledge, establishing it as a novel trait.

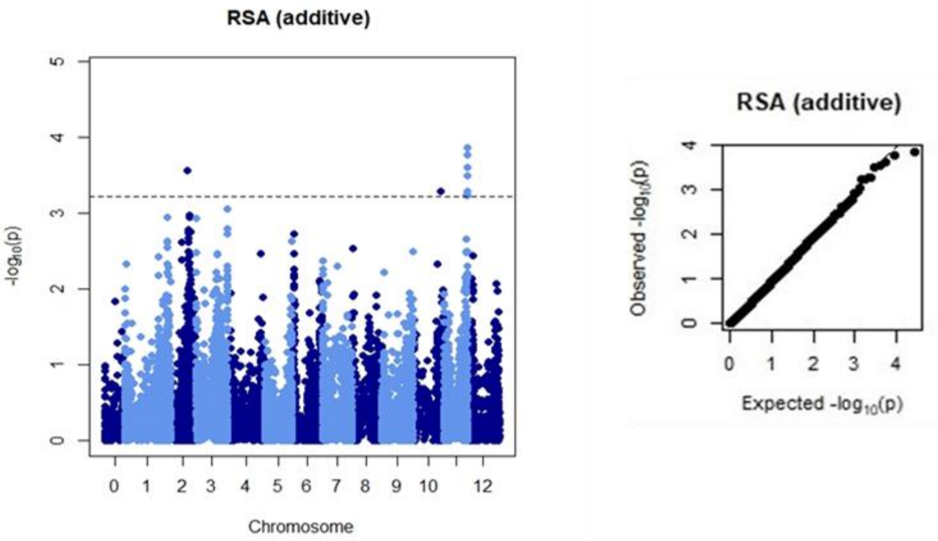


Figure 4.6. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) and Q-Q plot (right) for root surface area (RSA) of potato using BLUPs

Table 4.8. SNP markers along with chromosome number and position (bp) found by additive model using BLUPs data set for root surface area (RSA) with sequence ID and its annotation (threshold: -log10(P) ≥ 3.23; P ≤ 0.00059)

SNP Markers	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
solcap_snp_c2_51985	2	33352128	A/G	XM_006364229.2	Protein dehydration-induced 19
solcap_snp_c2_37963	10	53579712	A/C	CP046683.1	Uncharacterized
PotVar0008906	11	43871440	A/G	PGSC0003DMG400027379	ACI13
PotVar0124359	11	44648033	A/G	PGSC0003DMG400025365	Protein Kinase
solcap_snp_c2_51273	11	44683272	A/G	XM_006365087.2	Phototropin 1
PotVar0117909	11	45054279	C/T	PGSC0003DMG400015546	Endoplasmic reticulum [ER]-type calcium ATPase
PotVar0118016	11	45057709	C/T	PGSC0003DMG400015546	Endoplasmic reticulum [ER]-type calcium ATPase
solcap_snp_c1_10252	11	45059903	A/G	XM_006363281.2	Calcium transporting ATPase 4
solcap_snp_c2_34191	11	45085309	A/C	XM_006363283.2	Protein Kinase HERK 1
solcap_snp_c2_34193	11	45086032	A/G	XM_006363283.2	Protein Kinase HERK 1

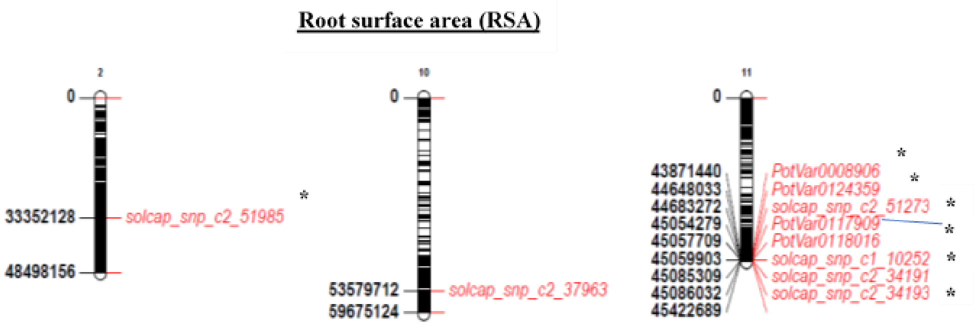


Figure 4.7. Physical chromosomal map exhibiting the localization of significant SNPs linked with RSA along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated with *

4.4.1.3 Average Root Diameter (RAD)

Average diameter of root was observed by high-throughput phenotyping and then combined with genotypic data in *GWASpoly* R to find the marker-trait association. Q-Q plot showed the normal distribution of data with sharp deviation of *p* values in the tail region depicting significant associations (Kaler et al., 2020). The observed vs expected p values were uniformly distributed till -log10(P)=3.5 (Fig. 4.8).

Manhattan plot at a threshold of -log10(P)=3.23 ($P \leq 0.00059$) showed significant marker-trait associations using additive model by employing BLUPs data. Eight significant SNP markers were found to be associated with average root diameter on chromosomes 5, 6, and 11, while one SNP marker was found an unmapped chromosome (Table 4.9). Out of 8 SNPs, five were associated with RAD and positioned on chr 5. SNPs found on chromosome 5 were present in the genes with a plausible function of WRKY transcription factor, magnesium transporter, dihydropterin pyrophosphokinase-dihydropteroate synthase and UDP-glucose:protein transglucosylase. WRKY transcription factors are major class of proteins and found to be associated with stress signalling in the roots of potato (Gallou et al., 2012). Koch et al. (2020) were of the view that magnesium transporters (*StMRS2*) played a vital role in the regulation of root growth through re-mobilization and photo assimilate partitioning of Mg in potato, from source to sink. A genomic region (solcap_snp_c2_37611) located on chromosome 6 had a gene annotation as mitogen-activated protein kinase kinase (MAPKK). MAPKK was involved in the regulation of abscisic acid and this cascade influence root architecture (such as root elongation and cell division) in plants (Li et al., 2017) (Fig. 4.8 and Table 4.9). A region spanning 0.512 Mbp (0.190 to 0.703 Mbp) located on chr 5 was linked to RAD. This genomic region is important and may contain a vital QTL (Fig. 4.9).

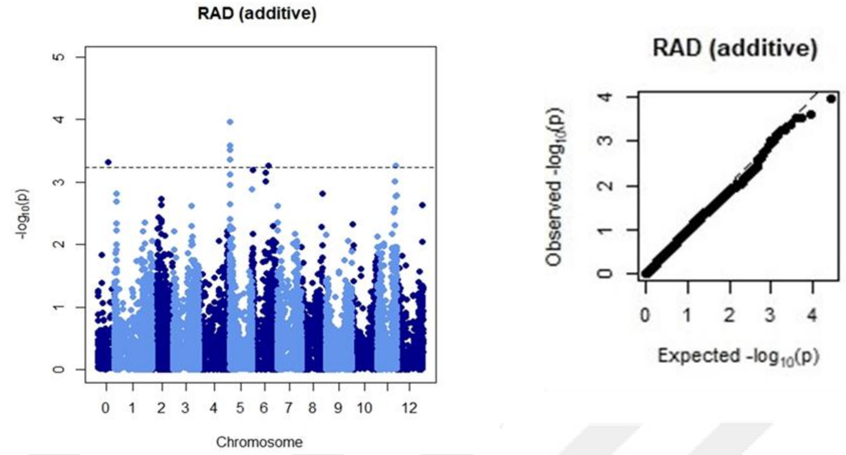


Figure 4.8. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) and Q-Q plot (right) for root average diameter (RAD) of potato using BLUPs

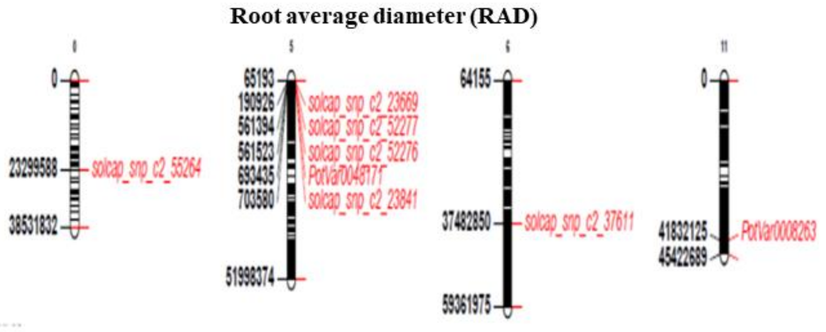


Figure 4.9. Physical chromosomal map exhibiting the localization of significant SNPs linked with RAD along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated with *

Table 4.9. SNP markers along with chromosome number and position (bp) found by additive model using BLUPs data set for average root diameter (RAD) with sequence ID and its annotation (threshold: -log10(P) ≥ 3.23; P ≤ 0.00059)

Marker	Chrom	Position	Variant Ref/Alt	Seq ID	Annotation
solcap_snp_c2_55264	0	23299588	A/C	CP055239.1	Uncharacterized
solcap_snp_c2_23669	5	190926	A/C	NM_001318555.1	WRKY transcription factor 4
solcap_snp_c2_52277	5	561394	C/T	XM_006348622.2	Magnesium transporter MRS2-5
solcap_snp_c2_52276	5	561523	C/T	XM_006348622.2	Magnesium transporter MRS2-5
PotVar0048171	5	693435	G/T	PGSC0003DMG400028362	Dihydropterin pyrophosphokinase-dihydropteroate synthase
solcap_snp_c2_23841	5	703580	C/T	NM_001288097.1	UDP-glucose:protein transglucosylase
solcap_snp_c2_37611	6	37482850	C/T	XM_006363265.2	mitogen-activated protein kinase kinase kinase YODA-like
PotVar0008263	11	41832125	C/T	PGSC0003DMG400001149	Allene oxide synthase 2

4.4.1.4 Root volume (RV)

Root volume is another critical trait, as it plays a significant role in the reproductive and vegetative growth of the plant. Root volume was observed phenotypically by high-throughput phenotyping and then combined with genotypic data in *GWASpoly* R for finding the marker-trait associations. Q-Q plot depicting expected versus observed *p* values at -log10 scale showed sharp deviations in the tail region exhibiting significant marker trait associations. The curve was found to be normal with uniform distribution of *p* values utilizing additive gene action model (Fig. 4.10).

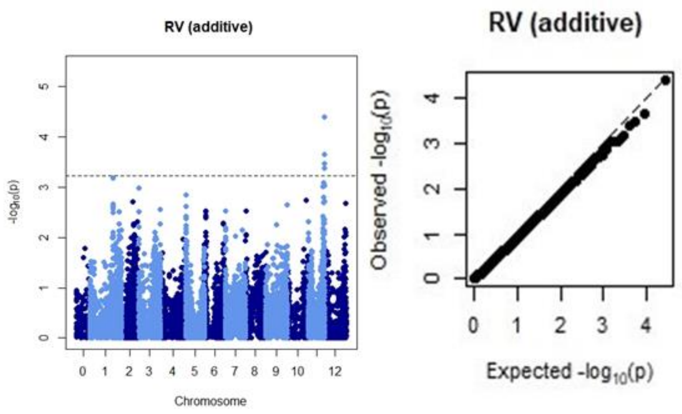


Figure 4.10. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) and Q-Q plot (right) for root volume (RV) of potato using BLUPs

Manhattan plots were created through MLM in GWASpoly R with additive gene action model using BLUPs. Four SNP markers were found to be associated with root volume revealed through additive model at threshold of -log10(P) ≥ 3.23 (P ≤ 0.00059). All of the identified SNPs were located on chromosome 11 (Fig. 4.10 and Table 4.10). Physical map of chromosomes is presented in Figure 4.11. A region spanning 0.72 Mbp (44.68 to 45.42 Mbp) encompassing 4 SNPs were linked to RV and explained the probable presence of a QTL. This region on chr 11 was also associated to RSA, thus all these 4 SNPs were termed as “Pleiotropic SNPs” and linked to both RSA and RV. These SNPs were present in the genes with putative gene function as protein kinase. Protein kinases are group of proteins that are involved in the development of root hairs and root tip growth in Arabidopsis (Wei and Li, 2018). Root hairs greatly enhances the surface area of the root and root volume, thus the SNPs with a plausible gene function as protein kinases in our study could potentially be tagged as a major QTL controlling RSA and RV in potato. Phototropin-1 impact root growth and enhances the efficiency of plants under drought stress (Galen et al., 2007). The SNP with similar gene annotation was present on chr 11 in our study. SNP named solcap_snp_c1_10252 with gene function of Ca^{+2}-ATPase played an important role in the transport and uptake of calcium ions in the root cells (Hong-Quang and Yu-Ling, 2005). Based on our results, it is envisaged the above-mentioned genes play a pivotal role in RV and RSA of potato. Thus, genomic regions found on chromosome 11 were considered as potential QTL associated with both RSA and RV (Fig. 4.11). No any QTLs associated with the studied trait were found in potato and closely related species to the best of our knowledge, establishing it as a novel trait.

As 04 SNP markers present to chromosome number 11 of potato in our studies so we could use these markers as candidate markers for our future breeding programs after being validated.

Table 4.10. SNP markers along with chromosome number and position (bp) found by additive model using BLUPs data set for average root volume (RV) with sequence ID and its annotation (threshold: -log10(P) ≥ 3.23; P ≤ 0.00059)

Marker	Chrom	Position	Variant Ref/Alt	Seq ID	Annotation
solcap_snp_c2_51273	11	44683272	A/G	XM_006365087.2	Phototropin-1
PotVar0117909	11	45054279	C/T	PGSC0003DMG400015546	Endoplasmic reticulum [ER]-type calcium ATPase
solcap_snp_c1_10252	11	45059903	A/G	XM_006363281.2	calcium-transporting ATPase 4, endoplasmic reticulum-type-like
solcap_snp_c2_34193	11	45086032	A/G	XM_006363283.2	receptor-like protein kinase HERK 1

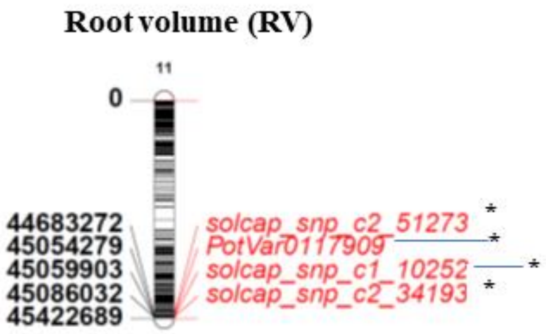


Figure 4.11. Physical chromosomal map exhibiting the localization of significant SNPs linked with RV along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated with *

4.4.1.5 Root branching pattern (RBP)

Q-Q plots revealed the normal distribution of the BLUPs data for RBP, as the observed vs expected *p* values were uniformly distributed as a straight-line till -log10(P)=3. Soon after 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). Furthermore, it illustrates that the model is controlling population stratification (Fig. 4.12).

Manhattan plots were created through MLM in GWASpoly R with additive gene action model using BLUPs. Six SNP markers were found to be associated with root branching pattern revealed through additive model at a threshold of -log10(P) ≥ 3.23 (P ≤ 0.00059). The identified SNPs were present on chr 1, chr 3 and chr 7 (Fig. 4.12 and Table 4.11). Physical map of chromosomes is presented in Figure 4.13. Out of six, 4 SNPs were located on chr 3 within a region spanning 2.96 Mbp (13.92-16.8Mbp) and at a position of 2.72 Mbp. These SNPs were present in genes with a putative gene function of phytoene synthase, glycine-rich RNA-binding protein RZ1C-like and histone. SNPs at chr 1 (solcap_snp_c1_9958 positioned at 53.26 Mbp) and chr 7 (solcap_snp_c1_10013 positioned at 45.14 Mbp) were annotated as DDB1- and CUL4-associated factor and Glucan endo-1,3-beta-glucosidase 12-like, respectively. Glycine-rich RNA binding proteins perform important roles in abiotic stress in the actively proliferating cells such as root tips and determined the root size (Wang et al., 2018). No any QTLs associated with the studied trait were found in potato and closely related species to the best of our knowledge, establishing it as a novel trait. Thus, such identified SNPs may be useful for further studies. These SNPs must be validated before implementing in future breeding studies at GS as well as at MAS.

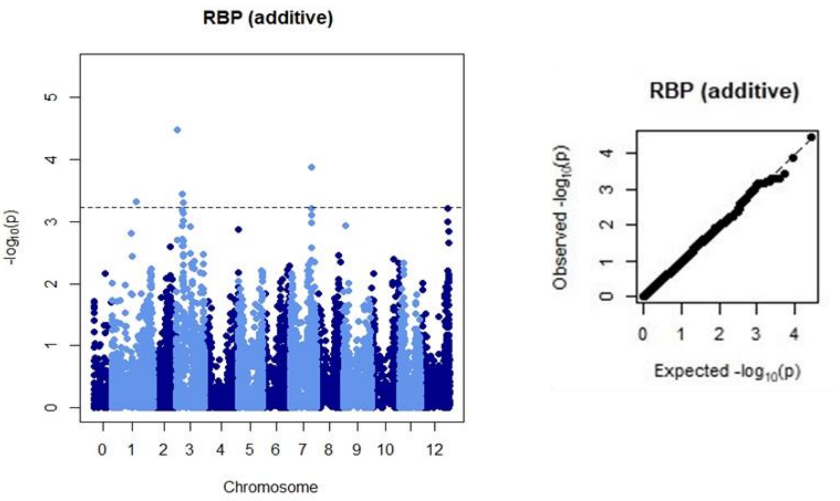


Figure 4.12. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) and Q-Q plot (right) for root branching pattern (RBP) of potato using BLUPs

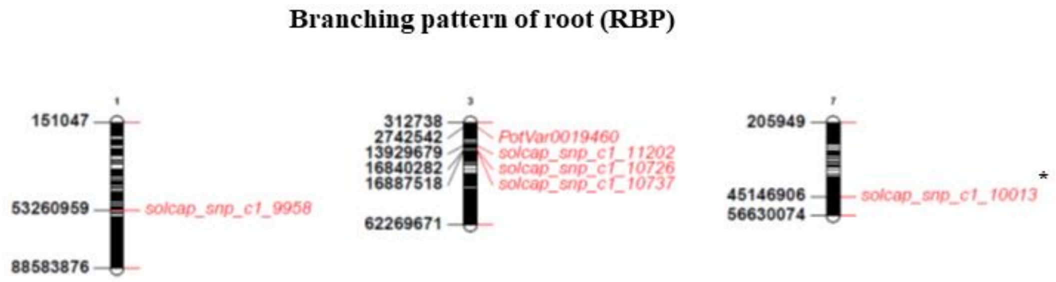


Figure 4.13. Physical chromosomal map exhibiting the localization of significant SNPs linked with RBP along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated with *

Table 4.11. SNP markers along with chromosome number and position (bp) found by additive model using BLUPs data set for average root branching pattern (RBP) with sequence ID and its annotation (threshold: -log10(P) ≥ 3.23; P ≤ 0.00059)

Marker	Chrom	Position	Variant Ref/Alt	Seq ID	Annotation
solcap_snp_c1_9958	1	53260959	A/G	XM_006341832.2	DDB1- and CUL4-associated factor 4
PotVar0019460	3	2742542	C/T	PGSC0003DMG400024063	Phytoene synthase 1, chloroplastic
solcap_snp_c1_11202	3	13929679	A/C	CP055236.1	Unknown
solcap_snp_c1_10726	3	16840282	A/G	XM_006364385.2	Glycine-rich RNA-binding protein RZ1C-like
solcap_snp_c1_10737	3	16887518	G/T	XM_006364383.2	Histone H2B
solcap_snp_c1_10013	7	45146906	A/G	XM_006357904.2	Glucan endo-1,3-beta-glucosidase 12-like

4.4.1.6 Root fresh weight (RFW)

Root fresh weight defines the ability of the plant to absorb water. It also defines the total biomass of the root in the soil. The marker-trait association was calculated for root fresh weight by using BLUPs data set along with genotypic data to find out significant SNP markers. Q-Q plots revealed the normal distribution of the data as the observed vs expected *p* values were uniformly distributed as a straight-line till -log10(P)=3. Soon after 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). Furthermore, it illustrates that the model is controlling population stratification (Fig. 4.14)

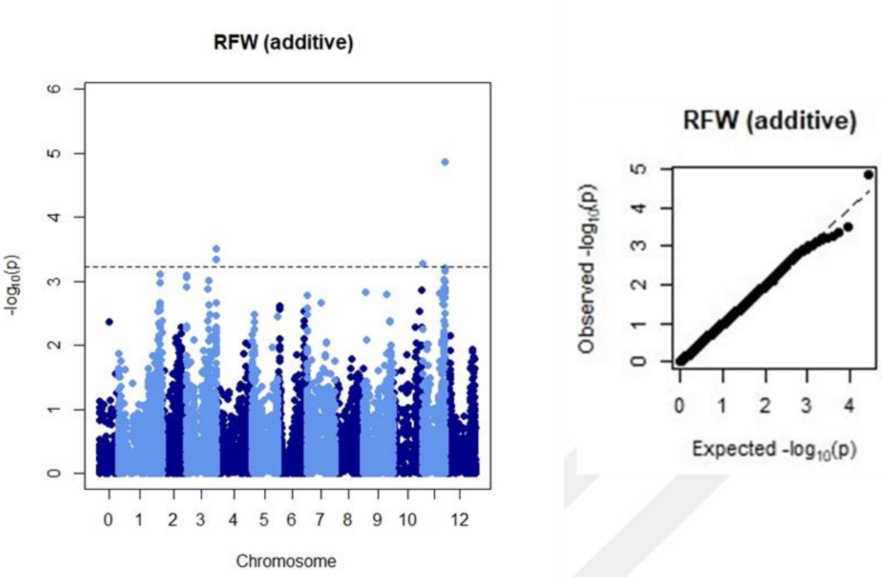


Figure 4.14. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) and Q-Q plot (right) for root fresh weight (RFW) of potato using BLUPs

Table 4.12. SNP markers along with chromosome number and position (bp) found by additive model using BLUPs data set for average root fresh weight (RFW) with sequence ID and its annotation (threshold: -log10(P) $\geq$ 3.23; P $\leq$ 0.00059)

Marker	Chrom	Position	Variant Ref/Alt	Seq ID	Annotation
PotVar0020802	3	61234155	A/G	PGSC0003DMG400002486	Threonine synthase, chloroplastic
PotVar0020782	3	61267788	A/C	PGSC0003DMG400002483	Phosphatidylcholine: Diacylglycerol Acyltransferase
R3a_m_LG11	11	0	C/T	-	-
solcap_snp_c2_51273	11	44683272	A/G	XM_006365087.2	Phototropin-1

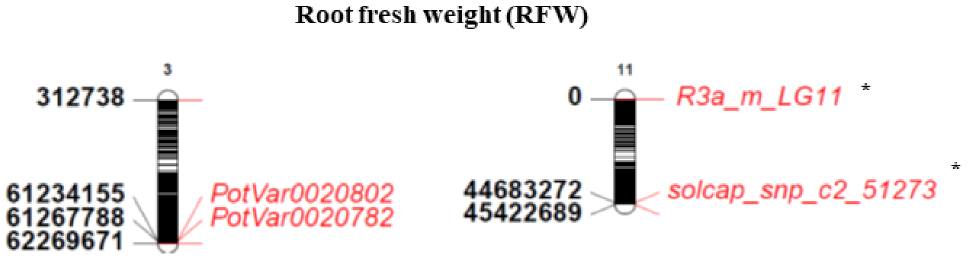


Figure 4.15. Physical chromosomal map exhibiting the localization of significant SNPs linked with RFW along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated with *

Manhattan plots were created through MLM in GWASpoly R with additive gene action model using BLUPs. Four SNP markers were found to be associated with root fresh weight revealed through additive model at a threshold of -log10(P) $\geq$ 3.23 (P $\leq$ 0.00059). The identified SNPs were present on chr 3 and chr 11 (Fig. 4.14 and Table 4.12). Physical map of chromosomes is presented in Figure 4.15. 2 SNPs positioned on chromosome 3 span a region of 0.033 Mbp (61.23 to 61.26 Mbp), while one SNP was located on chr 11 at a position of 44.68 Mbp. These SNPs were present in the genes with putative gene function of threonine synthase, phosphatidylcholine: diacylglycerol acyltransferase and phototropin-1. The SNP named (solcap_snp_c2_51273) showed putative gene annotation as “phototropin-1” that impact root growth and enhances the efficiency of plants under drought stress (Galen et al., 2007). In *Arabidopsis thaliana*, protein phosphatases of serine/threonine class enhanced sensitivity to osmotic stress (País et al. 2009) and regulate the transport of auxins playing critical roles in root elongation (Blakeslee et al. 2008). Roots and stolons are the primary sites of stress perception and signaling (País et al.

2009). In potato, StPP1 and StPP2 genes (belonging to serine/threonine protein phosphatase family) are involved in defense response against salt stress. No any QTLs associated with the studied trait were found in potato and closely related species to the best of our knowledge, establishing it as a novel trait.

4.4.1.7 Root dry weight (RDW)

Marker trait association for root dry weight was calculated by using BLUPs data set along with genotypic data to find significant SNPs. Q-Q plots revealed the normal distribution of the data as the observed vs expected *p* values were uniformly distributed as a straight-line till -log10(P)=3.5. Soon after 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). Furthermore, it illustrates that the model is controlling population stratification (Fig. 4.16).

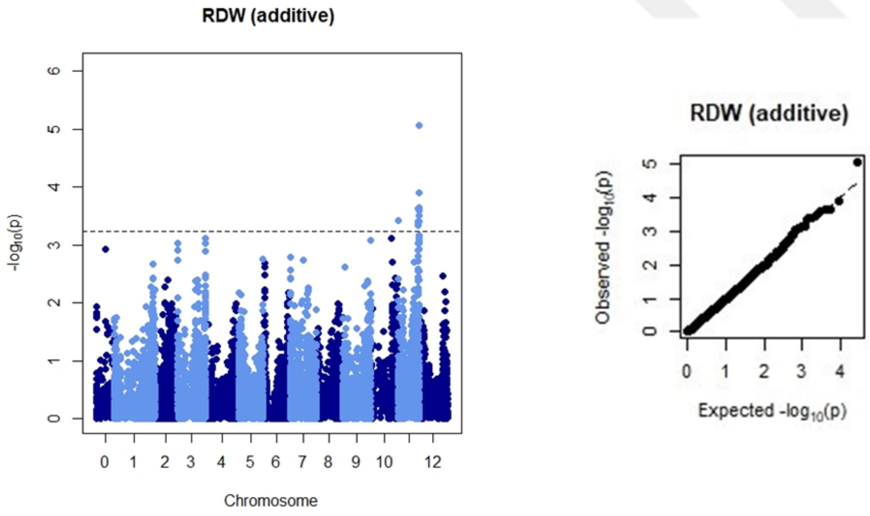


Figure 4.16. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) and Q-Q plot (right) for root dry weight (RDW) of potato using BLUPs

Table 4.13. SNP markers along with chromosome number and position (bp) found by additive model using BLUPs data set for average root dry weight (RDW) with sequence ID and its annotation (threshold: -log10(P) ≥ 3.23; P ≤ 0.00059)

Marker	Chrom	Position	Variant Ref/Alt	Seq ID	Annotation
R3a_m_LG11	11	0	C/T	-	-
solcap_snp_c2_39928	11	43126361	A/C	XM_015302885.1	Beta-glucosidase BoGH3B-like
solcap_snp_c2_39889	11	43298362	C/T	XM_015302950.1	Protein IQ domain 1
PotVar0008857	11	43868548	C/T	PGSC0003DMG400027379	ACI13
PotVar0008906	11	43871440	A/G	PGSC0003DMG400027379	ACI13
PotVar0008949	11	44072039	C/T	PGSC0003DMG400027403	ThiF family protein
PotVar0124359	11	44648033	A/G	PGSC0003DMG400025365	Protein Kinase
solcap_snp_c2_51273	11	44683272	A/G	XM_006365087.2	Phototropin 1
PotVar0117909	11	45054279	C/T	PGSC0003DMG400015546	Endoplasmic reticulum [ER]-type calcium ATPase
solcap_snp_c1_10252	11	45059903	A/G	XM_006363281.2	calcium-transporting ATPase 4, endoplasmic reticulum-type-like
solcap_snp_c2_34193	11	45086032	A/G	XM_006363283.2	receptor-like protein kinase

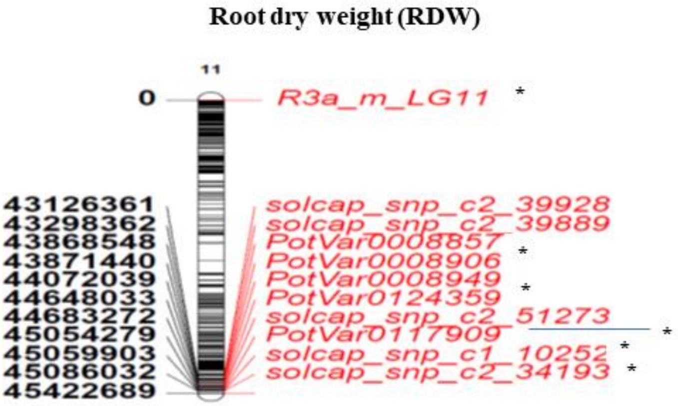


Figure 4.17. Physical chromosomal map exhibiting the localization of significant SNPs linked with RDW along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated with *

Manhattan plots were created through MLM in GWASpoly R with additive gene action model using BLUPs. Eleven SNP markers were found to be associated with root dry weight at a threshold of -log10(P) ≥ 3.23 (P ≤ 0.00059). All the identified SNPs were present on chromosome 11 (Fig. 4.16 and Table 4.13). Physical map of chromosomes is presented in Figure 4.17. A region spanning 2.30 Mbp (43.12 to 45.42 Mbp) on chromosome 11 was associated with RDW. It indicates the possible presence of QTL linked to RDW within this genomic region. The identified SNPs on chr 11 were present in the genes with putative gene function of Beta-glucosidase BoGH3B-like, Protein IQ domain 1, ACI13, ThiF family protein, Protein Kinase, Phototropin 1, Endoplasmic reticulum [ER]-type calcium ATPase, calcium-transporting ATPase 4, endoplasmic reticulum-type-like and receptor-like protein kinase. A genome wide analysis and expression profiling study in potato revealed that protein kinases especially calcium dependent protein kinases (*StCPK*$_{13}$ and *StCPK*$_{18}$) were expressed in all parts of potato plants including roots and stolons (Gromadka et al., 2018). Roots and stolons are the primary sites of stress perception and signalling (País et al. 2009). Gene ontology showed that receptor like protein kinase is responsible for the functioning of serine/threonine protein kinase cascade resulting in cell elongation in all vegetative parts including roots and provide defense response against salt stress. Genes found in protein kinase family are responsible for adaptive plant response in stress conditions. Additionally, receptor like protein kinases are involved in dynamic signalling complex for root hair and lateral development in plants (Duan et al., 2010; Ou et al., 2020). Moreover, pleiotropic SNPs were also present on chr 11 spanning a region of 1.55 Mbp (43.87-45.42 Mbp) associated with RDW, RFW, RSA and RV. Thus, it can be concluded that genomic regions located on chr 11 is associated with root architecture in potato and controls significant root traits. No any QTLs associated with the studied trait were found in potato and closely related species to the best of our knowledge, establishing it as a novel trait.

4.4.2 Stolon Traits

4.4.2.1 Total number of stolons (TNS)

The total number of stolons is one of the imperative traits influencing final tuber yield since swollen stolons referred to as tubers. Total number of stolons were analysed and found with normal distribution curve. Q-Q plot showed that the observed *p* values were uniformly distributed as the expected *p* values. Furthermore, sharp deviations at the tail showed the presence of some significant markers associated with the trait. Manhattan plot was obtained by additive model and showed eighteen SNP markers that were found to be significantly associated with total number of stolons. These SNPs were positioned on chromosomes 1, 4, 5, 10, 11, and 12. (Fig. 4.18 and Table 4.14)

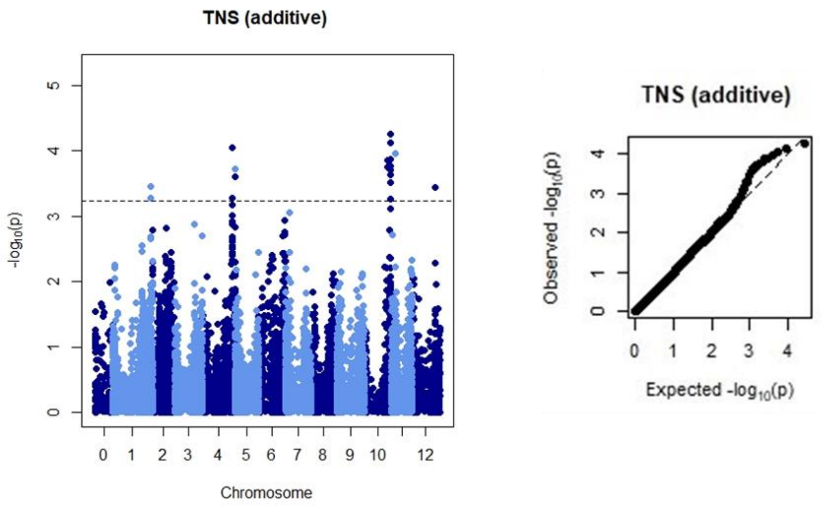


Figure 4.18. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for total number of stolons (TNS) of potato

Table 4.14. SNP markers found by additive model using BLUPs data set for total number of stolons (TNS) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Markers	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
PotVar0035753	1	84646761	A/G	PGSC0003DMG400025796	Longevity assurance factor
PotVar0035852	1	84727400	A/G	PGSC0003DMG400025801	Conserved gene of unknown function
PotVar0000812	4	64801926	C/T	PGSC0003DMG402012897	Unknown
PotVar0000800	4	64802757	A/C	PGSC0003DMG402012897	Unknown
solcap_snp_c1_3499	4	71826344	A/G	XM_006342094.2	Glyceraldehyde-3-phosphate dehydrogenase B
solcap_snp_c2_23832	5	694469	C/T	XM_006348607.2	Folate synthesis bifunctional protein, mitochondrial-like
solcap_snp_c2_27806	10	50615253	A/G	XM_006349411.2	Proteasome subunit alpha type-4-like
solcap_snp_c2_27808	10	50615474	C/T	XM_006349411.2	Proteasome subunit alpha type-4-like
solcap_snp_c2_44193	10	56828920	C/T	XM_006339178.2	Alpha-L-arabinofuranosidase 1-like
solcap_snp_c2_22588	10	57368730	A/G	XM_006351294.2	F-box/kelch-repeat protein At1g15670-like
solcap_snp_c2_22662	10	57644499	C/T	XM_006351263.2	Uncharacterized
PotVar0058153	10	57670719	C/T	PGSC0003DMG400023721	Remorin
solcap_snp_c2_22697	10	57698776	A/G	XM_006351257.2	Zinc finger AN1 and C2H2 domain-containing stress-associated protein 13
solcap_snp_c2_22699	10	57698893	C/T	XM_006351257.2	Zinc finger AN1 and C2H2 domain-containing stress-associated protein 13

solcap_snp_c2_22741	10	57823346	A/G	XM_006351245.2	EGF domain-specific O-linked N-acetylglucosamine transferase-like
PotVar0057984	10	57895786	G/T	PGSC0003DMG401029823	Integral membrane family protein
solcap_snp_c2_12334	11	8281236	C/T	XM_006351057.2	uncharacterized
PotVar0037665	12	50379400	A/G	PGSC0003DMG402031379	Unknown

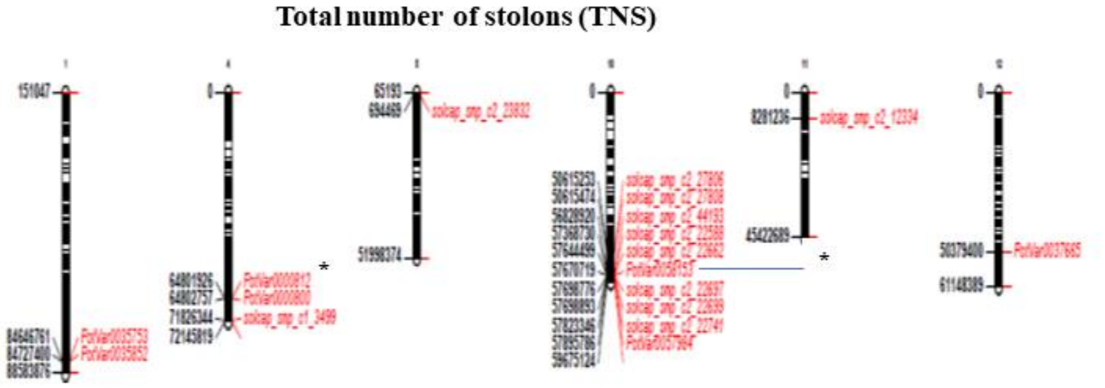


Figure 4.19. Physical chromosomal map exhibiting the localization of significant SNPs linked with TNS along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated by *

Figure 4.19 illustrated the chromosome number and physical base pair distance between the SNPs associated with TNS. On chr 1 a narrow region of 0.08 Mbp was identified. Similarly, on chr 4 a region spanning 0.01 Mbp was found to be associated with TNS. Due to their narrow presence on the chromosomes or closed linkage with each other it was thought these two chromosomes could be a possible QTLs controlling total number of stolons. Chromosome 10 constitutes a genomic region having 10 SNPs spanning a region of 9.06 Mbp linked to TNS. Seven SNPs within this region constitutes a narrow distance of 0.51 Mbp (57.38-57.89 Mbp) and indicates the presence of possible QTL.

Furthermore, these SNPs have their gene annotation like, Glyceraldehyde-3-phosphate dehydrogenase B, Folate synthesis bifunctional protein, Zinc finger protein, Longevity assurance factors, and Proteasome. Our identified SNPs are associated with folate synthesis. Folate are the important minerals that are involved in the better growth or development of living organisms. The genes such as *GTPCHI*, *ADCS*, *HPPK/DHPS*, *and/or FPGS* are involved in the folate enhancement in potato. It was indicated that the overexpression of these genes increased the folate contents up to 12-fold that ultimately enhanced stolon development followed by the number of tubers (De Lepeleire et al., 2018). Zinc finger proteins constitutes an important family of DEGs (differentially expressed genes) in stolons of potato under fluctuating nutrient and water conditions (Tiwari et al., 2020). No any QTLs associated with the studied trait were found in potato and closely related species to the best of our knowledge, establishing it as a novel trait. Similar is the case with rest of the stolon traits i.e., SL, SD, BS, SFW and SDW.

4.4.2.2 Stolon Length (SL)

An association mapping of stolon length was done by combining BLUPs data along with the genotypic data in GWASpoly R to find significant marker-trait associations. Normal distribution of data was analyzed through Q-Q plot and showed that the observed *p* values were uniformly distributed as the expected *p* values up to -log10(P)=3, soon after deviations were noticed indicating significant associations. Overall, Q-Q plot showed normal distribution of data. After this analysis, Manhattan plot was drawn, using BLUPs values using additive gene action and revealed eighteen SNP markers that was associated with the trait of interest at chromosome numbers 2, 4, and 7 (Fig. 4.20 and Table 4.15).

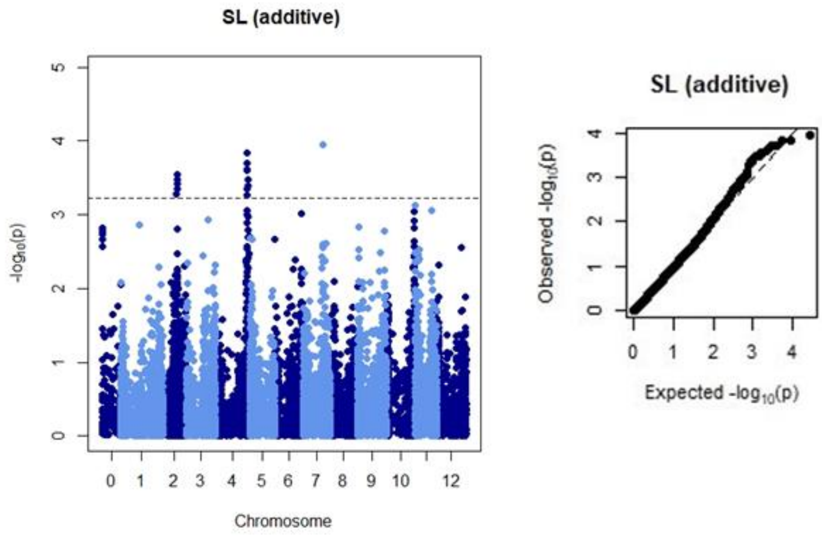


Figure 4.20. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for stolon length (SL) of potato.

Table 4.15. SNP markers found by additive model using BLUP data set for stolon length (SL) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Marker	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
PotVar0124339	2	27089130	A/G	PGSC0003DMG402009429	Taz protein
solcap_snp_c1_11580	2	29540500	C/T	XM_006352915.2	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12
solcap_snp_c2_46903	2	29922614	C/T	XM_006365495.2	Uncharacterized protein At2g34460
solcap_snp_c2_46904	2	29922863	A/G	XM_006365495.2	Uncharacterized protein At2g34460
solcap_snp_c1_13910	2	29990972	A/G	XM_006365502.2	Nuclear pore complex protein GP210
solcap_snp_c2_46890	2	30050056	C/T	XM_006365507.2	Transcription factor bHLH144-like
solcap_snp_c2_46898	2	30147347	C/G	CP046695.1	Unknown
PotVar0000800	4	64802757	A/C	PGSC0003DMG402012897	Unknown
solcap_snp_c1_6750	4	64973019	A/G	XM_006337999.2	Mechanosensitive ion channel protein 3
PotVar0000460	4	65304259	A/G	AFLP	AFLP
solcap_snp_c1_8316	4	65802638	A/G	XM_006364906.2	Probable beta-1,4-xylosyltransferase IRX9H
PotVar0123654	4	65867228	G/T	PGSC0003DMG200006377	DM_SUT4
solcap_snp_c2_25283	4	65867228	A/C	NM_001288141.1	Sucrose transporter 4
PotVar0087095	4	66149105	A/G	PGSC0003DMG400004956	Erg28
PotVar0087316	4	66212200	A/G	PGSC0003DMG400004953	Homeotic protein knotted-1
PotVar0111512	4	67171388	C/T	PGSC0003DMG400021527	Adenine phosphoribosyltransferase
solcap_snp_c2_52195	4	67631327	A/G	XM_006367359.2	Transcription factor MYB44-like
PotVar0069782	7	40642384	C/T	PGSC0003DMG400013546	Sucrose synthase 2

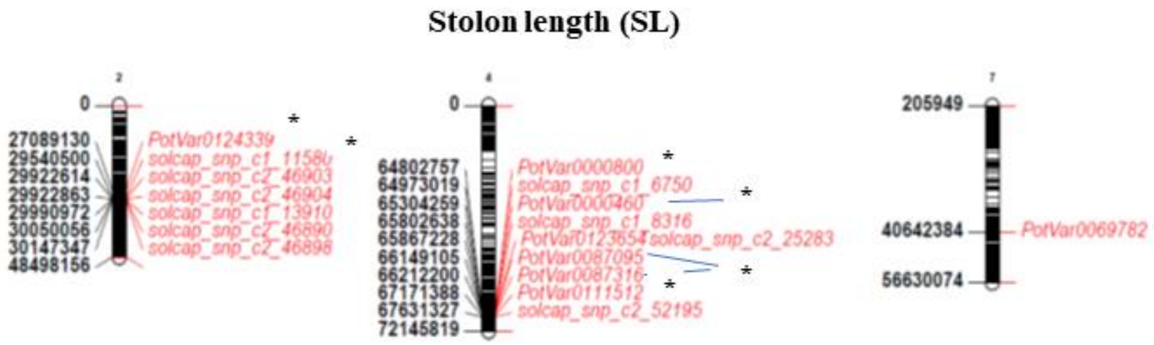


Figure 4.21. Physical chromosomal map exhibiting the localization of significant SNPs linked with SL along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated by *

The chromosome number and physical base pair distance between the SNPs associated with SL were depicted in the Figure 4.21. Furthermore, chromosome map also showed that the 4 SNPs present on the chr 2 has a narrow distance of 0.45 Mbp (29.54 to 29.99 Mbp), while 7 SNPs on chr 4 are closely linked within 1.41 Mbp distance (less than 2.31 Mbp) and there is a possibility of QTLs that are controlling the stolon length within this region.

Among of these SNPs some were showing pleiotropic effect with other traits. These SNPs have their gene annotation such as sucrose synthase 2 and sucrose transporter. Sucrose transporters (*StSUT1*) and sucrose synthase genes (*Sus3* and *SuSy*) are involved in the transport and storage of sucrose in sink organs like potato tuber and sugar beet (Fu and Park 1995; Kühn et al., 2003; Kühn and Grof 2010; Stein and Granot 2019). This might be the reason that SNPs linked to stolon traits (i.e., stolon length) possess the genes with plausible functions as sucrose transporter 4, sucrose synthase 2, and sucrose responsive element binding factor (Table 4.15).

4.4.2.3 Stolon diameter (SD)

Diameter of the stolons were measured manually with the help of digital compass. BLUPs data of phenotypic traits along with the genotypic data was analysed through *GWASpoly* R. Q-Q plots obtained showed non-uniform distribution of data, therefore log transformation was done. By implementing additive model, the Q-Q plot was obtained with nonlinear nature which showed some deviations from uniform distribution, this could be due to the reason of environment and phenotype interactions that affected the stolon characteristic. So, in this case the original data were log transformed and then Q-Q plot were obtained with normal distribution. Q-Q plots of log transformed data exhibited normal distribution of data (Fig. 22). Manhattan plot was drawn by using additive gene action in *GWASpoly* R package and revealed six SNP markers significantly associated with stolon diameter, on chromosomes 2, 5,7, and 8 as mentioned in Table 4.16 (Fig. 4.22).

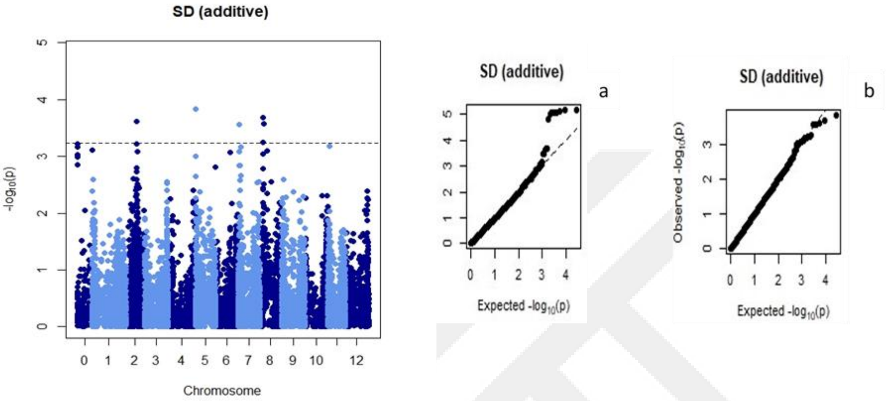


Figure 4.22. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for stolon diameter (SD) of potato. Q-Q plot obtained from normal BLUPs data set (a) and Q-Q plot obtained after log10 transformed data set (b)

Table 4.16. SNP markers found by additive model using BLUP data set for stolon diameter (SD) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Marker	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
solcap_snp_c1_13459	2	27143975	A/G	XM_006364935.2	Choline-phosphate cytidylyltransferase 1-like
solcap_snp_c2_23735	5	388873	C/T	NM_001288234.1	Probable mitochondrial-processing peptidase subunit beta-like
PotVar0102342	7	3170893	A/G	PGSC0003DMG400030748	Dnajc14 protein
solcap_snp_c2_17283	8	8980876	C/T	XM_006364195.2	aminoacyl tRNA synthase complex-interacting multifunctional protein 1
solcap_snp_c2_17294	8	9091210	A/G	XM_006364198.2	guanine nucleotide exchange factor SPIKE 1
solcap_snp_c1_5713	8	9226857	A/G	XM_006364199.2	uncharacterized

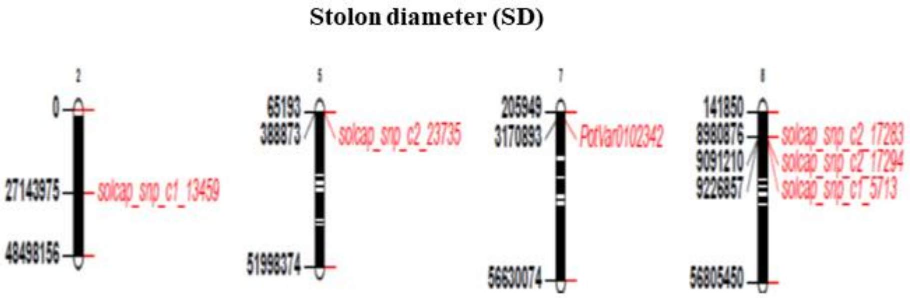


Figure 4.23. Physical chromosomal map exhibiting the localization of significant SNPs linked with SD along with the corresponding physical distance in base pair (bp).

After getting the SNPs associated with SD, the chromosome map was obtained having chromosomes number and physical base pair distance between the SNPs. A narrow region covering 0.246 Mbp (8.98 to 9.22 Mbp) on chr 8 was found to be linked with SD. It could be a possible QTL controlling stolon diameter. Furthermore, chromosome map also showed that the SNPs present on the chr 2 (27.14 Mbp), 5 (0.38 Mbp) and 7 (3.17 Mbp) (Fig. 4.23)

These SNPs have their gene annotation such as Choline-phosphate cytidylyltransferase, Probable mitochondrial-processing peptidase subunit beta-like, Dnajc14 protein, aminoacyl tRNA synthase complex-interacting multifunctional protein, guanine nucleotide exchange factor SPIKE 1 and one SNP identified with uncharacterized function. The SNP known as (solcap_snp_c2_17294) found on chr 8 positioned on 9.09 Mbp distance portraying the gene function as “guanine nucleotide exchange factor SPIKE 1” that is involved in the organization of cell shape as well as tissue development in *Arabidopsis thaliana.*

4.4.2.4 Branching of stolon (BS)

Branching of stolon plays a significant role in the tuber yield, providing sites for tuber formation. Phenotyping of BS was done manually. Q-Q plot showed that the observed *p* values is the same as the expected *p* values but at the end there were two points that were found above of the expected line for this specific trait. Manhattan plot was drawn by MLM model using additive gene action from *GWASpoly* R package. Fourteen SNP markers were found to be significantly associated with branching of stolon on chromosomes 1, 2, 6, 10, 11, and 12 (Fig. 4.24 and Table 4.17).

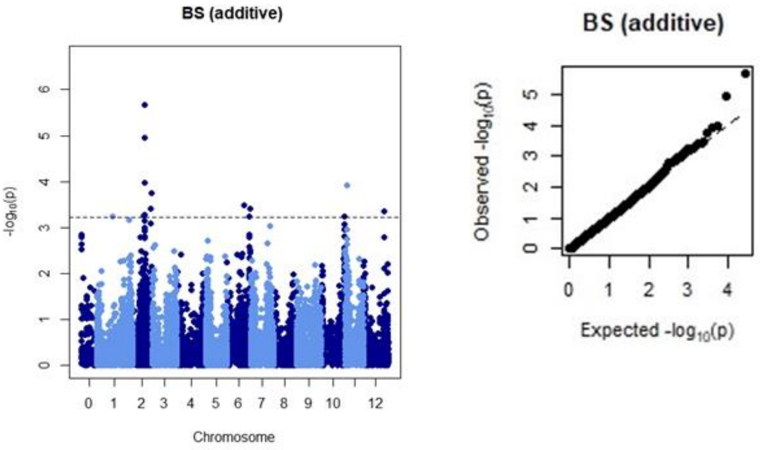


Figure 4.24. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for branching of stolons (BS) of potato and obtained from BLUPs data set

Table 4.17. SNP markers found by additive model using BLUP data set for branching of stolon (BS) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Marker	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
PotVar0047191	1	39256105	A/G	-	Unknown
PotVar0124339	2	27089130	A/G	PGSC0003DMG402009429	Taz protein
solcap_snp_c1_11580	2	29540500	C/T	XM_006352915.2	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12
solcap_snp_c2_51113	2	29665074	C/T	XM_006352908.2	F-box protein At5g46170-like
solcap_snp_c2_51115	2	29665296	A/G	XM_006352908.2	F-box protein At5g46170-like
PotVar0062085	2	29763626	G/T	PGSC0003DMG400021158	Ribosomal protein S14
solcap_snp_c2_15041	2	45652445	C/G	XM_006338315.2	50S ribosomal protein L7/L12
PotVar0002944	2	47625735	G/T	PGSC0003DMG400012642	3-ketoacyl-CoA reductase 1

PotVar0127225	6	42760056	A/G	PGSC0003DMG400011772	Mannose-6-phosphate isomerase
PotVar0041078	6	55569340	C/T	PGSC0003DMG400011997	CPN60A
solcap_snp_c2_50783	6	56978030	C/T	XM_006350754.2	Serine/arginine-rich splicing factor SR45a-like
PotVar0058153	10	57670719	C/T	PGSC0003DMG400023721	Remorin
solcap_snp_c2_47382	11	4250278	A/G	XM_006360453.2	Uncharacterized
PotVar0037683	12	50379146	A/G	PGSC0003DMG402031379	Unknown

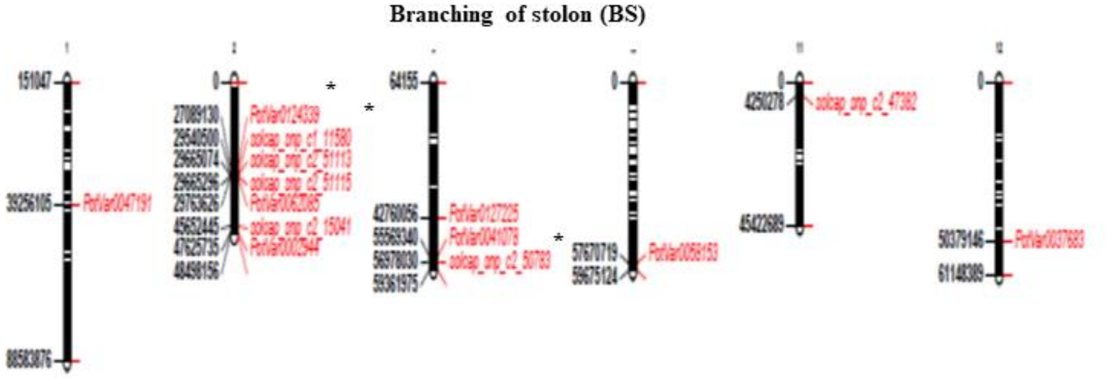


Figure 4.25. Physical chromosomal map exhibiting the localization of significant SNPs linked with BS along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated by *

Physical map showed that 4 SNPs positioned on chr 2 were located within a narrow distance of 0.22 Mbp (29.54 to 29.76 Mbp). Similarly, 2 SNPs on chr 6 were within the 1.41 Mbp distance (55.56-56.97 Mbp). It may represent a possible QTL bearing genomic regions. The SNP markers with asterisk* showed pleiotropic effect such as (PotVar0058153 linked with both TNS and BS), PotVar0124339 (SL, BS), solcap_snp_c1_11580 (SL and BS). A region spanning 2.46 Mbp (27.08 to 29.54) was found to be associated with TNS, SL and BS (Fig. 4.25).

Branching of stolon was associated with SNPs having putative gene function such as Serine/arginine-rich splicing factor SR45a-like. These are responsible for adaptive plant response in stress conditions. Li et al. (2021) came with the discovery that a conserved serine/arginine-rich (SR)-like protein, SR45a, was involved in post-transcriptional regulation of salinity tolerance in *Arabidopsis thaliana*. SR45a is a spliceosome and has two variants (i.e., SR45a-1a and SR45a-1b) and overexpression of these involved in salt stress tolerance. The other SNPs having Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12, Mannose-6-phosphate isomerase, 3-ketoacyl-CoA reductase 1, F-box protein At5g46170-like, Ribosomal protein S14, 50S ribosomal protein L7/L12 functions and some of them with unknown and uncharacterized functions.

4.4.2.5 Stolon fresh weight (SFW)

Q-Q plot showed that the observed *p* values were normally distributed as the expected *p* values. Manhattan plot was obtained by MLM from *GWASpoly* R package with additive gene action and nine SNP markers were found to be associated with the trait of interest (SFW) on chromosome 4. (Fig. 4.26 and Table 4.18). So, it is summarized that chr 4 is important regarding the presence of SNPs controlling SFW.

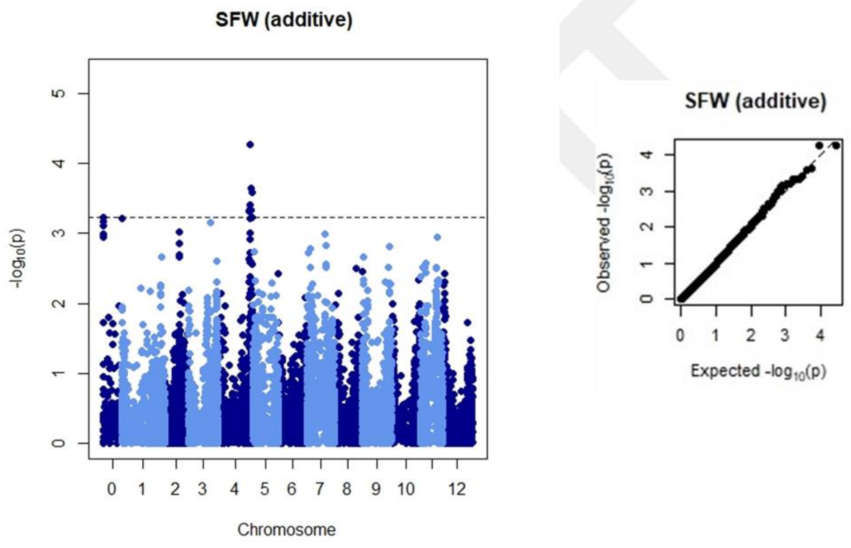


Figure 4.26. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for stolon fresh weight (SFW) of potato and obtained from BLUPs data set

Table 4.18. SNP markers found by additive model using BLUP data set for stolon fresh weight (SFW) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Marker	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
solcap_snp_c2_39453	4	63668434	C/T	XM_006367672.2	Probable pectin methyltransferase QUA2
PotVar0000495	4	65237296	C/T	-	Unknown
PotVar0000460	4	65304259	A/G	AFLP	AFLP
solcap_snp_c2_25283	4	65867228	A/C	NM_001288141.1	Sucrose transporter 4
PotVar0087095	4	66149105	A/G	PGSC0003DMG400004956	Erg28
PotVar0087316	4	66212200	A/G	PGSC0003DMG400004953	Homeotic protein knotted-1
PotVar0111512	4	67171388	C/T	PGSC0003DMG400021527	Adenine phosphoribosyltransferase
PotVar0075328	4	67822283	A/C	PGSC0003DMG400007947	WRKY transcription factor 2
solcap_snp_c2_12956	4	69148721	A/G	XM_006366393.2	BEL1-like homeodomain protein 4

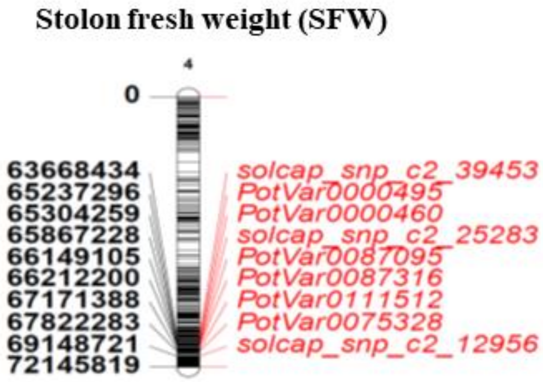


Figure 4.27. Physical chromosomal map exhibiting the localization of significant SNPs linked with SFW along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated by *

Figure 4.27 illustrated the chromosome number and physical base pair distance between the SNPs associated with SFW and these SNPs were spanning a distance of 8.48 Mbp on chr 4. Interestingly, the narrow region of 0.56 Mbp (65.30 to 65.86 Mbp) were showing a pleiotropic effect with SL and a region 0.07 Mbp (66.14 Mbp to 66.21 Mbp) with SL and SDW. Most of the SNPs on the chromosome 4 are closely linked (less than 2.31 Mbp) and indicates the presence of QTL controlling SFW.

Furthermore, these SNPs have their gene annotation like, Probable pectin methyltransferase QUA2. The study showed that OsQUA2 shares similar sequence with rice mutant (*AtQUA2*) and mutation in OsQUA2 resulted in the decrease of HG esterification in the culture sieve element and root cell walls, which ultimately affect the transport of sucrose and the growth of roots and other underground parts, respectively (Qu et al., 2016; Xu et al., 2017). Other SNP named (solcap_snp_c2_25283) identified with a putative function like sucrose transporter 4, sucrose transporters (*StSUT1*) and sucrose synthase genes (*Sus3* and *SuSy*) are involved in the transport and storage of sucrose in sink organs like potato tuber as discussed above. A study revealed that *POTH1* gene is involved in the development and regulation of underground traits by reducing the GA levels in vegetative meristems (Rosin et al., 2003). SNP having putative function as a WRKY transcription factor was also found. Gallou et al. (2012) conducted research and suggested that the WRKY transcription factor genes are involved in the mechanisms controlling the arbuscular mycorrhizal establishment by the regulation of plant defense genes that ultimately involved in the development of underground parts (i.e., stolons) of potato.

4.4.2.6 Stolon dry weight (SDW)

The curve was found to be normal and harp deviations were observed the tail region providing an indication of significant marker-trait associations. After getting Q-Q plot, the Manhattan plot was drawn by *GWASpoly* R package with additive gene action. Three SNP markers were found to be associated with stolon dry weight on chromosomes 3 and 4. While eight SNP markers were found on unmapped chromosome (Fig. 4. 28 and Table 4.19).

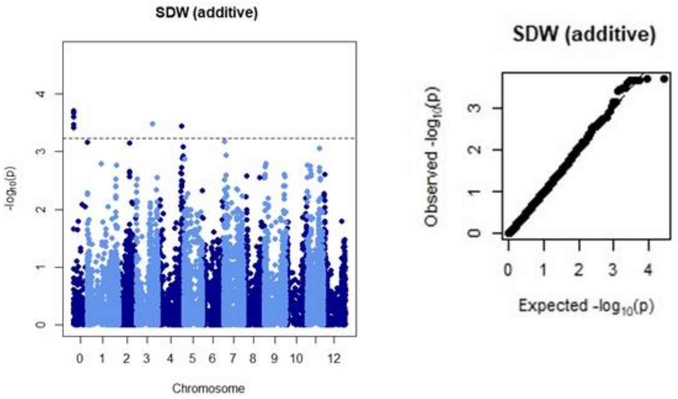


Figure 4.28. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for stolon dry weight (SDW) of potato and obtained from BLUPs data set.

Table 4.19. SNP markers found by additive model using BLUP data set for stolon fresh weight (SFW) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Marker	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
PotVarCP00005	0	0	C/T	-	Unknown
PotVarCP00017	0	0	A/G	-	Unknown
PotVarCP00027	0	0	C/T	-	Unknown
PotVarCP00029	0	0	A/G	-	Unknown
PotVarCP00071	0	0	A/G	-	Unknown
PotVarCP00081	0	0	G/T	-	Unknown
PotVarCP00122	0	0	A/G	-	Unknown
PotVarCP00219	0	0	G/T	-	Unknown
solcap_snp_c2_57863	3	46423284	A/G	XM_006347458.2	Protein TRANSPARENT TESTA GLABRA 1-like
PotVar0087095	4	66149105	A/G	PGSC0003DMG400004956	Erg28
PotVar0087316	4	66212200	A/G	PGSC0003DMG400004953	Homeotic protein knotted-1

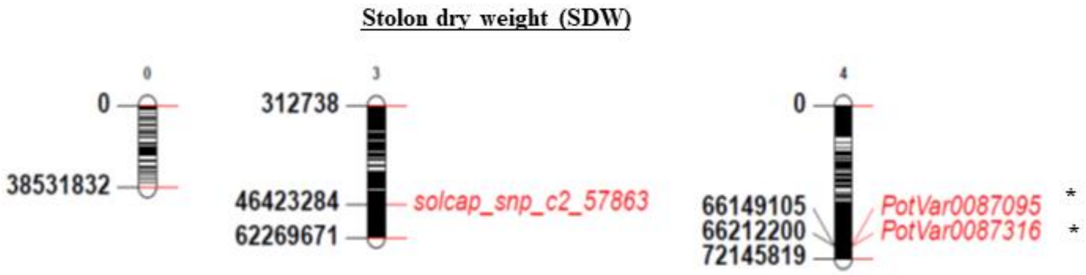


Figure 4.29. Physical chromosomal map exhibiting the localization of significant SNPs linked with SDW along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated by *

A physical map based on chromosome and physical base pair distance between the SNP markers associated with the studied stolon dry weight traits is portrayed in Figure 4.29. The narrow region of 0.07 Mbp (66.14 to 66.21 Mbp) on chr 4 (having a pleiotropic SNP) was found to be associated with SFW and SL.

These identified SNPs have their gene annotations such as, Protein TRANSPARENT TESTA GLABRA 1-like, Erg28, and Homeotic protein knotted-1.

4.4.3 Tuber Traits

4.4.3.1 Total number of tubers per plant (TNT)

The total number of tubers per plant was counted and then phenotypic BLUPs data was combined with genotypic data for marker-trait association studies. Before AM studies, Q-Q plot was drawn and noticed non-uniform distribution. This could be due to the reason of environment and phenotype interactions that affected formation of number of stems that ultimately caused the number of tubers per plant. The data was transformed by log10 transformation to normalize the data and then Q-Q plots were obtained with quite normal distribution. (Fig. 4.29). Manhattan plot was taken from *GWASpoly* R by using additive gene action and found three SNP markers that were associated with total number of tubers on chromosome 6 and 7 (Table 4.20 and Fig. 4.30).

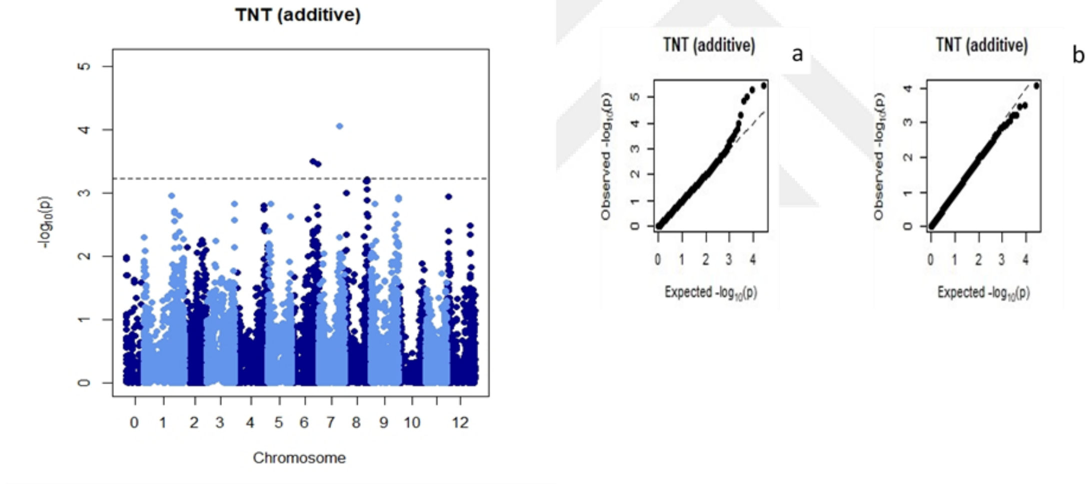


Figure 4.30. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for total number of tubers (TNT) of potato using BLUPs

Table 4.20. SNP markers found by additive model using BLUP data set for total number of tubers (TNT) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Markers	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
PotVar0085941	6	47270969	A/G	PGSC0003DMG400005177	NTGP4
solcap_snp_c2_9219	6	58219072	A/G	XM_006352609.2	GTP cyclohydrolase 1
solcap_snp_c1_10013	7	45146906	A/G	XM_006357904.2	Glucan endo-1,3-beta-glucosidase 12-like

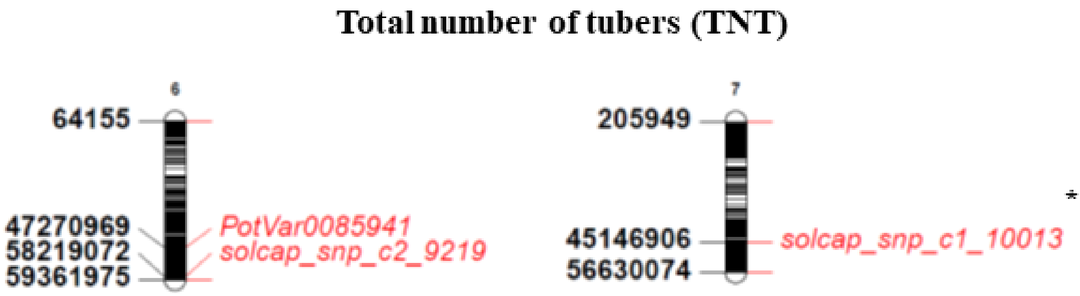


Figure 4.31. Physical chromosomal map exhibiting the localization of significant SNPs linked with TNT along with the corresponding physical distance in base pair (bp). Pleiotropic SNPs are indicated by *

According to Figure 4.31, the SNP markers named PotVar0085941 and solcap_snp_c2_9219 were located on chromosome 6 with a physical distance of 10.94 Mbp (47.27 to 58.21 Mbp) associated with TNT. Other SNP named solcap_snp_c1_10013 showed pleiotropic effect and associated with both TNT and RBP positioned at 45.14 Mbp.

These identified SNPs have their putative gene functions like NTGP4, GTP cyclohydrolase and Glucan endo-1,3-beta-glucosidase 12-like. The transcript (i.e., *GTPCHI*) of GTP cyclohydrolase 1 is involved in the synthesis of folate mineral that is important for better growth and development in living organisms. It was indicated that the overexpression of this transcript increases the folate contents up to 12-fold that ultimately increase the shelf life of tubers as well as tubers production (De Lepeleire et al., 2018). The identified SNP solcap_snp_c1_10013 showed putative gene function of Glucan endo-1,3-beta-glucosidase 12-like protein, the gene *GLUB3* (belonging to Glucan endo-1,3-beta-glucosidase 12-like) are involved in a defense response against fungal pathogens (Balasubramanian et al., 2012). According to literature Manrique-Carpintero et al., (2015) identified QTLs on chromosome number 5 associated with total number of tubers per plant by using diploid potato species. Rak et al., (2017) did QTL mapping for number of tubers per plant by using auto-tetraploid family, and found that the number of tubers per plant trait is associated to chromosome # 4, 5 and 10. In our results, we found an SNP linked with this trait on chromosome # 6 and 7 that are contradictory to the findings of Manrique-Carpintero et al., (2015) and Rak et al., (2017). Contradiction is quite normal because it may be possible due to the previous studies were conducted by using diploid mapping populations.

4.4.3.2 Tuber shape

Marker trait association for tuber shape was calculated by using BLUPs data set along with genotypic data to find significant SNPs. Q-Q plots revealed the normal distribution of the data as the observed vs expected *p* values were uniformly distributed as a straight-line till -log10(P)=3.5. Soon after 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). Furthermore, it illustrates that the model is controlling population stratification (Fig. 4.32)

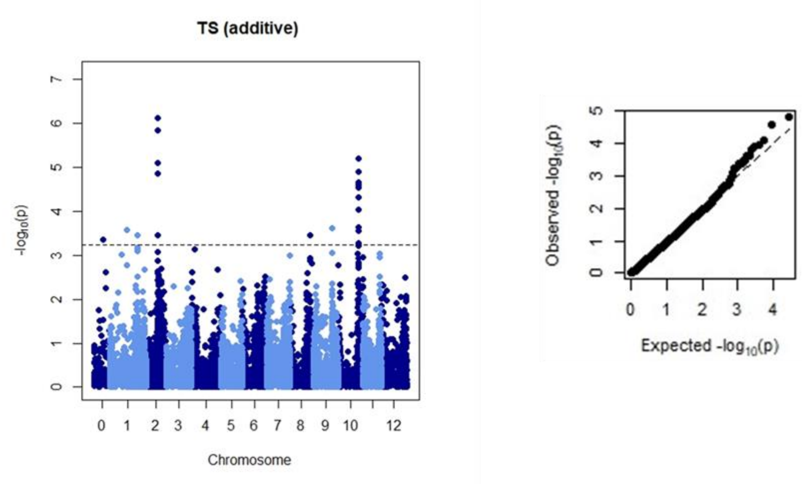


Figure 4.32. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for tuber shape (TS) of potato using BLUPs

Table 4.21. SNP markers found by additive model using BLUP data set for tuber shape (TS) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

Marker	Chrom	Position	Variant Ref/Alt	Seq ID	Annotation
solcap_snp_c2_56344	0	22129989	C/T	XM_006367337.2	Ferredoxin
PotVar0114094	1	42213437	C/T	AFLP	AFLP
PotVar0098536	1	67210899	A/G	PGSC0003DMG401031123	Utp-glucose-1-phosphate uridylyltransferase
solcap_snp_c2_41980	2	27557527	C/T	XM_006364983.2	Sulfiredoxin, chloroplastic/mitochondrial
solcap_snp_c1_12330	2	27618698	A/G	XM_006364974.2	50 S ribosomal protein L 30
solcap_snp_c2_42060	2	27679089	C/T	XM_006367829.1	Uncharacterized protein At4g19900
solcap_snp_c2_38942	2	27856828	A/C	XM_015303064.1	Glutathionyl-hydroquinone reductase YqjG
solcap_snp_c2_38936	2	27860001	A/T	XM_015303064.1	Glutathionyl-hydroquinone reductase YqjG
PotVar0063529	8	48935556	A/C	PGSC0003DMG400002398	Gamma-tocopherol methyltransferase
solcap_snp_c1_4090	9	46138944	C/T	XM_006355832.2	ABC transporter C family member 5
solcap_snp_c2_25526	10	48617149	A/G	XM_015302933.1	Uncharacterized
solcap_snp_c2_25522	10	48617457	C/T	XM_015302933.1	Uncharacterized
PotVar0111687	10	48721966	C/T	PGSC0003DMG200031229	-
solcap_snp_c2_25485	10	48737840	C/T	XM_006362277.2	Serine/threonine-protein kinase AtPK2/AtPK19
solcap_snp_c1_16351	10	48761642	C/T	XM_006362284.2	Phospholipid-transporting ATPase 1-like
solcap_snp_c2_25471	10	48808404	C/T	XM_006362286.2	Transmembrane protein 87B-like
solcap_snp_c2_25469	10	48808653	C/T	XM_006362286.2	Transmembrane protein 87B-like
solcap_snp_c1_8021	10	48862950	A/G	XM_006362290.2	B3 domain-containing transcription repressor VAL2
solcap_snp_c1_8019	10	48863165	A/G	XM_006362290.2	B3 domain-containing transcription repressor VAL2
solcap_snp_c2_55948	10	48982352	C/T	XM_006365292.2	Aspartate aminotransferase, mitochondrial-like
solcap_snp_c2_57640	10	49179309	A/G	XM_006365294.2	Cationic peroxidase 1-like

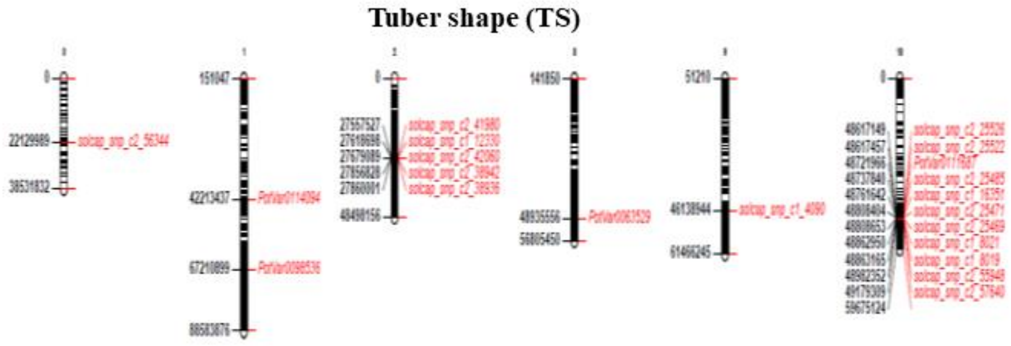


Figure 4.33. Physical chromosomal map exhibiting the localization of significant SNPs linked with TS along with the corresponding physical distance in base pair (bp).

Manhattan plots were created through MLM in GWASpoly R with additive model using BLUPs. Twenty-one SNP markers were found to be associated with tuber shape through additive model at a threshold of -log10(P) ≥ 3.23 (P ≤ 0.00059). These SNPs were located on chromosomes 1, 2, 8, 9 and 10, while one SNP was present on an unmapped chromosome (Fig. 4.32 and Table 4.21). Physical map of chromosomes is presented in Figure 4.33. Eleven SNPs were present on chr 10 within a narrow region of 0.56 Mbp (48.61 to 49.17 Mbp) and exhibited the presence of a possible QTL on chr 10 linked to tuber shape. Likewise, chr 2 also contain a narrow region within 0.31 Mbp (27.55-27.86 Mbp) associated with TS. The SNPs on chr 10 were located in the genes with a putative function as B3 domain-containing transcription repressor VAL2. It is involved in the signalling cascade that controls tuber development (Hannapel et al., 2017). Aspartate aminotransferase is involved in the formation of asparagine in potato tuber (Muttucumaru et al., 2014). The SNP named solcap_snp_c2_38942 found on chr 2 had a putative gene function of Glutathionyl-hydroquinone reductase that detoxify ROS species like H_2O_2 to H_2O and maintain cellular redox homeostasis during tuber development (Cheng et al., 2020). One SNP marker named (solcap_snp_c2_25485) was identified on chr 10 having a putative gene function as Serine/threonine-protein kinase. In *Arabidopsis thaliana*, serine/threonine class are involved to enhanced the sensitivity to osmotic stress (País et al., 2009) and regulate the transport of auxins playing critical roles during stress condition. A few studies have been conducted to find the genomic regions controlling tuber shape trait. As per existing literature, Bradshaw et al., (2008) performed mapping study to find the QTLs associated with tuber shape and identified 4 QTLs related to TS by using tetraploid full-sib family consisting of 227 clones after a crossing between table cultivar

Stirling and 12601ab1. Similarly, another genetic mapping study was carried out by utilizing heterozygous full-sib diploid potato population (06H1) based on the use of a set of 8,303 single nucleotide polymorphism (SNP) markers and identified a significant QTLs on chromosome number 2 and 10 (Parashar et al., 2014), that was accordance to our results. Van eck et al., 1994 and Endelman and Jansky, 2016 were also revealed some QTLs linked with tuber shape on chromosome number 2 and 10 by implementing RFLP markers in diploid potato population. Two more studies also showed the QTLs for tuber shape on chromosome 10 in diploid population of potato (Meijer et al., 2018; Hara-Skrzypiec et al., 2018). According to recent study by Zia et al., (2020), performed an association mapping by using 12K SolCAP array and found 2 SNPs on chromosome 10 and 1 SNP marker on chromosome 4 that is in line with our results as well as with Kreuze et al. (2015). We identified SNPs on chromosomes 1, 2, 8, 9 and 10. Thus, genomic regions found on chromosome 2 and 10 were considered as potential QTLs associated with TS in accordance with the previous literature.

4.4.3.3 Average tuber weight (ATW)

After Q-Q plot analysis we noticed that observed values did not follow normal distribution pattern. The data was transformed to log10 values for data normalization. Q-Q plot was drawn by using transformed data and found that the observed vs expected *p* values follow normal distribution. After -log10(P)=3, sharp deviation was observed in the *p* values at the tail region and *p* values curved towards normally distributed line indicating significant marker-trait associations (Fig. 4.34).

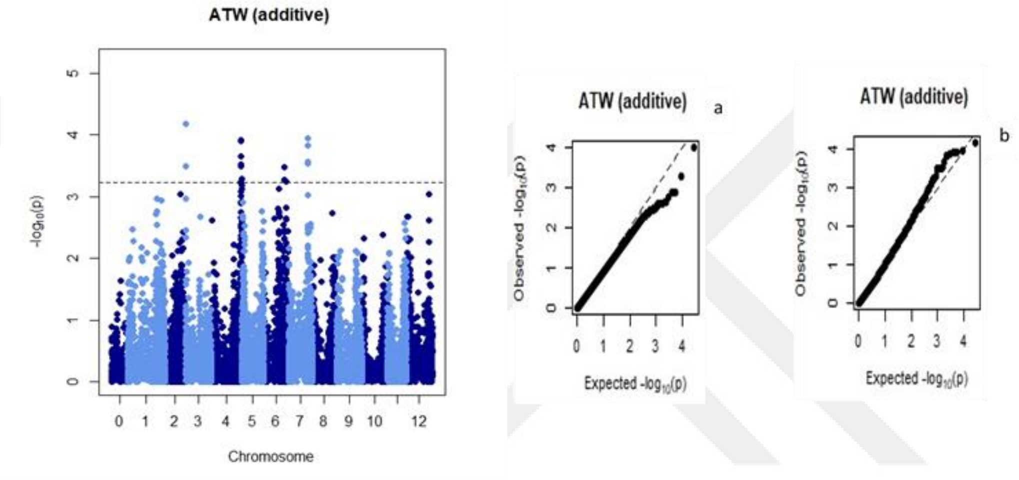


Figure 4.34. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for average tuber weight (ATW) of potato. (a) Q-Q plot obtained from BLUPs data set and (b) Q-Q plot obtained from log10 transformed data set.

Table 4.22. SNP markers found by additive model using BLUP data set for average tuber weight (ATW) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

SNP Marker	Chrom	Position	Variant Ref/Alt	Sequence ID	Annotation
solcap_snp_c2_52809	3	1575045	A/G	CP046682.1	Uncharacterized
solcap_snp_c2_52811	3	1580212	C/T	XM_006367716.2	transcription factor IIIB 60 kDa subunit
PotVar0015043	4	69623215	C/T	PGSC0003DMG400005140	GYF domain-containing protein
solcap_snp_c1_10211	4	70065735	C/T	XM_006341904.2	inositol-pentakisphosphate 2-kinase-like
solcap_snp_c1_10202	4	70396887	A/C	XM_006341937.2	coatomer subunit alpha-1-like
PotVar0015639	4	70760360	C/T	PGSC0003DMG400003779	Eukaryotic initiation factor 3 gamma subunit family protein
solcap_snp_c2_35959	4	70787279	C/T	NM_001288386.1	hexokinase-related protein 1
solcap_snp_c2_35958	4	70787357	C/T	NM_001288386.1	hexokinase-related protein 1
PotVar0015848	4	70790948	A/C	PGSC0003DMG400009862	Clathrin coat assembly protein AP17
PotVar0015898	4	70807382	A/G	PGSC0003DMG400009936	Beta-fructofuranosidase
PotVar0015907	4	70807924	C/T	PGSC0003DMG400009936	Beta-fructofuranosidase
PotVar0017551	4	72024197	A/C	PGSC0003DMG400010007	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha
solcap_snp_c2_16780	6	48020360	A/G	XM_006357393.2	chlorophyll a-b binding protein CP26, chloroplastic
solcap_snp_c2_16817	6	48131679	C/T	XM_006357375.2	Uncharacterized
solcap_snp_c2_22289	6	53307968	A/C	XM_006347290.2	CASP-like protein 1F1
PotVar0093790	7	45136020	A/G	PGSC0003DMG400000690	Conserved gene of unknown function
solcap_snp_c2_33495	7	45145932	C/T	XM_006357904.2	glucan endo-1,3-beta-glucosidase 12-like
solcap_snp_c2_33492	7	45146134	A/T	XM_006357904.2	glucan endo-1,3-beta-glucosidase 12-like
solcap_snp_c1_10001	7	45239915	A/T	XM_006357912.2	protein disulfide isomerase-like 2-3
solcap_snp_c1_10000	7	45242018	A/G	XM_006357912.2	protein disulfide isomerase-like 2-3

Average tuber weight (ATW)

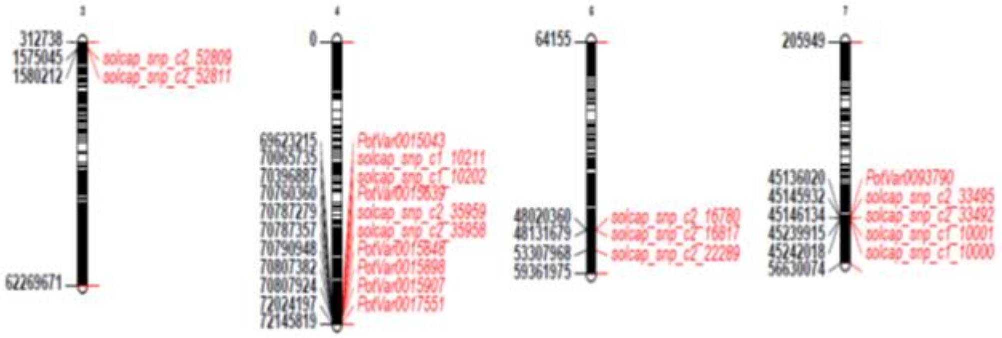


Figure 4.35. Physical chromosomal map exhibiting the localization of significant SNPs linked with ATW along with the corresponding physical distance in base pair (bp).

Manhattan plots were created through MLM in GWASpoly R with additive model using BLUPs. Twenty SNP markers were found to be associated with average tuber weight through additive model at a threshold of $-\log10(P) \geq 3.23$ ($P \leq 0.00059$). These SNPs were located on chromosomes 3, 4, 6 and 7 (Fig. 4.34 and Table 4.22). Physical map of chromosomes is presented in Figure 4.35. A region spanning 2.40 Mbp (69.62 to 72.02 Mbp) on chr 4 carry eight SNPs positioned within a narrow distance of 0.74 Mbp (70.06 to 70.80 Mbp) linked to ATW. Similarly, the narrow distance of 0.11 Mbp (45.13-45.24 Mbp) on chr 7 was associated with ATW. These genomic regions may contain a probable QTL linked to ATW. Chr 3 also contain two SNPs that are closely linked with each other (0.01 Mbp distance). The SNP on chr 4 were located in the genes with a putative function as inositol-pentakisphosphate 2-kinase. It is involved in biosynthetic pathway of phytic acid (Sun et al., 2007). Phytic acid is found in mature tubers and is a major reservoir of phosphorous mineral in tubers. Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha (PFPase) is involved in sucrose synthesis, glycolysis and starch metabolism in starchy crops like rice and potato (Chen et al., 2020). SNP with a putative gene function of Pyrophosphate--fructose 6-phosphate is located on chr 4. SNP (solcap_snp_c2_33495 and solcap_snp_c2_33492) found on chr 7 with putative gene function of glucan endo-1,3-beta-glucosidase 12-like is involved in carbohydrate metabolism in potato tubers (Wang et al., 2008). In previous study, QTL for tuber weight were detected on chromosomes 1, 4, 5, and 6 in a diploid potato mapping population comprising of 149 individuals (Hara-Skrzypiec et al., 2018) that is in accordance to our findings. Similarly, Rak et al., (2017) also draw a linkage map and identified 3 significant markers for average tuber weight on chromosome number 5 by utilizing bi-parental family W9817 from the University of Wisconsin potato breeding program consisting of 110 individuals obtained by a cross of chipping cultivar Liberator and Wisconsin breeding clone W4013-1. But unfortunately, in our studies we did not find any association of marker on chromosome number 5. It is quite normal because it may be due to differences in mapping populations used in the studies.

4.4.3.4 Average tuber yield (ATY)

Marker trait association for average tuber yield was calculated by using BLUPs data set along with genotypic data to find significant SNPs. Q-Q plots revealed the normal distribution of the data as the observed vs expected *p* values were uniformly distributed as a straight-line till -log10(P)=3. Soon after 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). Furthermore, it illustrates that the model is controlling population stratification (Fig. 4.36).

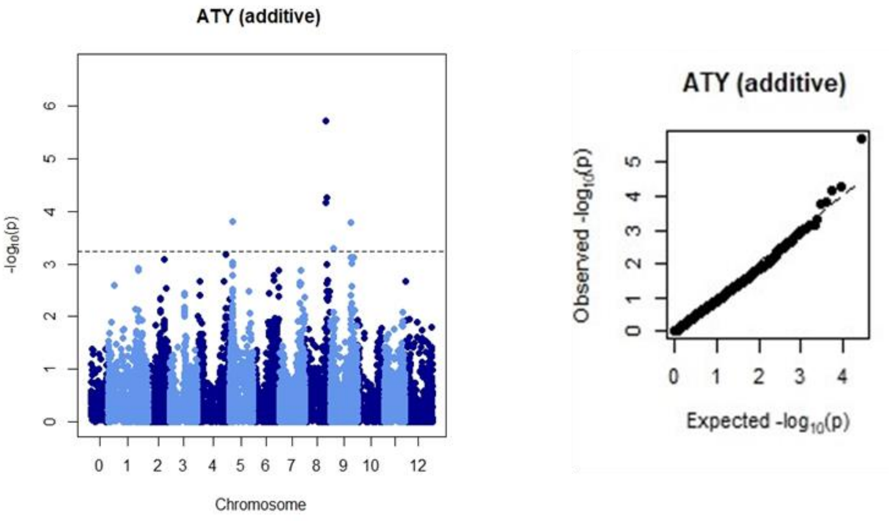


Figure 4.36. Manhattan plot (left) displaying significantly associated SNPs (-log10 (P) threshold of 3.23 in blue dotted line) Q-Q plot (right) for average tuber yield (ATY) of potato

Table 4.23. SNP markers found by additive model using BLUP data set for average tuber yield (ATY) along with their chromosome number, position (bp), variant, sequence ID, and gene annotations (threshold: -log10 (P) ≥ 3.23; P ≤ 0.00059)

Marker	Chrom	Position	Variant Ref/Alt	Seq ID	Annotation
solcap_snp_c2_12495	5	5463844	C/T	XR_001471742.1	F-box/kelch-repeat protein At3g23880-like
PotVar0103302	8	47376201	A/G	PGSC0003DMG400001969	Carotenoid cleavage dioxygenase 4
PotVar0103431	8	47378085	G/T	PGSC0003DMG400001969	Carotenoid cleavage dioxygenase 4
PotVar0122020	8	48019800	A/C	PGSC0003DMG400030849	Conserved gene of unknown function
PotVar0034218	9	7531739	G/T	PGSC0003DMG200023924	DIAMINOPIMELATE EPIMERASE
solcap_snp_c2_44815	9	46687355	A/C	XM_015312554.1	Isoamylase isoform 2

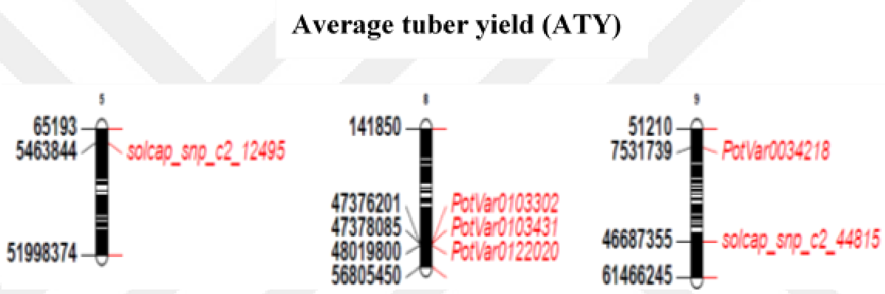


Figure 4.37. Physical chromosomal map exhibiting the localization of significant SNPs linked with ATY along with the corresponding physical distance in base pair (bp).

Manhattan plot showed six significant SNP markers at a threshold of -log10(P)=3.23 associated with ATY. These SNP markers were distributed on chromosomes 5, 8 and 9 (Fig. 4.36 and Table 4.23). A physical map based on chromosome and physical base pair distance between the SNP markers associated with the studied tuber trait (ATY) is depicted in Figure 4.37. A region spanning 0.64 Mbp (47.37 to 48.01 Mbp) located on chr 8 was linked with ATY, which indicates the presence of possible QTL in this particular genomic region controlling tuber characteristic. Furthermore, the identified SNP markers have their putative gene functions such as, F-box/kelch-repeat protein At3g23880-like, Carotenoid cleavage dioxygenase 4, DIAMINOPIMELATE EPIMERASE, Isoamylase isoform 2, and one SNP (PotVar0122020) showed gene annotation as Conserved gene of unknown function.

Our results are in line with the findings of Manrique-Carpintero et al., 2015 where they identified that tuber yield trait is linked on chromosome number 5 along with chromosome 2 and 12. we found that tuber yield is associated on chromosome number 5, 8 and 9. Likewise, according to Rak et al., (2017) QTL mapping of tuber yield trait by using the auto-tetraploid family, it was detected that QTLs were present on chromosome # 2, 5, and 11. Previous literature in line with our results revealed that the chromosome number 5 showed significantly important for ATY, which indicates the presence of possible QTL controlling tuber characteristic like tuber yield and can be used for future association mapping studies.

CHAPTER V

CONCLUSION

The main purpose of the current study was to find SNPs associated with roots, stolons, and tuber traits in diversified tetraploid potato panel by using an association mapping technique. We observed novel genomic regions that could be potentially utilized in future potato breeding programs. Our results showed that five SNPs were associated with TRL, ten with RSA, eight with RAD, four SNPs were related to RV, six with RBP, four with RFW, while eleven were linked to RDW on chr 1, chr 2, chr 3, chr 5, chr 6, chr 7, chr 10, chr 11, and chr 12. Eighteen SNPs were associated with TNS and SL each, thirteen SNPs were found related to SL, fourteen with BS, nine with SFW and eleven were linked with SDW on chr 1, chr 2, chr 3, chr 4, chr 5, chr 6, chr 7, chr 10, chr 11, and chr 12. Furthermore, fourteen SNPs were found associated with TNT, twenty-one with TS, only two with ATW and Six with ATY on chr 1, chr 2, chr 4, chr 5, chr 6, chr 7, chr 8, chr 9, and chr 10.

Out of these identified SNPs, twenty of them were found to be associated with multiple traits. The SNPs can be referred to as pleiotropic or overlapping since it was associated with more than one trait. **Root traits:** solcap_snp_c2_51985 (TRL and RSA), R3a_m_LG11 (RFW and RDW), PotVar0008906, PotVar0124359 (RSA and RDW), solcap_snp_c2_51273 (RSA, RV, RFW, and RDW) PotVar0117909, solcap_snp_c1_10252, solcap_snp_c2_34193 (RSA, RV, and RDW). **Stolon traits:** PotVar0000800 (TNS and SL), PotVar0058153 (TNS and BS), PotVar0124339 (SL, BS), solcap_snp_c1_11580 (SL and BS), PotVar0000460, PotVar0111512, solcap_snp_c2_25283 (SL and SFW), PotVar0087095, PotVar0087316 (SL, SFW, and SDW). **Tuber traits:** solcap_snp_c1_10013 (TNT and RBP). The identified SNPs had a putative gene function in root and stolon elongation, various plant signalling pathways, signal transduction, plant defense response, cell differentiation/proliferation, and disease resistance. Genomic regions related to underground traits identified in our study were novel, they can provide a new way to proceed for potato breeders. Shortly, the development of selection markers using allele-specific KASP marker validation studies of the identified SNPs in the present research will prove to be a ground-breaking approach for marker-assisted breeding of root, stolon, and tuber traits in potato.

After validation, these can be used in future potato breeding programs to accelerate the breeding process as well as to cope with the needs of the breeding objectives in potato such as potato productivity.

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APPENDIXES

APPENDIX-A Mean phenotypic data of root traits for the year 2019 (Aeroponic)

Genotypes	TRL	RSA	RAD	RV	RBP	RFW	RDW
GENO2	7706.50	1766.28	0.80	36.48	1.00	18.70	2.10
GENO3	13000.50	3777.58	0.90	91.66	2.00	43.55	5.05
GENO4	10977.00	3310.00	1.04	80.26	2.00	31.47	4.04
GENO5	10816.75	3429.83	1.06	88.62	2.00	37.66	4.93
GENO6	3407.00	593.90	0.54	7.74	5.00	5.20	0.90
GENO7	6083.00	1590.90	0.83	33.88	1.00	11.72	1.59
GENO9	NA	NA	NA	NA	NA	NA	NA
GENO10	5325.00	2062.90	1.24	63.30	5.00	18.59	2.39
GENO11	19674.00	4910.00	0.82	98.80	2.00	40.71	5.34
GENO12	9148.00	3432.20	1.21	106.27	4.00	24.45	3.66
GENO13	4145.00	1531.50	1.18	45.04	5.00	28.30	3.47
GENO14	12880.00	4663.10	1.16	137.43	2.00	76.47	7.97
GENO16	NA	NA	NA	NA	NA	NA	NA
GENO18	NA	NA	NA	NA	NA	NA	NA
GENO19	18065.00	3674.80	0.65	60.60	2.00	23.35	3.20
GENO20	15873.00	4411.20	0.90	101.39	2.00	41.16	5.44
GENO21	NA	NA	NA	NA	NA	NA	NA
GENO22	16538.00	7004.90	1.41	255.25	2.00	57.70	7.07
GENO23	10466.00	3278.30	1.00	83.37	2.00	43.96	2.71
GENO24	18107.00	4390.50	0.77	85.86	2.00	51.47	7.55
GENO25	13025.00	4292.20	1.05	113.31	1.00	52.57	8.25

GENO26	5344.00	1410.80	0.84	29.66	5.00	12.65	1.31
GENO27	7239.00	2505.10	1.15	70.08	1.00	24.82	3.11
GENO28	9344.00	3435.30	1.19	103.29	5.00	38.42	4.37
GENO29	17255.00	5948.50	1.17	171.45	2.00	50.21	7.32
GENO30	13527.00	2991.10	0.70	53.99	2.00	34.33	4.05
GENO31	12932.00	2719.40	0.67	45.89	2.00	12.60	1.77
GENO32	15683.00	3464.00	0.70	62.37	2.00	32.63	4.96
GENO33	6611.00	2426.50	1.22	71.99	5.00	32.55	4.86
GENO34	15024.00	4646.20	1.02	117.87	2.00	43.02	6.14
GENO35	13331.00	4296.00	0.97	115.48	2.00	55.42	7.17
GENO36	10466.00	2091.00	0.64	35.03	2.00	16.70	2.01
GENO37	9764.00	3048.70	1.00	76.84	5.00	34.37	4.11
GENO38	24619.00	5563.10	0.73	101.59	2.00	53.37	7.31
GENO39	NA	NA	NA	NA	NA	NA	NA
GENO41	16550.00	3465.80	0.66	58.04	2.00	28.50	3.25
GENO42	6720.00	1914.50	0.91	43.19	5.00	16.97	2.45
GENO43	10734.00	2426.90	0.72	43.75	2.00	28.95	3.93
GENO44	3177.00	825.00	0.82	17.40	4.00	6.33	0.87
GENO45	32240.00	8992.30	0.83	191.75	2.00	106.78	12.32
GENO46	10750.00	2785.90	0.83	58.34	2.00	25.63	3.17
GENO47	12154.00	3138.40	0.82	65.79	2.00	28.88	3.88
GENO48	2417.00	348.90	0.46	4.01	4.00	3.39	0.49
GENO49	7364.00	1978.20	0.92	43.94	5.00	11.20	1.70
GENO50	10710.00	2683.50	0.82	55.33	2.00	23.03	2.98
GENO52	14124.00	3165.60	0.72	56.59	2.00	24.50	3.02

GENO53	10740.00	4222.80	1.28	139.53	2.00	40.34	4.17
GENO54	8346.00	3490.70	1.34	117.47	1.00	40.65	4.91
GENO55	8637.00	2711.00	1.04	70.99	1.00	18.49	2.63
GENO56	13322.00	3487.10	0.83	73.95	2.00	70.86	9.10
GENO57	8014.00	2599.80	1.07	68.53	1.00	34.50	4.92
GENO58	8969.00	2384.30	0.84	51.05	2.00	20.82	3.56
GENO59	11145.00	2561.80	0.73	47.17	1.00	34.40	4.39
GENO60	33159.00	7714.10	0.75	146.64	4.00	76.38	8.77
GENO61	NA	NA	NA	NA	NA	NA	NA
GENO63	6470.00	1699.30	0.87	36.46	5.00	10.70	1.50
GENO64	5557.00	1615.60	0.92	38.03	5.00	21.05	3.20
GENO65	15594.00	3480.60	0.70	62.38	2.00	45.25	6.13
GENO66	18211.00	3901.40	0.68	67.32	2.00	43.65	4.48
GENO67	17032.00	5125.80	0.97	125.41	2.00	47.94	5.65
GENO68	4987.00	1680.00	1.07	45.06	4.00	26.38	3.04
GENO69	NA	NA	NA	NA	NA	NA	NA
GENO70	10210.00	4793.40	1.43	190.16	2.00	55.33	7.06
GENO71	14012.00	7104.40	1.59	311.55	2.00	93.21	9.11
GENO72	12260.00	4234.40	1.11	119.86	2.00	50.26	7.07
GENO73	10594.00	4780.00	1.49	183.48	2.00	78.61	6.00
GENO74	4888.00	952.90	0.65	16.44	5.00	7.13	0.92
GENO75	15724.00	4327.90	0.88	96.74	2.00	38.25	5.03
GENO76	14424.00	4126.00	0.90	94.78	2.00	59.93	7.28
GENO77	9523.00	3175.00	1.07	88.26	2.00	41.46	5.24
GENO78	13439.00	4520.10	1.14	144.62	2.00	69.43	8.55

GENO79	28244.00	9799.10	1.11	275.07	2.00	144.51	15.18
GENO80	9832.00	2813.00	0.91	64.49	2.00	37.09	3.80
GENO81	6402.00	2068.90	1.12	54.47	1.00	23.13	3.01
GENO82	9628.00	3654.00	1.20	131.99	2.00	36.67	4.75
GENO83	10559.00	3833.10	0.95	116.70	2.00	44.97	5.95
GENO84	7539.00	2990.30	1.30	96.65	1.00	37.68	4.43
GENO85	8561.00	2841.70	1.07	75.83	1.00	26.98	3.25
GENO86	13922.00	4190.00	0.96	102.14	2.00	39.21	4.47
GENO87	5069.00	1329.10	0.84	28.67	5.00	11.46	1.04
GENO88	6889.00	1727.10	0.80	35.19	5.00	8.39	1.08
GENO89	9209.00	3205.00	1.25	93.81	2.00	40.92	4.00
GENO90	NA	NA	NA	NA	NA	NA	NA
GENO91	NA	NA	NA	NA	NA	NA	NA
GENO92	10449.00	3211.40	0.98	81.76	2.00	30.16	4.61
GENO93	8746.00	3636.70	1.33	120.49	1.00	47.70	6.87
GENO94	11322.00	3774.80	1.10	104.01	1.00	33.03	4.21
GENO95	8485.00	2247.60	0.84	47.38	5.00	24.60	2.58
GENO96	6160.00	2382.00	1.18	78.21	5.00	31.38	3.42
GENO97	9195.00	2729.60	0.94	66.09	1.00	20.93	2.53
GENO98	6809.00	1840.00	0.83	40.27	1.00	13.05	1.60
GENO99	5158.00	1759.60	1.08	46.62	1.00	15.78	1.85
GENO100	4589.00	1396.80	0.94	32.96	4.00	12.80	1.22
GENO101	15366.00	4513.40	0.93	111.37	2.00	50.92	6.59
GENO102	13391.00	3337.20	0.83	69.19	2.00	32.57	4.17
GENO103	16349.00	4596.10	0.91	105.05	2.00	43.77	5.76

GENO104	11158.00	4472.10	1.25	148.99	2.00	73.03	8.61
GENO105	6842.00	2204.70	1.04	56.50	5.00	20.99	2.48
GENO106	4804.00	1260.60	0.84	26.34	5.00	26.70	2.55
GENO107	13469.00	4079.00	0.95	101.49	2.00	46.46	6.01
GENO108	15091.00	4183.80	0.89	91.63	2.00	26.70	3.79
GENO109	3093.00	672.20	0.65	11.64	4.00	5.36	0.67
GENO110	10048.00	3032.60	0.96	76.45	5.00	39.25	4.93
GENO111	6185.00	1526.40	0.78	30.06	5.00	10.17	1.58
GENO112	6358.00	1781.50	0.90	39.73	4.00	14.15	1.69
GENO113	4565.00	1014.20	0.71	17.94	4.00	7.52	1.11
GENO114	4732.00	1369.20	0.94	32.64	5.00	19.16	2.00
GENO115	7069.00	1492.80	0.68	25.65	5.00	12.31	1.43
GENO116	14674.00	3061.60	0.64	51.35	2.00	35.91	4.85
GENO117	5517.00	2407.40	1.34	85.21	5.00	23.80	3.26
GENO118	14183.00	3799.10	0.85	80.94	2.00	27.90	4.15
GENO120	14278.00	4055.70	0.90	93.10	2.00	68.10	8.63
GENO121	4876.00	893.10	0.58	13.04	5.00	5.94	0.77
GENO122	5918.00	1886.90	0.96	52.15	5.00	26.62	3.68
GENO123	6788.00	2317.60	1.02	66.27	5.00	24.91	2.83
GENO124	NA	NA	NA	NA	NA	NA	NA
GENO125	5109.00	1064.90	0.66	17.65	5.00	8.83	1.01
GENO126	3809.00	635.90	0.62	11.14	4.00	10.07	1.03
GENO127	20340.00	6313.30	0.83	136.05	2.00	53.38	6.55
GENO128	13999.00	5307.30	1.21	160.50	2.00	85.10	12.05
GENO130	4659.00	1305.80	0.92	32.48	5.00	7.87	1.18

GENO131	16009.00	5692.60	1.13	161.52	2.00	48.54	6.82
GENO132	7105.00	2263.50	1.01	58.43	5.00	13.95	2.08
GENO133	10514.00	3262.80	0.91	86.40	2.00	23.59	2.95
GENO134	7119.00	2307.50	1.00	62.52	5.00	25.70	2.89
GENO136	NA	NA	NA	NA	NA	NA	NA
GENO137	5576.00	1126.70	0.64	18.19	4.00	9.08	0.95
GENO138	4537.00	2031.50	1.43	73.86	4.00	31.42	3.67
GENO139	13524.00	4089.00	1.03	100.44	2.00	49.68	4.94
GENO140	12202.00	4482.80	1.19	135.74	2.00	48.41	6.10
GENO141	10330.00	3160.70	1.01	76.21	2.00	30.70	4.37
GENO142	17219.00	4341.90	0.81	87.89	2.00	38.59	5.09
GENO143	12646.00	2783.40	0.69	51.81	2.00	16.58	2.37
GENO144	NA	NA	NA	NA	NA	NA	NA
GENO145	4522.00	1167.40	0.82	23.21	5.00	8.77	1.19
GENO146	9599.00	3572.00	1.18	105.92	2.00	55.60	5.76
GENO147	18581.00	4465.20	0.76	85.63	2.00	44.18	5.44
GENO148	8800.00	3196.00	1.16	93.16	2.00	34.03	4.05
GENO149	3591.00	1607.10	1.41	57.83	5.00	18.28	2.55
GENO150	7387.00	2239.50	0.92	56.20	5.00	21.49	2.60
GENO151	6439.00	2032.00	0.99	51.23	5.00	12.15	1.73
GENO152	NA	NA	NA	NA	NA	NA	NA
GENO153	7714.00	2976.90	1.27	94.48	5.00	31.43	4.32
GENO154	5364.00	1581.10	0.94	37.10	5.00	15.67	2.38
GENO155	20512.00	6931.50	1.14	202.13	2.00	56.95	6.99
GENO156	4869.00	1764.80	1.17	51.60	5.00	17.83	2.52

GENO157	9575.00	3183.70	1.10	86.66	1.00	41.50	4.94
GENO158	4713.00	1173.30	0.79	23.24	4.00	6.18	0.75
GENO159	7083.00	2176.70	0.96	51.72	5.00	19.60	2.17
GENO160	4675.00	1807.30	1.22	56.08	5.00	15.00	2.03
GENO161	10284.00	2992.40	0.93	69.24	2.00	25.54	3.37
GENO162	19283.00	4901.00	0.76	100.07	2.00	38.73	5.57
GENO163	8724.00	2279.10	0.72	50.45	5.00	21.42	2.78
GENO164	6196.00	1745.80	0.90	39.66	5.00	17.17	1.93
GENO165	NA	NA	NA	NA	NA	NA	NA
GENO167	5224.00	1595.60	1.02	40.66	5.00	16.61	1.95
GENO168	4396.00	1339.80	0.99	32.75	5.00	13.97	1.95
GENO169	6448.00	1773.50	0.88	39.46	4.00	16.63	2.31
GENO170	4801.00	892.10	0.59	13.19	4.00	1.75	0.23
GENO171	4157.00	1609.60	1.23	49.60	4.00	17.18	2.22
GENO172	13644.00	3360.50	0.79	67.05	2.00	20.17	2.84
GENO173	10377.00	2683.20	0.86	55.95	5.00	16.31	2.71
GENO174	18809.00	4452.00	0.75	85.80	2.00	40.47	4.78
GENO175	14189.00	4349.30	0.99	107.90	5.00	35.40	4.67
GENO176	8792.00	2816.60	1.04	72.24	5.00	27.89	3.42
GENO177	11258.00	3306.80	0.99	79.61	2.00	32.16	3.72
GENO178	14110.00	4056.80	0.93	93.97	2.00	33.13	4.57
GENO179	5877.00	1671.20	0.86	37.74	5.00	11.51	1.50
GENO180	4764.00	1696.10	1.15	49.33	5.00	18.33	2.70
GENO181	4539.00	1375.30	0.98	33.21	5.00	10.78	1.29
GENO182	5776.00	2306.60	1.32	75.25	5.00	27.65	3.35

GENO183	11532.00	2619.50	0.72	47.69	2.00	18.05	2.46
GENO184	13443.00	4029.40	0.96	97.88	2.00	46.50	7.25
GENO185	10679.00	2966.40	0.88	66.30	2.00	29.61	3.95
GENO186	4500.00	1724.30	1.27	57.03	5.00	18.96	2.61
GENO187	7037.00	2226.90	1.07	60.51	1.00	22.39	2.70
GENO188	10198.00	2841.50	0.90	63.48	2.00	19.79	2.45
GENO189	3927.00	796.00	0.64	13.44	5.00	6.16	0.55
GENO190	7713.00	2628.50	1.09	76.13	1.00	30.51	4.05
GENO191	4906.00	1096.30	0.72	19.54	5.00	6.83	1.14
GENO192	4067.00	1817.20	1.43	65.09	5.00	21.95	3.13
GENO193	5170.00	1109.70	0.69	19.49	5.00	5.46	0.87
GENO194	10976.00	4004.60	1.18	133.07	2.00	56.13	5.66
GENO195	5651.00	1441.00	0.79	30.68	5.00	17.28	2.14
GENO196	NA	NA	NA	NA	NA	NA	NA
GENO197	7241.00	2381.30	1.02	63.76	1.00	35.90	4.57
GENO198	9174.00	2660.80	0.87	65.76	2.00	31.46	4.80
GENO199	4588.00	1728.50	1.21	52.45	5.00	23.90	3.60
GENO200	3687.00	993.90	0.87	22.31	5.00	5.90	0.83
GENO202	9803.00	3221.70	1.07	86.40	2.00	37.04	5.36
GENO203	5439.00	1230.20	0.71	22.61	5.00	10.52	1.41
GENO204	15453.00	5138.50	1.07	139.60	2.00	79.40	7.33

APPENDIX-B Mean phenotypic data of root traits for the year 2020 (Aeroponic)

Genotypes	TRL	RSA	RAD	RV	RBP	RFW	RDW
GENO2	8004.00	1735.90	0.64	28.09	1.00	18.87	2.41
GENO3	13943.00	3758.80	0.87	94.50	2.00	46.28	3.89
GENO4	11558.00	3080.20	1.09	61.42	2.00	26.20	1.35
GENO5	13257.00	2826.50	0.68	48.08	2.00	32.40	2.10
GENO6	9377.32	2191.00	0.74	41.11	1.00	24.50	2.27
GENO7	6247.00	1425.60	0.72	25.82	4.00	10.40	0.75
GENO9	6320.00	1025.50	0.51	13.38	4.00	20.20	1.25
GENO10	5786.00	1809.00	1.00	46.20	5.00	30.76	1.99
GENO11	7666.00	1672.90	0.66	26.68	1.00	11.40	1.77
GENO12	11519.00	2943.80	0.82	60.67	2.00	53.50	3.83
GENO13	6301.00	1698.70	0.86	36.09	4.00	27.74	1.96
GENO14	7172.00	1425.40	0.63	22.54	1.00	18.40	1.46
GENO16	NA	NA	NA	NA	NA	NA	NA
GENO18	NA	NA	NA	NA	NA	NA	NA
GENO19	5722.00	1303.00	0.73	23.64	5.00	7.25	0.67
GENO20	8097.00	2358.10	0.96	55.19	1.00	45.87	3.28
GENO21	NA	NA	NA	NA	NA	NA	NA
GENO22	9209.00	2589.40	0.87	58.25	1.00	52.57	3.30
GENO23	8314.00	2001.80	0.77	45.10	1.00	36.90	4.53
GENO24	12894.00	3595.30	0.88	79.17	2.00	25.90	2.07
GENO25	9098.00	2372.40	0.71	67.72	1.00	41.05	3.20
GENO26	6877.00	1773.20	0.83	36.99	1.00	37.37	2.43

GENO27	9990.00	3061.30	0.98	77.33	1.00	30.66	2.10
GENO28	9750.00	2374.20	0.85	49.28	1.00	39.28	3.59
GENO29	6765.00	1513.60	0.71	27.26	1.00	21.35	1.49
GENO30	8328.00	2708.90	0.83	63.28	1.00	32.12	2.72
GENO31	8361.00	1666.30	0.63	26.43	1.00	20.90	1.77
GENO32	15172.00	3818.40	0.74	76.60	2.00	39.36	3.47
GENO33	7060.00	1214.10	0.55	16.69	1.00	17.58	1.26
GENO34	5720.00	1437.00	0.80	28.82	5.00	16.37	1.57
GENO35	12452.00	2999.90	0.77	58.09	2.00	45.50	3.51
GENO36	14128.00	3563.20	0.81	72.08	2.00	51.90	3.34
GENO37	7305.00	1799.50	0.76	33.73	1.00	25.78	1.71
GENO38	NA	NA	NA	NA	NA	NA	NA
GENO39	8404.00	2309.60	0.85	50.97	1.00	43.07	3.37
GENO41	14897.00	3099.50	0.64	52.10	2.00	32.23	2.73
GENO42	6867.00	2037.30	0.95	48.21	1.00	28.15	2.83
GENO43	6181.00	1416.20	0.73	25.84	4.00	18.23	1.42
GENO44	4959.00	848.70	0.55	11.39	5.00	12.20	1.04
GENO45	7005.00	1500.20	0.59	26.75	1.00	18.20	1.45
GENO46	6997.00	1798.70	0.80	36.53	1.00	20.12	1.39
GENO47	11229.00	2841.10	0.80	58.05	2.00	39.14	3.00
GENO48	5734.00	1055.10	0.60	17.05	5.00	13.20	0.86
GENO49	9982.00	2324.70	0.74	43.23	1.00	18.11	1.54
GENO50	11958.00	2549.10	0.68	43.42	2.00	35.70	2.78
GENO52	10167.00	2155.00	0.66	38.21	2.00	17.77	1.67
GENO53	7784.00	2360.40	0.96	58.57	1.00	26.07	2.10

GENO54	9423.00	2213.20	0.76	41.40	1.00	29.53	1.80
GENO55	12249.00	2372.70	0.62	36.80	2.00	31.40	2.94
GENO56	6572.00	1384.40	0.67	23.25	1.00	17.43	1.15
GENO57	7837.00	2366.80	0.99	57.00	1.00	40.94	3.23
GENO58	6313.00	1549.60	0.79	30.71	4.00	18.46	1.46
GENO59	NA	NA	NA	NA	NA	NA	NA
GENO60	6363.00	1902.00	0.96	45.39	4.00	50.40	3.69
GENO61	NA	NA	NA	NA	NA	NA	NA
GENO63	10784.00	2314.90	0.69	39.75	2.00	35.26	4.02
GENO64	5257.00	1337.70	0.73	29.47	5.00	18.50	2.15
GENO65	11240.00	2890.00	0.79	60.15	2.00	31.00	2.64
GENO66	12524.00	3096.40	0.81	65.50	2.00	32.75	2.37
GENO67	6171.00	1402.50	0.72	25.37	4.00	20.00	2.43
GENO68	6894.00	1483.20	0.68	25.38	1.00	22.80	1.77
GENO69	6230.00	2136.60	1.09	58.33	4.00	44.60	2.72
GENO70	4943.00	1657.40	1.08	45.04	5.00	25.68	2.40
GENO71	6333.00	1763.90	0.91	40.14	4.00	24.14	1.98
GENO72	7348.00	1756.50	0.76	33.70	1.00	24.95	1.95
GENO73	6746.00	1682.10	0.80	33.72	1.00	24.47	1.83
GENO74	6443.00	1226.30	0.60	18.52	4.00	14.80	1.12
GENO75	11550.00	3280.60	0.91	78.60	2.00	51.85	3.94
GENO76	5630.00	1457.90	0.82	30.13	5.00	23.55	3.83
GENO77	6767.00	1486.90	0.70	26.32	1.00	20.69	1.82
GENO78	7100.00	1860.10	0.76	36.60	1.00	15.00	1.36
GENO79	12055.00	3066.00	0.82	63.04	2.00	53.72	3.78

GENO80	7859.00	1990.10	0.70	41.67	1.00	31.19	3.94
GENO81	6646.00	1733.20	0.83	35.82	1.00	25.45	1.86
GENO82	11431.00	1986.20	0.59	26.44	2.00	19.95	1.84
GENO83	6053.00	2229.10	1.05	67.66	4.00	31.26	2.60
GENO84	6085.00	1166.00	0.61	17.87	4.00	14.67	1.13
GENO85	7961.00	2743.70	1.11	76.55	1.00	21.40	1.43
GENO86	11519.00	1898.60	0.68	25.32	2.00	30.90	2.55
GENO87	5738.00	1482.00	0.82	30.48	5.00	10.70	0.95
GENO88	5963.00	1324.10	0.70	23.68	5.00	25.53	1.75
GENO89	8975.00	1811.60	0.63	29.40	1.00	29.93	2.03
GENO90	NA	NA	NA	NA	NA	NA	NA
GENO91	4115.00	1199.50	0.95	28.02	5.00	16.20	1.20
GENO92	11353.00	2953.70	0.83	61.43	2.00	22.22	2.55
GENO93	7741.00	2184.50	0.89	48.39	1.00	33.70	2.87
GENO94	8416.00	1979.60	0.76	38.59	1.00	23.53	2.85
GENO95	6341.00	1739.30	0.88	38.42	4.00	20.93	1.76
GENO96	7843.00	1991.50	0.86	43.13	1.00	30.04	2.18
GENO97	10257.00	2497.30	0.79	48.70	2.00	48.11	3.41
GENO98	6515.00	1171.40	0.57	16.76	4.00	7.60	0.59
GENO99	7360.00	1650.00	0.72	39.37	1.00	21.56	2.72
GENO100	10133.00	2931.50	1.00	72.70	2.00	41.62	3.08
GENO101	10119.00	2107.40	0.66	36.42	1.00	30.34	2.25
GENO102	7393.00	1572.40	0.65	27.69	1.00	27.70	2.22
GENO103	11018.00	2548.70	0.71	45.53	2.00	31.72	2.14
GENO104	9038.00	2517.10	0.94	58.09	1.00	35.82	3.08

GENO105	5377.00	1319.10	0.79	26.28	5.00	14.48	1.04
GENO106	6512.00	2044.20	1.01	52.85	4.00	40.60	3.01
GENO107	6375.00	1541.00	0.71	28.39	4.00	21.45	1.75
GENO108	6429.00	2568.50	1.22	88.67	4.00	36.27	2.86
GENO109	6832.00	1550.00	0.72	27.98	1.00	29.00	1.92
GENO110	6161.00	1582.40	0.80	31.84	4.00	26.75	1.69
GENO111	6336.00	1167.80	0.59	17.13	4.00	15.70	1.47
GENO112	8420.00	2166.60	0.77	41.50	1.00	42.13	3.23
GENO113	5599.00	1362.90	0.74	27.64	5.00	28.33	1.56
GENO114	6956.00	1585.00	0.73	28.85	1.00	25.50	1.71
GENO115	6014.00	1306.70	0.68	22.80	5.00	13.88	1.02
GENO116	14094.00	3182.40	0.72	58.28	2.00	50.23	3.71
GENO117	13850.00	3780.20	0.94	83.97	2.00	79.48	5.74
GENO118	9211.00	2837.80	0.98	69.97	1.00	47.55	3.20
GENO120	10259.00	2587.00	0.87	52.96	2.00	36.98	2.89
GENO121	6991.00	1292.20	0.59	19.05	1.00	12.33	1.12
GENO122	6405.00	2076.70	1.08	52.75	4.00	36.25	2.37
GENO123	4822.00	1333.10	0.88	29.33	5.00	17.45	1.49
GENO124	NA	NA	NA	NA	NA	NA	NA
GENO125	5834.00	1189.90	0.63	19.37	5.00	10.96	0.82
GENO126	4681.00	786.40	0.54	9.79	5.00	13.60	1.16
GENO127	16529.00	4094.10	0.74	80.90	2.00	43.22	3.41
GENO128	12245.00	3363.80	0.90	74.48	2.00	50.60	3.97
GENO130	6298.00	1579.30	0.78	30.49	4.00	11.78	0.89
GENO131	6080.00	1574.00	0.83	32.44	4.00	38.70	1.82

GENO132	12956.00	3413.60	0.85	74.87	2.00	41.91	2.19
GENO133	8923.00	2867.70	0.98	67.81	1.00	34.44	3.30
GENO134	6339.00	1213.80	0.60	18.09	4.00	15.10	1.51
GENO136	7632.00	1652.30	0.69	28.47	1.00	24.00	2.18
GENO137	8114.00	1731.50	0.69	29.87	1.00	27.92	2.25
GENO138	6341.00	1398.40	0.78	27.41	4.00	29.80	3.48
GENO139	13366.00	2969.20	0.71	54.44	2.00	34.44	2.95
GENO140	6078.00	1779.40	0.93	41.45	4.00	35.30	2.80
GENO141	9495.00	1902.80	0.65	29.90	1.00	29.95	2.18
GENO142	6024.00	1591.20	0.85	34.10	4.00	18.47	1.45
GENO143	5961.00	1538.70	0.72	30.39	5.00	24.18	1.97
GENO144	NA	NA	NA	NA	NA	NA	NA
GENO145	6839.00	1691.00	0.78	32.21	1.00	19.70	1.69
GENO146	13755.00	2538.60	0.61	38.38	2.00	25.83	2.71
GENO147	9874.00	2070.70	0.66	35.96	1.00	20.60	1.31
GENO148	16062.00	2810.10	0.56	39.15	2.00	43.50	3.70
GENO149	6228.00	1911.90	0.97	46.67	4.00	15.07	1.35
GENO150	6951.00	1709.50	0.79	33.91	1.00	21.76	1.72
GENO151	5995.00	885.70	0.47	10.43	5.00	9.70	0.92
GENO152	5936.00	1491.40	0.80	31.18	5.00	16.90	1.49
GENO153	9047.00	3084.00	1.10	85.26	1.00	27.35	1.41
GENO154	5341.00	1551.30	0.63	33.63	5.00	11.33	0.90
GENO155	8649.00	2107.50	0.76	45.66	1.00	31.70	3.99
GENO156	6639.00	1495.50	0.72	26.86	1.00	21.76	1.81
GENO157	6696.00	1134.60	0.54	16.07	1.00	9.60	0.81

GENO158	7007.00	1587.20	0.66	29.71	1.00	24.00	3.00
GENO159	13873.00	3611.60	0.87	82.38	2.00	52.10	4.60
GENO160	5579.00	1364.60	0.79	26.88	5.00	12.80	0.94
GENO161	6841.00	1812.20	0.79	37.11	1.00	22.08	1.81
GENO162	13565.00	3682.80	0.94	84.55	2.00	41.53	3.00
GENO163	NA	NA	NA	NA	NA	NA	NA
GENO164	4841.00	1153.30	0.68	21.23	5.00	8.18	0.73
GENO165	NA	NA	NA	NA	NA	NA	NA
GENO167	6785.00	1320.00	0.62	20.49	1.00	19.33	1.42
GENO168	6124.00	2021.00	1.04	52.58	4.00	20.93	1.56
GENO169	4653.00	923.30	0.67	14.59	5.00	9.00	0.73
GENO170	6334.00	1725.80	0.81	35.00	4.00	10.60	0.75
GENO171	7657.00	1736.80	0.72	31.35	1.00	26.60	3.10
GENO172	6065.00	1019.70	0.54	13.74	4.00	13.40	0.89
GENO173	5579.00	1180.90	0.67	20.12	5.00	10.45	1.12
GENO174	14160.00	3529.90	0.76	67.56	2.00	102.27	10.93
GENO175	10242.00	2167.60	0.70	36.86	2.00	39.55	3.27
GENO176	12775.00	3158.70	0.79	63.31	2.00	39.33	2.86
GENO177	6431.00	1231.70	0.61	18.79	4.00	20.25	1.55
GENO178	5975.00	1256.10	0.69	22.50	5.00	11.67	1.13
GENO179	8958.00	2127.50	0.75	40.39	1.00	32.63	2.31
GENO180	7772.00	1799.80	0.76	34.59	1.00	33.25	4.00
GENO181	9253.00	1926.80	0.68	32.34	1.00	24.83	1.72
GENO182	5139.00	1212.90	0.70	20.71	5.00	14.53	1.17
GENO183	6795.00	1249.80	0.65	22.18	1.00	8.50	0.62

GENO184	6748.00	1605.50	0.76	31.17	1.00	29.05	1.89
GENO185	8892.00	2036.20	0.71	38.13	1.00	35.70	2.57
GENO186	7098.00	1790.00	0.82	36.74	1.00	27.53	2.57
GENO187	8764.00	1873.10	0.64	32.78	1.00	35.37	2.61
GENO188	7466.00	2184.70	0.93	51.01	1.00	17.40	1.70
GENO189	7921.00	1995.80	0.76	40.22	1.00	20.24	2.34
GENO190	6862.00	1512.50	0.70	21.21	1.00	17.50	1.14
GENO191	6338.00	1463.00	0.69	25.16	4.00	15.54	3.56
GENO192	3372.00	1120.30	0.97	32.31	5.00	8.57	0.68
GENO193	8635.00	1934.10	0.73	36.03	1.00	35.83	2.71
GENO194	12875.00	2928.90	0.72	53.10	2.00	40.50	3.27
GENO195	3706.00	610.00	0.50	7.95	5.00	5.83	0.72
GENO196	4872.00	785.40	0.51	11.31	5.00	7.50	0.81
GENO197	11636.00	2460.10	0.69	42.51	2.00	50.60	4.08
GENO198	7568.00	1443.30	0.61	21.91	1.00	24.95	3.87
GENO199	6687.00	1725.70	0.83	35.61	1.00	33.47	2.42
GENO200	6119.00	1057.00	0.56	14.56	4.00	8.03	0.67
GENO202	7829.00	2011.00	0.80	42.54	1.00	25.33	2.01
GENO203	16098.00	3639.70	0.76	77.48	2.00	68.77	4.96
GENO204	7158.00	1519.00	0.68	25.69	1.00	25.00	1.71

APPENDIX-C Mean phenotypic data of root traits for the year 2020 (Pot experiment)

Genotypes	TRL	RSA	RAD	RV	RBP	RFW	RDW
GENO2	2985.90	491.88	0.51	6.27	4.00	13.70	1.40
GENO3	6283.30	1605.90	0.81	32.84	2.00	36.70	3.50
GENO4	3968.60	1044.50	0.85	21.92	1.00	41.80	1.45
GENO5	4367.40	1150.50	0.85	24.23	2.00	27.47	2.23
GENO6	3085.90	490.88	0.51	6.22	1.00	11.30	0.85
GENO7	3201.80	889.58	0.87	20.30	1.00	14.65	1.22
GENO9	NA	NA	NA	NA	NA	NA	NA
GENO10	4300.30	1076.40	0.79	21.57	2.00	27.40	2.60
GENO11	3442.20	1138.50	1.06	31.70	1.00	36.67	3.63
GENO12	4524.30	1145.30	0.80	21.57	2.00	37.35	3.40
GENO13	3588.20	660.10	0.59	9.72	1.00	9.50	0.95
GENO14	4421.50	1200.60	0.86	25.98	2.00	47.27	4.03
GENO16	NA	NA	NA	NA	NA	NA	NA
GENO18	NA	NA	NA	NA	NA	NA	NA
GENO19	3944.00	1012.80	0.81	20.97	1.00	52.63	4.33
GENO20	4276.80	1473.10	1.11	42.61	2.00	44.70	3.90
GENO21	4338.40	1393.90	1.03	35.73	2.00	36.87	3.40
GENO22	4375.10	1788.20	1.33	59.89	2.00	50.53	4.27
GENO23	5177.70	1483.20	0.92	33.81	2.00	53.45	4.25
GENO24	4244.20	865.13	0.64	14.36	2.00	39.50	3.83
GENO25	7404.20	1959.20	0.86	42.13	2.00	65.13	5.10
GENO26	4236.60	1106.40	0.84	23.07	2.00	34.85	2.80
GENO27	4024.10	1626.20	1.32	54.98	1.00	47.47	4.27

GENO28	3749.20	1146.60	0.98	28.73	1.00	31.37	2.17
GENO29	NA	NA	NA	NA	NA	NA	NA
GENO30	3037.50	1402.10	1.64	53.92	1.00	86.13	5.20
GENO31	3684.50	963.41	0.84	20.04	1.00	21.92	2.00
GENO32	4071.80	1079.20	0.84	22.83	2.00	23.20	1.80
GENO33	3572.60	821.35	0.73	15.03	1.00	30.40	3.30
GENO34	4049.70	1387.80	1.10	38.22	2.00	36.07	2.90
GENO35	5094.30	1455.80	0.91	33.43	2.00	46.75	4.65
GENO36	2619.20	627.30	0.76	11.96	4.00	7.20	1.00
GENO37	4497.80	1587.40	1.13	45.11	2.00	43.40	3.63
GENO38	NA	NA	NA	NA	NA	NA	NA
GENO39	NA	NA	NA	NA	NA	NA	NA
GENO41	1863.20	821.20	1.49	34.76	5.00	47.77	2.57
GENO42	2264.00	504.88	0.71	8.91	5.00	15.83	1.47
GENO43	4645.80	1411.80	0.96	34.15	2.00	34.73	3.50
GENO44	4380.60	1251.00	0.91	28.51	2.00	44.10	4.00
GENO45	2884.10	943.97	0.98	25.03	4.00	34.67	2.86
GENO46	4685.90	1037.70	0.70	18.37	2.00	50.23	4.27
GENO47	3575.60	1278.00	1.13	37.10	1.00	45.07	4.53
GENO48	4124.60	1414.30	1.09	38.75	2.00	37.07	3.07
GENO49	2747.40	587.62	0.68	9.40	4.00	26.05	2.40
GENO50	5313.50	1551.80	0.94	36.43	2.00	70.57	6.50
GENO52	4196.80	1656.30	1.29	53.32	2.00	44.95	2.43
GENO53	3765.50	1071.10	0.92	24.50	1.00	23.40	1.97
GENO54	3124.00	689.47	0.70	12.10	1.00	21.33	1.90

GENO55	7528.40	2396.90	1.04	60.88	2.00	64.75	5.85
GENO56	3365.90	1255.00	1.17	37.69	1.00	42.50	4.13
GENO57	3699.20	1074.20	0.93	25.07	1.00	24.90	2.50
GENO58	2262.20	840.03	1.27	28.18	5.00	36.00	3.27
GENO59	NA	NA	NA	NA	NA	NA	NA
GENO60	3481.60	883.00	0.81	18.06	1.00	29.87	2.27
GENO61	NA	NA	NA	NA	NA	NA	NA
GENO63	5255.60	1523.10	0.92	35.12	2.00	54.50	5.40
GENO64	6023.10	1669.20	0.87	37.79	2.00	53.80	4.10
GENO65	4377.70	1033.90	0.76	19.47	2.00	21.80	2.00
GENO66	4161.70	1183.10	0.91	27.15	2.00	25.10	2.00
GENO67	3740.90	1062.30	0.91	24.09	1.00	31.83	3.17
GENO68	NA	NA	NA	NA	NA	NA	NA
GENO69	NA	NA	NA	NA	NA	NA	NA
GENO70	4204.20	1033.10	0.79	20.47	2.00	26.30	2.17
GENO71	4182.10	1183.90	0.90	27.70	2.00	37.95	4.00
GENO72	3592.60	954.31	0.85	20.18	1.00	27.17	2.90
GENO73	4433.60	1226.60	0.86	25.28	2.00	33.05	2.76
GENO74	4270.00	1125.90	0.83	22.35	2.00	7.67	1.09
GENO75	3571.20	1429.10	1.30	48.64	1.00	41.30	3.50
GENO76	4472.30	1236.20	0.88	27.24	2.00	27.50	2.40
GENO77	3991.20	1219.90	0.97	30.90	1.00	32.23	2.73
GENO78	3710.70	782.31	0.67	13.17	1.00	37.80	2.47
GENO79	3915.30	786.96	0.64	12.74	1.00	24.60	1.80
GENO80	3367.10	1356.80	1.26	51.29	1.00	43.43	3.83

GENO81	3292.00	730.91	0.71	12.93	1.00	22.17	2.10
GENO82	4378.50	1294.20	0.93	31.28	2.00	43.43	3.40
GENO83	4290.60	1057.20	0.78	21.84	2.00	21.20	1.81
GENO84	5322.90	1568.70	0.95	36.98	2.00	48.23	3.96
GENO85	2654.60	583.91	0.71	10.23	4.00	17.95	1.75
GENO86	4152.00	1419.60	1.09	38.62	2.00	40.80	3.30
GENO87	5416.90	1465.40	0.86	31.55	2.00	12.10	0.89
GENO88	3613.00	1684.90	1.56	66.09	1.00	53.20	5.47
GENO89	4492.50	1138.90	0.80	23.60	2.00	25.67	1.77
GENO90	NA	NA	NA	NA	NA	NA	NA
GENO91	4324.00	1736.80	1.28	55.65	2.00	64.65	5.70
GENO92	4230.30	1181.80	0.90	26.42	2.00	35.05	3.35
GENO93	4887.30	1197.80	0.78	23.48	2.00	30.27	2.13
GENO94	5802.60	1597.60	0.88	35.85	2.00	62.00	5.40
GENO95	4871.90	1178.90	0.77	22.75	2.00	28.30	1.93
GENO96	3823.40	1197.90	1.00	29.87	1.00	36.57	3.30
GENO97	4084.10	1201.50	0.93	28.30	2.00	35.63	3.43
GENO98	3810.90	901.80	0.73	17.40	1.00	23.00	1.57
GENO99	4772.20	1768.30	1.18	52.35	2.00	74.77	6.90
GENO100	5149.50	1516.90	0.95	35.80	2.00	50.38	4.67
GENO101	3767.80	898.79	0.76	17.07	1.00	28.40	2.53
GENO102	4440.10	1003.30	0.72	19.12	2.00	24.93	2.20
GENO103	4382.00	1372.80	1.00	34.28	2.00	28.40	2.37
GENO104	4661.00	1408.60	0.96	34.74	2.00	51.17	4.13
GENO105	3402.30	805.62	0.75	15.19	1.00	18.85	1.45

GENO106	3848.70	857.39	0.71	15.21	1.00	22.78	2.03
GENO107	2249.60	400.86	0.68	9.57	5.00	19.43	1.77
GENO108	3412.40	893.19	0.83	18.60	1.00	24.70	2.20
GENO109	4252.30	1170.70	0.88	25.74	2.00	34.67	2.60
GENO110	2885.20	698.52	0.77	13.47	4.00	16.30	1.37
GENO111	2134.90	440.99	0.65	7.26	5.00	12.67	1.17
GENO112	NA	NA	NA	NA	NA	NA	NA
GENO113	3405.30	741.95	0.69	12.92	1.00	25.00	1.80
GENO114	4270.00	1492.30	1.11	41.50	2.00	15.30	2.03
GENO115	4149.00	920.97	0.71	16.30	2.00	35.15	2.75
GENO116	3974.90	936.97	0.74	17.34	1.00	21.57	1.03
GENO117	5103.80	1447.20	0.80	34.37	2.00	21.65	2.04
GENO118	3854.20	1074.00	0.88	23.86	1.00	27.80	2.43
GENO120	4790.70	1175.80	0.78	23.01	2.00	31.33	3.00
GENO121	3745.40	815.66	0.70	14.16	1.00	11.40	1.35
GENO122	2708.40	967.16	1.10	28.49	4.00	29.53	2.63
GENO123	2780.10	891.06	0.97	26.50	4.00	41.08	3.95
GENO124	NA	NA	NA	NA	NA	NA	NA
GENO125	4844.20	1103.20	0.73	20.12	2.00	27.92	3.25
GENO126	2911.70	616.38	0.67	9.78	4.00	10.75	0.90
GENO127	3311.00	723.82	0.70	12.62	1.00	18.93	1.10
GENO128	3774.40	1028.20	0.87	22.31	1.00	39.00	2.80
GENO130	NA	NA	NA	NA	NA	NA	NA
GENO131	3512.20	1536.20	1.40	54.45	1.00	42.29	4.47
GENO132	3985.30	1298.40	1.06	34.73	1.00	41.60	3.16

GENO133	2542.90	646.29	0.80	13.14	4.00	20.80	1.85
GENO134	4954.80	1123.50	0.73	20.40	2.00	42.67	4.13
GENO136	3750.60	1221.40	1.06	33.77	1.00	29.63	2.25
GENO137	3924.70	888.86	0.72	16.25	1.00	17.63	1.30
GENO138	3261.80	718.86	0.70	12.61	1.00	22.20	1.90
GENO139	5049.50	1368.80	0.86	30.09	2.00	21.00	2.15
GENO140	4946.50	1426.50	0.92	33.01	2.00	43.27	4.23
GENO141	4096.40	1179.40	0.92	28.01	2.00	32.14	2.92
GENO142	4466.20	1204.10	0.86	26.05	2.00	29.40	2.97
GENO143	3657.30	894.82	0.76	17.95	1.00	20.25	1.60
GENO144	NA	NA	NA	NA	NA	NA	NA
GENO145	4314.90	1372.70	1.22	38.93	2.00	42.35	4.65
GENO146	3662.00	821.40	0.72	14.72	1.00	18.30	1.20
GENO147	4533.50	1523.90	1.08	43.87	2.00	42.77	3.90
GENO148	2792.90	565.11	0.71	9.91	4.00	10.15	0.87
GENO149	3969.40	686.31	0.55	9.44	1.00	12.50	0.90
GENO150	3828.10	1403.30	1.17	41.63	1.00	49.50	4.70
GENO151	4667.60	1304.60	0.89	29.32	2.00	36.97	3.60
GENO152	4673.90	1295.80	0.88	28.65	2.00	33.50	2.80
GENO153	1925.10	695.19	1.19	20.45	5.00	10.80	0.85
GENO154	1842.10	381.62	0.66	6.29	5.00	15.60	0.30
GENO155	2434.60	530.12	0.69	9.19	5.00	22.20	1.70
GENO156	2575.10	571.28	0.74	10.83	4.00	15.10	1.50
GENO157	7246.50	2150.90	0.99	51.69	2.00	60.27	4.87
GENO158	4241.50	1448.80	1.09	39.40	2.00	35.08	3.97

GENO159	3968.80	1187.70	0.96	29.08	1.00	36.85	3.75
GENO160	3678.40	1111.80	0.93	27.90	1.00	24.75	2.20
GENO161	3800.40	1003.80	0.83	21.26	1.00	37.83	2.67
GENO162	5650.70	1579.50	0.89	35.24	2.00	57.00	4.67
GENO163	2509.90	717.84	0.96	17.25	5.00	13.23	1.53
GENO164	2498.70	585.22	0.73	11.14	5.00	23.17	1.77
GENO165	NA	NA	NA	NA	NA	NA	NA
GENO167	3783.90	877.81	0.74	16.21	1.00	26.40	1.70
GENO168	2395.70	770.13	0.99	18.67	5.00	17.18	2.00
GENO169	3909.40	1068.90	0.87	23.26	1.00	47.65	3.35
GENO170	3143.50	692.74	0.70	12.16	1.00	21.23	2.07
GENO171	4805.80	1333.00	0.88	29.62	2.00	33.47	2.97
GENO172	NA	NA	NA	NA	NA	NA	NA
GENO173	4039.50	886.54	0.70	15.49	2.00	21.27	1.63
GENO174	5043.80	1256.70	0.79	24.96	2.00	41.33	3.87
GENO175	2965.00	835.06	0.88	19.18	4.00	25.00	2.45
GENO176	4541.00	1406.10	1.00	33.48	2.00	27.10	2.55
GENO177	3441.30	1023.40	0.95	24.11	1.00	28.73	2.20
GENO178	4408.90	797.08	0.70	16.17	2.00	15.55	1.35
GENO179	2898.10	740.24	0.81	15.18	4.00	30.00	2.37
GENO180	2767.30	662.72	0.76	12.50	4.00	8.83	0.80
GENO181	4276.60	1314.80	0.98	34.34	2.00	28.45	2.50
GENO182	3259.30	728.15	0.71	12.95	1.00	26.33	1.93
GENO183	4210.50	1326.20	1.00	34.45	2.00	37.48	3.77
GENO184	3139.70	672.11	0.68	11.12	1.00	15.00	1.16

GENO185	4413.80	1427.20	1.03	37.54	2.00	44.50	4.10
GENO186	4159.60	1438.40	1.14	46.26	2.00	26.70	2.71
GENO187	5356.00	1241.50	0.74	22.27	2.00	44.38	4.15
GENO188	4578.00	1336.20	0.93	30.19	2.00	12.00	1.17
GENO189	3933.60	946.70	0.75	18.36	1.00	18.70	2.18
GENO190	2679.00	663.18	0.77	13.45	4.00	24.70	2.03
GENO191	3432.00	917.06	0.86	19.66	1.00	18.20	1.47
GENO192	3792.30	1895.60	1.59	75.40	1.00	28.18	4.05
GENO193	4446.00	986.93	0.73	17.23	2.00	16.62	1.72
GENO194	4312.20	959.84	0.73	17.11	2.00	15.83	1.53
GENO195	3975.20	1059.60	0.84	22.59	1.00	20.80	2.10
GENO196	NA	NA	NA	NA	NA	NA	NA
GENO197	3473.70	1150.50	1.03	31.24	1.00	47.57	4.23
GENO198	3141.70	680.80	0.69	11.78	1.00	22.65	2.20
GENO199	NA	NA	NA	NA	NA	NA	NA
GENO200	4563.30	1226.90	0.86	26.58	2.00	27.23	2.27
GENO202	3885.00	1913.30	1.72	84.13	1.00	68.73	6.13
GENO203	4337.20	1197.80	0.91	26.94	2.00	43.53	3.03
GENO204	3091.50	660.26	0.68	11.76	1.00	16.70	1.17

APPENDIX-D Mean phenotypic data of stolon and tuber traits for the year 2019 (Aeroponic)

Genotype	TNS	SL	SD	BS	SFW	SDW	TNT	TS	ATW	ATY
GENO2	2.46	12.14	1.15	5.92	1.23	0.09	0.58	3.00	2.20	2.33
GENO3	3.10	135.02	4.42	26.21	40.89	2.29	2.81	2.50	8.35	48.84
GENO4	3.33	57.91	3.35	17.42	13.77	0.87	2.58	3.75	14.47	50.29
GENO5	4.42	52.89	2.79	23.77	7.54	0.54	2.83	3.00	16.72	50.66
GENO6	3.25	22.00	1.67	11.75	1.24	0.08	1.00	1.00	9.21	9.21
GENO7	2.20	33.16	2.02	8.80	3.90	0.28	1.60	2.00	19.23	37.11
GENO9	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO10	1.00	10.00	1.17	5.67	0.88	0.05	0.33	2.00	6.99	6.99
GENO11	2.50	213.70	4.58	33.00	52.32	2.48	2.00	5.00	44.94	63.00
GENO12	0.50	6.40	2.22	2.50	1.25	0.07	0.00	0.00	0.00	0.00
GENO13	3.00	20.00	1.60	10.00	1.33	0.13	4.00	3.00	5.23	20.90
GENO14	8.33	551.53	4.55	65.33	147.83	7.57	2.00	3.00	0.79	4.77
GENO16	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO18	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO19	1.00	127.50	3.48	21.50	11.65	0.70	4.00	5.00	17.67	60.40
GENO20	3.00	27.77	1.77	6.00	2.25	0.16	0.00	0.00	0.00	0.00
GENO21	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO22	3.00	20.00	1.90	9.00	1.40	0.08	0.00	0.00	0.00	0.00
GENO23	5.33	31.67	2.39	14.00	6.23	0.40	1.00	1.00	4.09	6.65
GENO24	5.25	391.09	6.30	84.50	105.15	7.12	5.75	2.00	16.06	76.84
GENO25	3.00	258.17	5.43	58.00	89.00	6.71	1.00	4.00	0.28	0.85
GENO26	3.00	115.00	3.32	29.00	23.56	1.82	3.50	2.00	3.70	14.90
GENO27	6.67	140.77	5.00	45.33	28.12	2.24	0.00	0.00	0.00	0.00

GENO28	3.65	61.25	1.28	16.00	5.08	0.31	0.25	4.00	3.10	3.10
GENO29	2.67	270.67	5.56	54.33	77.47	4.08	2.33	2.00	9.97	23.23
GENO30	2.00	299.76	5.34	46.00	43.78	1.89	0.00	0.00	0.00	0.00
GENO31	3.00	15.00	0.90	6.00	0.32	0.02	3.00	1.00	11.83	35.50
GENO32	3.67	258.23	4.67	60.67	90.11	5.68	4.33	2.00	4.35	23.16
GENO33	2.67	129.50	3.43	28.33	21.16	1.07	0.67	2.00	13.12	13.12
GENO34	3.00	155.37	5.79	38.67	47.81	3.20	5.67	4.00	6.19	34.49
GENO35	4.67	229.87	5.69	46.00	72.10	4.56	5.33	2.00	13.59	75.91
GENO36	4.33	16.50	2.53	5.67	2.52	0.17	2.67	3.00	10.37	15.07
GENO37	4.00	189.44	4.50	44.00	43.44	2.66	1.67	2.00	9.52	23.06
GENO38	2.67	192.70	4.58	38.67	64.30	3.60	0.00	0.00	0.00	0.00
GENO39	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO41	1.33	14.93	1.12	5.33	1.19	0.06	1.00	4.00	14.64	20.85
GENO42	1.00	10.67	2.17	5.67	3.03	0.22	1.00	3.00	11.31	11.31
GENO43	1.67	11.67	1.68	7.33	1.23	0.07	1.33	1.00	14.40	16.83
GENO44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO45	0.33	1.97	0.57	1.00	0.30	0.17	2.00	4.00	0.31	1.83
GENO46	3.00	10.17	2.20	10.67	2.60	0.14	2.33	5.00	5.49	11.63
GENO47	2.50	232.50	5.99	58.25	81.68	4.60	0.50	4.00	2.90	5.81
GENO48	1.00	5.00	0.70	4.00	0.50	0.03	1.00	1.00	6.00	6.00
GENO49	1.67	8.35	0.63	4.33	0.36	0.02	0.33	2.00	12.67	12.67
GENO50	6.33	148.53	2.80	35.33	17.53	1.10	0.67	2.00	4.07	8.13
GENO52	2.50	187.95	3.95	29.00	35.90	2.64	0.50	1.00	1.65	1.65
GENO53	3.60	121.76	4.52	29.60	33.38	1.76	3.40	1.00	9.31	30.03
GENO54	3.75	119.18	4.59	28.00	14.14	0.91	8.00	2.00	14.49	117.15

GENO55	1.33	5.07	1.20	9.67	5.97	0.46	0.00	0.00	0.00	0.00
GENO56	6.00	303.97	5.09	71.33	117.94	7.04	6.33	3.00	11.09	74.63
GENO57	3.25	141.38	5.38	46.25	30.80	1.80	3.00	5.00	16.56	40.40
GENO58	2.67	207.67	3.01	44.67	48.63	3.74	3.33	1.00	2.57	15.66
GENO59	3.33	310.83	4.87	54.33	74.23	4.63	0.00	0.00	0.00	0.00
GENO60	4.00	27.50	2.55	16.00	1.67	0.09	0.00	0.00	0.00	0.00
GENO61	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO63	1.50	10.78	1.50	6.25	0.60	0.18	1.00	1.00	4.67	5.94
GENO64	1.33	15.39	4.06	8.33	5.07	0.35	2.00	3.00	7.25	16.31
GENO65	4.00	148.00	4.58	49.00	52.94	3.96	12.00	6.00	5.16	61.92
GENO66	2.50	145.00	4.35	35.00	51.70	3.02	4.00	1.00	10.06	40.23
GENO67	3.67	80.00	3.32	31.00	26.17	2.62	9.00	4.00	13.76	125.63
GENO68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO69	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO70	6.33	98.30	2.97	46.33	28.97	1.92	3.00	3.00	12.62	37.37
GENO71	1.67	50.97	4.30	17.33	26.67	1.27	1.00	2.00	1.23	1.73
GENO72	4.25	13.75	2.94	10.75	1.09	0.06	4.75	3.00	13.92	32.98
GENO73	4.50	65.80	3.95	37.75	37.90	1.97	4.50	2.00	15.77	69.54
GENO74	2.00	7.50	2.56	4.00	1.38	0.10	2.00	4.00	15.15	28.53
GENO75	2.50	37.48	2.98	11.00	8.06	0.53	2.25	2.00	11.51	23.94
GENO76	2.33	48.60	2.78	16.67	25.47	1.48	0.00	0.00	0.00	0.00
GENO77	4.00	41.75	2.91	26.75	5.75	0.38	2.50	2.00	21.28	45.83
GENO78	5.00	183.90	3.83	34.33	44.54	2.52	1.33	1.00	1.97	4.44
GENO79	4.00	182.67	4.62	43.67	34.15	1.63	0.33	4.00	2.17	2.17
GENO80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

GENO81	1.67	173.64	2.38	29.33	29.90	1.82	1.00	1.00	2.88	4.59
GENO82	0.67	8.67	2.69	4.00	7.30	0.41	0.67	2.00	5.63	11.26
GENO83	2.67	145.33	3.47	33.33	39.41	2.29	0.00	0.00	0.00	0.00
GENO84	1.33	166.90	6.71	25.00	57.77	3.69	2.00	4.00	25.12	50.23
GENO85	1.80	112.36	4.49	28.20	34.00	2.16	1.20	2.00	2.50	7.66
GENO86	3.25	217.93	5.06	55.00	57.26	3.43	2.50	1.00	3.23	10.25
GENO87	3.75	67.63	2.64	25.00	12.25	1.31	3.00	4.00	16.34	34.68
GENO88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO89	2.40	131.96	4.35	27.80	30.88	1.74	5.40	6.00	21.72	70.32
GENO90	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO91	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO92	2.25	129.78	5.46	28.75	27.03	2.06	3.00	5.00	13.20	38.05
GENO93	1.00	140.00	6.10	56.00	45.00	3.91	0.00	0.00	0.00	0.00
GENO94	1.25	116.35	6.15	26.25	33.30	2.58	1.00	2.00	2.43	4.85
GENO95	2.00	6.00	4.06	4.00	2.10	0.13	2.00	4.00	8.60	17.20
GENO96	2.00	189.33	3.24	42.33	58.60	2.96	4.33	3.00	2.26	17.57
GENO97	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO98	5.00	21.80	1.76	12.50	3.19	0.28	1.00	5.00	1.42	2.84
GENO99	0.33	40.00	0.32	8.33	3.13	0.23	0.67	1.00	0.53	1.07
GENO100	0.33	5.10	0.65	2.33	1.90	0.10	0.67	1.00	0.55	1.10
GENO101	3.67	163.74	5.41	39.00	33.33	2.31	1.00	3.00	1.53	2.43
GENO102	2.00	15.50	1.44	9.00	1.60	0.09	2.00	5.00	15.45	31.25
GENO103	3.67	31.50	2.72	14.00	4.12	0.34	1.67	2.00	3.19	8.20
GENO104	2.33	121.96	6.63	42.00	41.31	2.60	4.67	3.00	21.31	103.28
GENO105	1.67	51.23	2.45	10.33	5.39	0.24	0.67	3.00	1.03	2.07

GENO106	4.50	40.15	2.59	16.00	6.75	0.41	3.00	4.00	14.17	33.62
GENO107	3.33	326.70	5.99	55.33	76.40	4.54	3.33	2.00	21.98	71.70
GENO108	2.00	81.23	5.17	23.67	16.20	1.33	1.67	4.00	7.29	18.12
GENO109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO110	3.00	120.43	3.94	33.33	51.48	2.52	0.00	0.00	0.00	0.00
GENO111	4.33	15.00	1.90	11.00	1.50	0.08	1.67	1.00	9.07	13.66
GENO112	1.50	5.00	0.95	4.00	0.94	0.06	0.50	1.00	1.25	1.25
GENO113	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO114	4.00	336.00	4.09	61.50	60.00	2.86	2.00	4.00	8.38	16.76
GENO115	2.00	14.93	1.02	8.00	0.92	0.08	1.00	1.00	8.29	8.29
GENO116	5.00	253.33	4.99	53.67	84.44	4.61	1.67	5.00	6.04	16.94
GENO117	0.00	0.00	0.00	0.00	0.00	0.00	0.33	5.00	1.26	1.26
GENO118	1.75	16.31	2.61	6.50	1.30	0.11	2.75	5.00	58.25	128.68
GENO120	3.00	370.00	5.90	54.00	94.00	4.27	0.00	0.00	0.00	0.00
GENO121	1.33	6.00	1.07	3.67	1.22	0.07	1.00	3.00	20.87	20.87
GENO122	1.00	14.33	0.52	9.67	2.63	0.14	0.00	0.00	0.00	0.00
GENO123	1.50	64.34	2.75	16.75	31.28	1.75	2.25	3.00	2.65	12.17
GENO124	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO125	0.33	1.70	0.50	1.00	0.37	0.03	0.33	1.00	0.40	0.40
GENO126	2.00	51.63	1.07	17.33	5.30	0.29	1.33	5.00	21.11	26.26
GENO127	1.67	99.62	4.95	27.67	65.67	4.40	4.33	3.00	42.14	184.23
GENO128	4.00	440.00	7.60	83.00	222.00	13.27	1.00	1.00	10.00	10.00
GENO130	3.33	11.90	1.17	10.00	1.17	0.05	0.67	2.00	1.18	1.18
GENO131	3.67	63.60	2.23	20.33	8.21	0.53	1.67	2.00	3.78	18.90
GENO132	5.33	10.00	2.17	11.00	2.32	0.13	1.33	4.00	13.94	17.91

GENO133	2.00	58.00	4.50	16.33	10.23	0.91	3.33	2.00	30.26	107.46
GENO134	1.33	9.40	1.00	2.33	1.13	0.06	1.00	3.00	9.97	15.70
GENO136	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO137	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO138	1.67	249.63	5.19	46.33	48.14	2.70	0.00	0.00	0.00	0.00
GENO139	1.50	122.85	3.10	13.50	17.08	1.04	0.50	5.00	1.70	10.16
GENO140	2.50	146.35	4.93	31.00	37.78	2.17	4.25	3.00	14.08	50.56
GENO141	1.00	115.97	3.10	19.33	16.50	1.55	2.33	1.00	23.94	54.99
GENO142	4.00	27.70	1.60	14.67	4.11	0.39	2.00	2.00	11.14	33.72
GENO143	3.50	74.18	4.08	21.75	13.05	1.18	5.50	1.00	8.19	47.89
GENO144	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO145	2.33	83.00	2.06	14.67	8.47	0.56	2.33	2.00	6.75	15.88
GENO146	2.00	254.96	5.45	69.33	117.04	7.00	3.33	1.00	2.51	8.43
GENO147	0.67	5.00	1.15	2.33	1.17	0.06	0.67	2.00	1.77	1.77
GENO148	3.00	126.50	2.48	32.33	19.90	1.42	4.00	2.00	17.56	71.72
GENO149	1.33	8.17	1.63	3.33	2.60	0.12	1.00	4.00	20.37	20.37
GENO150	2.67	194.33	4.22	51.33	27.43	1.77	4.00	2.00	9.28	40.97
GENO151	2.25	107.95	2.86	31.50	13.99	1.13	6.00	2.00	7.75	53.61
GENO152	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO153	3.33	169.65	2.42	38.33	13.85	0.53	5.33	2.00	4.52	24.33
GENO154	3.00	31.57	1.70	8.67	2.70	0.15	1.00	4.00	19.19	19.19
GENO155	2.67	166.57	6.33	31.67	52.75	3.14	0.67	2.00	3.47	6.93
GENO156	1.33	58.10	2.45	17.33	5.80	0.42	3.00	1.00	1.94	17.49
GENO157	3.00	369.92	4.97	47.00	104.67	5.64	0.33	1.00	0.31	0.31
GENO158	2.00	5.00	0.90	2.00	0.19	0.01	0.00	0.00	0.00	0.00

GENO159	0.25	23.28	1.21	5.25	8.95	0.29	1.00	4.00	0.77	3.08
GENO160	2.33	96.77	5.55	53.33	25.90	1.40	3.33	1.00	6.82	23.29
GENO161	3.33	166.10	4.19	45.00	39.32	2.70	0.00	0.00	0.00	0.00
GENO162	4.00	385.62	5.97	61.00	61.60	4.12	4.67	2.00	10.79	51.32
GENO163	2.33	48.33	4.24	30.67	13.05	0.93	1.33	2.00	1.24	2.52
GENO164	2.00	18.50	1.37	4.00	2.38	0.13	1.67	2.00	24.15	37.79
GENO165	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO167	4.33	36.33	3.32	14.67	3.10	0.27	5.00	5.00	22.11	94.97
GENO168	2.50	122.55	4.24	36.00	25.60	1.38	3.00	3.00	19.16	57.47
GENO169	3.00	82.57	2.76	21.33	5.50	0.45	3.00	1.00	1.05	3.19
GENO170	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO171	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GENO172	3.00	308.23	4.60	63.33	72.44	4.66	2.33	2.00	5.52	19.01
GENO173	2.50	195.22	6.13	32.50	59.56	3.22	2.00	1.00	10.46	22.47
GENO174	1.33	78.23	3.56	23.67	15.20	1.08	0.00	0.00	0.00	0.00
GENO175	2.00	123.70	3.94	29.00	28.28	2.43	3.00	4.00	18.08	54.22
GENO176	3.25	71.60	3.55	23.25	8.77	0.56	2.50	1.00	13.45	30.19
GENO177	1.33	40.00	2.07	12.33	3.44	0.26	1.67	1.00	9.39	24.00
GENO178	3.67	123.90	4.26	30.00	26.17	1.53	5.33	4.00	11.53	68.70
GENO179	1.20	73.30	3.25	13.00	6.80	0.44	2.60	3.00	6.27	24.94
GENO180	2.67	291.93	6.90	68.33	106.67	6.66	5.00	2.00	13.90	76.33
GENO181	1.50	29.13	2.67	11.00	3.02	0.19	0.50	1.00	4.00	4.00
GENO182	1.67	173.69	4.70	45.33	60.40	3.58	0.33	5.00	0.92	0.92
GENO183	2.67	45.00	3.80	18.33	8.18	0.53	3.00	1.00	16.63	45.77
GENO184	4.00	78.90	2.30	19.00	6.42	0.39	3.00	2.00	14.16	42.70

GENO185	5.67	25.50	2.60	9.33	2.90	0.15	1.33	4.00	5.52	11.03
GENO186	3.33	52.27	2.25	20.33	7.41	0.47	3.00	3.00	7.06	21.33
GENO187	1.33	77.97	3.47	19.67	9.52	0.81	1.00	4.00	10.86	17.91
GENO188	2.33	20.00	1.95	11.33	8.17	0.45	3.67	4.00	11.86	46.80
GENO189	2.50	18.55	1.37	8.75	1.85	0.13	2.25	1.00	17.80	41.90
GENO190	5.25	163.02	3.75	35.25	28.77	1.99	2.50	5.00	13.44	33.78
GENO191	1.33	10.63	1.77	5.00	0.57	0.04	0.67	1.00	5.52	11.03
GENO192	4.67	81.70	3.07	24.33	9.02	0.70	4.33	2.00	11.19	47.14
GENO193	2.20	14.00	1.88	5.00	2.47	0.14	2.25	2.00	4.79	10.45
GENO194	3.60	189.36	5.20	67.60	73.91	4.63	4.80	1.00	15.68	62.14
GENO195	2.33	18.50	2.83	9.33	2.86	0.15	2.33	3.00	20.83	50.60
GENO196	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO197	4.00	140.27	4.33	25.67	31.57	2.08	1.67	1.00	22.04	30.93
GENO198	2.00	55.75	4.23	21.50	12.71	0.69	1.75	5.00	73.03	117.76
GENO199	4.00	188.62	3.98	45.50	38.86	2.32	2.25	2.00	16.36	33.95
GENO200	2.00	123.93	2.96	40.00	14.62	1.23	0.00	0.00	0.00	0.00
GENO202	3.33	343.43	3.54	63.33	176.31	11.40	1.33	2.00	3.11	12.44
GENO203	0.67	4.37	0.70	2.00	0.69	0.07	0.33	1.00	2.81	2.81
GENO204	3.00	268.35	5.56	41.00	76.30	3.68	1.00	4.00	3.75	7.50

APPENDIX-E Mean phenotypic data of stolon and tuber traits for the year 2020 (Aeroponic)

Genotypes	TNS	SL	SD	BS	SFW	SDW	TNT	TS	ATW	ATY
GENO2	5.00	26.65	1.71	14.00	2.40	0.19	3.00	3.00	8.72	26.15
GENO3	5.33	90.28	2.56	27.67	22.10	2.00	6.00	2.50	22.25	136.98
GENO4	4.00	38.50	2.60	20.10	8.35	0.58	6.00	3.75	14.80	88.79
GENO5	5.33	76.33	2.17	21.33	8.87	0.33	2.67	3.00	31.17	82.70
GENO6	1.50	10.00	1.17	4.75	0.80	0.06	2.50	1.00	32.51	56.35
GENO7	1.00	13.00	0.90	4.00	0.90	0.06	3.00	2.00	31.58	94.75
GENO9	4.50	25.00	1.85	8.00	2.10	0.17	2.00	3.00	19.68	39.35
GENO10	2.80	36.40	1.04	17.20	4.26	0.26	4.60	2.00	16.39	75.42
GENO11	2.67	22.65	1.42	6.67	0.65	0.04	2.33	5.00	2.19	7.40
GENO12	3.75	22.25	1.83	7.25	3.70	0.21	4.00	5.00	44.65	174.15
GENO13	5.33	143.33	2.16	22.67	9.43	0.62	5.00	2.00	9.73	50.57
GENO14	4.00	55.00	2.98	8.00	9.00	0.73	4.00	6.00	3.38	13.50
GENO16	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO18	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO19	1.50	9.40	1.45	7.00	1.65	0.13	2.50	5.00	2.00	10.00
GENO20	3.67	95.67	2.40	26.67	9.57	0.51	3.00	3.00	27.81	74.17
GENO21	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO22	7.50	110.28	3.40	36.50	14.88	0.86	5.25	1.00	29.46	153.68
GENO23	2.00	20.15	2.91	9.00	8.12	0.15	3.00	1.00	5.20	15.60
GENO24	6.00	181.25	2.48	41.50	11.10	0.61	3.75	4.00	10.20	37.13
GENO25	5.00	130.10	1.16	20.00	8.70	0.73	3.00	4.00	6.82	20.46
GENO26	5.00	39.00	1.83	13.33	3.50	0.27	6.67	4.00	22.38	124.57
GENO27	3.00	72.42	2.15	26.40	6.85	0.43	5.40	3.00	23.01	112.00

GENO28	4.75	133.75	2.47	67.25	17.95	1.45	4.25	5.00	27.92	118.18
GENO29	3.50	104.00	2.79	53.25	14.23	0.84	3.25	6.00	5.87	18.53
GENO30	5.80	196.00	2.13	69.80	15.34	0.89	7.20	5.00	23.98	149.76
GENO31	7.00	45.00	1.60	18.00	3.50	0.24	5.00	1.00	15.82	79.10
GENO32	3.80	19.40	2.15	6.80	2.94	0.21	6.20	2.00	13.57	86.88
GENO33	4.25	39.00	1.80	14.50	5.58	0.33	2.50	3.00	19.88	50.78
GENO34	5.33	75.00	1.97	20.00	2.97	0.16	4.00	4.00	12.64	52.10
GENO35	5.00	159.00	3.58	44.00	32.14	2.14	5.00	2.00	18.14	90.70
GENO36	6.50	180.32	3.21	44.50	25.00	1.63	10.00	2.00	10.34	105.30
GENO37	5.00	53.62	3.31	12.33	8.29	0.49	7.33	3.00	13.32	99.72
GENO38	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO39	4.67	29.67	1.91	12.67	3.90	0.22	5.67	4.00	25.89	156.07
GENO41	4.00	19.70	1.40	7.00	1.07	0.05	3.00	4.00	25.17	75.51
GENO42	2.50	11.00	2.15	6.00	2.03	0.15	3.50	3.00	30.39	99.03
GENO43	2.33	16.67	1.07	3.67	1.43	0.12	3.00	3.00	19.26	58.37
GENO44	3.00	5.10	1.50	5.00	1.12	0.09	1.00	2.00	4.21	4.21
GENO45	2.00	5.70	1.07	3.33	0.87	0.06	1.67	3.00	19.46	28.97
GENO46	3.00	12.80	1.56	5.00	1.05	0.06	2.60	5.00	31.00	79.24
GENO47	4.00	60.80	2.56	28.80	7.30	0.45	4.20	4.00	28.21	121.32
GENO48	2.50	14.64	1.68	8.00	1.73	0.12	2.00	1.00	10.32	18.92
GENO49	6.00	16.10	1.95	10.00	1.10	0.09	2.00	2.00	25.01	50.01
GENO50	3.00	65.00	4.05	53.50	17.30	0.93	8.00	2.00	7.66	62.90
GENO52	1.00	104.97	2.10	19.33	14.50	1.01	4.00	1.00	4.03	16.11
GENO53	2.25	12.58	1.29	8.50	2.18	0.13	2.00	4.00	27.63	50.73
GENO54	14.00	199.00	2.77	55.50	14.90	0.72	14.00	2.00	8.74	124.70

GENO55	3.00	22.00	1.90	7.00	2.70	0.15	2.00	5.00	14.85	29.70
GENO56	3.67	29.00	1.90	13.33	3.03	0.20	1.00	3.00	8.10	8.10
GENO57	9.20	196.00	3.26	56.20	20.30	1.44	6.60	5.00	12.06	79.10
GENO58	2.00	14.43	1.18	6.20	1.68	0.09	2.60	3.00	17.94	44.56
GENO59	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO60	5.00	43.00	1.80	14.50	6.40	0.28	4.00	3.00	19.14	72.75
GENO61	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO63	5.00	108.40	2.28	12.60	7.83	0.43	7.20	1.00	14.51	103.70
GENO64	4.00	280.50	2.60	195.00	26.60	2.06	12.00	5.00	5.05	60.60
GENO65	5.00	155.90	2.80	75.00	24.50	1.85	3.00	6.00	14.97	44.90
GENO66	6.00	32.00	1.69	23.50	4.70	0.24	3.50	1.00	14.58	49.85
GENO67	4.00	65.00	3.20	38.00	19.70	0.79	5.00	2.00	14.68	73.40
GENO68	2.00	25.72	1.63	9.67	1.63	0.13	2.00	4.00	12.93	38.80
GENO69	6.50	47.00	3.20	25.25	7.25	0.43	4.00	3.00	22.92	90.18
GENO70	8.60	420.31	3.37	90.60	75.92	3.73	13.00	3.00	5.88	75.70
GENO71	5.40	48.60	2.41	21.40	5.70	0.37	5.60	2.00	16.78	89.86
GENO72	2.00	22.53	1.43	7.50	1.96	0.13	2.50	3.00	19.39	51.35
GENO73	3.67	29.67	1.53	11.33	1.33	0.08	4.33	4.00	16.78	48.33
GENO74	3.50	8.75	1.53	4.75	0.98	0.07	2.50	4.00	21.16	52.90
GENO75	5.50	67.50	1.84	4.50	2.80	0.17	3.50	4.00	7.20	50.40
GENO76	4.00	76.00	2.02	18.00	4.95	0.36	6.00	3.00	7.82	40.15
GENO77	8.25	75.25	2.19	35.00	7.05	0.47	4.25	2.00	17.01	70.38
GENO78	1.50	10.00	0.89	8.50	0.76	0.04	1.50	3.00	9.84	29.50
GENO79	9.25	177.75	2.93	48.25	37.23	3.28	9.25	2.00	11.74	114.70
GENO80	1.00	26.14	2.50	7.00	10.92	0.58	3.00	0.00	4.23	12.70

GENO81	2.00	37.00	1.61	9.50	3.80	0.30	3.50	1.00	45.36	134.15
GENO82	2.50	24.50	2.09	8.00	2.75	0.16	1.50	3.00	10.23	16.70
GENO83	2.00	25.40	1.93	10.20	3.60	0.21	3.00	4.00	36.81	103.90
GENO84	4.00	19.44	1.30	11.00	12.60	0.72	3.67	4.00	5.55	20.43
GENO85	4.00	83.00	2.20	19.00	19.60	1.23	5.00	2.00	12.23	61.15
GENO86	6.00	235.00	1.80	120.00	25.60	1.95	4.00	1.00	5.88	23.50
GENO87	2.25	6.76	1.34	10.25	1.30	0.16	2.00	1.00	11.00	20.30
GENO88	3.25	19.75	1.50	6.25	2.70	0.15	2.75	3.00	30.82	84.90
GENO89	7.00	34.68	2.80	28.67	18.14	0.48	3.67	5.00	28.48	105.63
GENO90	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO91	2.33	14.33	1.58	5.33	0.77	0.05	2.00	4.00	30.86	45.30
GENO92	3.00	125.10	2.95	17.00	15.50	1.20	5.00	5.00	13.15	65.76
GENO93	3.00	157.15	3.10	45.00	29.15	1.65	1.00	0.00	6.12	6.12
GENO94	4.00	84.67	2.07	17.33	3.47	0.17	5.67	2.00	24.10	128.37
GENO95	4.33	45.00	1.77	17.33	4.60	0.33	3.33	4.00	28.26	88.70
GENO96	4.40	121.60	2.11	43.80	10.06	0.67	4.00	3.00	29.79	114.34
GENO97	2.50	17.00	1.75	5.00	2.10	0.15	3.00	4.00	57.75	173.25
GENO98	4.00	8.00	0.75	2.00	0.80	0.04	2.00	5.00	5.10	10.20
GENO99	2.00	65.01	2.05	14.00	5.40	0.38	4.00	1.00	8.93	35.70
GENO100	5.80	72.54	2.12	24.20	10.77	0.62	7.40	4.00	19.44	147.14
GENO101	5.00	42.07	1.70	17.60	3.62	0.20	4.80	3.00	19.97	84.76
GENO102	4.00	183.09	1.47	66.67	10.83	0.68	7.67	6.00	6.16	46.80
GENO103	4.00	34.00	2.31	15.67	10.99	0.70	4.00	2.00	7.55	30.21
GENO104	6.00	176.25	1.56	108.25	18.03	1.05	3.00	3.00	9.68	27.10
GENO105	3.80	3.60	1.95	2.80	0.65	0.03	1.60	3.00	25.39	38.46

GENO106	9.00	320.00	2.55	105.00	20.35	1.36	6.33	5.00	21.83	136.00
GENO107	1.00	35.00	1.65	10.50	1.45	0.10	4.00	2.00	11.35	45.40
GENO108	4.00	95.00	1.55	22.75	8.95	0.52	4.25	4.00	20.04	94.20
GENO109	4.00	16.00	1.71	4.00	1.10	0.04	3.00	6.00	27.70	83.10
GENO110	3.50	36.50	1.53	14.00	2.25	0.13	4.50	4.00	19.56	86.80
GENO111	2.00	18.00	1.16	5.00	2.20	0.21	4.00	1.00	4.55	18.20
GENO112	3.67	48.33	2.39	15.00	1.97	0.17	3.00	1.00	30.57	92.90
GENO113	4.00	83.84	1.77	27.67	2.52	0.22	6.00	2.00	14.30	79.83
GENO114	5.50	43.00	2.35	24.00	2.95	0.24	1.50	3.00	61.95	79.85
GENO115	3.80	16.00	1.55	5.20	1.93	0.13	2.20	6.00	38.54	74.46
GENO116	3.67	162.25	4.70	71.33	21.59	1.74	3.00	5.00	12.21	36.63
GENO117	4.25	45.53	2.47	18.75	5.65	0.33	5.25	5.00	33.86	185.68
GENO118	2.67	30.46	2.02	5.67	2.53	0.16	5.67	5.00	19.51	99.63
GENO120	2.50	147.50	2.63	23.75	13.73	0.77	4.25	2.00	10.35	37.10
GENO121	3.25	21.75	2.08	7.25	1.43	0.08	2.00	4.00	23.34	46.03
GENO122	3.50	71.13	2.11	20.50	4.15	0.23	3.00	2.00	18.82	53.50
GENO123	6.00	65.74	1.89	13.00	9.10	0.43	5.00	3.00	8.18	40.90
GENO124	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO125	3.00	13.40	1.32	6.00	1.06	0.07	1.60	1.00	10.51	13.22
GENO126	1.00	39.10	0.90	12.00	3.70	0.20	2.00	5.00	18.73	37.45
GENO127	3.00	135.55	2.95	30.00	31.10	2.44	6.00	3.00	36.18	217.09
GENO128	6.33	410.30	3.10	210.00	39.53	2.32	3.33	2.00	4.66	25.47
GENO130	2.67	17.70	3.00	8.67	3.30	0.18	1.67	2.00	7.95	13.43
GENO131	3.00	49.52	2.67	10.50	3.87	0.17	4.00	2.00	32.50	130.00
GENO132	8.00	110.67	3.51	45.00	17.17	1.10	4.33	4.00	13.66	66.93

GENO133	3.80	43.00	1.94	8.80	4.32	0.26	3.80	2.00	20.75	88.60
GENO134	3.33	19.23	1.63	5.33	3.10	0.20	2.00	6.00	12.96	23.27
GENO136	2.00	8.00	2.03	4.00	1.20	0.10	3.00	2.00	13.60	40.80
GENO137	4.80	30.60	1.69	8.60	2.58	0.19	4.40	1.00	21.67	84.50
GENO138	2.00	30.00	1.50	12.00	12.40	1.18	4.00	3.00	5.70	22.80
GENO139	2.80	55.83	2.62	8.80	6.96	0.37	4.40	5.00	26.25	119.56
GENO140	4.00	28.00	2.13	14.00	2.80	0.13	3.00	6.00	33.63	100.90
GENO141	4.50	49.09	2.63	17.50	8.10	0.46	2.00	6.00	18.49	37.35
GENO142	2.67	17.33	1.93	7.33	1.70	0.08	3.33	2.00	15.82	55.17
GENO143	3.33	42.72	2.29	21.00	6.60	0.65	6.00	4.00	6.33	40.50
GENO144	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO145	5.00	16.00	1.37	4.67	1.30	0.09	3.33	2.00	18.81	63.13
GENO146	3.00	24.05	1.17	7.67	2.87	0.17	2.67	1.00	5.38	12.03
GENO147	2.00	14.33	1.22	5.00	2.10	0.15	2.33	5.00	14.44	30.47
GENO148	8.00	175.10	1.80	67.00	10.60	0.57	9.00	2.00	12.80	115.20
GENO149	4.00	13.55	1.31	7.00	1.90	0.10	4.00	4.00	24.19	96.75
GENO150	3.20	59.97	1.92	23.80	9.02	0.83	3.40	5.00	13.82	52.26
GENO151	4.67	32.33	1.07	12.33	2.20	0.18	4.67	1.00	3.23	15.30
GENO152	3.50	126.50	2.05	26.50	7.80	0.45	6.50	2.00	8.13	53.56
GENO153	5.00	125.01	2.15	37.00	8.50	0.38	6.00	2.00	8.00	48.00
GENO154	2.67	23.67	1.50	11.33	1.50	0.07	3.33	4.00	13.08	44.27
GENO155	1.67	24.44	2.54	9.00	10.70	0.47	1.00	2.00	0.62	1.87
GENO156	5.33	60.13	1.54	15.33	4.69	0.27	7.00	2.00	7.44	53.34
GENO157	2.25	28.06	1.38	12.00	1.83	0.12	3.25	1.00	6.21	19.65
GENO158	1.50	9.00	1.00	3.50	1.33	0.08	2.25	4.00	33.94	68.93

GENO159	4.00	109.84	2.00	43.25	18.18	1.02	10.00	4.00	17.20	165.43
GENO160	4.50	75.00	1.45	16.00	3.40	0.31	3.50	5.00	14.27	45.10
GENO161	5.50	155.75	1.60	71.25	8.63	0.56	5.25	5.00	14.95	52.00
GENO162	6.75	174.00	1.94	22.75	11.20	0.64	4.00	2.00	12.87	42.95
GENO163	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO164	2.50	20.25	1.28	10.50	3.80	0.23	1.75	2.00	6.50	11.28
GENO165	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO167	2.33	73.33	2.66	17.67	9.47	0.52	3.00	5.00	21.17	61.47
GENO168	3.00	60.67	2.78	19.33	7.57	0.41	4.67	3.00	7.50	36.28
GENO169	2.00	9.80	1.45	3.50	1.05	0.07	3.00	1.00	8.33	24.70
GENO170	4.75	47.25	1.40	19.25	3.33	0.23	5.25	1.00	6.83	35.10
GENO171	7.00	460.00	3.01	255.00	38.30	2.02	0.00	0.00	0.00	0.00
GENO172	2.00	19.03	2.10	13.00	2.61	0.21	4.00	1.00	8.89	35.30
GENO173	4.00	25.00	2.08	12.50	3.05	0.16	2.50	3.00	7.39	21.40
GENO174	3.67	128.40	2.27	22.00	31.50	2.11	9.00	4.00	18.65	149.07
GENO175	0.50	40.01	2.00	22.50	7.20	0.29	1.00	3.00	2.02	4.04
GENO176	11.25	138.50	2.64	51.00	9.10	0.51	9.00	1.00	9.83	93.43
GENO177	1.00	35.00	2.67	14.00	5.30	0.37	2.00	3.00	5.55	11.10
GENO178	3.00	15.84	1.73	5.33	7.31	0.46	2.67	4.00	14.51	41.97
GENO179	6.67	349.33	2.69	90.33	24.87	1.55	0.00	3.00	0.00	0.00
GENO180	2.00	13.29	0.96	5.50	0.37	0.03	7.50	2.00	13.02	93.30
GENO181	4.67	29.12	1.88	12.00	2.23	0.40	3.33	1.00	21.97	60.03
GENO182	1.67	3.33	0.87	2.33	0.98	0.13	1.33	2.00	4.38	5.47
GENO183	3.00	31.94	1.56	13.50	2.60	0.16	3.50	1.00	13.65	35.55
GENO184	5.00	21.50	1.25	8.00	3.05	0.19	7.50	2.00	12.06	88.80

GENO185	4.50	34.50	2.20	14.00	6.33	0.47	4.00	5.00	10.02	40.05
GENO186	4.50	106.00	3.61	21.25	13.48	0.88	10.50	2.00	11.10	113.60
GENO187	1.67	35.67	2.07	9.33	3.17	0.20	2.00	4.00	9.39	28.17
GENO188	4.00	14.00	1.69	4.50	2.35	0.14	3.00	4.00	15.20	47.80
GENO189	4.80	19.80	1.42	8.60	2.36	0.12	5.00	2.00	15.50	74.50
GENO190	4.50	36.75	2.06	19.00	6.41	0.30	5.50	5.00	4.92	27.21
GENO191	3.00	8.10	1.30	5.00	0.30	0.02	2.00	1.00	16.55	33.10
GENO192	1.67	25.85	1.94	10.00	2.45	0.15	3.33	1.00	5.33	21.38
GENO193	1.50	53.82	2.07	13.25	5.23	0.35	3.50	4.00	19.54	67.48
GENO194	6.50	114.50	1.30	47.00	7.15	0.39	7.00	1.00	18.08	126.55
GENO195	4.50	22.50	2.05	16.00	1.50	0.08	1.50	3.00	20.00	26.50
GENO196	2.00	9.00	1.40	3.00	1.10	0.86	1.00	5.00	5.20	5.20
GENO197	15.00	273.67	2.39	91.00	31.93	1.78	9.67	2.00	11.64	113.20
GENO198	4.50	9.25	1.30	6.50	1.80	0.10	2.00	3.00	16.49	29.45
GENO199	10.67	193.66	2.67	64.67	16.93	1.00	6.00	2.00	13.13	65.20
GENO200	1.50	68.72	2.55	13.75	9.80	0.97	2.75	1.00	7.07	18.90
GENO202	4.67	133.33	2.05	21.33	17.30	0.88	6.33	2.00	8.55	51.57
GENO203	2.67	181.67	5.48	35.67	59.60	3.99	2.00	1.00	3.60	21.62
GENO204	5.00	73.33	1.70	13.67	2.70	0.18	4.00	4.00	17.15	59.50

APPENDIX-F Mean phenotypic data of stolon and tuber traits for the year 2020 (Pot experiment)

Genotypes	TNS	SL	SD	BS	SFW	SDW	TNT	TS	ATW	ATY
GENO2	2.50	16.50	2.25	8.50	3.40	0.18	6.00	2.00	18.02	108.10
GENO3	1.00	49.50	2.51	16.50	4.30	0.35	9.00	4.00	19.07	171.65
GENO4	5.50	20.44	2.21	13.50	2.25	0.24	7.00	4.00	31.52	198.50
GENO5	7.00	27.08	2.08	12.67	3.00	0.25	5.33	3.00	46.23	209.77
GENO6	4.50	18.50	1.45	7.00	1.45	0.10	4.50	1.00	9.63	44.60
GENO7	2.67	35.07	2.10	7.33	3.57	0.25	5.33	2.00	11.28	73.90
GENO9	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO10	6.00	26.50	3.09	14.00	3.70	0.45	4.50	2.00	54.52	251.10
GENO11	5.33	21.00	1.07	9.33	2.47	0.17	8.00	4.00	32.88	277.33
GENO12	5.00	17.00	0.80	6.50	1.30	0.09	4.00	1.00	16.37	62.05
GENO13	4.00	43.50	2.40	19.50	3.75	0.35	2.50	5.00	21.66	59.25
GENO14	5.67	28.33	2.83	15.67	3.93	0.48	5.67	3.00	30.25	92.30
GENO16	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO18	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO19	8.67	72.33	2.20	34.00	5.27	0.27	7.67	3.00	25.28	172.70
GENO20	8.67	120.00	1.95	50.67	6.73	0.39	3.33	2.00	12.48	42.20
GENO21	9.00	46.00	2.83	14.33	5.10	0.38	13.67	2.00	26.81	342.67
GENO22	5.00	48.33	2.36	21.67	4.07	0.45	1.67	2.00	5.22	17.97
GENO23	16.00	145.50	2.60	27.00	11.60	0.95	8.00	3.00	9.28	74.20
GENO24	4.67	24.67	2.54	13.00	3.80	0.29	11.00	2.00	26.75	300.17
GENO25	4.33	53.33	4.00	23.33	10.00	0.88	3.33	5.00	49.01	140.20
GENO26	6.00	100.00	3.51	41.00	7.00	0.28	3.67	3.00	30.05	120.47
GENO27	9.67	108.67	3.61	56.00	10.40	0.84	6.33	3.00	9.86	62.23

GENO28	11.00	56.33	3.95	33.33	13.25	0.93	4.67	2.00	19.35	88.47
GENO29	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO30	10.67	71.67	1.92	27.00	2.97	0.29	8.33	2.00	6.13	53.37
GENO31	7.50	49.00	2.45	18.50	10.75	0.34	8.50	2.00	24.35	197.65
GENO32	5.33	24.67	2.67	10.33	4.70	0.21	3.00	3.00	19.34	57.83
GENO33	7.00	52.00	2.10	25.00	4.70	0.32	12.00	3.00	12.53	150.40
GENO34	8.00	75.33	2.78	42.00	4.29	0.26	5.00	2.00	11.16	46.10
GENO35	8.00	213.50	3.74	67.00	36.40	3.20	7.50	4.50	43.08	326.15
GENO36	14.00	187.00	3.03	12.00	17.60	0.50	2.00	3.00	25.70	51.40
GENO37	5.67	44.67	1.70	14.00	5.57	0.29	8.33	2.00	14.22	72.83
GENO38	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO39	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO41	7.00	27.67	2.20	15.00	3.23	0.24	9.67	3.00	12.38	124.27
GENO42	4.67	22.00	1.13	6.67	0.87	0.05	2.67	3.00	6.75	19.17
GENO43	6.00	46.33	3.48	21.00	6.27	0.27	6.67	3.00	20.97	136.73
GENO44	7.00	19.00	1.53	6.33	3.17	0.47	6.00	2.00	12.10	87.40
GENO45	3.33	13.33	1.97	6.33	1.67	0.09	5.67	3.00	9.19	65.23
GENO46	5.67	30.67	3.30	14.67	4.63	0.47	8.33	3.00	29.96	132.70
GENO47	10.67	156.00	3.55	77.67	11.40	1.37	2.00	3.00	8.26	14.53
GENO48	14.00	231.67	3.33	126.00	25.87	1.80	2.67	3.00	12.83	32.40
GENO49	3.50	11.00	0.55	3.50	0.70	0.04	3.00	2.00	13.08	37.10
GENO50	15.33	229.33	2.10	34.33	16.17	1.30	12.00	1.00	19.75	241.67
GENO52	10.33	220.00	4.16	148.33	30.60	3.41	4.67	3.00	12.83	54.87
GENO53	5.00	21.33	2.70	12.00	2.57	0.13	3.33	3.00	60.96	210.47
GENO54	5.00	16.00	1.84	8.67	1.70	0.09	5.33	3.00	14.22	59.23

GENO55	8.00	52.50	5.72	33.00	14.66	0.90	10.00	3.00	29.75	270.15
GENO56	15.00	131.67	2.67	79.67	6.50	0.57	4.00	2.00	21.86	83.90
GENO57	12.00	230.67	2.88	129.67	15.53	1.07	4.67	2.00	15.68	70.27
GENO58	8.67	35.33	3.97	18.00	6.41	0.34	5.33	2.00	56.79	304.83
GENO59	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO60	4.33	26.33	1.74	15.00	2.23	0.13	3.00	1.00	6.43	13.20
GENO61	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO63	8.00	33.00	5.10	9.00	9.20	0.50	15.00	4.00	29.48	442.20
GENO64	4.67	15.00	2.00	9.33	2.23	0.13	3.67	4.00	32.50	121.69
GENO65	5.00	12.00	0.90	7.50	0.90	0.08	4.50	1.00	14.21	58.95
GENO66	8.00	40.33	2.30	19.33	3.53	0.46	6.00	3.00	18.05	118.47
GENO67	5.67	40.33	3.58	20.00	6.77	0.62	8.33	4.00	29.60	254.70
GENO68	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO69	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO70	9.67	100.67	2.83	40.00	15.27	1.02	5.00	3.00	20.57	113.57
GENO71	8.50	77.00	2.45	30.00	11.05	1.02	7.50	3.00	25.99	168.05
GENO72	5.00	59.33	2.03	38.67	3.97	0.20	4.00	2.00	10.80	43.20
GENO73	3.00	22.00	1.94	12.50	2.50	0.14	4.00	2.00	14.99	66.15
GENO74	2.00	7.50	2.47	3.50	1.00	0.08	5.00	3.00	19.31	96.55
GENO75	6.67	63.33	1.82	28.67	3.47	0.20	4.67	4.00	22.82	99.73
GENO76	8.67	157.67	3.27	80.67	15.63	1.37	5.67	4.00	29.21	165.80
GENO77	5.67	18.67	1.83	7.00	2.40	0.13	3.33	2.00	61.02	200.93
GENO78	5.33	36.67	1.80	19.00	3.60	0.21	5.00	4.00	10.73	53.40
GENO79	16.00	123.00	1.75	19.00	5.50	0.15	4.00	1.00	10.49	38.20
GENO80	7.00	62.67	2.61	29.67	6.77	0.61	4.33	2.00	18.85	67.93

GENO81	5.33	72.33	4.25	42.67	11.93	0.86	7.67	3.00	27.82	212.93
GENO82	11.33	30.00	3.27	13.67	6.47	0.45	5.67	2.00	44.85	217.30
GENO83	6.00	20.00	2.33	16.67	2.63	0.18	6.67	4.00	10.00	68.97
GENO84	8.67	136.33	1.98	43.00	6.97	0.43	5.67	1.00	12.06	69.13
GENO85	4.00	28.00	1.50	7.50	1.15	0.08	6.00	4.00	14.07	74.25
GENO86	15.00	162.00	3.21	71.00	11.60	1.00	3.00	1.00	32.13	96.40
GENO87	4.00	55.00	1.30	21.00	2.60	0.20	1.00	1.00	6.70	6.70
GENO88	12.67	31.00	3.33	30.00	6.70	0.49	10.33	2.67	30.78	302.63
GENO89	9.00	69.33	2.22	41.00	5.27	0.29	8.33	2.00	13.43	111.50
GENO90	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO91	15.00	156.00	2.23	83.50	17.70	1.25	8.50	2.00	20.94	172.15
GENO92	6.50	15.50	1.44	9.00	1.60	0.09	13.00	4.00	33.14	433.75
GENO93	2.33	24.47	1.07	4.67	1.33	0.12	3.00	1.00	4.80	21.57
GENO94	6.00	60.00	3.80	28.50	11.55	0.80	7.50	4.00	51.18	360.25
GENO95	7.33	27.67	2.75	18.67	3.73	0.80	6.00	3.00	22.60	128.87
GENO96	9.00	178.33	3.50	49.67	15.57	1.07	6.33	3.00	18.62	117.63
GENO97	9.00	32.61	2.41	19.00	4.33	0.33	5.00	3.00	20.73	105.57
GENO98	3.00	13.33	0.68	3.33	0.57	0.24	6.00	3.00	4.28	40.20
GENO99	12.33	71.67	3.90	44.00	22.40	1.98	5.67	3.00	71.24	371.19
GENO100	20.33	110.67	2.03	48.67	14.70	1.20	6.67	3.00	23.40	150.70
GENO101	4.00	21.00	2.03	9.00	2.80	0.22	8.00	4.00	24.89	197.83
GENO102	6.33	91.00	3.27	37.00	9.43	0.72	6.67	3.00	50.57	293.83
GENO103	4.33	21.67	1.90	9.67	2.00	0.12	3.67	2.00	6.84	26.77
GENO104	6.33	35.67	1.79	20.33	3.23	0.18	6.33	2.00	16.58	99.70
GENO105	5.00	2.25	1.75	3.50	0.85	0.05	2.50	2.00	38.59	94.25

GENO106	5.67	65.67	3.10	30.00	6.83	0.46	7.33	3.00	35.35	244.80
GENO107	5.33	22.00	2.53	13.67	4.10	0.22	10.00	3.00	34.69	315.73
GENO108	4.00	60.00	1.40	12.00	5.70	0.32	6.00	2.00	6.08	36.50
GENO109	3.00	12.33	1.18	3.67	0.73	0.06	4.00	1.00	2.78	11.93
GENO110	8.00	26.67	1.26	12.33	2.27	0.09	3.33	3.00	4.79	10.70
GENO111	4.33	16.67	2.00	12.33	1.48	0.08	4.00	3.00	29.07	107.30
GENO112	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO113	3.50	18.50	1.40	6.00	1.55	0.10	4.00	2.00	30.38	121.50
GENO114	5.00	20.00	1.80	4.00	1.50	0.13	5.00	3.00	9.18	45.90
GENO115	3.00	19.80	1.00	8.50	1.16	0.12	8.00	3.00	33.54	255.95
GENO116	3.67	12.00	1.40	9.00	2.30	0.11	4.00	4.00	8.77	38.00
GENO117	3.00	9.00	2.93	6.50	3.50	0.28	2.50	4.00	20.21	59.10
GENO118	4.00	18.67	1.18	7.33	1.40	0.10	3.67	4.00	32.15	114.17
GENO120	7.67	47.67	1.50	13.00	4.13	0.22	4.00	2.00	6.65	24.53
GENO121	3.50	23.00	2.35	8.00	1.70	0.12	4.00	2.00	36.74	127.70
GENO122	6.00	22.00	1.79	11.00	2.47	0.15	5.33	3.00	9.35	48.73
GENO123	7.50	25.00	2.65	12.00	6.45	0.49	6.50	6.00	57.27	354.80
GENO124	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO125	7.50	99.05	1.80	32.00	6.95	0.54	6.00	2.00	12.98	73.30
GENO126	1.00	8.00	0.87	3.50	1.40	0.09	1.50	5.00	2.78	4.40
GENO127	8.00	56.67	2.27	21.67	4.30	0.30	9.00	4.00	24.62	221.73
GENO128	11.50	120.50	2.45	18.00	7.10	0.34	6.00	3.00	21.83	136.50
GENO130	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO131	6.67	85.67	1.80	38.67	8.97	0.76	2.00	4.00	23.81	55.73
GENO132	8.50	144.50	2.08	50.00	6.05	0.36	9.00	3.00	14.53	134.20

GENO133	4.00	8.00	1.75	6.50	1.70	0.10	4.00	4.00	22.51	68.85
GENO134	10.00	60.00	2.44	28.33	6.23	0.56	6.33	3.00	34.17	212.80
GENO136	6.33	34.33	2.23	24.33	2.57	0.15	4.00	3.00	11.84	34.73
GENO137	4.67	26.33	1.99	14.67	2.10	0.12	1.67	1.33	1.98	5.80
GENO138	1.00	50.00	3.20	26.00	7.20	0.70	4.00	1.00	6.93	27.70
GENO139	6.00	37.50	2.24	11.50	3.55	0.16	5.50	3.00	18.08	99.40
GENO140	15.33	320.00	3.24	181.67	25.87	1.80	4.33	2.00	9.67	46.70
GENO141	3.00	58.84	2.11	25.04	4.88	0.39	1.67	2.00	27.62	37.37
GENO142	3.67	28.90	1.90	12.67	2.90	0.22	7.67	3.00	29.97	213.63
GENO143	5.50	20.00	1.55	10.00	2.30	0.12	7.50	2.00	10.30	77.50
GENO144	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO145	8.50	41.50	1.65	20.50	3.90	0.25	8.00	3.00	11.98	92.00
GENO146	6.50	159.00	3.63	100.00	15.30	1.46	16.00	2.00	8.03	128.95
GENO147	6.00	45.00	2.07	20.00	5.37	0.43	4.33	4.00	16.14	72.17
GENO148	3.50	15.00	1.67	8.50	1.23	0.09	4.00	2.00	9.19	36.75
GENO149	3.00	10.00	1.00	4.00	1.90	0.47	5.00	5.00	34.54	172.70
GENO150	9.00	28.00	1.80	9.50	9.05	0.53	8.50	4.00	51.31	406.05
GENO151	5.67	23.67	2.25	11.67	3.10	0.25	3.67	1.00	4.85	14.40
GENO152	9.33	61.00	3.30	33.33	9.70	0.66	9.00	2.00	24.90	196.47
GENO153	3.50	52.65	2.07	9.50	2.65	0.23	5.50	1.00	5.84	32.90
GENO154	3.00	15.00	2.69	10.00	1.60	0.10	2.00	1.00	0.90	1.80
GENO155	9.00	73.00	1.50	29.00	4.10	0.22	9.00	2.00	3.77	33.90
GENO156	3.50	53.50	1.64	13.00	4.04	0.25	4.50	2.00	3.17	14.30
GENO157	15.00	156.00	3.29	53.67	19.10	1.53	7.33	2.00	12.65	89.80
GENO158	5.00	101.67	5.01	52.00	34.47	2.38	3.67	2.00	18.98	69.60

GENO159	5.00	17.00	2.51	10.00	2.45	0.16	1.50	3.00	15.78	23.85
GENO160	6.00	20.00	1.33	8.50	1.50	0.08	5.00	3.00	8.65	44.70
GENO161	7.00	31.67	2.73	22.33	4.20	0.18	8.33	4.00	34.95	281.37
GENO162	12.67	75.33	1.45	35.67	8.83	0.71	10.00	1.00	15.47	138.47
GENO163	5.00	25.00	2.53	19.67	4.83	0.27	5.67	3.00	6.09	37.23
GENO164	7.33	23.67	1.65	10.67	3.40	0.23	4.33	3.00	12.38	58.50
GENO165	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO167	6.00	18.00	1.80	12.00	2.10	0.12	6.00	3.00	17.12	102.70
GENO168	3.67	41.33	2.45	18.00	4.20	0.25	19.33	3.00	25.52	492.67
GENO169	16.00	44.00	1.05	12.00	3.05	0.17	7.50	3.00	28.15	247.00
GENO170	3.67	35.00	1.37	13.33	1.73	0.10	6.67	2.00	22.60	144.73
GENO171	5.67	18.33	1.40	10.00	2.10	0.14	9.67	1.00	12.79	149.80
GENO172	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO173	6.67	44.00	3.12	19.00	3.97	0.31	2.33	2.00	37.78	54.10
GENO174	4.00	20.00	4.21	11.00	9.76	0.79	2.00	3.00	59.20	109.37
GENO175	3.50	23.00	3.10	14.00	2.05	0.15	7.00	4.00	46.81	337.95
GENO176	6.50	58.50	2.95	28.50	13.70	0.76	5.50	3.00	19.61	107.40
GENO177	6.00	152.37	4.63	75.67	23.38	1.45	3.33	4.00	55.33	199.33
GENO178	4.00	40.10	1.88	16.50	3.50	0.28	3.00	2.00	13.30	39.90
GENO179	3.67	42.20	2.67	15.00	6.10	0.42	7.00	1.00	15.33	105.20
GENO180	4.50	15.20	1.40	3.50	3.00	0.17	7.50	1.50	20.00	142.85
GENO181	9.00	21.00	0.90	10.50	3.75	0.30	9.00	4.00	24.12	238.60
GENO182	6.00	31.00	1.83	13.33	2.03	0.13	7.00	2.00	7.05	45.43
GENO183	8.67	58.67	1.99	24.33	8.13	0.48	5.00	2.00	29.72	124.33
GENO184	5.50	47.05	1.79	17.50	2.90	0.17	3.50	2.00	5.71	20.35

GENO185	8.33	33.33	1.37	17.67	2.90	0.23	6.67	3.00	16.21	98.07
GENO186	4.33	17.83	1.70	8.33	1.93	0.13	6.67	4.00	34.35	220.33
GENO187	2.50	53.50	3.10	14.00	4.75	0.30	6.00	3.00	45.30	271.80
GENO188	4.00	10.00	1.40	10.00	2.90	0.16	5.00	2.00	5.36	26.80
GENO189	5.50	20.00	1.55	10.00	2.30	0.12	6.50	2.00	7.87	51.05
GENO190	6.33	93.17	2.64	45.05	12.80	0.45	9.67	3.00	34.60	320.93
GENO191	6.67	66.00	3.57	40.00	17.35	1.30	8.33	2.00	16.84	131.07
GENO192	8.00	50.00	2.24	15.00	4.00	0.36	7.00	2.00	8.54	59.80
GENO193	4.00	11.50	1.71	4.67	2.00	0.11	4.00	2.00	11.65	44.10
GENO194	6.67	109.67	2.01	19.00	8.53	0.38	6.00	2.00	6.17	39.67
GENO195	5.00	25.00	2.57	15.00	3.07	0.26	7.00	3.00	19.45	145.37
GENO196	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO197	5.00	26.67	2.17	14.67	3.17	0.20	12.67	2.00	17.67	221.17
GENO198	6.00	123.00	1.95	23.00	6.90	0.56	7.50	3.00	13.26	98.00
GENO199	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GENO200	15.33	230.00	3.57	80.33	28.53	1.67	3.67	2.00	30.14	99.40
GENO202	10.67	145.00	2.90	41.67	15.60	5.91	9.33	2.00	18.58	177.93
GENO203	6.67	37.33	2.60	15.67	3.40	0.18	2.67	0.67	10.14	40.57
GENO204	5.00	47.50	1.60	16.50	2.95	0.73	7.50	4.00	28.69	206.75

APPENDIX-F Name of genotypes with their codes used in this study

Code	Gonotype Name	Code	Gonotype Name	Code	Gonotype Name
GENO2	Jelly	GENO30	DT14091.04	GENO57	DT14034.03
GENO3	Rumba	GENO31	DT14083.28	GENO58	DT14057.36
GENO4	Hermes	GENO32	DT14015.22	GENO59	DT14062.08
GENO5	Alegria	GENO33	DT14051.15	GENO60	DT14079.02
GENO6	ROYAL	GENO34	DT14047.38	GENO61	DT14053.03
GENO7	Electra	GENO35	DT14026.04	GENO63	DT13088.03
GENO9	DT14007.11	GENO36	DT14068.07	GENO64	DT14051.66
GENO10	DT14038.01	GENO37	DT14063.12	GENO65	DT13100.02
GENO11	DT14010.18	GENO38	DT14036.01	GENO66	DT13162.15
GENO12	DT14004.17	GENO39	DT14055.25	GENO67	DT13162.12
GENO13	DT14010.14	GENO41	L.olympia	GENO68	DT11107.01
GENO14	DT14085.03	GENO42	Banba	GENO69	Zirve
GENO16	DT14013.15	GENO43	V.GOGH	GENO70	DT12012.02
GENO18	DT14018.32	GENO44	DT14049.10	GENO71	DT13136.22
GENO19	DT14042.27	GENO45	DT14061.23	GENO72	DT13045.74
GENO20	DT14005.09	GENO46	DT14006.07	GENO73	DT13124.21
GENO21	DT14030.11	GENO47	DT14046.19	GENO74	Borwina
GENO22	DT14057.37	GENO48	DT14014.27	GENO75	BROOKE
GENO23	DT14065.01	GENO49	DT14011.18	GENO76	TESSA
GENO24	DT14016.01	GENO50	DT14069.13	GENO77	DT13143.49
GENO25	DT14016.34	GENO52	DT14026.21	GENO78	DT13130.48
GENO26	DT14078.03	GENO53	DT14042.24	GENO79	DT13143.54

GENO27	DT14028.03	GENO54	DT14090.11	GENO80	DT13007.03
GENO28	DT14054.11	GENO55	DT14071.19	GENO81	Kutup
GENO29	DT14037.18	GENO56	DT14027.08	GENO82	DT13028.01

GENO83	DT13093.92	GENO108	Laura	GENO108	Laura
GENO84	DT13051.10	GENO109	SHEPODY	GENO109	SHEPODY
GENO85	DT13143.58	GENO110	43-111-11	GENO110	43-111-11
GENO86	DT13026.10	GENO111	karlena	GENO111	karlena
GENO87	DT13049.50	GENO112	139-101-11	GENO112	139-101-11
GENO88	DT13072.19	GENO113	84-105-11	GENO113	84-105-11
GENO89	DT13083.01	GENO114	NANDU	GENO114	NANDU
GENO90	LadyRosetta	GENO115	882-202-10	GENO115	882-202-10
GENO91	DT11007.01	GENO116	Talent	GENO116	Talent
GENO92	DT11108.02	GENO117	57-104-11	GENO117	57-104-11
GENO93	Doruk	GENO118	878-202-10	GENO118	878-202-10
GENO94	DT13085.01	GENO120	146-103-11	GENO120	146-103-11

GENO95	DT12068.21	GENO121	salute	GENO121	salute
GENO96	DT11088.01	GENO122	68-105-11	GENO122	68-105-11
GENO97	DT13045.42	GENO123	63-113-11	GENO123	63-113-11
GENO98	DT13147.17	GENO124	106-105-11	GENO124	106-105-11
GENO99	DT13048.10	GENO125	939-201-10	GENO125	939-201-10
GENO100	DT13052.23	GENO126	NEXE	GENO126	NEXE
GENO101	DT13037.31	GENO127	51-109-11	GENO127	51-109-11
GENO102	DT13045.103	GENO128	No Code	GENO128	No Code
GENO103	DT13037.35	GENO130	40-103-11	GENO130	40-103-11
GENO104	DT13047.08	GENO131	99-115-11	GENO131	99-115-11
GENO105	DT13162.16	GENO132	141-104-11	GENO132	141-104-11
GENO106	DT13067.03	GENO133	89-105-11	GENO133	89-105-11
GENO107	SORAYA	GENO134	Nautilus	GENO134	Nautilus
GENO136	157-103-11	GENO161	84-107-11	GENO187	Solist

GENO137	133-112-11	GENO162	128-105-11	GENO188	Lolita
GENO138	944-208-10	GENO163	140-107-11	GENO189	karatop
GENO139	Privilige	GENO164	PELIKAN	GENO190	Innara
GENO140	966-203-10	GENO165	KOLIBRI	GENO191	Acapella
GENO141	904-212-10	GENO167	82-119-11	GENO192	Allora
GENO142	Betina	GENO168	wendy	GENO193	Arkulla
GENO143	125-104-11	GENO169	Romanze	GENO194	Tokio
GENO144	SWING	GENO170	PRESTIGE	GENO195	BIRTE
GENO145	758-109-09	GENO171	Maxi	GENO196	900-205-11
GENO146	735-102-09	GENO172	Fasan	GENO197	MAXILLA
GENO147	99-102-11	GENO173	Madalene	GENO198	Tucan
GENO148	TERANA	GENO174	Pomqueen	GENO199	946-202-10
GENO149	104-103-11	GENO175	Mungo	GENO200	kormoron
GENO150	SF-HIT	GENO176	ALBATROS	GENO202	jumbo

GENO151	kiwi	GENO177	Fedelia	GENO203	Logo
GENO152	KIEBITZ	GENO178	Tacoma	GENO204	102-102-11
GENO153	Bonus	GENO179	BONZA		
GENO154	509-104-09	GENO180	Adretta		
GENO155	43-118-11	GENO181	power		
GENO156	BEO	GENO182	Gold Marie		
GENO157	Baltic Cream	GENO183	Rita		
GENO158	868-201-10	GENO184	Summer Gold		
GENO159	860-201-10	GENO185	Diplomat		
GENO160	Dukata	GENO186	cascada		

CURRICULUM VITAE

Muhammad Farhan Yousaf was born on …. , …. In ….. , …... . He completed his higher-secondary education in 2005 from Punjab College, Multan. Then he enrolled for his undergraduate studies in 2005 from Bahauddin Zakaria University (BZU), Multan, Pakistan. He did his bachelor’s degree B.Sc. (Hons.) Agriculture with agronomy major from Department of Agronomy in 2009. After bachelor’s he continued his education and started masters in 2009 in the same department. In 2011 he graduated from the university. He enrolled in Graduate School of Natural and Applied Sciences, Department of Agricultural Genetic Engineering at Niğde Ömer Halisdemir University, Niğde, Turkey to pursue his Ph.D. education under the supervision of Prof. Dr. Mehmet Emin ÇALIŞKAN. During his doctoral thesis research, he worked on association mapping of underground traits in potato.

PUBLICATIONS PRODUCED DURING THESIS WORK

Yousaf, M.F., Demirel, U., Naeem, M. and Çalışkan, M.E., "Association mapping study reveals novel genomic regions controlling some root and stolon traits in tetraploid potato (*Solanum tuberosum* L.)" ***3 Biotech*** 11, 4, 1-16, 2021.

International Conferences/Congress

Yousaf, M.F., Demirel, U., Naeem, M., Çalışkan, M.E., "Association mapping study reveals novel genomic regions c-ontrolling some root and stolon traits in tetraploid potato (*Solanum tuberosum* L.)" In: ***International horticulture e-conference,*** University of Agriculture Faisalabad, Pakistan, 22-23 February, 2021

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