

Genetic Variation In Solanum

Tomato (*Solanum lycopersicon* Mill.) is an important vegetable crop belongs to family solanaceae. It is well known and very popular vegetable among farmers and grown successfully throughout the world. It is used as vegetable and ripe fruits are also utilized into salad, soups, pickles, sauce, ketchups etc. Yield of tomato crop is primarily governed by the genetic makeup of the variety. Thus, full genetic potential of the variety can be utilized through recommended cultural practices. To develop the variety, existence of significant heritable variability is of prime importance. Some biometric techniques like variability, correlation and path analysis provide information about the relative contribution of various yield related traits. Genetic and phenotypic correlation coefficients seek out the association between yield and yield contributing traits in tomato. Thus, these biometric techniques help in selection of superior plant genotypes for breeding programme.

Solanum lycopersicum (cultivated tomato) is one of the most important vegetable crops worldwide. Improvement of cultivated tomato is limited because it has little genetic variation compared to its diverse wild relatives. There is therefore great interest in studying and leveraging the genetic diversity of closely related wild tomato species. *Solanum habrochaites* is a wild tomato species with several advantageous traits such as tolerance to chilling and water stress. One of the goals of the St. Clair research group is to understand the genetic and genomic basis for chilling tolerance in wild tomato. Previous studies used an interspecific population derived from chilling-susceptible *S. lycopersicum* cv. T5 and chilling-tolerant *S. habrochaites* acc. LA1778 to map QTL controlling tolerance to rapid-onset water stress induced by root chilling. The largest effect QTL for this trait is located in a 0.32-cM region on chromosome 9, which was named QTL *stm9* for "shoot turgor maintenance, chromosome 9". The two studies in this thesis describe our efforts to identify the genetic and genomic bases for the functional differences between *S. lycopersicum* and *S. habrochaites* in the QTL *stm9* region. In the first study, we sequenced BACs isolated from a *S. habrochaites* acc. LA1778 genomic library using probes corresponding to the *stm9* region. Unfortunately, the targeting was inaccurate, and only one of the 30 BACs sequenced aligned to *stm9*. Fortunately, we were able to use the 30 BACs and ~1x shotgun sequencing of LA1778 to examine the global repeat content of the *S. habrochaites* genome. We found that it has greater repeat content and diversity than *S. lycopersicum*. In the second study, we created a genomic scaffold of the *stm9* region using the recently publicly released contigs from a *S. habrochaites* accession LYC4 genome sequencing project. We found that the *S. habrochaites* LYC4 *stm9* region is relatively gene-rich and repeat-poor compared to the genome average of *S. lycopersicum*. Based on the alignment of LA1778 random shotgun sequences, the LYC4 scaffold appears to be nearly complete. We find that there are many sequence differences between the LYC4 *stm9* scaffold and its syntenic sequence in *S. lycopersicum*. It is currently unclear which of these differences may impact the biology of the organism, specifically tolerance to chilling. While one might expect the critical polymorphisms to be within the approximately one dozen genes located in this region, it may be that regulatory elements, RNAs, and/or repeat structure also play a significant role.

This book describes the historical importance of potato (*Solanum tuberosum* L.), potato genetic resources and stocks (including *S. tuberosum* group Phureja DM1-3 516 R44, a unique doubled monoploid homozygous line) used for potato genome sequencing. It also discusses strategies and tools for high-throughput sequencing, sequence assembly, annotation, analysis, repetitive sequences and genotyping-by-sequencing approaches. Potato (*Solanum tuberosum* L.; $2n = 4x = 48$) is the fourth most important food crop of the world after rice, wheat and maize and holds great potential to ensure both food and nutritional security. It is an autotetraploid crop with complex genetics, acute inbreeding depression and a highly heterozygous nature. Further, the book examines the recent discovery of whole genome sequencing of a few wild potato species genomes, genomics in management and genetic enhancement of *Solanum* species, new strategies towards durable potato late blight resistance, structural analysis of resistance genes, genomics resources for abiotic stress management, as well as somatic cell genetics and modern approaches in true-potato-seed technology. The complete genome sequence provides a better understanding of potato biology, underpinning evolutionary process, genetics, breeding and molecular efforts to improve various important traits involved in potato growth and development.

Assessment of Genetic Variation in Tomato (*Solanum Lycopersicum* Mill.) Genetic Diversity in Plants IntechOpen

Tomato (*Solanum lycopersicum* L.), broadly divided into two varieties: *Solanum lycopersicum* var. *lycopersicum* (domesticated tomato) and the weedy *Solanum lycopersicum* var. *cerasiforme* (cherry tomato), is closely related to the wild tomato species *Solanum pimpinellifolium*. Studies show presence of a very low genetic diversity among tomato cultivars, which is estimated to be lower than 5% of that available in nature. With the estimation of such a low level of genetic variability in the germplasm, assessment of the extent and nature of the genetic variation in tomatoes would be important for breeding and genetic resource conservation programs. I used AFLP data to analyze the genetic variability within the germplasm of *Solanum lycopersicum* var. *cerasiforme* (112 accessions), and genetic variability along with fruit morphological diversity in the accessions of *Solanum lycopersicum* var. *lycopersicum* (219 accessions) from different parts of the World. Cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) in terms of genetic distance and molecular variance (1% molecular variance) was very close to *Solanum lycopersicum* var. *lycopersicum* than its wild sister taxa *Solanum pimpinellifolium* (20% molecular variance). It also showed more genetic diversity (H_j , 0.42052-0.48361) than that of *S. l. lycopersicum* (H_j , 0.26008-0.42017); and among its geographic groups, South American accessions had more genetic diversity (H_j , 0.43703-0.48361) than that of Mesoamerican (H_j , 0.42052-0.46946) and Caribbean accessions (H_j , 0.42287). The germplasm of *S. l. lycopersicum* showed presence of more genetic diversity in the accessions from Western South America, Caribbean and Mediterranean regions (H_j , 0.42017), and Mesoamerica (H_j , 0.41790), the places associated with tomato domestication and subsequent dispersal after domestication. Studied tomato germplasm was divided into three genetically distinct clusters ($K=3$), and one of the clusters (cluster 3) in *S. l. lycopersicum*.

As a result of selecting for high yield, the tomato fruit lost its flavor. Last two decades, big efforts have been put in increasing the tomato fruit quality. In this MSc thesis report we assessed the association between existing and tomato fruit quality related traits. Also, de novo genetic variation in an EMS derived TILLING population has been assessed. After two sequence experiments, we could confirm 8 mutations in genes that are involved in the tomato fruit quality. Protein prediction programs have predicted that these point mutations will alter the translated protein. The mutations were found in pools, which contain DNA of 64 individual plants. The SNP genotyping technique Kompetitive Allele Specific PCR (KASPTM) was domesticated and used to detect the one mutated plant out of the pool of 64 plants. Due to chimerism, the mutant SNP was present at low quantities in the mutant plant. KASP showed to not work when the mutant SNP is present at low quantities. Therefore we were not able to find the one mutant plant in the pool of 64 plants. It is discussed that other SNP genotyping techniques like castPCRTM or ddPCRTM could give a more satisfying outcome. In silico experiments have revealed statistically significant clues that some existing variation in the promoter region of glycosyl transferase genes of *Solanum lycopersicum* accessions show an association with several tomato fruit quality related compounds. However, in vivo confirmations are still needed.

Genetic variation in *Leptinotarsa decemlineata* (Say) for adaptation to *Solanum berthaultii* Hawkes. Selection of the Colorado potato beetle, *Leptinotarsa decemlineata* (Say) for adaptation to *Solanum berthaultii* Hakes. Resistance of *Solanum berthaultii* Hawkes and advanced hybrids to the Colorado potato beetle: two-year no-choice and choice tests in the field. Influence of photosynthetically active radiation (PAR) on Colorado potato beetle.

Eggplant (*Solanum melongena* L.) is an important crop and has a growing reputation and is now cultivated globally. It is a valuable member of the human diet in Asia, especially in India, which is a primary diversity center of the species. Turkey is the first in Europe and is in the first five countries around the world in terms of eggplant production. The Solanaceae family to which *S. melongena* belongs is an important family, too. Tomato, potato, tobacco and petunia are some example species of the Solanaceae family. This important family with 3000-4000 species shows a high level of morphological diversity which results in confusion about its systematics and this diversity is at the level of genera, species and cultivars. The aims of the studies reported in this thesis were to analyze genetic diversity of Turkish eggplants and wild relatives in separate studies with different molecular tools. To reveal genetic diversity among eggplant cultivars grown in Turkey, the AFLP marker system was applied to the sample genotypes. For the investigation of genetic variation between *S. melongena* and its wild relatives, though, the SSR marker system was used. For the AFLP data for Turkish eggplants, an *r* value of 0.97 was obtained which was in the best scale. Eigen values reported here were also informative. These results showed that the first component analysis explained 64.34% of the variation between samples. For three axes, though, a total of 72.21% variation was explained. According to the statistical results of SSR analysis, the *r* value of *Solanum* species. genotypic data was found to be 0.88. That means the correlation between sample genotypic data and dendrogram was found to be high. Due to the other statistical results which were Eigen values explained 46.12% of genotypes for first component analysis. With a total value of 55.28%, the 47 different genotypes were explained by the three principle component axes. The results of AFLP studies showed that although a high similarity value was observed, diversity was detectable among the accessions. The results of SSR studies were also meaningful with their concordance with previous studies and observed diversity with a good fit to statistical results.

Solanum ($2n = 2x = 24$) species (*Solanum chacoense*) when used as male self-compatible donor can be easily hybridized with other wild species ($2n = 2x = 24$) and dihaploids of *Solanum tuberosum* ($2n = 4x = 48$). Previous work carried out using diploid breeding techniques has had success and this has culminated into potato breeding platforms that exploit the $2n$ gamete breeding scheme with a focus on creating genetic diversity. In a diploid breeding program, the spontaneous occurrence of tetraploid progeny complicates the breeding process. Thirty-five $2x \times 2x$ crosses were made to examine spontaneous incidences of tetraploid progeny in the F1 hybrid progeny of $2x \times 2x$ *S. tuberosum* dihaploids by self-compatible donors *S. chacoense* (M6) and DRH S6-10-4P17. In these $2x \times 2x$ crosses we expect both diploid and tetraploid progeny. Results showed that by using chloroplast counting and SNP genotyping, the frequency of tetraploid progeny ranged from 0 to 40% in the 35 crosses between Atlantic or Superior dihaploids to self-compatibility donors. This result is attributed to bilateral sexual polyploidization (BSP) which is the result of $2n$ egg and pollen formation. The results of this study will inform breeders developing diploid germplasm the potential consequences of $2x \times 2x$ crosses between *Solanum* species and dihaploids of *S. tuberosum*. Bacterial wilt, caused by *Ralstonia solanacearum* (Rs), is a major disease in most tropical, subtropical and temperate potato producing regions of the world. Breeding for bacterial wilt disease resistance in potatoes is challenging due to the pathogen's aggressive nature and persistence in the environment. Accessions of *S. commersonii* are known to harbor resistance, therefore, breeding for genetic resistance to bacterial wilt may be an effective strategy to control bacterial disease. The genetic variation among S1 selfed progeny of *S. commersonii* line MSEE912-08 was characterized by artificially inoculating them with an isolate of Rs. One hundred and twenty individual S1 selfed progeny were screened for Rs resistance by artificial inoculation with Rs isolate NAK66 in a glasshouse replicating each line three times in the experiment. Percent disease reaction was calculated as the relative area under disease progress curve (RAUDPC). RAUDPC was fitted to a random effects mixed model and the means were transformed as a Best linear unbiased prediction (BLUP) score for each clone. BLUP values ranged from -19.25 for the most resistant to 16.83 for the most susceptible clones. Genotyping S1 individuals using the V3 Illumina Infinium Array generated 117 polymorphic single nucleotide polymorphic (SNP) markers from the selfed population. Using 98 of the 120 progeny the significance of the markers was confirmed by single marker analysis from WindowsQTL Cartographer 2.5, as well as a single marker ANOVA test using JMP®, Pro13. Significant markers were identified on Chromosome 4 which explained 9.8% to 13% of the phenotypic variation. SNP markers identified resistance associated with a homozygous genotype. Specifically, the genotypic value prediction from BLUP scores in single marker ANOVA showed that the homozygous genotype of the SNP markers in solcap_snp_c2_35970, PotVar0015326, PotVar0075537, solcap_snp_c1_10181, solcap_snp_c1_4109 and solcap_snp_c2_12904 were significantly associated with Rs resistance. This study was able to discover self-compatibility in *S. commersonii*. This study provides potential germplasm that can be used in marker assisted breeding in potato. Secondly, self-compatibility was identified in *S. commersonii* and should be further evaluated for use in a diploid breeding program.

This book describes the strategy used for sequencing, assembling and annotating the tomato genome and presents the main characteristics of this sequence with a special focus on repeated sequences and the ancestral polyploidy events. It also includes the chloroplast and mitochondrial genomes. Tomato (*Solanum lycopersicum*) is a major crop plant as well as a model for fruit development, and the availability of the genome sequence has completely changed the paradigm of the species' genetics and genomics. The book describes the numerous genetic and genomic resources available, the identified genes and quantitative trait locus (QTL) identified, as well as the strong synteny across Solanaceae species. Lastly, it discusses the consequences of the availability of a high-quality genome sequence of the cultivated species for the research community. It is a valuable resource for students and researchers interested in the genetics and genomics of tomato and Solanaceae.

This first volume of the Handbook of Plant Breeding book series is devoted to vegetable crops breeding. Each chapter is dedicated to a major vegetable crop. Each chapter contains a comprehensive review of the diversity, breeding techniques, achievements and use of the most advanced molecular techniques in the genetic improvement of these crops. The purpose of the book is to provide breeders and researchers from the public and private sectors with updated information and the latest novelties in the breeding of specific crops of economic relevance. Also, it serves as a major reference book for post-

graduate courses and PhD courses on breeding vegetable crops.

Genetic diversity is of fundamental importance in the continuity of a species as it provides the necessary adaptation to the prevailing biotic and abiotic environmental conditions, and enables change in the genetic composition to cope with changes in the environment. Genetic Diversity in Plants presents chapters revealing the magnitude of genetic variation existing in plant populations. The increasing availability of PCR-based molecular markers allows the detailed analyses and evaluation of genetic diversity in plants and also, the detection of genes influencing economically important traits. The purpose of the book is to provide a glimpse into the dynamic process of genetic variation by presenting the thoughts of scientists who are engaged in the generation of new ideas and techniques employed for the assessment of genetic diversity, often from very different perspectives. The book should prove useful to students, researchers, and experts in the area of conservation biology, genetic diversity, and molecular biology.

Potato (*Solanum tuberosum* L.) is one of the world's most important food crops. It is widely grown throughout the world ranking fourth in food production after wheat, maize and rice. Over a billion people consume potato as a staple food in Europe and a principal vegetable in developing countries. India is a major producer of potato along with China, Russia, Ukraine and Poland. Peru Bolivian region in the Andes (South America) is reported to be the centre of its origin. Potatoes were introduced to Europe during the second half of the sixteenth century by Spanish seamen. Potatoes were introduced to India in the seventeenth century by Portuguese and to Africa in the late eighteenth century by Christian missionaries. Potato belongs to the family Solanaceae, genus *solanum* and species *tuberosum*. The genus *Solanum* comprises of 2000 species. About 170 species produce under ground stem tubers and cultivated species differing in chromosome numbers from 24 (diploid), 36 (triploid), 48 (tetraploid) to 60 (pentaploid). The tetraploid *Solanum tuberosum* has an outstanding agricultural importance and has a worldwide distribution in the form of sub-species *tuberosum*.

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