

Genetic Variation In Solanum

Genetic Diversity in Microorganisms presents chapters revealing the magnitude of genetic diversity of microorganisms living in different environmental conditions. The complexity and diversity of microbial populations is by far the highest among all living organisms. The diversity of microbial communities and their ecologic roles are being explored in soil, water, on plants and in animals, and in extreme environments such as the arctic deep-sea vents or high saline lakes. The increasing availability of PCR-based molecular markers allows the detailed analyses and evaluation of genetic diversity in microorganisms. The purpose of the book is to provide a glimpse into the dynamic process of genetic diversity of microorganisms 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 microbial phylogeny, genetic diversity, and molecular biology.

We are entering a particularly fruitful period in evolutionary genetics, as rapid technological progress transforms the investigation of genetic variation within and between species. *Molecular Methods for Evolutionary Genetics* is a collection of advanced molecular biology protocols and general overviews intended to represent the essential methods currently bringing evolutionary genetics to fruition. Divided into six thematic sections, this volume covers methods for characterizing genomes, diverse approaches to enrich DNA for subsets of the genome prior to sequencing, and state-of-the-art protocols for sampling genetic variation for genetic mapping studies and population genetic studies (RAD sequencing, Sequenom, microarrays, etc.). The volume concludes by focusing on methods to study candidate genes, from obtaining their sequences and analyzing their transcripts to experimentally manipulating their activities in vivo. Written in the highly successful *Methods in Molecular Biology*TM series format, chapters contain introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and notes on troubleshooting and avoiding known pitfalls. Authoritative and accessible, *Molecular Methods for Evolutionary Genetics* serves as a rich resource to biologists interested in evolution, whether they be specialists or beginners in molecular biology.

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 F_1 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 WindowsQTLCartographer 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 in the series "Sustainable Development and Biodiversity" contains peer-reviewed chapters from leading academicians and researchers around the world in the field of horticulture, plant taxonomy, plant biotechnology, genetics and related areas of biodiversity science centered on genetic diversity. This book includes original research reviews (national, regional and global) and case studies in genetic diversity in fruits and vegetables, horticulture, and ecology from sub-tropical and tropical regions. It is unique as it covers a wide array of topics covering global interests and will constitute valuable reference material for students, researchers, extension specialists, farmers and certification agencies who are concerned with biodiversity, ecology and sustainable development.

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.

Genetic Diversity in PlantsIntechOpen

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.

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.

The Galápagos Islands are renown for their unique flora and fauna, inspiring Charles Darwin in the elaboration of his theory of evolution. Yet in his Voyage of the Beagle, published in 1839, Darwin also remarked on the fascinating geology and volcanic origin of these enchanted Islands. Since then, the Galápagos continue to provide scientists with inspiration and invaluable information about ocean island formation and evolution, mantle plumes, and the deep Earth. Motivated by an interdisciplinary Chapman Conference held in the Islands, this AGU volume provides cross-disciplinary collection of recent research into the origin and nature of ocean islands, from their deepest roots in Earth's mantle, to volcanism, surface processes, and the interface between geology and biodiversity. Volume highlights include: Case studies in biogeographical, hydrological, and chronological perspective Understanding the connection between geological processes and biodiversity Synthesis of decades of interdisciplinary research in physical processes from surface to deep interior of the earth In-depth discussion of the concept of the island acting as a natural laboratory for earth scientists Integrated understanding of the Galápagos region from a geological perspective Collectively, The Galápagos presents case studies illustrating the Galápagos Archipelago as a dynamic natural laboratory for the earth sciences. This book would be of special interest to a multidisciplinary audience in earth sciences, including petrologists, volcanologists, geochronologists, geochemists, and geobiologists.

For the last eighteen years we have been deeply involved in a cooperative effort with our Latin American colleagues in genetics, biochemistry, physiology, and molecular biology. We have been in close contact with scientists in a number of centers and have helped to organize symposia, workshops, and so forth, in an effort to accelerate their development and make their substantial work known. These symposia in Latin America have been quite successful. The fifteenth will take place in Brasilia in 1977. At the request of colleagues, we are in the process of developing a similar series in Asia. The first very successful symposium was held in Calcutta in 1973. We were most pleased when Dr. Amir Muhammed, Vice Chancellor of the University of Agriculture, Lyallpur suggested that we hold a symposium on a topic of great importance to Pakistan, Genetic Control of Diversity in Plants, under the auspices of the University of Agriculture. It is our hope that this symposium will be followed by additional ones in Pakistan as well as in other countries in the Far East. Leadership is quickly developing in the hands of outstanding scientists in these countries, and we appreciate the opportunity to cooperate with them. We are especially grateful to the National Science Foundation for making PL- 480 funds available which made this symposium possible.

The photosynthetic fixation of carbon dioxide into organic compounds is mediated by the enzyme ribulose 1,5-bisphosphate (RuBP) carboxylase. The diversity of current research on this protein attests to its central role in biomass productivity, and suggests the importance of a timely and broadly based review. This Symposium was the first devoted exclusively to RuBP

carboxylase and was attended by agronomists, plant physiologists, biochemists, molecular biologists, and crystallographers. Special efforts were made to involve young scientists in addition to established investigators. It is a pleasure to acknowledge financial support provided by the Department of Energy, the United States Department of Agriculture, and the National Science Foundation, and the valued assistance of agency representatives, Drs. Joe Key, Robert Rabson, Elijah Romanoff, and Donald Senich. Thanks are due to Mrs. Margaret Dienes, without whose editorial skills this volume could not have been produced, and to Mrs. Helen Kondratuk as Symposium Coordinator. Finally, we wish to record our indebtedness to Dr. Alexander Hollaender for his tireless efforts in support of all aspects of this Symposium.

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.

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 (Hj, 0.42052-0.48361) than that of *S. l. lycopersicum* (Hj, 0.26008-0.42017); and among its geographic groups, South American accessions had more genetic diversity (Hj, 0.43703-0.48361) than that of Mesoamerican (Hj, 0.42052-0.46946) and Caribbean accessions (Hj, 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 (Hj, 0.42017), and Mesoamerica (Hj, 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*.

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. 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.

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