

Genetic Variation In Solanum

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Genetic Variation In Solanum

The evolutionary history of Solanum genomes has also been investigated from the perspective of chromosome organization. The study by Szinay et al. involving cross species BAC FISH painting of Solanum species revealed few large rearrangements in the short arm euchromatin of chromosomes 6, 7 and 12, whereas Anderson et al.

Exploring genetic variation in the tomato (Solanum section ...

We explored genetic variation by sequencing a selection of 84 tomato accessions and related wild species representative of the Lycopersicon, Arcanum, Eriopersicon and Neolycopersicon groups, which has yielded a huge amount of precious data on sequence diversity in the tomato clade.

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The first eight principal components accounted for 90.26% of the observed variations among 24 potato genotypes. The first three PC accounted for 60.43% of the variation.

Genetic Diversity in Potato (Solanum tuberosum L ...

Exploring genetic variation in the tomato (Solanum section Lycopersicon) clade by whole-genome sequencing. This is the prepeer reviewed version of the following ...

Exploring genetic variation in the tomato (Solanum section ...

In this study, we screened DNA markers that are specific to tomato (Solanum lycopersicum L.) and Solanum lycopersicoides Dunal for their interspecific transferability to *S. elaeagnifolium* and determined the applicability of the transferable DNA markers in assessing the extent of genetic variation in populations from Lubbock, Littlefield, and Blackwell, TX.

Cross-species transferability of Solanum spp. DNA markers ...

Fgr in tomato is a phenotypically characterized genetic trait with natural genetic variability for modified fructose accumulation in fruit.

Natural genetic variation for expression of a SWEET ...

A wide range of genetic variability was observed in shelf life (5-106 days) and fruit firmness (0.55-10.65 lbs/cm (2)).

Phenotypic and molecular characterization of a tomato ...

genetic variation in solanum can be one of the options to accompany you next having extra time.

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Tomato (Solanum lycopersicum L.) is an economically important vegetable crop worldwide and a pre-eminent plant genetic analysis system. Genetic marker development for tomato has been conducted over 30 years through various approaches, including restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), simple sequence repeat (SSR), cleaved amplified polymorphisms (CAPs), and conserved ortholog sets (COSs).

In Silico Identification and Experimental Validation of ...

Intraspecific genetic variation underlying postmating reproductive barriers between species in the wild tomato clade (Solanum sect. Lycopersicon)

Intraspecific genetic variation underlying postmating ...

principal characteristic of tuber-bearing wild Solanum species. The hypotheses to explore this observation have been developed based on the presence of genetic variation. In this context, evolutionary changes and adaptation are impossible without genetic variation. However, epigenetic effects, which include DNA methylation and microRNAs

Changes in micro RNA expression in a wild tuber-bearing ...

Eight Bulgarian accessions were studied: variety Plovdivska karotina of a Solanum chillense background, variety IZK Alya (cherry type) of a Solanum pimpinellifolium background and six tomato breeding lines (L21 , L53 , L1140, L1116, L975, L984) from the Maritza Institute of Vegetable Crops (Plovdiv, Bulgaria). Each genotype was presented by seven individual plants.

Assessment of genetic variation in Bulgarian tomato ...

Genebanks seek to understand the partitioning of genetic diversity among species, populations, and individuals in their collections since this informs decisions for adopting the most effective sampling strategy. Recent reports have suggested that diploid wild species have much less heterogeneity within populations than cultivated forms. We here review past empirical phenotypic trait variation ...

Assessing under-Estimation of Genetic Diversity within ...

Three hundred and eighty genotypes of tomato were investigated for genetic diversity for nine seedling traits and considerable genetic variation was observed for all the traits except pubescence. Only two genotypes (19901 and 6836-9) were glabrous, whereas all others had hair on the hypocotyl.

Genetic Divergence for Seedling Traits in Tomato (Solanum ...

Considering that genetic variation between the tomato reference genome *S. lycopersicum* and *S. pimpinellifolium* is larger than genetic variation within *S. lycopersicum*, mapping parameters were set as 0.5 for the length fraction and 0.9 for the similarity fraction. The reads of the same individual in different lanes were merged.

Assessment of Genetic Differentiation and Linkage ...

The objective of this work was to genetically analyze somaclonal variants and gamma induced mutants of potato (*Solanum tuberosum* L.) cv. Diamant using RAPD-PCR technique. In the present work, callus was induced from nodes, internodes and leaf explants in MS medium supplemented with NAA (1.0 mg/l) and BAP (0.5 mg/l) and plants were regenerated from 14-20 weeks old calli.

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.

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*.

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 syntnc 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.

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.