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(PDF) Genetic and bioclimatic variation in Solanum ...

Genetic Diversity and Population Structure of Tomato ...

Solanum pimpinellifolium; genetic differentiation; linkage disequilibrium; RADseq; The wild tomato species *Solanum pimpinellifolium* is a native perennial shrub in Ecuador and Peru, ranging along the western Andean slopes to the coastal regions. It is believed that *S. pimpinellifolium* originated in northern Peru and then diversified into several subpopulations after it migrated to Ecuador and ...

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weight,...

Solanum pimpinellifolium, due to its close relationship to *S. lycopersicum*, has been a genetic source for many commercially important tomato traits. It is a wild species found in the coastal areas of Peru and Ecuador. In this study, the genetic variation of *S. pimpinellifolium* was studied using the diversity found in 10 microsatellites in 248 plants spread throughout its entire distribution ...

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For tomato (*Solanum lycopersicum* L), breeding has involved the competing forces of narrowed genetic variation due to best by best crosses followed by selection, and the expansion of genetic variation due to the introgression of genes for biotic stress resistance from wild species.

We calculated the pairwise genetic distance matrix for the 322 tomato genotypes in TASSEL

v5.2.52. Genetic distance between tomato genotypes ranged from 0.092 to 0.443, with an average distance of 0.270 (Table 1 and Table S2). Among them, the combination of genotypes TAM-CS-138 and USDA-273 revealed the smallest genetic distance (0.092).

High-Density SNP Genotyping of Tomato (*Solanum* ...

Population genetics of eggplants (*Solanum* species) was studied using RAPD (Random Amplified Polymorphic DNA) markers in six states (populations) within Nigeria, Tropical West Africa. The aim was to estimate the actual amount of polymorphism in each population and the overall population combined together.

A molecular genetic linkage map based on tomato cDNA, genomic DNA, and EST markers was constructed for eggplant, *Solanum melongena*. The map consists of 12 linkage groups, spans 1480 cM, and contains 233 markers. Comparison of the eggplant and tomato maps revealed conservation of large tracts of colinear markers, a common feature of genome evolution in the Solanaceae and other plant families. *Fgr* in tomato is a pheno-

typically characterized genetic trait with natural genetic variability for modified fructose accumulation in fruit. Considering both the rarity of the fructose accumulation trait as well as its potential importance in contributing to fruit quality, we undertook a map-based cloning of the *Fgr* gene, leading to its functional identification as a member of the SWEET family of sugar transporters.

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