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▶ To cite this version:

Mathilde M. Causse, Nicolas N. Ranc, Stephane Munos, Sophie Rolland, Marie-Christine Le Paslier, et al.. Linkage disequilibrium mapping for tomato fruit quality traits. 5. Solanaceae Genome Workshop, Oct 2008, Cologne, Germany. hal-02751766

HAL Id: hal-02751766 https://hal.inrae.fr/hal-02751766

Submitted on 3 Jun 2020

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Session IV: Biodiversity and Evolution

#158: Linkage Disequilibrium mapping for tomato fruit quality traits

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Linkage Disequilibrium (LD) mapping links the natural variability present in germplasm collections to molecular polymorphism and allows the identification of candidate genes. We assessed the possibilities of such approach for the study of candidate genes for tomato fruit quality. Knowledge of the genetic diversity and structure of the germplasm is necessary before implementing LD mapping. We genotyped 360 tomato accessions with 20 SSR markers for highlighting the genetic structure of the sample. A genetic continuum between cultivated tomato and wild ancestor S. pimpinellifolium was established by a part of S. lycopersicum var. cerasiforme accessions. The other part of cherry tomato accessions was closer to cultivated accessions. Nested core collections from 8 to 64 accessions of S. lycopersicum var. cerasiforme were built using molecular and phenotypic data. Cherry tomato accessions were tested for association genetics because (i) they exhibit a large range of variation for fruit quality traits, (ii) they show valuable amount of genetic diversity and (iii) their admixed position between wild and cultivated forms is supposed to increase mapping resolution. Fifty gene fragments from chromosome 2 were sequenced on the largest core collection and SNPs were recorded. LD decreases slowly with genetic distance but the S. lycopericum var. cerasiforme admixture group showed reliable results for association genetics even when a limited number of accessions is used. Association could thus be used either to find or to validate candidate genes. SNPs were identified by sequencing 27 fragments of candidate genes for quality traits on the smallest core collection incremented with accessions from S. lycopersicum and S. pimpinellifolium. SNPs were much more frequent in S. lycopersicum var cerasiforme (1 SNPs every 220 bp) than S. lycopersicum accessions (1 SNPs every 1000 bp). These SNPs will be used in future studies to genotype the entire collection.

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