

## MARKER-TRAIT ASSOCIATIONS IN A COLLECTION OF DIVERSIFIED TOMATO (*SOLANUM LYCOPERSICUM* L.) LANDRACES AND CULTIVARS

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The tomato (*Solanum lycopersicum* L.) has long served as a model species in the study of fruit growth and development. Conventional quantitative trait loci (QTL) analysis led to the identification of many of the regions controlling complex traits such as fruit size, shape and quality. In addition to genotyping suitable segregating populations, the identification of QTLs for important traits may be addressed through association genetics, after the phenotypic and genotypic characterization of germplasm collections, provided that a suitable amount of phenotypic and molecular variation is available.

In this research, we exploited the genetic diversity maintained in Italian landraces and in selected cultivars to implement association mapping in tomato addressing plant, flower and fruit characters. Fifty-nine accessions highly diversified as for fruit size, shape and destination were phenotyped for 15 morpho-physiological traits and genotyped at 20 microsatellite (SSR) polymorphic loci. SSR markers were selected in order to obtain a rough coverage of the tomato genome; in addition, nine SSRs were linked to regions harboring reported QTLs affecting fruit size and/or shape (Q-SSRs), whereas 11 had no a priori known linkage with genes affecting fruit traits (NQ-SSRs).

Significant marker-trait associations were first detected by a non-parametric test. The matrix revealed 29 significant combinations, among which 22 (15.6%) were due to Q-SSRs and seven (4.2%) to NQ-SSRs. When only traits directly describing fruit dimensions and shape were considered, the proportion of significant associations revealed by Q-SSRs raised to 28.6%, whereas the other groups of combinations ranged between 3.4 and 5.6%. Results obtained in parallel by GLM analysis widely overlapped those revealed by non-parametric test. In some cases associations were obvious if population structure among accession was factored into the analysis, in others the associations were structure-independent pointing to previously reported QTLs or to new associations between markers and phenotypes.

Although based on a relatively small number of accessions and marker loci, the study demonstrates that the level of diversity encountered in this material made it very attractive to implement association analysis in tomato and that such analysis may represent a useful tool for both

validating the function of known QTLs and for highlighting genetic effects not previously reported. Such power was evident because the proportion of significant associations was much higher when markers chosen as localized near QTLs controlling the trait were compared with variables related to the trait itself. It can therefore be reasonably predicted that a suitable choice of markers, accessions, and traits may provide an analytical platform useful to get insights into the function of specific QTLs over the phenotypic germplasm variation. To translate this information into tools for marker assisted breeding would then be straightforward.