ASSESMENT OF QUANTITATIVE TRAIT LOCI AFFECTING TOMATO BIOMASS

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Tomato is an important vegetable cultivated worldwide and a well-studied crop species in terms of genetics, genomics, and breeding. In particular, a mapping population composed of 76 introgression lines (ILs) of *L. pennelli* have been used extensively for identification and mapping of many biologically and agriculturally important traits. Considering its wide cultivation the possibility to use their biomass for biofuel production is being explored. In this study, were assessed agronomic parameters (earliness, plant coverage, LAI, fruit weight, fruit yield, and weight plant) of ILs mapping population identifying four genotypes with high biomass production. To select candidate genes involved in biomass, we mapped enzymes reported as involved in polysaccharides synthesis (GO annotation) in different ILs by means of *in silico* analysis. Thirty genes previously located on tomato genome were selected and further analysed. Comparison between phenotypic characteristics and candidate gene loci indicated a few candidate genes may influence the variation of biomass composition.