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# A CANDIDATE GENE APPROACH FOR IDENTIFYING QUANTITATIVE TRAIT LOCI AFFECTING TOMATO BIOMASS CHEMICAL COMPOSITION

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Tomato is the most important vegetable cultivated in Italy and a well-studied crop species in terms of genetics, genomics, and breeding. In particular, a permanent 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 in our country the possibility to use their biomass for biofuel production is being explored. Successful use of biomass for biofuel production depends on not only pretreatment methods and efficient processing conditions but also physical and chemical properties of the biomass. In this study, 4 genes previously located on the tomato map using an introgression lines, involved in sugar metabolism were selected and further analyzed. Expression changes among selected ILs (IL 4-4; IL 6-2; IL 7-2) were assessed by Real-time PC. The ADH2 gene shows expression significantly increased in fruit than in leaf while the Ppc1 gene is highly expressed in leaf IL 6-2. Comparison between phenotypic characteristics and candidate gene loci indicated a few candidate genes may influence the variation of biomass composition.