

A BSA-SEQ APPROACH TO IDENTIFY CANDIDATE GENES CONTROLLING STIGMA POSITION IN CULTIVATED TOMATO

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Domesticated tomato (*Solanum lycopersicum* L.) is characterized by a pistil usually shorter than the staminal cone, resulting in an inserted stigma position (SP). This feature ensures fertility and autogamy and represents a domestication trait typical of cultivated tomato. However, several traditional and vintage genotypes show an SP at the level of the staminal cone or even slightly exerted. Moreover, also genotypes with inserted SP, can undergo stigma exertion as a response to high temperature (HT). Shift in stigma position thus represents an important breeding issue because SP exertion increases cross-pollination, generates fertility problems, and decreases crop yield. Identification of genetic and physiological mechanisms controlling SP will be useful in breeding, to adopt strategies to reduce style growth and ensure a high level of fertility and yield even under HT conditions. To this purpose, two landraces phenotypically similar for both vegetative and fruit traits, but contrasting for having stably inserted (Scatolone di Bolsena, SCA) or exerted (Marmande ancienne, MAR) SP were crossed. F1 plants were self-pollinated and the F2 offspring phenotyped to obtain two groups contrasting for the SP trait. DNA from the selected specimens of each group were extracted and pooled to obtain an inserted (INS) and exerted (EXE) bulk. 20X resequencing was performed on the bulk samples and on the parental lines. After filtering, a SNP dataset of ≈ 400 k was used to calculate the genetic similarity between SCA and MAR, that corresponded to 57%. The BSA-seq analysis on F2 bulks revealed that in the INS bulk 19% of the homozygous alleles were peculiar to SCA on chromosome 3. In addition, a dataset of parental lines contrasting SNPs was developed to select SCA private SNPs in the INS bulk and MAR private SNPs in the EXE bulk. Using SNPeff, a total of 227 SNPs with a putative high,

moderate and modifier impact on the protein function were found. Among these, six modifier SNPs and one with high impact were found to be related with genes highly expressed in flower tissues according to the TomExpress expression database and thus are promising as candidate genes involved in style length regulation within cultivated tomatoes. Quantitative expression analysis was also performed to evaluate the possible differential expression of the selected genes between the parental lines. In addition to the quantitative analyses, according to the SNP dataset, over 5,000 SNPs/InDels were detected in eight previously identified QTL regions, mostly on Chr 8, which will be further investigated on F3 specimens.