

## CHARACTERIZATION OF A COLLECTION OF TOMATO LINES INTROGRESSING FRUIT MUTATIONS IN SAN MARZANO

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Tomato represents a food crop of increasing importance all over the world and many efforts have been invested in diversifying the tomato fruit phytonutrients, as potential promoters of dietary benefits. In addition, considerable attention was given to the ripening process, to improve both the quality and the marketability of the fruit. In the development of lines and cultivars commercialized to date, tomato breeders used mutations that delay fruit aging (*rin*, *nor*, *Nr*) and increase the synthesis of pigments (*hp-1*, *hp-2*, *Ip*), mostly at the heterozygous state. In the early seventies, G.P. Soressi started an introgression program to develop repertoires of about 30 tomato fruit mutations into five diversified genetic backgrounds. The present work describes the characterization of the collections of tomato fruit variants in the San Marzano background. The collection represents a unique material in which useful genes are gathered into a well know italian traditional landrace. In addition to the original San Marzano line, the collection includes near-isogenic lines with genes for delayed ripening (*rin*, *nor*, *Nr*), with altered content of all pigments (*hp-1*, *hp-2*, *pd*), of carotenoids (*r*, *t*, *B*, *at*) and of other pigments such as chlorophyll (*gf*) and flavonoids (*y*). Double mutant lines have been selected, with new phenotypes of interest such as "*gf hp-2*" ( brown berry), "*gf r*" (green berry), "*gf y*" (red wine berry), "*y r*" (pale yellow berry), "*Aft atv*" (black berry, anthocyanic). Phenotypic aspects of vegetative growth, reproductive development and fruit quality were analysed. Phenotypes of mutants involving all pigments were consistent with the result that high pigment mutations intensify chlorophyll and flavonoid contents, whereas the genetically anonymous variant *pd* dilute them. GBS data have been used to shed light on the differences between each line and the San Marzano recurrent parent as related to the various degrees of backcross of each line. PCA plotting on the first three axes showed that all the introgression lines are distributed in a tight group together with the wild type with genetic distances ranging from 0.027 (*hp-2*) to 0.119 (*rin*). The *t* and *Aft atv* lines made exception showing genetic distances close to 0.200. The genetic distance between each line and the recurrent parent was not significantly correlated with the number of backcrosses.