

SELECTION OF ONE SUPERIOR TOMATO SUB-LINE CARRYING A *SOLANUM PENNELLII* WILD REGION ON CHROMOSOME 7

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The *Solanum pennellii* Introgression Line (IL) population has been exploited to map useful QTLs and to identify favourable alleles that can improve yield and fruit quality traits in commercial tomato varieties. Over the past few years, in our laboratory we have selected ILs and sub-ILs that exhibit increased content of antioxidant compounds in the fruit, compared to the cv. M82, which represents the genetic background in which the different wild regions of *S. pennellii* ILs were included. Recently, we have identified seven sub-lines of IL7-3 accumulating different amounts of ascorbic acid and carotenoids in the mature fruit. Since it was demonstrated that the wild region carried on chromosome 7 also induces a low production of IL7-3, the aims of the present work was to evaluate yield performances of the seven sub-lines in three different experimental fields. Another aim was to confirm the higher levels of antioxidants and evaluate other fruit quality traits in different environmental conditions.

On red ripe fruit, the level of soluble solids content (Brix), firmness and ascorbic acid was highly variable between the sub-lines and between the three environmental conditions, and evidenced a significant genotype x environment interaction for Brix ($p=0.008$). Only one sub-line (R182) exhibited a significantly higher firmness in all the trials, even though no differences were observed for this trait between the parental lines M82 and IL7-3. The same sub-line showed significant higher ascorbic acid content in all the three fields compared to M82, thus resembling IL7-3. As for the yield, even though IL7-3 always exhibited a significant lower production of fruit *per* plant, with a lower fruit weight, and consequently a lower yield, the sub-lines showed a consistent variability of yield over the three fields. Interestingly, the sub-line R182, selected for its better performances in terms of fruit quality, in all the trials showed a production comparable to that of the control line M82.

In order to better define the wild genomic regions carried by each sub-line, a group of species-specific molecular markers are being tested on the seven sub-lines and their parental genotypes. Moreover, a GBS analysis is in progress in order to identify SNPs on the different sub-lines.