Poster Communication Abstract – 6.41

DEVELOPMENT OF MOLECULAR MARKERS ASSOCIATED WITH DESIRABLE AGRONOMIC TRAITS TO IMPROVE PROCESSING TOMATO PRODUCTION

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processing tomato, SNP, chilling, earliness, blossom-end rot

Tomato (*Solanum lycopersicum* L.) is one of the most widely cultivated vegetable crops, and its production for both processing and fresh market is widespread in the Mediterranean area, especially in Italy. With 26,500 ha cultivated with processing tomato, Emilia-Romagna region is the Italian leader in production.

Low temperature stress and blossom-end rot (BER) physiopathy are two of the major limiting factors for the local processing tomato production, while length of growth cycle strongly influences the fructification timeframe, an essential trait for transformation industry. Understanding the molecular basis of chilling tolerance, BER resistance and crop earliness would be crucial to identify the correlated molecular markers and to characterize their allelic variants: this would allow developing new processing tomato cultivars carrying these desirable traits.

A thorough literature survey allowed us to identify candidate genes and QTLs linked to the three mentioned traits. The position of candidate genes was directly inferred from the annotated genome (version SL2.50), while QT loci were physically positioned using the sequences of associated flanking and peak markers. This allowed the detection of genomic regions putatively associated with the 3 selected traits, and SolCAP database was searched to identify a set of SNPs located within or nearby the genomic regions of interest. In total 1,564 and 312 SNPs putatively correlated to chilling and BER tolerance, respectively, while identification of SNPs linked to crop cycle length is still in progress.

A processing tomato collection of 124 accessions (both lines and hybrids) with a wide phenotypic range for the three traits was assembled and grown in filed and in controlled conditions during 2017. Phenotyping and genotyping using SNPs putatively associated with the studied traits of these accessions are currently in progress, aiming at the identification of a set of locus specific SNPs (and respective allelic variants) that could be used for assisted selection in breeding programs.

European ERDF fund supported this research as a part of Emilia Romagna regional project GENBACCA.