Proceedings of the LXV SIGA Annual Congress
Piacenza, 6/9 September, 2022
ISBN: **978-88-944843-3-5**

Poster Communication Abstract – 1.07

DEVELOPMENT OF IMPROVED PINK TOMATO (SOLANUM LYCOPERSICUM L.) LINES FOR THE CREATION OF REMARKABLE HYBRIDS AND SUPPORTED BY GENE EXPRESSION ANALYSIS

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pinktomato, germplasm, SlMYB12, breeding

The "pink" color fruit trait in tomato is associated with a recessive monogenic y locus on chromosome 1. The pink skin phenotype is due to the lack of naringenin chalcone (NarCh), the predominant yellow pigment that accumulates during ripening. SlMYB12 is the transcription factor involved in the regulation of the NarCh biosynthesis, and its suppression causes the pink phenotype. This project aims to improve the ISI Sementi pink germplasm by generating new tomato fixed lines. During 2020, different heterozygous F1 generations with red phenotype were obtained by crossing a pink-fruited line (ISI 1) with three different red-fruited lines (ISI 2, ISI 3, ISI 4). These hybrids were then used to make a first backcross with ISI 1 and other 12 parental lines with similar characteristics. More than 20 BC1F1 lines were obtained. Expression analysis of the MYB12 gene was carried out by quantitative Real-Time PCR on 3 BC1F1lines, also considering a hybrid and a control red-fruited line. In the pink-fruited lines, MYB12 expression was almost completely abolished. Since various sequence modifications localized in MYB12 of different commercial pink lines have been reported in literature, a 591 bp portion of MYB12 cDNA was amplified and sequenced. The results showed no differences in the sequence between all the germplasm tested and the accessions of the MYB12 genes deposited in the database; therefore, the reduction in gene expression in the lines generated by ISI Sementi could be attributable to modifications present in other points of the gene. Currently the project is still in progress: we are developing BC2F1 generations and will continue with the stabilization of future

parental lines useful for the development of new commercial hybrids.