

## EXPLORING PHENOTIPIC VARIABILITY IN A G10 MAGIC POPULATION OF TOMATO

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Climate changing, soil fertility deterioration, increasing soil salinity and water pollution are just some of the many challenges that the [MB1] current and future agriculture are going to face. The combination of good agricultural practices and innovative plant breeding techniques are needed to overcome these problems. In particular, the development of crops capable of producing in sub-optimal conditions, will be crucial, so as the mapping of quantitative traits loci (QTLs) will play a fundamental role. In this framework, a new crossing scheme to obtain a multi-parent advanced generation inter-cross (MAGIC) populations was planned, to increase germplasm allelic diversity, track down specific sequence in the genome and develop new molecular markers associated to future high value agricultural traits.

In this research, a MAGIC population of tomato (*Solanum Lycopersicum L.*) was produced crossing 8 parental lines, selecting for specific phenotypical traits of breeding relevance. 7 parental line were derived from breeding programs of ISI Sementi and one from a wild accession of *Solanum cheesmaniae* (LA1407) obtained from TGRC (<http://tgrc.ucdavis.edu>). This last, was selected for its resiliency and tolerance to abiotic stress. All the lines were genotyped with a genotyping by sequencing (GBS) approach.

After the first phase of parental lines intercrossing (G0 – G4), the MAGIC population is now in the self-crossing phase (G10) and all accessions are reproduced with a single seed descent approach (SSD). In order to analyse lines stability an activity of phenotyping was performed during season 2021 using classical tomato breeding tools.

The population was phenotyped in two location: one field in the headquarter of Isi sementi (Fidenza, PR) and a previous generation in Monsampolo del Tronto (AP) at the Research Centre for Vegetable and Ornamental Crops (CREA).

A statistical analysis was performed with R and R-Studio to verify phenotypical segregations still present in SSD sister-lines and to find correlations between scored traits.