Poster Communication Abstract – 5.34

EXPLOITATION OF GENETIC DIVERSITY OF A TOMATO MAGIC POPULATION THROUGH GENOME WIDE ASSOCIATION ANALYSIS

PALMA D.*, BERETTA M.**, LETEO F.*, CAMPANELLI G.*, SESTILI S.*

*) CREA - Centro di Ricerca Orticoltura e Florovivaismo
**) ISI Sementi

tomato, participatory plant breeding, GWAS, organic farming

The Multiparent Advanced Generation Intercross (MAGIC) population represent an important genetic material to be analyzed and provide increased recombination and mapping resolution. MAGIC population has great potential to discover the genetic architecture of complex traits by Genome-wide association studies (GWAS). A tomato MAGIC population developed by crossing eight founder lines chosen to include a wide range of variability, was used to develop genotypes with important agronomic traits and adapted to different environmental conditions. From the 400 G4 plants of the MAGIC population, 412 G10 RILs selected by SSD (two generation cycle per season) and 10 G7 lines selected by Participatory Plant Breeding (PPB) were cultivated at three different farms located throughout Italy. All the plant material developed and the 8 founder lines were phenotyped and genotyped using the Single primer enrichment technology (SPET). The RILs were phenotyped for 9 qualitative descriptor and 10 quantitative traits related to plant architecture and fruit characteristics, while the PPB lines were visual phenotyped RILs genotypic data were analysed by applying a filtering procedure based on MAF (Minor Allele Frequency) and presence of missing data (NA), and a total of 18.372 high quality single-nucleotide polymorphisms (SNPs) were obtained. The PCA analysis confirms the absence of genetic structure in the MAGIC population, since the first two principal components (PCs) account for 8.01% (PC1) and 7.41% of the total variation, respectively, while the first 5 PCs explain together 31.24% of the total variation. The phenotypic data collected were used for GWAS analysis. Significant associations were detected for Healthiness and Green shoulder traits. In detail, the PTI5, SUMM2, RGA3, glutamate receptor 3.2 and sus3 genes, involved in resistance to abiotic stress, were detected. These genes

resulted highly associated also from the GWAS analysis of the lines derived from PPB for which the major trait visualized was Healtiness. The SUN family genes, mainly SlSUN13, LYC-B, CTP synthase 2, SlUVR8 and GGPS, involved in physiological and biochemical changes, during tomato fruit development (i.e.production 4of plastidial isoprenoids as carotenoid), resulted highly associated to the Green Shoulder trait.