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Oral Communication Abstract – 1.04

DECIFERING THE RECOMBINATION SPOTS SCENARIO IN A MAGIC POPULATION OF CULTIVATED AND WILD TOMATO

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In recent years, the development of MAGIC (Multiparent Advanced Generation InterCross) populations led to major progress in the understanding of the genetics of several crops. Compared to bi-parental or multiple parents-based crosses, MAGIC populations result in a higher level of recombination, increasing the precision and resolution of QTL detection and genetic mapping. Moreover, a higher number of parents allows the investigation of more traits from each specific parent.

The MAGIC population developed in this study was named “SABER” and was generated from seven highly divergent *Solanum lycopersicum* determinate elite lines (chosen to maximize the phenotypic diversity) and one *Solanum cheesmaniae*. *S. cheesmaniae* originates from Galapagos Islands and it was selected for a very large dataset of traits as biotic and abiotic stress tolerance, yield and resiliency. The plants resulting from the 8-way crosses (G3) were self-pollinated for six generations to obtain stable lines (G9).

A genotyping by sequencing (GBS) was performed through ez-RAD on the eight parental lines. The reads were aligned against the reference genome of *S. lycopersicum* build SL4.0, allowing to detect > 500,000 SNPs. The variants that better represented the variability across the eight parental lines were then selected through a local clustering analysis and used to design a Single Primer Enrichment Technology (SPET)-based assay consisting of 7567 SNPs. The newly designed assay was used to genotype ~480 G9 plants.

By taking advantage of both GBS and SPET data, we reconstructed the

haplotypes of the G9 samples and we obtained a high-density genetic map, highlighting regions with different recombination rates. The characterization of the meiotic recombination spots is becoming a hot topic, having both practical and theoretical relevance, as it enables the identification of informative markers, building of genetic maps, association studies on important alleles and profiling linkage drags. Subsequently, a kinship matrix was computed, using the alleles sharing between samples as a measure of their similarity. This helped to estimate the contribute of each parent to the genomes of the G9 offspring.

Finally, since during the self-crossing cycles some of the individuals were sterile or died in the early stage of development, we searched for a possible genomic explanation of the phenomenon.