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Poster Communication Abstract – 2.10

GENOME SELECTION FOR TOMATO HEAT TOLERANCE IN MEDITERRANEAN AREA

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In the light of the forecasted world global climate changes and demographic growth, it is becoming a major challenge to provide sufficient amounts of food for all the population. The H2O20 Project TomGEM applies a multi-actor approach involving tomato producers and breeders to provide new targets and innovative breeding strategies to obtain new tomato cultivars with improved yield under suboptimal temperature conditions. In this work, genomic selection protocols to identify superior individuals correlating phenotype and genotype were build up. A breeding population of 130 individuals obtained from a tomato variety, previously selected for its production capacity in conditions of high temperatures, has been characterized at the phenotypic level. Traits related to flowering and fruit set were carefully phenotyped under heat stress conditions. PCA analysis based all phenotypic parameters analyzed allowed to select 20 superior genotypes. All individuals have been sequenced through GBS approach, producing a total of 117.798.988 reads. After quality check, all reads were mapped onto the reference genome (Solanum lycopersicum cv. Heinz 1706), and the results were used for SNP calling using STACKS (Catchen et al., 2013). The mapped genotypes were used to infer an haplotype map. Genotypic data revealed differences in the number and size of haplotype blocks, as well as contrasting chromosome haplotypes in phenotypically contrasting individuals. Alternative prediction models are beign tested to identify a high confidence statistical model that can predict plant performance based on the plant genotype. In particular, these data are used to calculate a "genome estimated breeding value" (GEBV). Individuals across our population with the highest GEBVs will be selected to produce the next generation, where the individuals will be only genotyped to validate the model. Complementary approaches such as collection of pedigree data, QTL search and genomic analysis among large datasets will integrate for enhancing the genetic gain for the traits of interest.