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SIGNIFICANT ASSOCIATIONS FOR SEED WEIGHT TRAIT IN TOMATO WERE REVEALED BY GWAS STUDY

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Domestication had a high impact on desirable qualitative traits in crops. For several domesticated crops the edible part is represented by the fruit and/or the seed; for some species, the seed weight is a fundamental yield component due to its use in the human diet. Specifically, breeding has acted in favour of larger seed size, germination uniformity and higher seedling vigour. In tomato (*Solanum lycopersicum*), domestication determined an improvement of desirable quality traits such as the fruit size, total soluble solid content and lack of alkaloids; subsequently, it led to an increase of seed weight (SW) in the cultivated forms compared to wild ancestors, due to the selective pressure of cultivation and breeding. However, high variability in the seed size is present in the tomato germplasm worldwide; indeed, many modern varieties still have a small seed, deriving from interspecific crosses with wild species pursued to introgress genes of interest. In this context, we purposed the phenotyping for SW of 185 genotypes selected in the European project TRADITOM and, in parallel, a GWAS approach to partially explain the origin of this trait. For three years (2015-2017) data regarding the SW were collected, sampling the weight of 50-seed replicates. Using a linear regression approach, the seed weight stability (sSW) over the years was calculated and used for the GWAS in addition to the SW trait. A filtered dataset of 2,709 SNPs retrieved from Genotyping-by-Sequencing (GBS) analysis was used for the genotyping experiment. The population structure was calculated using STRUCTURE 2.3.4 and, for the GWAS analysis, the R package Genomic Association and Prediction Integrated Tool (GAPIT) was adopted. For the identification of the associated SNPs, we used four different models (MLM, Blink, FarmCPU and

SUPER). The SNPs showing p-value < 104 in at least two models were regarded as associated. The phenotypic analysis revealed a high range of SW variability that varied from 1.35 mg and 4.65 mg in 2015, 1.38 and 4.34 mg in 2016 and between 1.36 and 4.17 mg in 2017. Regarding sSW, the values recorded showed a wide range of variation and the analysis revealed eight genotypes showing high stability of SW over the years. Crossing the phenotypic and genotypic data, the GWAS analysis revealed 26 SNPs (25 associated to SW and one to sSW). Moreover, a prediction analysis of the SNP revealed that four variants falling in the coding sequence of genes, led to a putative significant effect on protein function. Presently, some of these markers are in course of validation in an interspecific population (*S. lycopersicum* x *S. pimpinellifolium*) characterized by contrasting SW phenotype.