Deciphering the genetic control of tomato fruit quality in the resequencing era

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DECIPHERING THE GENETIC CONTROL OF TOMATO FRUIT QUALITY IN THE RESEQUENCING ERA

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Identifying the genes controlling the variation of quantitative traits is a key goal for breeders. Genetic variations underlying quantitative traits (QTL) have been mapped by traditional linkage mapping for years and positional cloning identified several QTLs. However linkage mapping is limited to the analysis of traits differing between two lines and the impact of genetic background on QTL effect has been underlined. Thanks to the increase in molecular markers, genome-wide association studies were then proposed to circumvent QTL limitations. In tomato, a self-pollinated crop, we have shown that association studies are possible, using the admixed nature of cherry tomato genomes that limits the impact of population structure in such an approach. Nevertheless, the results might be limited by linkage disequilibrium, which varies greatly along the genome. Multi-allelic Advanced Generation Inter-Cross (MAGIC) populations allow a wide range of variability to be analyzed and avoid dealing with population structure.

We have constructed a MAGIC population by crossing 8 tomato lines, representing a wide range of genetic diversity within the species. The large range of phenotypic variability represented by these lines was then characterized at different scales, metabolomic, proteomic and transcriptomic. The variation of a few genes/proteins, involved in primary metabolism and stress response, was related to metabolite content by network reconstruction. The whole genomes of the 8 founder lines were resequenced identifying more than 4 millions SNPs when mapped onto the reference genome. A set of 1536 SNPs markers was then selected to genotype the MAGIC population and used to construct a linkage map. A large increase in recombination frequencies compared to bi-parental populations was shown. QTLs for fruit quality traits were mapped and related to the variations detected at the genome sequence and expression levels in the parental lines. The advantages and limits of the three types of population, in the context of the available genome sequence and resequencing facilities, will be discussed.