

DISSECTING GENETIC FACTORS UNDERLYING STYLE POSITION IN TOMATO

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Plant domestication led to considerable phenotypic modifications of floral traits in the transition from wild species to modern varieties. A change in style position with respect to stamens represents one of these adaptations, leading from allogamy of ancestor species (style exerted), to the autogamy of modern counterparts (style inserted). The cultivated tomato is a clear example of such a change. However, genetic or environmental conditions, as heat stress, allow the observation of an exerted style in some domesticated tomato varieties, too. For modern breeding activities, style exertion is important to evaluate because it increases events of cross-pollination and can give rise to fertility problems.

In our research, the genetic control of style exertion in tomato has been studied with two different approaches. The first was based on the phenotypic study of the style in different tomato populations (the 224-accession core collection selected within the EU project Traditom, a 255-line MAGIC population developed at INRA Avignon, France). Phenotypic data collected from different fields were merged with genotypic information (GBS and 1500 SNP, respectively) to assess phenotype-genotype relationships by a genome wide association study (GWAS). The screening yielded QTL positions that confirmed previous studies (eg. the cloned *Style2.1* locus on Chr2) as well as novel positions (eg. on Chr1 and Chr11).

The second approach aimed to study transcriptomic differences in genotypes contrasting for style behaviour. Two groups of 13 accessions, each showing constantly inserted or exerted style, were selected from the Traditom core collection and a bulk RNAseq experiment was carried out using pistil tissue collected during flower development. The analysis, aimed to discover specific differentially expressed genes (DEGs) implicated in the style growth, yielded 566 up- and 235 down-regulated transcripts. A subgroup of them was validated by qPCR on bulks and on individual genotypes. Enrichment analysis indicated that up-regulated DEGs were enriched of metabolism-related processes at the membrane and extracellular level, whereas down-regulated DEGs were rich in translation-related terms.

Molecular analyses, compared to a fine phenotyping of style development in the studied genotypes, promise to give a significant contribution in the understanding of the genetic control of style growth in cultivated tomato, a very important trait in breeding activities and improvement for heat stress tolerant varieties.