

TOWARDS PHENOMICS OF THE SEQUENCED GENOMES OF THE CULTIVATED TOMATO AND ITS WILD ANCESTOR *SOLANUM PIMPINELLIFOLIUM*

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The genomes of tomato (*Solanum lycopersicum*) and its wild progenitor, *Solanum pimpinellifolium*, have been sequenced (<http://solgenomics.net/>). In contrast to most wild tomato species, which produce green inedible fruits, *Solanum pimpinellifolium* yields small (~1 gram) brightly colored red fruits commonly known as “currant” tomatoes. Until now *Solanum pimpinellifolium* remained largely inaccessible to high-resolution genetic dissection due to its low level of marker polymorphism. However, the recent sequencing efforts revealed multiple SNPs that could be used for the mapping as well as for the identification of the functional SNPs that differentiate the cultivated tomato from its wild progenitor. Our objective was to re-visit the phenotypic diversity in a Backcross Inbred Line (BIL) population (178 lines) derived from a *Solanum lycopersicum* (cv. E6203) x *Solanum pimpinellifolium* LA1589 cross. This will create an extremely valuable data resource for directly associating SNPs with domestication phenotypes. Towards this aim we have anchored the BIL population to a framework of PCR-based markers covering the entire genome, and we are now in the process of phenotypic evaluation of the BIL population for numerous traits of interest. By combining the large phenotypic databases with the *Solanum pimpinellifolium* genome sequence that is now available we aim to shed light on numerous QTL that underlie phenotypic variation in different biological areas.