ABSTRACT

“RNA-seq analysis in tomato and its wild relatives”

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Wild tomato species are native to diverse habitats in South America and show wide morphological and ecological diversity that has proven useful in breeding programs. The current high throughput sequencing technologies have the ability to characterize genome-wide genetic variation in sequences, expression profiles and other molecular events with an effect in adaptation and development.

We have used RNA-seq and smallRNA-seq to sequence cultivated tomato (*Solanum lycopersicum*) and three wild relatives: *S. pennellii*, *S. habrochaites* and *S. pimpinellifolium*, generating up to 50x -150x coverage of their transcriptome. Since only a draft of the genome sequence of cultivated tomato is currently available, it was required to combine well-established methodologies with custom protocols to effectively obtain relevant information from the short reads generated from the wild species. Our approaches have allowed us to infer genome-wide polymorphisms, species-specific expression differences and small RNA landscapes in tomato. I will present the rationale behind the bioinformatic protocols used for our analysis and the results obtained. In addition, we are now integrating the functional and evolutionary information obtained to identify candidate genes underlying phenotypic variation between tomato and its wild relatives.