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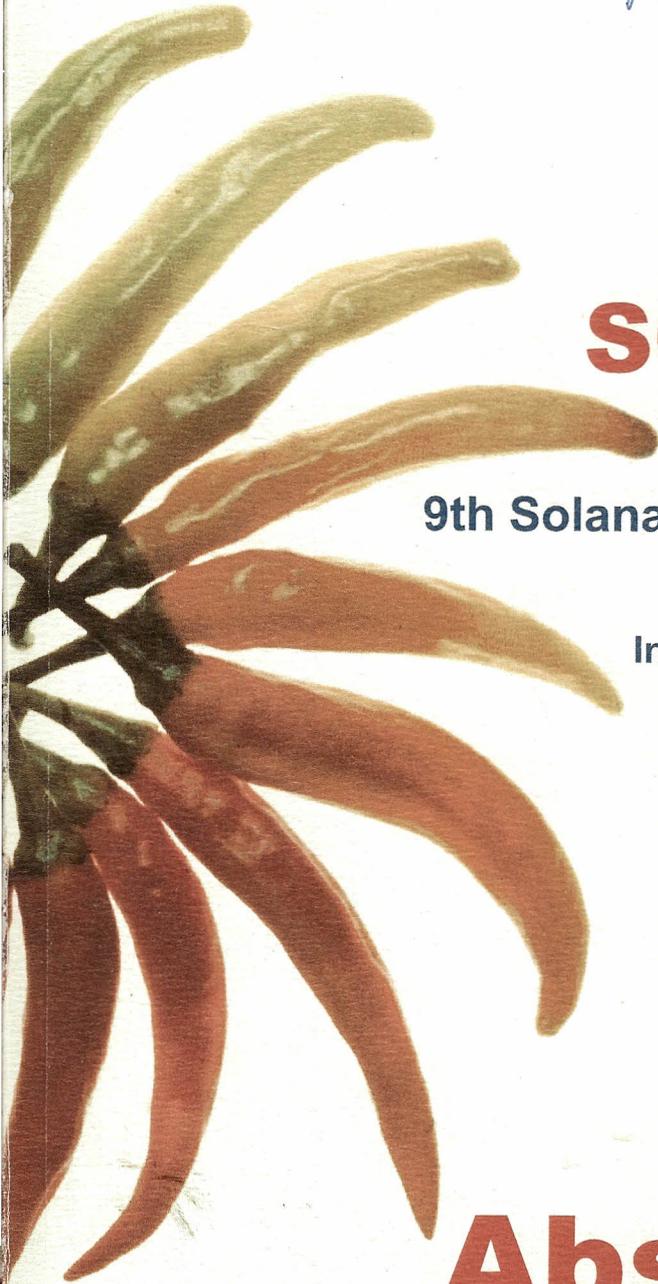
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Veronique Lefebvre



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From the Bench to
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Abstract
Book

Molecular genetic analysis of floral meristem diversity in tomato.

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Over history, domestication and selection of food crops have reshaped fruit morphology. With its large phenotypic diversity, Tomato (*Solanum lycopersicum*) illustrates this evolutive trend. Genes involved in flower meristem development are known to regulate traits related to fruit morphology.

To decipher genetics underlying tomato fruit morphology, we used a candidate gene approach and performed association studies. Thirty candidate genomic regions were selected according to orthology and known causal regions tomato genome. Regions were sequenced on a core collection maximizing the diversity (96 libraries) using Roche 454 technology. A total of 18 Mb were sequenced.

Sequence mapping detected 4460 polymorphisms. Annotation (ITAG.2.3) identified 234 exons and 517 related polymorphisms. Combining SNP detection results and population stratification (SolCAP array), association studies were performed using mixed linear model and tested on 49 fruit traits. Two associations co-localized with previously identified QTN: LC (locule number) and Ovate (fruit shape). Newly identified associations were confirmed on an extended set of 180 accessions. Two new associations were confirmed for fruit size. Subsequently, each region was tested for its molecular diversity and neutrality under selection.

These results (1) validate association approach with candidate genes in tomato; (2) identify new loci putatively involved in fruit size, (3) provide an efficient method for multilocus resequencing.