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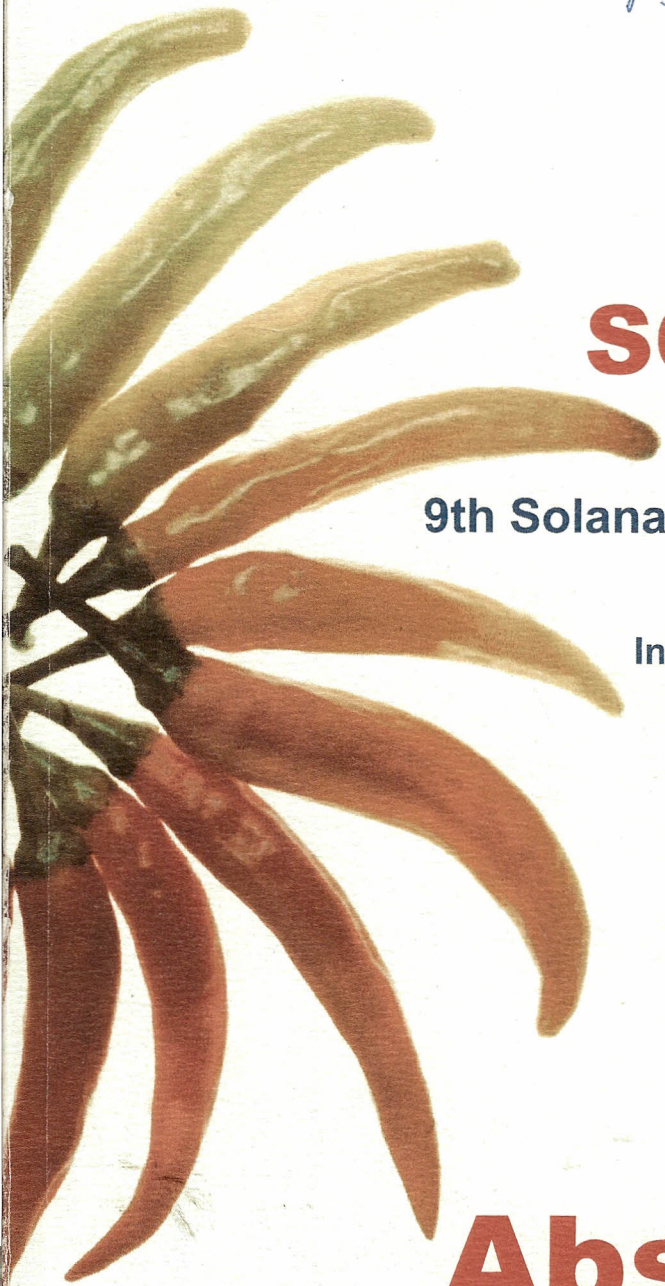
Veronique Lefebvre



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From the Bench to Innovative Applications

Abstract Book

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P19 Comparison of metabolomic, proteomic and genomic variability in tomato fruit

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Tomato fruit quality is an important trait for tomato consumers, but complex to improve due to the number of components involved and by their polygenic nature. In order to decipher the genetic diversity and the inheritance of fruit quality components at a global level, we have conducted a large multi-level omic experiment. A set of 8 contrasted lines and 4 of their F1 hybrids were phenotyped for fruit development traits. Fruits were harvested and pericarp samples analysed at 2 stages (cell expansion and orange) and different scales: (1) primary and secondary metabolome profiles, (2) activities of 28 enzymes involved in primary metabolism, (3) proteome profiles revealed by 2D-PAGE and sequencing of 470 spots showing quantitative variations and (4) gene expression analysis by Digital Gene Expression. In parallel, the 8 lines were resequenced and more than 4 millions SNPs identified when aligned on the reference tomato genome. These data are managed in the FlagDB++.

This experiment allowed us to address several question. The range of variability for the metabolic traits and expression data were compared. Correlation networks were constructed within and between levels of analysis to identify regulatory networks. Diversity of chosen candidate genes was analysed, relating the polymorphisms at the sequence levels with their expression. Some examples will be presented.