

XVI SOLANACEAE CONFERENCE

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Our lab focusses on understanding the genetic bases of plant metabolism; we combine metabolomics, linkage mapping, and metabolome-based genome-wide association studies (mGWAS) to provide insights into the genetic architecture underlying natural variation in tomato primary and secondary metabolism. We have profiled several mapping populations of introgression lines (ILs) and back crossed inbred lines (BILs) derived from crosses between the cultivated tomato Solanum lycopersicum and the wild species; Solanum Pennellii, Solanum neorickii, Solanum pimpinellifolium and Solanum lycopersicoides. In addition, we have explored the genetic diversity in a core collection of 550 tomato accessions composed of S. lycopersicum, S. lycopersicum var cerasiforme, and revealed the chemical diversity and genetic control of tomato metabolites