

## T001 – José Blanca

### *Tomato variation, origin and domestication*

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A collection of 949 accessions composed by *S. lycopersicum* var. *lycopersicum* (SLL; 514), *S. l.* var. *cerasiforme* (SLC; 291), *S. pimpinellifolium* (SP; 128), *S. galapagense* (SG;3), *S. neorickii* (SN; 1), *S. chmielewski* (Schm; 1) and 11 crosses between SP, SLC, SLL and *S. pennellii* was analyzed. The genotyping was carried out using the 7720 markers of the SolCAP genotyping platform and some key genes involved in the domestication process (CNR/FW2.2, SIKLUH/FW3.2, LC, FAS, OVATE and SUN). Using Principal Component Analyses (PCAs) based on the genetic data a new genetic-based classification divided the accessions in SP (121), SLC (236), SLL (492) and mixture (100). Within SP and Andean SLC a complex geographical structure correlated with the climate was found. Ecuadorian SP was remarkably differentiated from the rest of SP. In non-Andean SLC the structure found was not as marked. In a neighbor phylogenetic network SLC appeared intermediate between SP and SLL. Thus SLC was found to be a semi-domesticated with a key role in the tomato domestication. Andean SLC had a diversity comparable to SP while the non-Andean SLC had a lower diversity comparable to vintage SLL, indicating that the main bottleneck in the tomato domestication happened in the migration from the Andean region to Mesoamerica. Most SLC accessions were reported to have cherry-sized fruit, but interestingly some South American SLC were collected in markets as full-sized vintage tomatoes. Thus the vintage tomato in South America included SLC as well as SLL materials.