52. Complete genome sequence of the tropical-adapted Brazilian tomato (Solanum lycopersicum) cultivar IAC Santa Clara

Maria Esther N. Fonseca² & <u>Leonardo S. Boiteux</u>^{2,3*}.

¹ Embrapa Hortaliças, CP 0218, 70359-970; Brasilia-DF, Brazil,

Email: leonardo.boiteux@embrapa.br

Here we described the completion of the genome sequencing of the tropical adapted Brazilian cultivar 'IAC Santa Clara'. This genetic material was a leader tomato cultivar in the Brazilian market during over two decades and displays many traits of interest for breeding purposes. especially improved fruit set and fruit red color under high temperatures. The raw data that has been generated (via the Illumina platform) was employed for the identification of single nucleotide polymorphisms (SNPs) and insertion/deletions (indels) between the cultivars 'IAC Santa Clara' and 'Heinz 1706' (the reference S. lycopersicum genome). Chromosomal distribution of the SNPs and indels was quite variable. Polymorphisms were observed within many disease resistance genes, including the Sw-5 gene cluster in the chromosome 9 and also in members of a major resistance gene cluster in the chromosome 6. Polymorphisms were also within major structural genes of the carotenoid and biosynthetic pathways. Our results provide high-resolution DNA polymorphic information about 'IAC Santa Clara' and represent a significant contribution to molecular breeding programs and genomics resources aiming to develop new cultivars adapted to tropical and subtropical areas of the world.