## Citrus Genomics in Brazil (CitEST): experiences and future perspectives

Marcos A. Machado, Gustavo Astua-Monge, Maria L.P.N Targon, Marco A.Takita, Juliana Freitas-Astua, Alessandra A. Souza, Helvécio D. Coletta Filho, Alexandre M. Amaral, Mariangela Cristofani, Marines Bastianel, Darío A. Palmieri, Ana Carolina Basilio

In 2001, the Centro APTA Citros Sylvio Moreira launched its citrus genomics program with the purpose of integrating this new information into its citrus breeding program. Since then, more than 240,000 EST sequences have been produced expanding several Citrus species such as sweet orange, mandarins, sour orange, sweet lime, Rangpur lime, Persian lime; other related genera like <i>Poncirus</i> spp. and Fortunella spp., and fungal pathogens such as Phytophthora parasitica and Guignardia citricarpa. Even though most of the conditions used to construct the cDNA libraries included leaf tissue infected or not with several important pathogens, 20 new libraries were recently added to the project including new tissues or organs such as roots, bark, seeds, cotyledons, fruits, and flowers. The CitEST database and the bioinformatics tools developed have allowed the identification of more than 50,000 candidate microsatellite markers and more than 3,000 SNPs, some of which have already been proven to be polymorphic in silico. In addition, digital gene expression profiles have been characterized for citrus plants in response to infection with Xylella fastidiosa, Xanthomonas axonopodis pv. citri, Citrus leprosis virus, Citrus tristeza virus and P. parasitica, and to abiotic stresses such as drought. The knowledge accumulated so far on metabolic pathways in citrus plants has also allowed the beginning of a biofortification program focusing on the enhancement of the nutritional quality of citrus fruits and its derivatives. Preliminary efforts to sequence the entire genome of Citrus sinensis are underway. More than 9,000 genomic clones have been generated so far.