



W144: Capturing Next-Generation Genome Wide Molecular Markers in Cassava Helps to Untangle the Crop's Genetic Improvement History

Tuesday, January 16, 2018

04:40 PM - 05:00 PM

📍 Sunrise - Meeting House

The release of the cassava reference genome by Prochnik et al. in 2012 has allowed cassava geneticists identifying tens of thousands genome-wide sequence variations across multiple cultivars. These genomic variations have helped to develop a new generation of molecular markers for the crop's genetics research either by re-sequencing using restriction-site associated DNA-sequencing (RAD-seq) or by the SNPtype™ allele-specific PCR assays technology. Today CIAT's [cassava program](#) using these technologies has characterized at the DNA level more than 3000 cassava cultivars used by farmers in South East Asia or Latin America; including improved cultivars, LAC landraces, and its potential wild close relatives conserved at the [world's largest collections of the crop](#). These next generation molecular markers along with the analytical methods implemented in the [Cassava Genome Hub](#) has allowed to analyze the crop's genetic diversity, performed population and family structure analyses, unravel the crop's phylogenetic and phylogeographic history and confirm its recent introduction histories in Africa and South East Asia. Also, using these genomic and bioinformatics resources, the SNPtype™ technology has allowed us to examine the factors affecting the adoption of improved cassava varieties in the Cauca Department in southwest Colombia, as well as, six regions of Vietnam where most of the cassava is grown. These analytical approaches have showed the power of our next-generation sequencing analytical methods could have in identifying both historical population structure and recent colonization history along with the identification of clones recently adopted including its pedigree. But more importantly, it is guiding our efforts to understand the nature of complex traits in cassava such as whitefly resistance, post-harvest physiological deterioration of the roots, starch stability and content and its resistance to diseases such as frog skin disease.

Authors

[L. Augusto Becerra Lopez-Lavalle](#)

*International Center for Tropical Agriculture,
CIAT*

[Fausto Villafrade Rodriguez Zapata](#)

CIAT

[Tatiana Ovalle](#)

CIAT

[Manuel Ruiz](#)

CIRAD, UMR AGAP

[Anestis Gkanogiannis](#)

CIAT

[Joe Tohme](#)

*International Center for Tropical Agriculture
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