



W971: Greater Yam (*Dioscorea alata* L.) Pre-Breeding and Breeding: Use of Genomic Tools to Decipher the Genetic Diversity and Identify Wild Relatives.

Tuesday, January 16, 2018

05:30 PM - 05:45 PM

📍 Pacific Salon 1

The greater yam (*Dioscorea alata* L.) is the most widespread edible yam species and is cultivated throughout sub-tropical and tropical areas. The species is an important food in West Africa, the Caribbean and the Pacific where it has considerable social and cultural importance, and it is also grown in parts of upland Asia. Although *D. alata* production is expanding in West Africa because of its ease of cultivation, one of the major constraints to further development is its suitability for "fufu", a traditional dish necessitating tubers with high dry matter and specific starch contents. Moreover, some varieties with agronomic importance are susceptible to anthracnose (*Colletotrichum gloeosporioides*). Added to that, *D. alata* genetic improvement is constrained by access to well documented germplasm. Nevertheless, collections of *D. alata* and related species exist in international and national genebanks. Thus, to overcome these main limitations, rationalise the ex situ collections, and facilitate breeding for tuber quality and anthracnose tolerance, using Genotyping By Sequencing (GBS), we are investigating the genetic diversity of a worldwide sample of more than 500 *D. alata* accessions. Using targeted genotyping approaches on chloroplast and nuclear genomes, we are also investigating the relationship between *D. alata* and *D. nummularia* considered as one of its wild relatives from the Pacific. To identify gene/QTLs related to key agronomic traits, genetic mapping is on-going as well. Finally, the genomic resources produced are assembled to build up a "Yam Genome Hub"

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