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Meeting Information

When: January 08 - 13, 2016

Where: San Diego, CA

W902

CIRAD, IRD and INRA Yam Genomic Initiatives: Unlocking Genetic Diversity and Accelerating Yam

Breeding

Date: Wednesday, January 13, 2016

Time: 12:05 PM

Room: Sunset - Meeting House

Hana Chaour, CIRAD, Montpellier, France

Nora Scarcelli, IRD, Montpellier, France

Gemma Arnau, CIRAD, Montpellier, France

Claudie Pavis, INRA Antilles-Guyane, Petit-Bourg, France

Roland Akakpo, IRD, Montpellier, France

Alexandre Dansi, University of Parakou, Parakou, Benin

Dalila Petro, INRA Antilles-Guyane, Petit-Bourg, France

Karine Alix, AgroParisTech, Gif-sur-Yvette, France

Vincent Lebot, CIRAD, Port-Vila, Vanuatu

Yves P. Vigouroux, IRD, Montpellier, France

The fast development of new sequencing technologies allows unlocking diversity of tropical crops. The French institutes CIRAD, IRD and INRA have worked together the last 7 years to improve the yam's genomics toolkit. Using RNASeq from leaves and flower tissues, we have assembled the transcriptomes of three yam cultivated species: *Dioscorea rotundata*, *D. alata* and *D. trifida*. Genotyping by sequencing approaches are currently used to develop a genetic map from four half-sibling families of *D. alata*. Such tools will allow refining genome assembly and identifying QTL related to anthracnose resistance. The study of genomics diversity of *D. alata* using sampling covering the four continents Asia, Pacific, Africa and America is currently underway. Using similar approaches, we obtained 600K SNPs in *D. rotundata*, *D. abyssinica* and *D. praehensilis*. We will present result of this study documenting both the relationship and diversity in these three African species and the detection of genes under selection, genes that may be of importance for yam improvement. We further investigated the important role of wild to cultivated gene flow between *D. nummularia*/*D. alata* and *D. abyssinica*/*D. praehensilis*/*D. rotundata* could play in yam improvement.

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