

W079**The Banana Genome Hub**

Date: Tuesday, January 14, 2014

Time: 11:50 AM

Room: Pacific Salon 6-7 (2nd Floor)

Gaëtan Droc , CIRAD, UMR AGAP, F-34398 Montpellier, France

Delphine Larivière , CIRAD, UMR AGAP, F-34398 Montpellier, France

Valentin Guignon , Bioversity International, Commodity Systems & Genetic, F-34397 Montpellier, France

Nabila Yahiaoui , CIRAD, UMR AGAP, F-34398 Montpellier, France

Dominique This , Montpellier SupAgro, UMR AGAP, F-34060 Montpellier, France

Olivier Garsmeur , CIRAD, UMR AGAP, F-34398 Montpellier, France

Alexis Dereeper , IRD, UMR RPB, F-34394 Montpellier, France

Chantal Hamelin , CIRAD, UMR AGAP, F-34398 Montpellier, France

Xavier Argout , CIRAD, UMR AGAP, F-34398 Montpellier, France

Jean-François Dufayard , CIRAD, UMR AGAP, F-34398 Montpellier, France

Juliette Lengelle , UPS, UMR LRSV, F-31326 Castanet-Tolosan, France

Franc-Christophe Baurens , CIRAD, UMR AGAP, F-34398 Montpellier, France

Alberto Cenci , Bioversity International, Commodity Systems & Genetic, F-34397 Montpellier, France

Bertrand Pitollat , CIRAD, UMR AGAP, F-34398 Montpellier, France

Angélique D'hont , CIRAD, UMR AGAP, F-34398 Montpellier, France

Manuel Ruiz , CIRAD, UMR AGAP, F-34398 Montpellier, France

Mathieu Rouard , Bioversity International, Commodity Systems & Genetic, Montpellier, France

Stéphanie Bocs , CIRAD, UMR AGAP, F-34398 Montpellier, France

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The banana (*Musa acuminata* DH Pahang) reference genome sequence was released. To support post-sequencing efforts, an integrative genome information system, <http://banana-genome.cirad.fr/> accessible through the South Green Bioinformatics Platform, was articulated around a Community Annotation System. Our strategy was to exploit, whenever possible, generic software (e.g. GMOD tools) interconnected to establish a reliable framework. It is composed as follow.

A core comprises a relational database connected to a genome browser with an advanced search and an annotation editor. A controller allows access restriction, annotation quality and history. Authenticated curators can thus improve the automatic annotation of genes and transposable elements.

A gene report allows quick search and fosters interoperability with other South Green tools that manage molecular makers, genetic maps, gene families, ESTs, SNPs, metabolic pathways and cross-genome syntenic dotplots; and give access to sequence analysis workflows.

Thus, the Banana Genome Hub (BGH) aggregates various information systems and projects like the sequencing of the genome, in order to provide a unified access, which in turn encourages the integration of new tools. It can sustain re-sequencing efforts as recently done for the *Musa balbisiana* PKW.

We described use cases that illustrate the use of the BGH to retrieve data, benefit from pre-computed analyses, edit incorrect predictions, update analyses in order to refine the gene evolutionary history and the polypeptide function and finally to help to solve issues of agronomic interest. Since the BGH launch mid-2012, about 728 out of 36,542 genes were manually curated. Training on *Musa* bioinformatics was done in

November 2013.

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Meeting Information

When:

January 10 - 15, 2014

Where:

San Diego, CA