SAVE THE DATE !
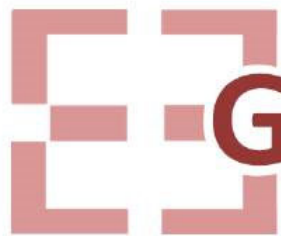
Flagship Project of **agropolis** fondation **2016 / 2021**

23rd(pm) and 24th(pm) of June

GenomeHarvest
diversity, organization and dynamics

Registration link

Project Closing Conference

Looking at **crops with a multiple genomic foundation**, such as banana, citrus, coffee or rice, we have **developed bioinformatics methods** and **tools** that shed **new light** on the dynamics of **genetic diversity**.

These may be relevant and applicable for many other species.

Registration link : https://evento.renater.fr/survey/genomeharvest-project-closing-conference-oluuo1jj

GenomeHarvest
diversity, organization and dyn

Flagship Project of agropolis fondation 2016

Project Closing Conference
Day 1

June 23rd
Synthesis of results on the project's plant models

14:00 Project presentation (A. D'Hont)

14:15 Diagnostic SNPs of citrus species reveal their origin, phylogenomic structures and ancestral haplotype expression (F. Curk *et al.*)

14:45 Genome ancestry mosaics reveal cryptic contributors and patterns of interspecific genome recombinations in banana cultivars (N. Yahiaoui)

15:15 Chromosome reciprocal translocations have accompanied subspecies evolution in bananas and impact chromosome segregation in hybrids (G. Martin)

15:45 Break

16:00 Clarifying genetic foundations of Asian rice cultivar diversity (J.-C. Glaszmann)

16/30 Phenotypic novelty in allopolyploids: gene expression analyses in developing seeds of *Coffea arabica* (M.-C. Combes)

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GenomeHarvest
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Flagship Project of agropolis fondation **2016**

Project Closing Conference
Day 2

June 24th
Tools developed during the project

14:00 Introduction (M. Ruiz)

14:15 Tools for fine characterization of genome ancestry mosaic architecture and chromosome painting (G. Martin, F. Curk,, M. Summo)

14:55 Resolving genome history with machine learning and local ancestry inference methods in rice (A. Beye)

15:25 SNAPPNET, phylogenetic networks in case of profuse introgression (C.-E. Rabier)

15:55 Break

16:10 Panache: a Web Browser-Based Viewer for Linearized Pangenomes (E. Durant)

16:40 RedOak: a reference-free and alignment-free structure for indexing a collection of similar genomes (C. Agret)

17:20 Conclusion

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