Cirad contribution to international training in crop omics

- We are giving a « BigOmics » course for MSc students at the University of Montpellier on the use of large genome sequence data sets to analyse the diversity in a range of important crops.

- We are building international partnerships with universities to propose comparable courses adjusted to local curricula.

- We hope to contribute to a sustainable process that will expose young scientists worldwide to the potential of genomic research for making the best use of genetic resources.
The current course in Montpellier

• Lectures on genomic diversity in rice, banana, sugarcane, three highly contrasting crops, by leading researchers

• Mini research projects on rice introgressions using the 3K resequencing data set

• Over 40 MSc2 students per year
Three important crops to illustrate contrasting crop genomic and biological features

**Rice**
A diploid autogamous crop with a compact genome, contrasted varietal groups growing in diverse environments, resulting from a multiple genetic foundation and profuse genetic exchanges.

**Musa:**
Banana and plantain, sterile parthenocarpic polyploid plants where genome differentiation and dosages determine crop domestication and evolution, and options for varietal improvement.

**Sugarcane:**
Highly polyploid, aneuploid plants derived from interspecific hybridization a century ago, involving two major founder species with 2n S. officinarum female gametes.

<table>
<thead>
<tr>
<th></th>
<th>DNA amount per cell</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
</tr>
<tr>
<td>rice</td>
<td>$2n = 2x = 24$</td>
</tr>
<tr>
<td>banana</td>
<td>($2n = 2x, 3x, 4x$ = $22, 33, 44)$</td>
</tr>
</tbody>
</table>

Rice: 373 Mb, Musa: 484 Mb, Sugarcane: 950 Mb
the principle for rice mini research projects

Rice introgression patterns and genome bioinformatic tools for students

**INPUT:** approximate position of an introgression, either between groups or open

Visualization of the genomic context
- introgression site
- SNP-Seek Haplotype view
- Gigwa Flapjack
- ecogeographic polarity of the introgression
- Gigwa DARwin
- local diversity patterns
- SNIPaly?
- local selection patterns
- REHH 2?

Documented links with phenotypic variation
- SNP-Seek / QTLs
- SNP-Seek / GWAS
- Q-TARO

**Visualization of the genomic region**
- Genome browsers
  - JBrowse Rice Genome Hub
  - JBrowse SNP-Seek (indels, duplisis, SNPs)
- Local syteny (paralogs & orthologs)
- CoGe Synmap (Dotplots)
- Grass Genome Hub

**Characterization and selection of candidate genes**
- synthetic table by S Bocs, Google Drive
- litterature search with key words
- Fun Rice Genes
- functional characterization
  - RAP-DB
  - Oryzabase
  - Uniprot
  - Smart
  - String
  - Riceexpro (expression)
- comparative genomics
  - Greenphyl
  - Salad
  - Genomicus
- prioritization (semantic web)
  - Knetminer

**OUTPUT:** candidate genes for adaptive functions with arguments and perspectives to explore

likely introgressions, potentially bearing genes and alleles with adaptive value
Emerging international partnerships

- Senegal, ISRA-CERAAS, Universités UCAD et Thiès
- Madagascar, Université d’Antananarive, FOFIFA
- Saudi Arabia, KAUST
- Portugal, CIBIO

Information

https://www.youtube.com/watch?v=DWZ05vhKbew
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