

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

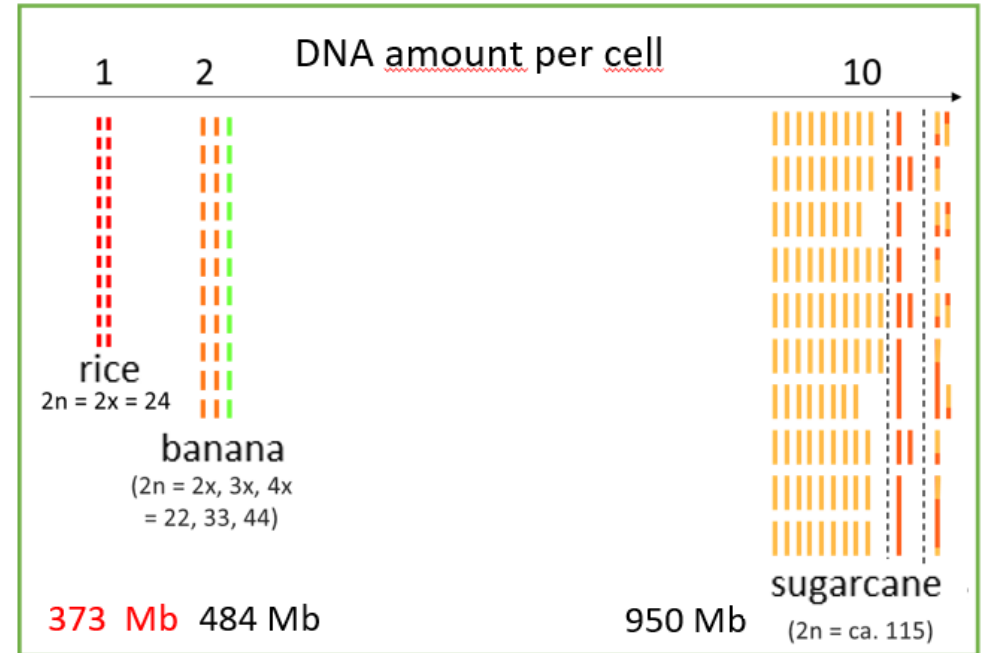


Three important crops to illustrate contrasting crop genomic and biological features



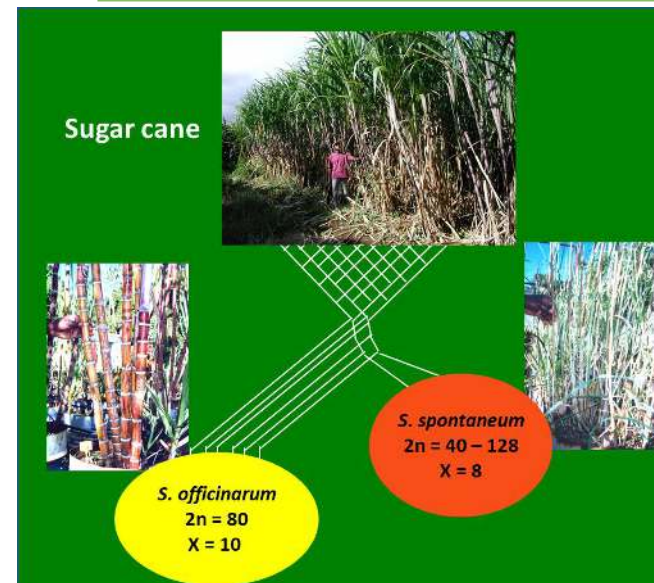
Rice

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.



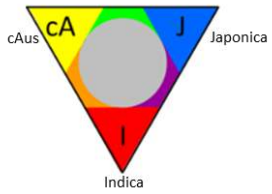
Musa:

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

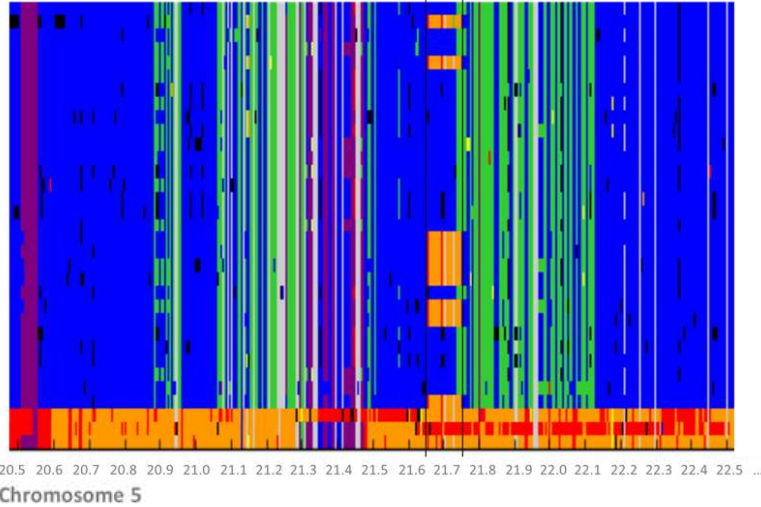


Sugarcane:

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



Chromosome painting
for subspecies
assignment



Chromosome 5



likely introgressions,
potentially bearing
genes and alleles
with adaptive value

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
 - SNIPlay?
- 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, duplis, SNPs)
- Local synteny (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
 - Ricexpro (expression)
- comparative genomics
 - Greenphyl
 - Salad
 - Genomicus
- prioritization (semanic web)
 - Knetminer



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

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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