

# Development of Chromosome Segment Substitution Lines in two interspecific *Oryza sativa* x *Oryza glaberrima* populations

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## INTRODUCTION

Gene mapping of underlying quantitative traits have progressed considerably however the development of new population structures has been poorly documented (Eshed and Zamir, 1995).

New mapping populations called Chromosome Segment Substitution Lines (CSSLs) have been developed in rice (Ebitani *et al.*, 2005). These lines are characterized to contain one or a few contiguous chromosomal segments of the donor genotype in the genetic background of a recurrent genotype.

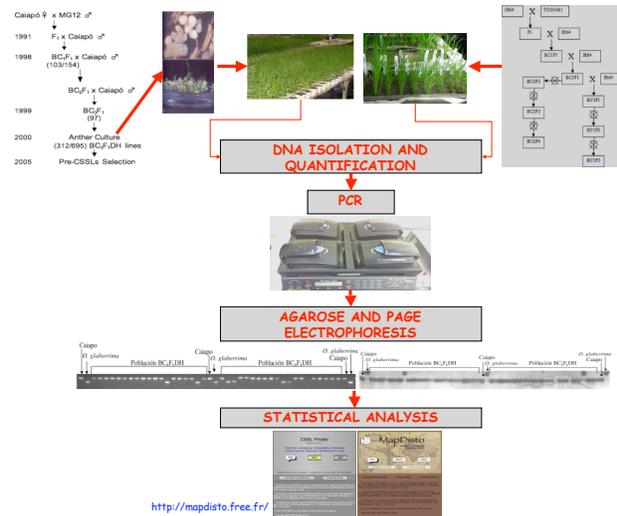
Two populations of CSSLs between the two cultivated species of rice, *Oryza sativa* L. and *O. glaberrima* Steud were developed. We present a QTLs detection analysis for yield, yield components and resistance to Rice Stripe Necrosis Virus (RSNV) in order to illustrate the advantages of using this kind of materials in genetic analysis and breeding of rice.

## METHODOLOGY

Two interspecific crosses: *Oryza sativa* x *Oryza glaberrima*

1. Caiapó (*japonica*) x MG12 (acc. IR6C103544)

2. IR64 (*indica*) x TOG5681 (2 populations)



## RESULTS AND DISCUSSION

1. Caiapó (*japonica*) x MG12 cross



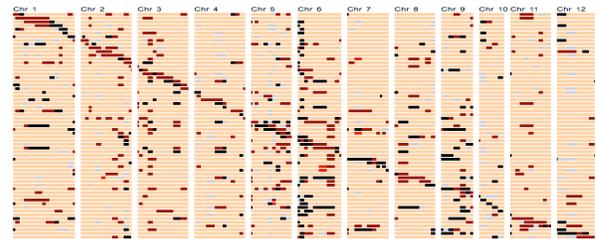
Genotyping of 312 lines with 200 SSRs (125 SSRs automatically selected by CSSL Finder program)  
 64 lines covering the whole *Oryza glaberrima* genome  
 Strong segregation distortion on Chr. 6

4200 BC<sub>4</sub>F<sub>2</sub> lines in field and molecular identification of target lines.



True CSSLs

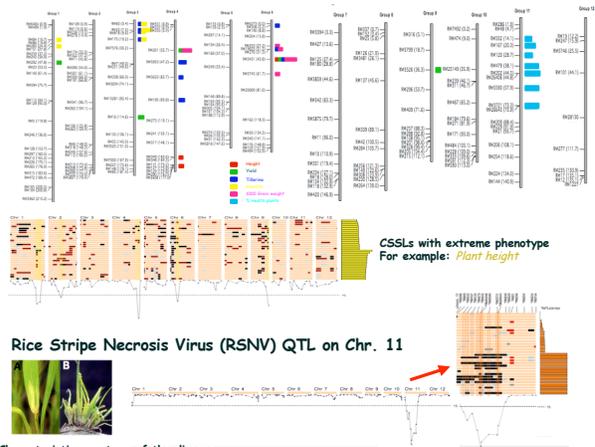
2. IR64 (*indica*) x TOG5681 cross



BC<sub>3</sub>F<sub>3</sub> and BC<sub>2</sub>F<sub>4</sub> population. 363 lines genotyped with 143 SSRs selected from the Universal Rice Core Map (115 SSRs automatically selected by CSSL Finder program) 61 lines covering 95% *O. glaberrima* genome.

## QTLs Mapping

Yield, yield components and RSNV



## CONCLUSIONS AND PERSPECTIVES

This work allowed us to advance significantly in the construction of CSSLs between the two cultivated species of rice, in both *indica* and *japonica* genetic backgrounds.

Fifteen QTLs in each interspecific population were located

Furthermore, CIAT also has available CSSLs populations with Wild species to explore allelic diversity, using the same SSRs from the Universal Rice Core Map and the same genetic background (acc. Curinga, tropical *japonica* elite line):

- Curinga x *O. meridionalis* acc. W2112/OR44 (CIAT, Colombia)
- Curinga x *O. barthii* acc. IR6C101937 (WARDA, Africa)
- Curinga x *O. rufipogon* acc. IR6C105491 (Fedearroz and CIAT, Colombia)
- Curinga x *O. glumaepatula* acc. 6EN1233 (CNPAP, Brazil)

BAR libraries for each of the Wild species have been constructed (Arizona University)

## REFERENCES

- Eshed Y. and Zamir D. (1995) An Introgression Line Population of *Lycopersicon pennellii* in the Cultivated Tomato Enables the Identification and Fine Mapping of Yield-Associated QTL. *Genetics* 141: 1147-1162
- Ebitani T., Takeuchi Y., Nonoue Y., Yamamoto T., Takeuchi K. and Yano M. (2005) Construction and Evaluation of Chromosome Segment Substitution Lines Carrying Overlapping Chromosome Segments of *indica* Rice Cultivar "Kasalath" in a Genetic Background of *japonica* Elite Cultivar "Koshihikari". *Breeding Science* 55: 65-73