Universal Rice Genetic Core Map

Orjuela J[1*], Garavito A[1 2], Bouniol M[1 2], Tranchant C[2], Wilson G[3], McCouch S.R[3], Tohme J[1], Ghesquière A[2], Lorieux M[1 2].

[1]CIAT, Biotechnology Research Unit, AA6713, Cali, Colombia. [2]UMR UP-IRD-CNRS 5096 Centre IRD, 911, Av Agropolis BP 64501, 34394 Montpellier Cedex 5

[3]Cornell University,146 Hemerson Hall, Ithaca N.Y., 14853-1901. [*]julieaorjuela@gmail.com

INTRODUCTION

As response to the higher requirements in rice production, the world's growing population, and the drawbacks caused by biotic and abiotic stresses, it is necessary to increase the genetic base of cultivated rice through the introduction of foreign alleles. Traits of interest can be transferred from other rice-related species of AA genome (Tohme, 2004).

This variability can be detected by Gene/QTL mapping. For this, new populations are created to identify genomic regions of potential use. Chromosome Segment Substitution Lines (CSSLs) populations allow to have a complete set of substitution lines that represent the whole donor genome separated into segments. Each segment is only present in one line, restricting the interactions between donor alleles only to substituted regions (Lorieux, 2000).

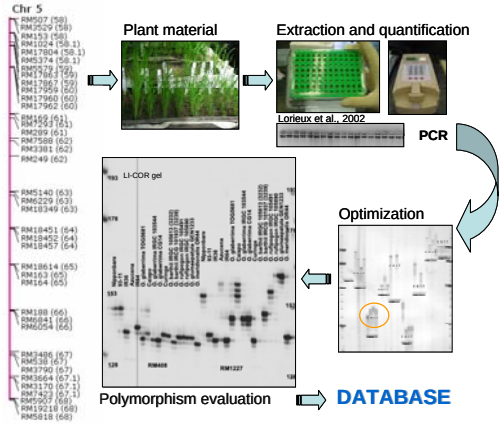
Integrating information about gene and QTL locations on different genetic maps has been an issue since molecular markers were discovered. One of the main difficulties is that the genetic maps of populations under study do not share the same set of markers. In order to facilitate the creation and comparison of CSSLs, we are developing a core map using a set of tightly linked SSR groups, defined as "anchors".

MATERIALS AND METHODS

•Genetic materials

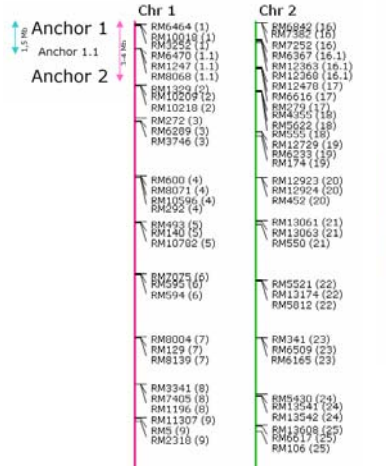
To evaluate anchors and their level of polymorphism, 16 lines with AA genomes where selected. These lines are the parents of the different populations developed in the framework of the Generetation Challenge Program project and CIAT's rice breeding program.

•Evaluation



RESULTS AND DISCUSSION

•Framework core map: Anchors.



	Cross 1	Cross 2	Cross 3
Anchor 1-SSR1	x	x	x
Anchor 1-SSR2	x	x	x
Anchor 1-SSR3	x	x	x
Anchor 2-SSR1	x	x	x
Anchor 2-SSR2	x	x	x
Anchor 2-SSR3	x	x	x

P(1 SSR to be polymorphic)= 0,8

P(1 anchor de 3 SSR to be polymorphic)= 0,9920
P(100 anchors to be polymorphic)= 0,45

P(1 anchor de 4 SSR to be polymorphic)= 0,9984
P(100 anchors to be polymorphic)= 0,85

P(1 anchor de 5 SSR to be polymorphic)= 0,9997
P(100 anchors to be polymorphic)= 0,97

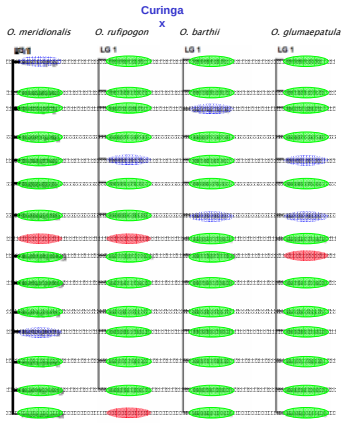
165 anchors composed by 3 SSRs were developed. A total of 511 SSR markers were selected based on *O. sativa* accession Nipponbare genomic sequence, using the annotation data from The Institute for Genomic Research-2004 or TIGR (http://www.tigr.org/index.shtml) version 4, and with the CHARM tool of Cornell University (http://sliver.plbr.cornell.edu/ssr). Finally, the class I markers were validated using the Primerblaster tool from Orygenes database, CIRAD France (http://orygenesdb.cirad.fr).

•Percentages of polymorphism in crosses of interest.

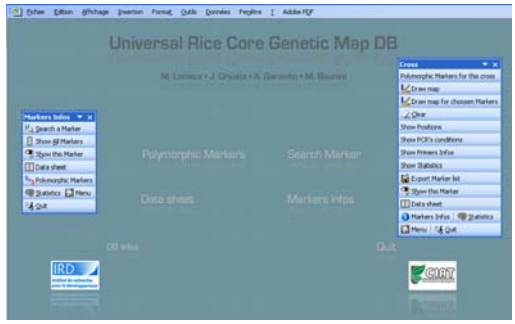
Cross	% Polymorphism
indica x *japonica*	45,2
O. sativa x *O. barthii*	82.8
O. sativa x *O. glaberrima*	80.1
O. sativa x *O. rufipogon*	81.8
O. sativa x *O. glumaepatula*	82.3
O. sativa x *O. meridionalis*	89.0
Mean	83,2

•Validation of Framework core map using six CSSLs real populations

The core map was validated with the development of six CSSLs populations derived from the following interspecific crosses: *O. sativa* ssp. indica cv. IR64 x *O. glaberrima* acc. TOG5681; *O. sativa* ssp. *japonica* acc. Caiapo x *O. glaberrima* acc. MG12; *O. sativa* ssp. *japonica* cv. Curinga x *O. rufipogon* acc. IRGC105491, *O. meridionalis* acc. OR44, *O. glumaepatula* acc. GEN1233 and *O. barthii* acc. IRGC101937. In these populations a similar genome size was observed between the physical and the genetic linkage maps of each populations. In addition, the molecular marker positions are indicated as the reference genome.



•Universal Rice Core Genetic Map Database.



The Universal Rice Core Genetic Map Database was created to provide the scientific community with an easy access to the information. Polymorphic markers for any cross and their localization in the genome can be displayed, as well as the definition of a set of markers enabling to screen a given population.

CONCLUSIONS

•The Universal Rice Core Genetic Map allows useful comparisons of different genetic maps in order to localize QTLs/genes throughout populations from interspecific crosses of interest. Moreover, the construction of CSSL, RIL and NIL lines is facilitated by the use of physical distances in the core map, allowing easier map comparisons.

•The Universal Rice Core Genetic Map provides the necessary allelic information from each parent of a given cross, saving time in the definition of a set of polymorphic markers uniformly dispersed in the genome.

PERSPECTIVES

In the perspective to develop the Universal Rice Core Genetic Map for indica-japonica intraspecific crosses, it is necessary to increase the number of markers of each anchor in order to assure that at least one marker per anchor will be polymorphic.

The Universal Rice Core Genetic Map database will be soon available through a free internet access.

Following SSR evaluations, SNPs will be used as new resource to find genomic variability. A core map based on SNP markers will be then developed to integrate all the information of QTL/gene localizations.

REFERENCES

TOHME, J. *et al.* Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives: A proposal to the Generation Challenge. In : *Program Standard Grant*: (2004); P.51-59.

LORIEUX, M., M.-N. Ndjiondjop, and A. Ghesquière. 2000. A first interspecific Oryza sativa × Oryza glaberrima microsatellite-based genetic linkage map. Theoretical and Applied Genetics 100:593-601.