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## INTRODUCTION

Rice blast, caused by *Magnaporthe grisea* is the most destructive fungal disease of rice worldwide (Fig.1). Genetic resistance is the most effective way to control the disease but major gene resistance is typically quickly broken by new races of the pathogen. Quantitatively inherited resistance can provide effective control under field conditions and is considered to be potentially more durable than qualitative resistance. Oryzica Llanos 5 (OL5) has been one of the most cultivated rice varieties in Colombia and has remained highly resistant to blast disease for over 15 years. However, the genetic basis of this resistance is not well known. In this work we used two different populations from the same cross (Fanny and OL5) to do a QTL (quantitative trait loci) detection approach with multiple *M. grisea* isolates to localize major and minor genes controlling the resistance of OL5. The main reason for a second map was to determine the reliability of the QTL estimates and identify QTL with consistent effects.

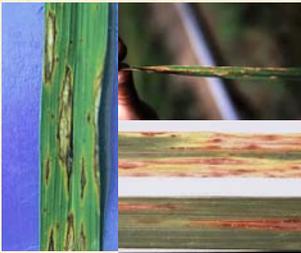


Fig 1. Typical blast leaf lesions



Fig 2. Lesion Type Scale

## MATERIALS AND METHODS

### Genetic material

Two linkage maps were constructed using 280 molecular markers: SSR, RFLP and RGAs for the first population (120 RIL's) and 200 SSR for the second population (231 RIL's). To detect QTL, nine Colombian blast isolates from 5 different lineages were used for inoculation studies. One isolate, FL440, was recovered from OL5 and was observed to be highly aggressive and have a very broad virulence spectrum in other experiments. Two evaluations methods i.e., lesion type (LT) Fig. 2 and disease leaf area (DLA) were used to score the blast resistance.

### QTL detection

Both composite interval mapping (CIM) and multiple interval mapping (MIM) techniques were used for QTL detection using QTL Cartographer package v2.0 (Wang *et al.* 2004). For CIM, each data set was analyzed with 1000 permutations, to 1 cM walking speed. When needed, MIM was performed in order to resolve ambiguous QTL positions or to try to identify linked QTL.

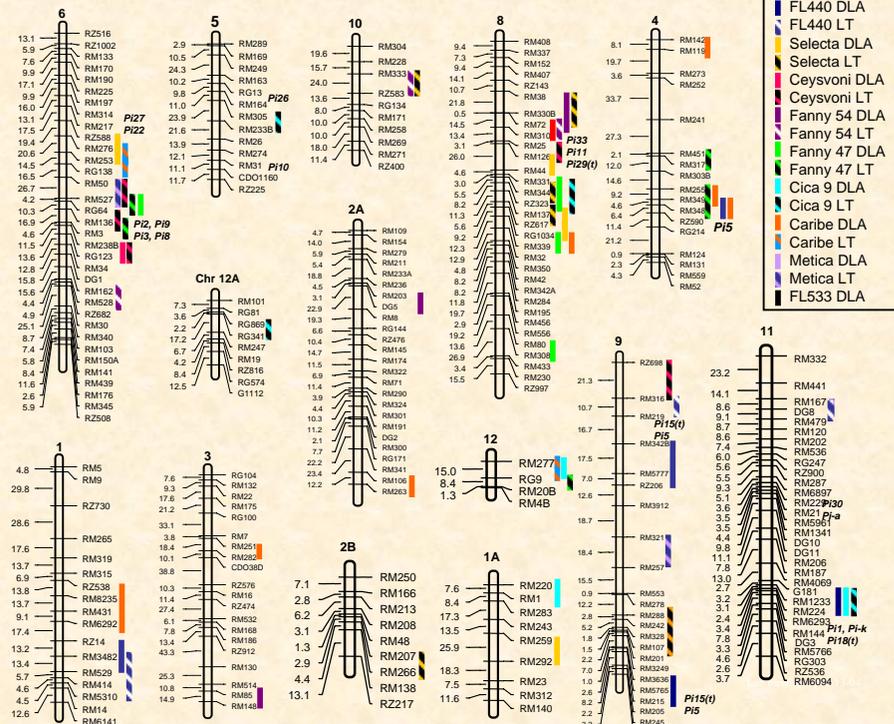


Fig. 3 Linkage maps of rice chromosomes based on 120 RIL derived from a cross between Fanny and OL5. Positions of QTLs for blast LT and DLA with different isolates are shown as colored bars.

## RESULTS

Twenty five loci distributed on 11 rice chromosomes in the first population (Fig 3) and nineteen loci distributed on 8 rice chromosomes in the second population (Fig 4) were associated with the quantitative expression of one of two resistance traits (lesion type and disease leaf area) to nine isolates *M. grisea*. QTL with the largest effects for the first population were on chromosomes 6 (LOD 3.2 explaining 67.7% of the phenotypic variance) and 8 (LOD 10.0 explaining 63.8.0% of the phenotypic variance). The largest effects for the second population were on chromosome 8 (LOD 30.8 explaining 62.9% of the phenotypic variance) and 2 (LOD 8.2 explaining 65.4.0% of the phenotypic variance). Other QTL (LOD 2.0 – 22.3) explained 2.4-45.4% of the phenotypic variance. In some of the QTL locations (i.e. chromosome 4, 6, 5, 8, 9 and 11) there are blast resistance major genes that have been reported to confer high levels of resistance to several *M. grisea* isolates. However, some of the QTL have small effects, indicating the presence of minor genes. A number of these genes are located in areas previously determined to be associated with QTL with large effects.

Most of the QTL detected in this study for the nine isolates were for both quantitative traits. LT is typically associated with QTL with large effects (major, or "R" genes). We identified an isolate, FL440, which appeared able to overcome all the major genes in OL5, but OL5 is still highly resistant. This resistance appears to be controlled by genes with small main effects. FL440 apparently allows these genes to be identified.

The main effect QTL on chromosome 9 and 11 for the DLA FL440 isolate were mapped in both populations to the RM3249-RM205 and G181-RM224 intervals confirming the presence of those QTL to the FL440 isolate; which possibly overcomes all major genes that were identified using the other isolates. One QTL with major effect (20.1%) for the same isolate in chromosome 1 was not identified in the second population even after the region was saturated with the same SSR markers.

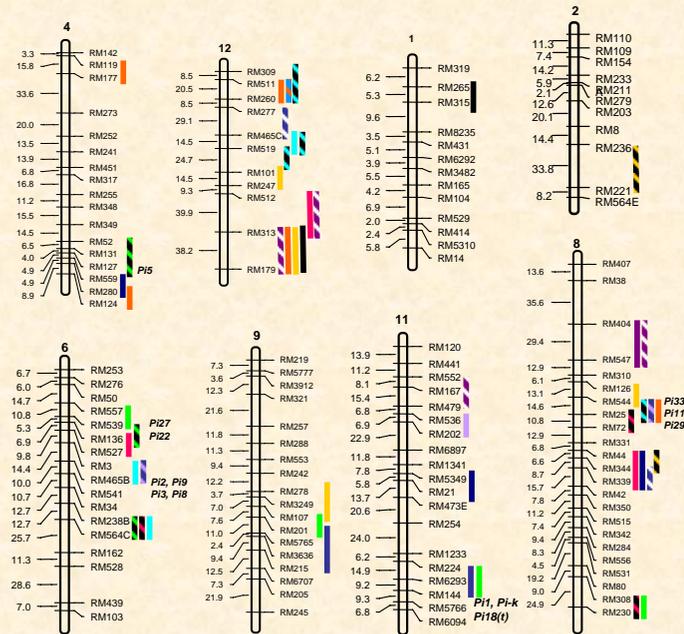


Fig. 4 Linkage maps of rice chromosomes based on 231 RIL derived from a cross between Fanny and OL5. Positions of QTLs for blast LT and DLA with different isolates are shown as colored bars.

## CONCLUSIONS AND FUTURE PROSPECTS

- The durable broad spectrum resistance of OL5 is associated with both major genes inducing hypersensitive reactions and minor genes causing less distinctive differences as in FL440.
- The chromosome 1, 9 and 11 carries genes with small effects for resistance to blast isolate FL440, which we appears to overcome all major genes.
- Comparison of the QTL in both populations identified 11 loci which were statistically significant in both experiments.
- We are in the process of fine mapping some QTL identified with isolate FL440 to characterize potentially non-specific genes. Advanced backcrosses lines are now being tested for ability to confer detectable levels of resistance to FL440.