Molecular Characterization of the RIL Population of *Japonica* Lemont Crossed with *Indica* Jasmine 85 for Mapping Rice Disease Resistance

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Fig.1 Two major rice diseases in the USA.

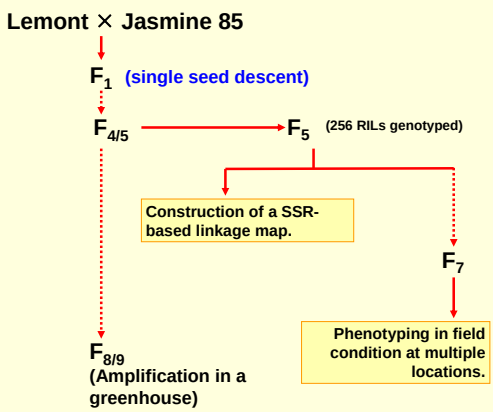

Fig. 2 Methodology for development of RILs.

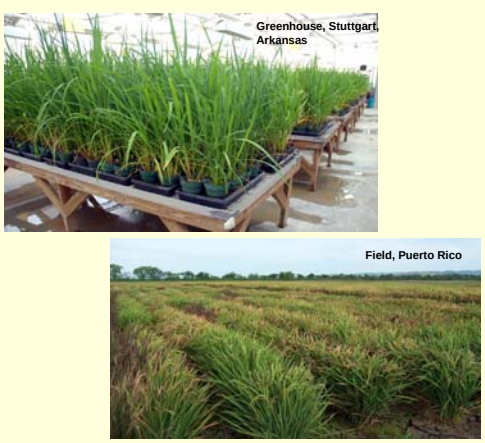

Fig.3 RILs grown in greenhouse and field.

RiceCAP (http://www.uark.edu/ua/ricecap/) is a multi-disciplinary and multi-institutional coordinated agricultural project funded by USDA-CSREES. It targets two of the most difficult rice traits: milling quality and sheath blight resistance.

Abstract

A population of $F_{8/9}$ 800 recombinant inbred lines (RIL) derived from a cross of Lemont with Jasmine 85 is being developed. A subset of 256 RIL was genotyped using 199 polymorphic simple sequence repeat (SSR) markers. A linkage map was constructed, representing a total of 1684.2 c*M* of genetic distance at an average of 8.5 c*M* per marker. This map is being used for mapping quantitative trait loci (QTL) responsible for rice sheath blight (RSB) and rice blast (RB) resistance.

Introduction

The complete genome sequences of both *indica* (Science, 2002, 296:74-92) and *japonica* (Science, 2002, 296:92-100) rice present a unique opportunity for determining sequence and trait relation. A RIL population of rice is commonly used in mapping agronomically important traits, and is particularly useful for analyzing QTL since phenotypes can be assessed over years. 'Jasmine 85', a midseason aromatic long-grain *indica* rice cultivar developed at the International Rice Research Institute, Philippines, is resistant to the RB races IB1, IB49, IC17 and ID1, susceptible to the races IB45 and IB54 of RB (Fig. 1), resistant to RSB (Fig. 1), to narrow brown leaf spot (NBLS), and susceptible to panicle blight (PB). 'Lemont', an early maturing, semi-dwarf tropical *japonica* cultivar is resistant to RB races IB45 and IB54, susceptible to the races IB1, IB49, IC17 and ID1, resistant to PB, susceptible to NBLS and RSB.

The objective of this study was to develop this RIL population for Identifying QTL for the above mentioned traits

Results and Discussion

A cross of Lemont with Jasmine 85 is being advanced to $F_{8/9}$ in Stuttgart, Arkansas using single seed descent in a greenhouse (Fig. 2 & 3). A subset of 256 RIL population at F_5 generation was genotyped with 199 SSR markers across 12 chromosomes. A SSR map was constructed, representing a total of 1684.2 c*M* of genetic distance at an average of 8.5 c*M* (Fig. 4) for mapping. Thus far, the QTLs responsible to RSB and RB resistance have been mapped using this population. In addition, candidate genes for RSB were identified at known RSB-QTLs (MGG, 2007, 278:421-431) and known RB QTLs.

Development and release of this population will benefit the rice scientific community to map other segregating traits. Limited amounts of seed can be obtained by writing to Dr. Yulin Jia.

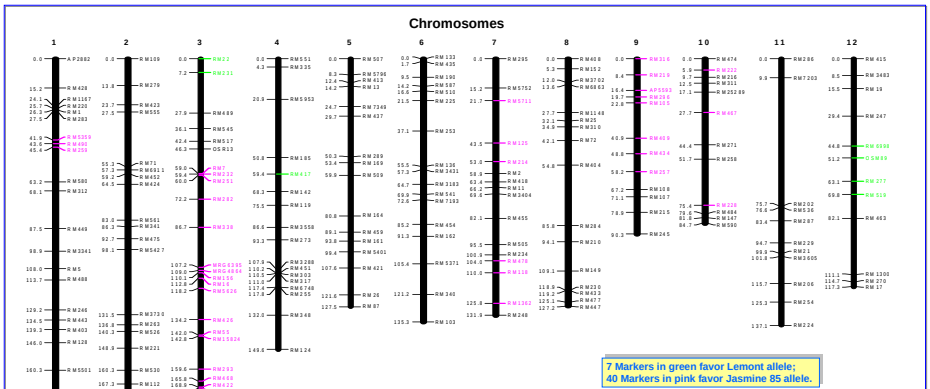

Fig.4 A SSR linkage map of rice showing the locations of 199 SSR markers based on 256 F_5 RILs of Lemont/Jasmine 85.

The genetic distances of SSR markers in cM are shown on the left side of each chromosome.

Acknowledgements

This work was supported in part by the USDA Cooperative State Research, Education and Extension Service – National Research Initiative – Applied Plant Genomics Program entitled "RiceCAP: A coordinated research, education, and extension project for the application of genomic discoveries to improve rice in the United States" (USDA/CSREES grant 2004-35317-14867). We thank Tony Beaty and Michael Lin for excellent technical support.

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