Asian J. of Bio Sci. (April, 2008) Vol. 3: (24-29)

Identification of candidate genes for bacterial leaf blight resistance in rice by integration of genetic QTL map with the physical map

B.P. NIRANJAN REDDY[1]*, R.K. DESHMUKH[2], BHAVNA GUPTA[1], N.K. DESHMUKH[2], G. BHAGANAGARE[1], S.M. SHIVRAJ[1], T. SINGH[1] AND A.S. KOTASHANE[1]

[1] Dept. of Boitechnology, Indira Gandhi Krishi Vishwavidhyalaya., RAIPUR, (C.G.), INDIA

[2] Dept. of Boitechnology, Swamy Ramanand Teerth Marathwada University, NANDED (M.S.) INDIA

(Accepted : October, 2007)

To identify putative candidate genes involved in BLB disease resistance, we performed *in silico* anchoring of the generated QTL genetic marker data to the rice physical map. In total, one QTL responsible for resistance specificity to *Xanthomonas oryzae* pv. *oryzae* iso 6 was identified using CT 9993-5-10-1-M / IR 62266-42-6-2 double haploid population. The QTL qBB 10.1, on chromosome 10 RG 4561-EM 14-10 was saturated with 108 markers, 1097 ESTs, and 201 genes. In total, 28 putative positional candidate genes were identified and were classified based on their function. it is suggested that, the generated data can further be used for the dissection and validation of the QTL to understand the molecular mechanisms of the plant pathogen interaction and to develop a resistant variety.

Key words: QTL, Bacterial leaf blight, Expressed Sequence Tags, Candidate genes, Physical map.

INTRODUCTION

Xanthomonas oryzae pv. *oryzae* is one of the most devastating pest of rice which causes bacterial leaf blight BLB (Wen *et al*., 2003). It acts as notoriously "shifty enemy" through mutation, recombination, migration, complemented with random genetic drift and selection pressure and are often circumvented with disease management strategies. One among the best disease management strategy followed is, development of resistant varieties utilizing both horizontal and vertical resistances (Zhang and Mew, 1985). Vertical resistance, govern by the single major gene, is race specific and can be broken down easily (Mew *et al*., 1992). In contrast, horizontal resistance is govern by polygenes, presumably non-race specific and inherited quantitatively (Nelson, 1972). Achieving/or developing long durable resistant variety needs deeper understanding of molecular principles underlining the quantitative trait loci QTL. Several QTLs responsible for the BLB resistance have been identified using different mapping populations across the different environmental backgrounds, which provide paved starting for candidate gene mining. Cloning of a QTL is necessary for a better understanding of the genetic and functional basis of the plant responsible to BLB resistance (Causse *et al*., 1994; Li *et al*., 1999).

* Author for Correspondence (Present Address) National Research Center on Plant Biotechnology,IARI, NEW DELHI (INDIA)

However, positional cloning of a candidate gene normally requires fine scale mapping with large mapping population (Wang *et al*., 2005; Tuberosa and Salvi, 2006). Availability of the whole rice genome sequence (IRGSP, 2005) provide a new tool for this task, along with a means of characterizing the associated molecular function of candidate genes. In this study, we exploited this new source of data by anchoring the QTL regions responsible for the resistance against the BLB on rice physical map and construct a high resolution map with molecular markers, ESTs, and genes to identify candidate genes and linked markers.

MATERIALS AND METHODS

QTL identification and selection for construction of high resolution map :

The present study was conducted at the Research Farm of Indira Gandhi Krishi Vishwavidhyalaya, Raipur, India 21.15° N latitude, 81.86° E longitude and 289.6 m above MSL. The plant material used in the present study consisted of 154 double haploid lines derived from CT 9993-5-10-1-M *Japonica* cultivar X IR 62266-42-6-2 *Indica* cultivar, developed at Centro International de Agricultura Tropical CIAT, Columbia, and International Rice Research Institute IRRI, Philippines. 154 DH lines were planted along with parents in Randomized Block Design with two replications. The row to row and plant