

Cloning and analysis of QTL linked to blast disease resistance in Malaysian rice variety Pongsu seribu 2

ABSTRACT

Blast, caused by *Magnaporthe oryzae*, is considered to be a global rice disease around the world including Malaysia. Limited information is available on the identification of quantitative trait loci (QTL) and linked markers associated with blast resistance within local rice varieties e.g. Pongsu Seribu 2. Partial resistance against blast disease is widely observed in this variety with mapping of QTLs linked to resistance genes. However, knowledge about the blast resistance genes on chromosome 3 is very limited and no specific blast resistance gene have been identified on chromosome 3 in rice genome of Pongsu Seribu 2. In order to find the similarity of sequence, QTL qRBr-3.1 located on chromosome 3 in Pongsu Seribu 2 was cloned and compared with identified blast resistant genes from other varieties. Sequence analysis of cloned fragment revealed a tandem of (CA)₂₃ repeats. The similarity of sequence was searched in Basic Local Alignment Search Tool (BLAST), which expressed similarity with different clones of rice located on chromosome 3. The cloned QTL fragment also expressed the similarity of 46% with Pi-b, 52% with Pi-kh, 23% with Pi-9 and 38% with Pi-zt, blast resistance genes located at different chromosomes in rice. The QTL fragment produced none of distribution of leucine rich repeats (LRRs) and nucleotide binding site (NBS-LRR). However, the domain contains maximum distribution of leucine amino acid which is responsible for the pathogen recognition in host-plant interaction and play important role in resistance mechanism against diseases. This result concluded that Pongsu Seribu 2 has homology to other resistant genes which are allelic to Pi-b, Pi9, Pi-zt and Pi-kh at different chromosomes.

Keyword: Partial resistance; QTL; Microsatellite marker; Six frame translation; Leucine rich repeat