

Molecular mapping of leaf rust resistance in C14.16/Aus91433 RIL population

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Leaf rust, caused by *P. triticina* (Pt) is one of the most wide-spread diseases of wheat. This pathogen was introduced into Australia by first migrant settlers. Due to its wide range of adaptation, rapid evolution of *P. triticina* (Pt) pathotypes in Australia has defeated many leaf rust resistance genes. Deployment of genetically diverse sources of resistance in wheat cultivars with the help of tightly linked molecular markers is the most quickest and eco-friendly means of rust control. Seedling resistant and adult plant leaf rust susceptible cultivar Aus91433 was crossed with the selection C16.14 and recombinant inbred line population was developed. The C16.14/Aus91433 RIL population was screened with Pt pathotype 104-2,3,6,(7),12 at the seedling stage in greenhouse. Resistant RILs and Aus91433 expressed IT 12C and susceptible RILs and C16.14 exhibited IT 3+. Monogenic segregation for leaf rust response was observed. The resistance locus was temporarily named *LrPak*. Genomic DNA extracted from the Resistance RILs and Susceptible RILs were processed with high throughput 90K SNP Array-based BSA to detect the chromosomal location of the resistance. 90K SNP Array identified association of 32 SNPs from chromosome 2B with *LrPak*. These SNPs spanned across 6.0 cM to 27.0 cM interval of the 90K consensus map. Based on the parental polymorphic screening, final linkage map of 17.4 cM showing marker order and position of the gene was drawn. *KASP_80930* and *KASP_51150* flanked *LrPak* 2.1 cM and 2.5 cM proximally and distally, respectively. Identified closely linked molecular markers in this study will be used for marker assisted back crossing of *LrPak* into modern wheat varieties to create diversity for leaf rust resistance.

Key words: ASR, BSA, Leaf rust, SNP markers