Molecular Mapping of Leaf Rust Resistance Genes *Lr41* and *Lr42* in Wheat

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INTRODUCTION

Leaf rust, caused by *Puccinia triticina*, is an important foliar disease of wheat (*Triticum aestivum*) worldwide. Breeding wheat for leaf rust resistance is a challenging task, because resistance built into a wheat variety can be completely overcome by a shift in predominant pathogenic races in the rust pathogen population. The successful control of rust epidemics using genetic resistance has two dimensions: monitoring the dynamic changes of rust pathogen populations to identify new virulent races and discovering the corresponding resistance genes from plant sources and pyramiding them into elite breeding lines to defeat the new races. Currently, more than 60 leaf rust resistance genes have been identified from wheat and its relatives, and identifying molecular markers linked to the genes can definitely facilitate efficient and effective use of these genes in breeding programs.

OBJECTIVES

Determine the chromosome locations of leaf rust gene *Lr41* and *Lr42* and identify DNA markers closely linked to the genes for marker-assisted gene pyramiding in breeding programs.

MATERIALS AND METHODS

❖95 selected near-isogenic lines were developed by selecting $F_{2:6}$ from crosses of KS93U62 (*Lr41*) and KS93U50 (*Lr42*) to OK92G205, respectively. KS93U62 and KS93U50 are selected backcross progenies of Century*3/TA2460 and Century*3/TA2450, respectively. TA 2460 and TA2450 are two *T. Tauschii* accessions carrying *Lr41* and *Lr42*, respectively.

Fig. 1 Leaf rust reaction on the leaves of plants with different rust resistant genes when inoculated with race *P.* 25. Name of resistance genes are shown in parenthesis.

❖Leaf rust of the mapping populations and their parents was evaluated through natural infection in the field of Stillwater, OK, and leaf rust reaction was recorded using modified Cobb scale (Martin et al. 2002). In addition, the population was also evaluated for rust resistance using a local isolate *Puccinia*. 25 in greenhouse at Kansas State University, Manhattan KS, 2007.

❖DNA was isolated from 1 week old seedling using CTAB protocol.

❖Simple sequence repeats (SSR) markers were analyzed in the ABI PRISM 3730 DNA Analyzer. The data were scored using the GeneMarker® version1.5 (SoftGenetics LLC.) and rechecked twice manually for accuracy.

❖Genetic linkage among SSR makers and leaf rust loci was determined by using Joinmap® 3.0(Van Ooijen and Voorrips 2001) with the LOD score of 3.0 and recombination fraction of 0.4.

❖Chromosome arm locations of *Lr41* and *Lr42* were determined by analyzing the markers linked to the two genes in nullitetrasomic and ditelosomic genetic stocks of Chinese Spring.

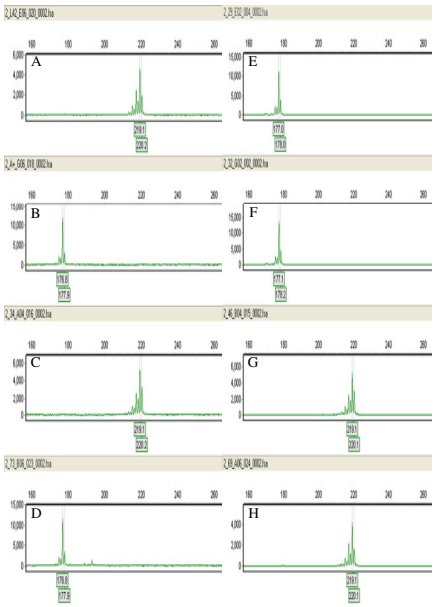

Fig. 2. ABI electropherograms of SSR marker Xcfd15 on chromosome 1D showing polymorphism between KS93U50 (A, *Lr42*), OK92G206 (B, susceptible parent) and selected segregating lines from population KS93U50/OK92G206 (C-H).

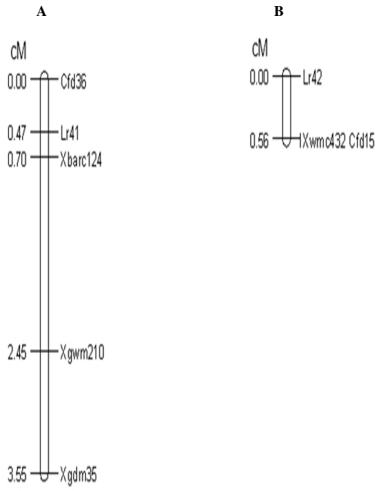

Fig. 3 A genetic linkage map for *Lr41* and *Lr42*, showing the linkage groups with leaf rust resistance gene *Lr41* (A) on chromosome 2DS and *Lr42* (B) on chromosome 1DS.

RESULTS

❖Parents carrying the *Lr41* and *Lr42* were resistant while the parent without the genes was highly susceptible to leaf rust when infected with natural rust inocula from Oklahoma and inoculated with a local isolate *P.* 25 from Kansas (Fig.1).

❖17 out of 160 SSR markers from chromosomes 1DS and 2DS were polymorphic between parents and segregating among NILs (Fig.2).

❖Four SSR markers together with *Lr41* were mapped on 2DS that covered 4 cM genetic distance with the closest marker Xbarc124 about 0.23 cM proximal to *Lr41* (Fig. 3).

❖Two markers were mapped closely to *Lr42* on 1DS (Fig.3).

❖Analysis of the 6 markers from 1DS and 2DS in nullitetrasomic and ditelosomic stocks of Chinese Spring confirmed that *Lr41* and *Lr42* were on chromosome 2DS and 1DS, respectively (Fig.4).

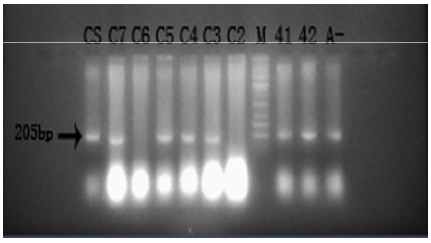

Fig. 4. SSR marker Xwmc432 amplified a 205 bp band in all tested entries except Chinese Spring nullitetrasomic line N1D-T1B and ditelosomic line 1DL-N1DS. C2 to C7 stand for N1D-T1B, N2D-T2A, N2D-T2B, 1DS-N1DL, 1DL-N1DS, 2DL-N2DS, respectively. 41, 42 and A- represent parents KS93062, KS93U50 and OK92G205, respectively. CS is Chinese Spring.

Summary

❖Chromosome location of *Lr41* was confirmed on 2DS and two new flanking markers for *Lr41* were identified within 1cM interval.

❖*Lr42* was located on chromosome 1DS using molecular markers and one new SSR marker linked to *Lr41* within 0.6 cM.

❖Physical mapping of linked markers to the genes further confirmed map location of *Lr41* and *Lr42*.

❖New markers linked to the two genes are useful for marker-assisted gene pyramiding in breeding programs.

Reference

Martin et al. (2003). Crop Sci. 43:1712-1717.

Acknowledgement

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