Identification and Molecular Characterization of Leaf Rust Resistance Gene *Lr14a* in Durum Wheat

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ABSTRACT

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Leaf rust, caused by *Puccinia triticina*, is an important disease of durum wheat (*Triticum turgidum* subsp. *durum*) and only a few designated resistance genes are known to occur in this crop. A dominant leaf rust resistance gene in the Chilean durum cv. Llaleta INIA was mapped to chromosome arm 7BL through bulked segregant analysis using the amplified fragment length polymorphism (AFLP) technique, and by mapping three polymorphic markers in the common wheat (*T. aestivum*) International Triticeae Mapping Initiative population. Several simple sequence repeat (SSR) markers, including *Xgwm344-7B* and *Xgwm146-7B*, were associated with the leaf rust resistance gene. Resistance response and chromosomal position indicated that this gene is likely to be *Lr14a*. The SSR markers *Xgwm344-7B* and *Xgwm146-7B* and one AFLP marker also differentiated common wheat cv. Thatcher from the near-isogenic line with *Lr14a*, as well as durum 'Altar C84' from durum wheat with *Lr14a*. This is the first report of the presence of *Lr14a* in durum wheat, although the gene originally was transferred from emmer wheat 'Yaroslav' to common wheat. *Lr14a* is also present in CIMMYT-derived durum 'Somateria' and effective against Mexican and other *P. triticina* races of durum origin. *Lr14a* should be deployed in combination with other effective leaf rust resistance genes to prolong its effectiveness in durum wheat.

Leaf rust, caused by *Puccinia triticina*, is an important disease of durum wheat (*Triticum turgidum* subsp. *durum*) worldwide (44). Growing resistant cultivars is the most effective way to control this disease. Enhanced knowledge of the presence and identity of leaf rust resistance genes in breeding materials and cultivars greatly improves the efficiency of developing and deploying resistant cultivars. Therefore, determining the chromosomal locations of resistance genes is a fundamental step toward identifying diverse resistance sources and utilizing them efficiently.

Only a few of the more than 50 designated leaf rust resistance genes (*Lr* genes; <http://www.shigen.nig.ac.jp/wheat/komugi/genes/macgene/supplement2007.pdf>) are known to have originated from or be present in durum wheat lines (43). *Lr23* was transferred to common wheat from durum wheat cv. Gaza and cytogenetically mapped to chromosome 2BS by McIntosh and Dyck (26). This gene was mapped

with molecular markers by Nelson et al. (31) using a population developed from the synthetic hexaploid 'W-7984' (durum wheat Altar C84/*T. taushii*) and 'Opata M85.' This gene is thought to be present in several durum wheat cultivars, but virulence to *Lr23* is common in *P. triticina* races isolated from durum wheat (11,34,43).

Hussein et al. (13) identified the chromosomal locations of two novel adult plant resistance genes from cultivated emmer (*T. turgidum* subsp. *dicoccum*) and durum wheat that are effective against South African *P. triticina* races. These genes, temporarily designated as *Lrac104* and *Lrac124*, were located in chromosomes 6B and 4A, respectively, using the durum wheat D-genome disomic substitution lines developed by Joppa and Williams (15) and Joppa (14).

Marais et al. (22) determined that a novel gene, *Lr53*, introduced to common wheat from wild emmer wheat (*T. turgidum* subsp. *dicoccoides*), was located in common wheat chromosome 6BS using monosomic and telosomic analysis, C-banding, and restriction fragment length polymorphism (RFLP) mapping. This gene was effective against several South African and Canadian *P. triticina* races (22).

Herrera-Foessel et al. (10) identified five different resistance sources effective

against BBG/BN, a *P. triticina* race from durum wheat predominant in Mexico. Two of these genes were mapped to chromosome 6BL by bulked segregant analysis and partial linkage mapping (9). One of them was confirmed to be *Lr3* using a previously known marker from common wheat (40), and the second gene appeared to be a novel gene.

Other genes postulated to be present in durum wheat through multi-pathotype seedling tests and comparing infection types with common wheat differentials carrying known *Lr* genes are *Lr10* (1), *Lr13* (41), and *Lr16* and *Lr17a* (49). In addition, a gene transferred from wild emmer wheat (*T. turgidum* subsp. *dicoccoides*) was reported to have the same infection types as *Lr33* (4,6). Of these genes, *Lr10* and *Lr33* are not considered effective, because virulence to them was reported to be frequent among *P. triticina* races affecting durum wheat (11,34).

The gene *Lr14a* is thought to have originated from emmer wheat cv. Yaroslav and transferred to the hexaploid wheat lines Hope and H-44 by McFadden (25). McIntosh et al. (27) reported that this incompletely dominant gene conferred 'X' infection type in common wheat cvs. Hope and H-44, and derived lines Spica, Renown, and Redman. Gene *Lr14a* is linked to stem rust and powdery mildew resistance genes *Sr17* and *Pm5*, respectively; cytogenetic analysis established their locations to chromosome 7BL (18–20,27). Interestingly, this gene is not known to be present in any durum wheat cultivar and has not been detected in tetraploid wheat by formal genetic studies (28). In addition, the original Yaroslav accession that carried the relevant genes (i.e., *Sr17*, *Lr14a*, and *Pm5*) and the slow-rusting stem rust resistance gene *Sr2* (chromosome 3B) has been lost (28).

P. triticina populations prevalent in durum wheat fields were shown in several studies to be different from those present in common wheat fields (8,24,34,41, 42,44). Ordóñez and Kolmer (34,35) found that the prevalent races on durum wheat in North America, South America, and Europe are very similar in avirulence and virulence patterns based on the North American common wheat differential set and on molecular characterization using simple sequence repeat (SSR) markers. In

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addition to *Lr23*, *Lr10*, and *Lr33*, seedling resistance genes that were not considered effective due to frequent virulence among *P. triticina* races from durum wheat were *Lr14b*, *Lr20*, *Lr41*, and *Lr44* (34). A characteristic feature of durum wheat leaf rust races is virulence to most durum wheat lines and avirulence to most *Lr* genes present in common wheat lines (11,34). The resistance genes that are effective in durum wheat germplasm could be genes that are widely ineffective in common wheat lines.

Herrera-Foessel et al. (10) identified a dominant leaf rust resistance gene in the popular Chilean durum wheat cv. Llaleta INIA (D67.54.4^a.9A//Jori 'S' × Rosner Durum 119-200-4Y) Sahel 77) (38). This race-specific resistance gene is effective against the predominant durum *P. triticina* race BBG/BN present in Mexico and confers near immunity (zero or trace severity) under field conditions (10). Under greenhouse test conditions, this gene conferred '3C' to 'X+' and 'X-' to 'X' infection types (39) in seedlings and adult plants, respectively (10). Identification of the gene in Llaleta INIA was based on field evaluations under artificially induced leaf rust epidemics of F₁ hybrids, 222 F₂ plants, and 98 F₃ families from a cross with the susceptible Atil C2000. Allelism tests indicated that the same leaf rust resistance gene also was present in Somateria (Srn_1/6/Fgo/Dom//Nach/5/Altar84/4/Garza/Afn//Cra/3/Ggovz394/7/Eudocimus), a resistant International Maize and Wheat Improvement Center (CIMMYT) durum wheat line (10).

The objective of our study was to enhance the knowledge of leaf rust resistance genes present in durum wheat by establishing the chromosomal location of the resistance gene present in the durum wheat cv. Llaleta INIA.

MATERIALS AND METHODS

Plant materials and leaf rust evaluations. The 98 F₃ lines developed by Herrera-Foessel et al. (10) from the Atil C2000 × Llaleta INIA cross and characterized for resistance to *P. triticina* race BBG/BN were used as the mapping population in this study for identifying molecular markers associated with the leaf rust resistance gene. The common wheat cv. Thatcher and its near-isogenic line Thatcher+*Lr14a* (RL6013) were used in this study for comparing molecular markers with the durum parents. The susceptible Mexican durum wheat cv. Altar C84 and the Altar C84+*Lr14a* line, developed by Huerta-Espino et al. (12) by crossing RL6013 with Altar C84, also were included.

Genomic DNA extraction, bulked segregant analysis, and amplified fragment length polymorphism assay. Twenty seeds from each of the 98 F₃ families of the Atil C2000 × Llaleta INIA population, together with the parents, were planted in

the greenhouse. RL6013, Thatcher, Altar C84+*Lr14a*, and Altar C84 also were included. Three weeks after sowing, leaf tissues were harvested and freeze dried, and DNA was extracted according to a cetyltrimethylammonium bromide-based procedure (3).

The bulked segregant analysis approach according to Michelmore et al. (29) was used for identifying markers associated with the leaf rust resistance gene. Equal quantities of DNA from 14 homozygous resistant (genotype AA) and 14 homozygous susceptible (genotype aa) F₃ families from the Atil C2000 × Llaleta INIA cross were pooled to obtain susceptible and resistant bulks. The amplified fragment length polymorphism (AFLP) technique was adapted for complex genomes (two-step amplification) according to Vos et al. (47) but with some modifications (3,48). Genomic DNA was digested with restriction enzymes *Pst*I and *Mse*I, and double-stranded *Pst*I and *Mse*I adaptors were ligated to the ends of the restriction fragments. The two-step amplification strategy included a preamplification step using primers specific to the *Pst*I and *Mse*I adaptors, including one selective nucleotide. Primers used for the preamplification step were (*Mse*I) GAT GAG TCC TGA GTA A and (*Pst*I) GAC TGC GTA GGT GCA G. The single selective nucleotides for the preamplification step were either C and A or G and T, for *Mse*I and *Pst*I, respectively. A main amplification step then was used with three selective nucleotides for each of the *Mse*I and *Pst*I primers. In total, 96 different AFLP primer–enzyme combinations were applied to Atil C2000, Llaleta INIA, and the two bulks. The AFLP bands were designated according to the nomenclature described in Herrera-Foessel et al. (9). The nomenclature for an AFLP marker is derived from the enzyme–primer combination and the relative molecular weight of the product. The molecular weight was estimated with help of a size marker.

For visualization of AFLP products, the *Pst*I selective amplification primers and the size marker were end labeled with digoxigenin (Sigma-Genosys Ltd., UK). A chemiluminescent detection system was used for observing amplification products separated on sequencing gels (BioRad) according to protocols available from CIMMYT (3). This system included three steps: (i) the amplification product was transferred to a nylon membrane, (ii) the membrane was washed with anti-dig/alkaline phosphatase and CSPD, and (iii) the membrane was exposed to X-ray film. When polymorphisms were identified between the bulks and the parents, the same primer combination was used for screening the individual families that constituted the bulks. If linkage was established between the AFLP marker and the resistance gene, the entire F₃ population,

including the segregating families that originated from heterozygous F₂ plants, was used for estimating the distance between the AFLP marker and the resistance gene.

Partial linkage mapping. The AFLP primer combinations that produced any band associated with the leaf rust resistance gene in the Atil C2000 × Llaleta INIA population were tested on the two common wheat parents, 'Opata M85' and 'Synthetic W-7984,' of the International Triticeae Mapping Initiative (ITMI) population (30). If the same band detected polymorphisms in the parents of the ITMI mapping population, the 114 recombinant inbred lines of the population were genotyped with the same marker. The chromosomal position of the AFLP band was determined by comparing the scoring data of the AFLP band with the publicly available scoring data of markers included in the genetic maps of the ITMI population. For the linkage analysis, MAPMAKER Version 3.0 at minimum 3.0 log of odds (LOD) score (17) was used. The genetic linkage maps based on the ITMI population consist of more than 1,000 genetic markers, of which approximately 800 were used (23,30,32,33,46); the scoring marker data for the genetic maps of the ITMI population are available at the GrainGenes website (<http://wheat.pw.usda.gov/GG2/index.shtml>). We have also included the scoring information on several defense response genes mapped by Li et al. (21). MAPMAKER was used to establish the linkage relationship between AFLP and other markers and the leaf rust resistance gene in Atil C2000 × Llaleta INIA population at a minimum 3.0 LOD score. The χ^2 test for goodness-of-fit was used for assessing the deviation of observed data from theoretically expected segregations.

SSR analysis. Once the chromosomal location of the AFLP markers associated with leaf rust resistance was established, the SSR markers *Xgwm146*, *Xgwm344*, *Xwmc276*, and *Xwmc273*, located on the long arm of chromosome 7B, were mapped in the Atil C2000 × Llaleta INIA population. In addition, *Xwmc273*, described by Somers et al. (45), was genotyped in the ITMI population because segregation scores were not available for this marker in the GrainGenes database. Polymerase chain reactions (PCRs) were performed according to protocols available from CIMMYT (3); the PCR program used depended on the optimal annealing temperature for each primer. Amplification products were separated on either 3% agarose gels with two parts SeaKem to three parts MetaPhor agarose, or 8% acrylamide (29:1) gels, depending on the nature of the polymorphisms observed. Visualization of the amplification products was done on agarose gels with ethidium bromide and with silver staining for acrylamide gels (3).

RESULTS AND DISCUSSION

Bulked segregant analysis was conducted with 96 AFLP primer combinations. Three markers, *P87/M67*₁₅₁, *P88/M76*₁₅₈, and *P84/M76*₂₃₄, were identified to be associated with the leaf rust resistance gene present in the Atil C2000 × Llareta INIA population (Fig. 1). Based on the phenotypic and molecular data of 93 F₃ families from the Atil C2000 × Llareta INIA population (including the segregating families originating from heterozygous F₂ plants), *P87/M67*₁₅₁ was completely linked in repulsion to the leaf rust resistance gene, displaying a dominant nature of inheritance (Table 1). *P88/M76*₁₅₈ was located at a distance of 13 centimorgans (cM) from the resistance gene but showed the same pattern of inheritance as *P87/M67*₁₅₁ (a dominant band linked in repulsion). In contrast to the above markers, *P84/M76*₂₃₄ was associated with the resistance gene in coupling, at a distance of 4.2 cM.

All three AFLP markers were polymorphic in common wheat parents Opata C85 and Synthetic W-7984; hence, all of them could be mapped using the ITMI population (Fig. 2). Mapping conducted with the three markers, along with scoring data of markers available at the GrainGenes website, established the chromosomal location of the three markers on the long arm of chromosome 7BL (Fig. 2). Consequently, the single, completely dominant, leaf rust resistance gene identified in Llareta INIA by Herrera-Foessel et al. (10) was located on 7BL.

The SSR markers *Xwmc276-7B*, *Xgwm344-7B*, and *Xgwm146-7B* positioned in 7BL were polymorphic in the Atil C2000 × Llareta INIA population and, therefore, used for establishing their position with respect to the leaf rust resistance gene (Fig. 1). The SSR marker *Xwmc273-7B* (45) was polymorphic in ITMI, as well as the durum population and, therefore,

Fig. 1. Distance in centimorgans between amplified fragment length polymorphism and simple sequence repeat markers linked to the leaf rust resistance gene *LrLla* (*Lr14a*) using the molecular and phenotypic responses of 98 Atil C2000 × Llareta INIA F₃ families.

Table 1. Number of present band for each identified marker associated to the leaf rust resistance gene on the entire Atil C2000 × Llareta INIA F₃ population (98 lines)^a

Marker	Phase ^b	Homozygous susceptible (25 lines)	Segregating (48 lines)	Homozygous resistant (25 lines)
<i>P87/M67</i> ₁₅₁	Repulsion	25	47 (1 ND)	0 (4 ND)
<i>P88/M76</i> ₁₅₈	Repulsion	24	44 (1 ND)	5
<i>P84/M76</i> ₂₃₄	Coupling	2	48	25
<i>Xwmc273-7B</i>	Repulsion	24	44	5
<i>Xwmc276-7B</i>	Repulsion	20 (3 ND)	39	5
<i>Xgwm344-7B</i>	Coupling	1 (1 ND)	48	25
<i>Xgwm146-7B</i>	Coupling	3 (1 ND)	45 (1 ND)	25

^a ND = no data.

^b Repulsion = band present in the susceptible parent Atil C2000 and in the homozygous susceptible lines, as well as in the segregating lines, of the F₃ population; and Coupling = band present in the resistant parent Llareta INIA and in the homozygous resistant lines, as well as in the segregating lines, of the F₃ population.

Fig. 2. Chromosome arm 7BL linkage map for simple sequence repeat, amplified fragment length polymorphism, and other markers associated with leaf resistance gene *Lr14a* based on the hexaploid Opata 85 × Synthetic International Triticeae Mapping Initiative mapping population. Markers identified to be associated to the leaf rust resistance gene in the durum population (Atil C2000 × Llareta INIA) are underlined.

included in both maps (Figs. 1 and 2). The SSR marker *Xgwm344-7B* was most closely linked to the leaf rust resistance gene in Llaraeta INIA, at a distance of 1 cM (Fig. 1). Marker *Xgwm146-7B* was located at 7.5 cM from the resistance gene, whereas other SSR markers were located further away. The three AFLP markers and the four SSR markers associated with the leaf rust resistance gene in the durum population (Fig. 1) conformed to the expected ratio of 3:1 ($P = 0.09$ to 0.91). The four SSR markers *Xwmc273-7B*, *Xwmc276-7B*, *Xgwm344-7B*, and *Xgwm146-7B* were dominant in nature. The AFLP marker *P87/M67₁₅₁* and SSR markers *Xwmc273-7B* and *Xwmc276-7B* were linked to the resistance gene in repulsion (Table 1). Markers *Xgwm344-7B* and *Xgwm146-7B* were linked to the resistance gene in coupling in a similar way as the AFLP marker *P84/M76₂₃₄*.

In the ITMI population, the AFLP marker *P84/M76₂₃₄* and the SSR marker *Xwmc273-7B* conformed to the expected ratio of 1:1 ($P = 0.62$). However, the segregation of *P88/M76₁₅₈* was barely acceptable at the 1% probability level ($P = 0.012$), and *P87/M67₁₅₁* showed a distorted segregation in the ITMI population ($P = 0.001$). The distorted segregation of the AFLP marker *P87/M67₁₅₁* that co-segregated with the leaf rust resistance gene probably explains why, on the ITMI map, this marker was positioned at a distance from the other markers, *Xgwm344-7B*, *P84/M76₂₃₄*, and *Xgwm146-7B*, which were closely linked to the resistance gene. Due to this distorted segregation, we believe that the position in 7BL, according to the ITMI genetic map (Fig. 2), was better defined by markers *Xgwm344-7B*, *P84/M76₂₃₄*, and *Xgwm146-7B*.

Positions of the molecular markers were in agreement with the position of the known leaf rust resistance gene *Lr14a*, previously reported in common wheat. Therefore, we tested common wheat Thatcher and the near-isogenic line with *Lr14a* (RL6013) and durum wheat lines Altar C84 and Altar C84+*Lr14a* with markers identified to be associated with the leaf rust resistance gene in Llaraeta

INIA (Table 2). Both RL6013 and Altar C84+*Lr14a* displayed a mesothetic response 'X' in seedlings to the Mexican *P. trititica* race BBG/BN in the greenhouse that was similar to that of Llaraeta INIA. Altar C84+*Lr14a* also was reported to display a near immune response similar to that of Llaraeta INIA in the field by Huerta-Espino et al. (12).

The AFLP marker *P87/M67₁₅₁*, found co-segregating with the leaf rust resistance gene in Llaraeta INIA, did not produce clear results in the differential set carrying *Lr14a* and in Altar+*Lr14a* and their respective controls. However, markers *Xgwm344-7B* and *P84/M76₂₃₄*, closely linked to the resistance gene, clearly discriminated genotypes that varied for *Lr14a*. It is interesting to note that only the markers linked in coupling were able to discriminate lines carrying *Lr14a* (Table 2). The utility of *Xgwm344-7B*, the most closely linked SSR, as a diagnostic marker for assisting durum wheat breeding in the future should be investigated by an allelic diversity study.

In durum wheat, *Xgwm344-7B* is reported to be associated with yellow pigment kernel content in cv. Omrabi 5 (7). Omrabi 5 was developed from a cross between Haurani and Jori C69 (7). Interestingly, Mexican cv. Jori C69 also is present in the pedigree of Llaraeta INIA (10,38). Ortiz et al. (36) identified a recessive leaf rust resistance gene in Jori C69 and a recessive stem rust resistance gene. However, Jori C69 is moderately susceptible to *P. trititica* race BBG/BN (J. Huerta-Espino, unpublished), which excludes the possibility of those resistance genes being *Lr14a* and *Sr17*, respectively. The origin of *Lr14a* in durum wheat cannot be traced back to any common wheat cultivar because neither Llaraeta INIA nor Somateria, which carry the same gene (10), seem to have any common wheat in their pedigrees (10,38). *Lr14a* also is not widely present in durum wheat cultivars, given that a large proportion of CIMMYT durum wheat germplasm and cultivars of diverse origins were found to be susceptible to Mexican *P. trititica* race BBG/BN from durum wheat (44).

In common wheat, *Lr14a* and the linked genes *Sr17* and *Pm5* were mapped cytogenetically to chromosome 7BL in cv. Hope and related lines (18–20,27). *Lr14b* is a very closely linked gene that is catalogued as an allele of the same locus (28) despite the low frequency of recombinants reported by Dyck and Samborski (5). *Lr14b* was first detected in common wheat lines Maria Escobar and Bowie and gives the same type of reaction as *Lr14a*, but to different races (5). Virulence against *Lr14b* is common among *P. trititica* races from durum wheat, including Mexican races BBG/BN and BBB/BN (44).

Lr14a also was mapped in common wheat in additional studies. Koebner et al. (16) mapped *Lr14a* at a distance of 9.6 cM from endopeptidase isozyme *Ep-B1* in 7BL. Chao et al. (2) developed RFLP-based genetic maps of group 7 and established the association between *Lr14a* and RFLP *Xpsr121(Glb3)*. *Lr14a* was mapped at 22 to 36 cM distal to the *Pm5* locus (2,27,28) and at 18 cM from *Sr17* (27). Li et al. (21) detected a cluster of defense response genes, *Tha1*, *Tha2*, *Cht1b*, *Cat*, and *Grp94*, in the same region of the long arm of chromosome 7B. Several of these defense response genes were included in the same linkage group that was generated in the ITMI population (Fig. 2).

Because virulence to *Lr14a* is very common in *P. trititica* races from common wheat, this gene is not considered valuable in common wheat (28,37). The predominant *P. trititica* races collected from durum wheat in Mexico, the United States, and Spain are avirulent to *Lr14a* (34) and, as found for *Lr3* (9), *Lr14a* also can be considered a valuable source of resistance in durum wheat in these countries. Although *Lr14a* confers a similar mesothetic seedling infection type 'X' to '3C' in both durum and common wheat, in the field this gene confers near immunity to avirulent Mexican durum wheat races BBG/BN and BBB/BN. However, Ordóñez and Kolmer (34) reported virulence to *Lr14a* among certain *P. trititica* isolates from durum wheat collected in Argentina, France, and Ethiopia. Therefore, the resistance gene *Lr14a* should be used with caution. In addition, Ordóñez and Kolmer (34) reported virulence to *Lr14a* in some Chilean durum *P. trititica* isolates, which should be further investigated, given that Llaraeta INIA continues to be highly resistant in Chile (I. Matus, personal communication). The leaf rust resistance of the Mexican durum wheat cv. Samayoa C2004 from the cross Inter × Somateria could be due to *Lr14a*, given that our present study found that Somateria carries *Lr14a*. One of the reasons why *P. trititica* races from common wheat continue to be avirulent on durum wheat in Mexico and other countries could be the presence of an unknown resistance gene which, in 2001, became ineffective to race BBG/BN in Mexico

Table 2. Genotype characterization of durum wheat cvs. Atil C2000, Llaraeta INIA, Altar C84, and Altar C84+*Lr14a* and common wheat cvs. Thatcher and its near-isogenic line with *Lr14a* (RL6013) for molecular markers associated with the leaf rust resistance gene present in Llaraeta INIA^a

Genotype ^b	<i>Lr14a</i>	<i>Xwmc276-7B</i>	<i>Xwmc273-7B</i>	<i>Xgwm344-7B</i>	<i>Xgwm146-7B</i>
Atil C2000	–	–	–	–	–
Altar C84	–	–	–	–	–
Thatcher	–	+	+	–	–
Llaraeta INIA	+	+	+	+	+
RL6013	+	+	+	+	+
Altar C84+ <i>Lr14a</i>	+	+	+	+	+

^a Simple sequence repeat markers *Xgwm344* and *Xgwm146* are dominant markers linked in coupling with the leaf rust resistance gene in Llaraeta INIA, whereas *Xwmc276* and *Xwmc273* are dominant markers linked in repulsion; – = Atil C2000 allele and + = Llaraeta INIA allele.

^b Atil C2000, Altar C84, and Thatcher are susceptible, and Llaraeta INIA, Thatcher+*Lr14a*, and Altar C84+*Lr14a* are resistant to the Mexican *Puccinia trititica* race BBG/BN.

(44) and is present in very high frequency in CIMMYT durum wheat lines. To reduce genetic vulnerability of durum wheat to leaf rust, *Lr14a* should be used in combination with other effective leaf rust resistance genes.

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