Genetic diversity for leaf rust resistance in durum wheat (Triticum durum)

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ABSTRACT: Studies were undertaken to find out the inheritance and extent of diversity for leaf rust resistance at seedling stage in four durum wheat (Triticum durum Desf.) genotypes using Puccinia triticina pathotype 12-5 (29R45). The F2 and F3 analyses showed that resistance was controlled by one dominant gene each in durum genotypes ‘HD 4672’ and ‘RS 749’, and by two dominant genes each in ‘MPO 615’ and ‘Raj 6562’. Allelic tests revealed that these genes were different from each other, except one common between ‘MPO 615’ and ‘RS 749’. Thus, a total of five diverse genes for leaf rust resistance were identified among the four genotypes. The identity of the genes is not known. However, they should be different from Lr23 which is common in Indian durum germplasm; and also from Lr3, Lr14a, Lr27+Lr31, and Lr72 among Lr genes reported in durum wheat, since pathotype 12-5 (29R45) is virulent to all these genes. These genotypes can contribute towards enriching diversity for leaf rust resistance in durum wheat improvement.

Key words: Leaf rust resistance, genetic diversity, Triticum turgidum ssp. durum, Puccinia triticina, Lr genes

India produces more than 90 million tonnes of wheat from 25 million ha. but contribution of durum wheat (Triticum durum Desf.) is about 5%. However, durum wheat has a special niche in Indian wheat economy. Durum wheat is mainly grown in central and southern parts of India, where leaf rust is one of the major diseases. Broadening of resistance base through utilization of genetically diverse resistance sources is necessary for enhancing the durability of resistance in view of the continued evolution of leaf rust pathogen (Puccinia triticina). Relatively little work has been done on inheritance of rust resistance in durum wheat, compared to bread wheat. However, durum wheat generally showed resistance to leaf rust pathotypes virulent to bread wheat, and vice versa (Paradies, 1980; Casulli et al., 1983; Pandey and Rao, 1984; Sharma et al., 1986; Huerta-Espino and Roelfs, 1992; Singh et al., 1992; Honrao and Rao 1996; Sharma et al., 1996; Mishra et al., 2001a,b; Singh et al., 2004; Mishra et al., 2009). The inheritance and extent of diversity for seedling resistance to leaf rust pathotype 12-5 (29R45) were studied in four durum genotypes, viz. ‘HD 4672’, ‘MPO 615’, ‘Raj 6562’ and ‘RS 749’ which showed seedling resistance to all the 40 leaf rust pathotypes tested (Mishra et al., 2011). Hence, studies were undertaken to evaluate genetic diversity for leaf rust resistance in durum wheat.

MATERIALS AND METHODS

Four resistant durum genotypes, viz. ‘HD 4672’, ‘MPO 615’, ‘Raj 6562’ and ‘RS 749’ were crossed among themselves, and with susceptible durum land race Local Red which served as female parental line. The parents, F1s, F2 populations and F3 families were tested at seedling stage with leaf rust pathotype 12-5 (29R45). This pathotype was chosen for study as it showed high degree of virulence to durum wheat genotypes (Bhardwaj et al., 2005; Mishra et al., 2009). Its avirulence (P) virulence (p) formula based on seedling tests is as follows (Bhardwaj et al., 2006):

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P = 12(29R45) / Lr_{P} \\
p = 12(29R45) / Lr_{p}
\]

Seedling tests were conducted in a glasshouse at 20-22°C ± 2°C using standard glasshouse procedures (Roelfs et al., 1992). The test seedlings were raised in 10 cm clay pots. Seedlings with primary leaf fully expanded and second leaf just emerged (generally 8-10 days old) were spray inoculated with aqueous suspension of uredospores of the test pathotype, freshly collected from the actively sporulating leaves of ‘Agra Local’ maintained in isolation in glasshouse. Agra Local served as ‘susceptible check’. Inoculated plants in pots were incubated in moist chambers for 16-24 h, and were then transferred to glasshouse benches. Infection types (ITs) on seedlings were recorded 12-15 days after inoculation on a 0-4 scale. The Infection Types (ITs) ‘3’, ‘3+’, and ‘34’ produced on a host line indicated latter’s susceptibility to test pathotype, whereas lower ITs indicated resistance (Roelfs et al., 1992).

The F2 plants were grouped into ‘resistant’ (R) and ‘susceptible’ (S) classes to determine the F2 ratios. The F3 families were classified as homozygous resistant (HR), segregating (SEG), or homozygous susceptible (HS), based on the presence of exclusively resistant plants, both resistant and susceptible plants, and exclusively
susceptible plants, respectively. The chi-square test was used to test the goodness-of-fit of observed F2 and F3 ratios to the expected ones on the basis of Mendelian segregation.

RESULTS AND DISCUSSION

The F1s from all of the ‘susceptible parent/resistant parent’ crosses were almost as resistant as the resistant parent, indicating dominant inheritance of seedling resistance to leaf rust pathotype 12-5 (Table 1). A single dominant resistance gene was identified in HD 4672, and in RS 749 [15R:1S F2 plants (P=0.30, 0.25); 7HR:8SEG:1HS F3 families (P=0.63, 0.34)] (Table 2). Two independent dominant genes each conditioned resistance in MPO 615, and in Raj 6562 [15R:1S F2 plants (P=0.30, 0.25); 7HR:8SEG:1HS F3 families (P=0.63, 0.34)] (Table 2). Among resistant parents inter-crosses, no susceptible segregants were observed in F2 population derived from the MPO 615/RS 749 cross (Table 3), showing that one of the genes in MPO 615 was common with that of RS 749. The remaining resistant parent/resistant parent crosses showed F2 segregation for expected ratio of 15R:1S, 63R:1S or 255R:1S (Table 3) based on the inheritance respectively of two, three, or four independent dominant genes, showing that the genes involved were different from each other. Thus, a total of five diverse dominant genes were identified for seedling resistance to the leaf rust pathotype 12-5 among the four durum genotypes studied.

In all, 72 leaf rust resistance genes have so far been catalogued and mapped to chromosome location in wheat (McIntosh et al., 2013; Herrera-Foessel et al., 2014). Only Lr14a derived from Triticum turgidum subsp. dicoccum cv. Yaroslav and Lr23 derived from Triticum turgidum subsp. durum cv. Gaja were known to be of tetraploid (AABB genomes) origin (McIntosh et al., 1995). The gene Lr23 is long known to occur in CIMMYT durum cultivar Altar C84 (Nelson et al., 1997). Presence of Lr14a in any durum lines (Chilean durum cultivar Llareta INIA and CIMMYT derived durum Somateria) was reported later (Herrera-Foessel et al., 2008a). Linked markers suggested that Lr14a has been present in about 95% CIMMYT lines developed since 2001 (Loladze et al., 2014). The gene Lr23 has commonly been postulated in Indian durum germplasm through comparison of seedling infection types with lines carrying known Lr genes (Nayar et al., 2001; Bhardwaj et al., 2013). However, leaf rust resistance genes identified in present study should be different from Lr23 and Lr14a as both of them are ineffective against the test pathotype 12-5. Some Lr genes known to be present in bread wheat like Lr3 (Herrera-Foessel et al., 2007), and Lr27 + Lr31 (Huerta-

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**Table 1.** Infection types (ITs) of the parental lines and their F1s in response to seedling tests with leaf rust pathotype 12-5 (29R45)  

<table>
<thead>
<tr>
<th>Wheat genotypes and the respective F1s</th>
<th>Seeding ITs</th>
</tr>
</thead>
<tbody>
<tr>
<td>HD 4672, Local Red/HD 4672</td>
<td>‘22’C’, ‘23’C’</td>
</tr>
<tr>
<td>MPO 615, Local Red/MPO 615</td>
<td>‘0’, ‘0;1’</td>
</tr>
<tr>
<td>Raj 6562, Local Red/Raj 6562</td>
<td>‘1;1’, ‘2’</td>
</tr>
<tr>
<td>RS 749, Local Red/RS 749</td>
<td>‘1;1’, ‘2’</td>
</tr>
<tr>
<td>Local Red, Agra Local (check)</td>
<td>‘34’, ‘34’</td>
</tr>
</tbody>
</table>

ITs on 0-4 scale; IT ‘34’ indicates susceptibility, others indicate resistance  
C = pronounced chlorosis

**Table 2.** Segregation for seedling resistance to leaf rust pathotype 12-5 (29R45) in F2 plants and F3 families derived from crosses of resistant parents with susceptible parent ‘Local Red’ (‘LR’)

<table>
<thead>
<tr>
<th>Cross</th>
<th>Number of F2 plants</th>
<th>Number of F3 families</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>R</td>
<td>S</td>
</tr>
<tr>
<td>HD 4672/RS 749</td>
<td>480</td>
<td>9</td>
</tr>
<tr>
<td>HD 4672/Raj 6562</td>
<td>475</td>
<td>11</td>
</tr>
<tr>
<td>HD 4672/RS 749</td>
<td>492</td>
<td>30</td>
</tr>
<tr>
<td>MPO 615/Raj 6562</td>
<td>618</td>
<td>2</td>
</tr>
<tr>
<td>MPO 615/RS 749</td>
<td>1036</td>
<td>0</td>
</tr>
<tr>
<td>Raj 6562/RS 749</td>
<td>563</td>
<td>4</td>
</tr>
</tbody>
</table>

R = Resistant, S = Susceptible  
HR = Homozygous resistant, SEG = Segregating, HS = Homozygous susceptible

**Table 3.** Segregation for seedling resistance to leaf rust pathotype 12-5 (29R45) in F2 populations derived from inter-crosses of resistant parents

<table>
<thead>
<tr>
<th>Cross</th>
<th>R</th>
<th>S</th>
<th>$\chi^2$</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>HD 4672/MPO 615</td>
<td>480</td>
<td>9</td>
<td>0.25 (63R:1S)</td>
<td>0.62</td>
</tr>
<tr>
<td>HD 4672/Raj 6562</td>
<td>475</td>
<td>11</td>
<td>1.56 (63R:1S)</td>
<td>0.21</td>
</tr>
<tr>
<td>HD 4672/RS 749</td>
<td>492</td>
<td>30</td>
<td>0.22 (15R:1S)</td>
<td>0.63</td>
</tr>
<tr>
<td>MPO 615/Raj 6562</td>
<td>618</td>
<td>2</td>
<td>0.07 (255R:1S)</td>
<td>0.79</td>
</tr>
<tr>
<td>MPO 615/RS 749</td>
<td>1036</td>
<td>0</td>
<td>16.45 (63R:1S)</td>
<td>0.00005</td>
</tr>
<tr>
<td>Raj 6562/RS 749</td>
<td>563</td>
<td>4</td>
<td>2.71 (63R:1S)</td>
<td>0.10</td>
</tr>
</tbody>
</table>

R = Resistant, S = Susceptible
Espino et al., 2009) were also found in durum wheat. Presence of recently designated gene Lr72 was confirmed in Mexican durum cultivars Atli C2000 and Altar C84 (Herrera-Foessel et al., 2014). The presently identified genes should be different from all of these genes as well since pathotype 12-5 showed virulence to Lr3, Lr27+Lr31, and Altar 84 (Bhardwaj et al., 2006). Resistance in Australian durum cultivar Wollaroi (Singh et al., 2010) and Italian durum Trinakria (Gireesh et al., 2014) was controlled by a dominant gene each which was thought to be Lr52 or its allele or a closely linked gene. A partially dominant leaf rust resistance gene mapped to the chromosome arm 6BS in Chilean durum Guayacan INIA and its sister line Guayacan 2 was named Lr61 (Herrera-Foessel et al., 2008b). While ‘Trinakria’ showed seedling resistance to pathotype 12-5 (Mishra et al., 2011; Gireesh et al., 2014), ‘Wollaroi’ and lines carrying Lr61 have not been tested with Indian leaf rust pathotypes. Allelic relationship of the gene(s) present in ‘Trinakria’ / ‘Wollaroi’, and of Lr61 with the identified genes is not known. Leaf rust resistance genes identified in the present study need to be characterized. However, reported genotypes can meanwhile be utilized for enriching diversity for leaf rust resistance in durum wheat improvement programme.

ACKNOWLEDGEMENTS

Receipt of the rust inoculum from Directorate of Wheat Research, Regional Station, Flowerdale, Shimla, is gratefully acknowledged. We thank the Director, ICAR-Indian Agricultural Research Institute, New Delhi, for providing facilities.

REFERENCES


Received for publication: December 22, 2014
Accepted for publication: April 27, 2015