Genetics of rust resistance in the Australian wheat germplasm

Shankar M1, McLean R1, Cakir M2, Gotzar H1, Bariana H1 and Loughman R1

1 Department of Agriculture and Food, 3 Baron-Hay Court, South Perth, WA 6151, Australia. 2 WA State Agricultural Biotechnology Centre, Murdoch University, Murdoch, WA 6150, Australia. 3 The University of Sydney Plant Breeding Institute-Cobbitty, PMB11 NSW 2750, Australia

ABSTRACT

F2 and F2:3 populations targeting leaf rust resistance genes (Lr13, Lr21, Lr28) and stem rust resistance genes (Sr32 and Sr33) were phenotyped for seedling resistance. In populations targeting Lr13 (Leichardt/WAWHT2071), Lr21 (Tincurrin+Lr21/EGA2248) and Lr28 (Sunland/Arrino), parents Leichardt, Tincurrin+Lr21 and Sunland were resistant (R) while parents WAWHT2071, EGA 2248 and Arrino were susceptible (S) to leaf rust. F2 progeny in crosses Leichardt/WAWHT2071 and Sunland/Arrino showed a 3R:1S segregation ratio ($\chi^2 = 0.3$ and 1.3; $P = 0.6$ and 0.3) while F2 families segregated as 1:2:1 (true breeding R (TR): segregating (seg): true breeding S (TS)) ($\chi^2 = 1.8$ and 1.0; $P = 0.4$ and 0.6) indicating the single dominant nature of Lr13 and Lr28. Population Tincurrin+Lr21/EGA 2248 targeting Lr21 showed a 13R:3S F2 segregation ($\chi^2 = 0.4$; $P = 0.5$) indicating the presence of one dominant and one recessive independent genes. The hypothesis was confirmed in F3 where families arising from resistant F2 plants segregated in a ratio of 7:6 (TR:seg) while families from susceptible F2 plants were all true breeding susceptible ($\chi^2 = 1.4$; $P = 0.5$). In populations targeting Sr32 and Sr33 parents C77.19/3*77W:549-163658 and Sr33/2*Shortim//4*Jacup//3/Calingiri were used as the sources of resistance, respectively, while parents WAWHT2046 and Calingiri were susceptible to stem rust. The F2 progeny in both crosses segregated into a 3R:1S ratio ($\chi^2 = 0.1$ and 3.3; $P = 0.8$ and 0.1) and the F3 families showed a segregation of 1:2:1 (TR:seg:TS ) ($\chi^2 = 5.5$ and 1.2; $P = 0.1$ and 0.6) indicating the single dominant nature of Sr32 and Sr33.

INTRODUCTION

Resistance to stem rust (Puccinia graminis Pers. f. sp. Triticum Eriks. & E. Henn.) and leaf rust (Puccinia recondita Rob. ex Desm. f. sp. tritici Eriks. & Henn.; Prt) is of high priority in the InterGrain wheat (Triticum aestivum L.) breeding program. Breeding for durable resistance against these diseases is based on the combination of different resistance genes in one cultivar (Van Ginkel and Rajaram, 1993). The selection of genotypes containing several rust resistance genes using infection with rust isolates with defined avirulence genes is very time-consuming. The development of molecular markers for specific genes allows the detection of these genes independently of the phenotype. Detailed genetic knowledge increases the efficiency of development of molecular markers which can be used in marker-assisted selection for an efficient combination of genes in the pyramiding strategy to create a more durable resistance (Roelfs et al., 1992).

The objectives of this study were genetic analysis of F2 and F2:3 breeding populations for leaf rust and stem rust resistance and provision of phenotypic data for the development and validation of molecular markers linked to known rust resistance genes in the Australian germplasm.

MATERIALS AND METHODS

F2 and F2:3 populations were developed from the following crosses:

(a) Leichardt/WAWHT2071 for targeting leaf rust resistance gene Lr13
(b) Tincurrin+Lr21/EGA2248 for targeting leaf rust resistance gene Lr21
(c) Sunland/Arrino for targeting leaf rust resistance gene Lr28
(d) C77.19/3*77W:549-163658//WAWHT2046 for targeting stem rust resistance gene Sr32
(e) Sr33(R.L.5405)/2*Shortim//4*Jacup/3/Calingiri for targeting stem rust resistance gene Sr33

Generation and management of plant material. Ninety four lines from each F2 population and parental lines were grown in a glasshouse with 22/18°C day/night temperatures and natural lighting in 96-cell trays containing a sand-loam mix with 1 g of Osmocote (slow release fertiliser). A single seed was planted per cell. A set of susceptible and resistant lines were included with each experimental set as controls.

Inoculation and scoring. Plants were inoculated at the two-and-a-half-leaf stage with a spore suspension of urediniospores in paraffin oil using an air brush. For crosses targeting leaf rust resistance genes Lr13 and Lr21 and Lr28 urediniospore suspension of P. recondita f.sp. tritici pathotype 104-1,2,3,(6),(7),11 +Lr37 was used while for crosses targetting stem rust resistance genes Sr32 and Sr33 urediniospore suspension of P. graminis f.sp. tritici pathotype 98-1,2,3,5,6,7 was used. Inoculated plants were placed in a humid chamber at 22°C for 48 hours for establishment of infection. Disease was assessed 12 to 14 days after inoculation using a 0 to 4 scale (McIntosh et al. 1995), where a scores of 0, 1 and 2 was classified as resistant (R) and 3 and 4 as susceptible (S). Infection type 3n (pustule accompanied by necrosis) was also classified as R.
Plants were grown to maturity and single heads harvested from each F2 plant. Twelve F2:3 seed per family were sown in 10-cm pots, inoculated and assessed as described above. Segregation of resistance alleles in the F2 and F2:3 was analysed by comparing the observed ratio of resistant:susceptible with the expected ratio by the chi-square method (Snedecor and Cochran, 1967).

RESULTS AND DISCUSSION

In populations targeting Lr13 (Leichardt/WAWHT2071), Lr21 (Tincurin+Lr21/EGA2248) and Lr28 (Sunland/Arrino), parents Leichardt, Tincurin+Lr21 and Sunland were resistant (R) while parents WAWHT2071, EGA2248 and Arrino were susceptible (S) to leaf rust. F2 progeny in crosses Leichardt/WAWHT2071 and Sunland/Arrino showed a 3R:1S segregation ratio ($\chi^2 = 0.3$ and 1.3; $P = 0.6$ and 0.3) (Table 1) while F3 families segregated as 1:2:1 (true breeding R (TR): segregating (seg): true breeding S (TS)) ($\chi^2 = 1.8$ and 1.0; $P = 0.4$ and 0.6) indicating the single dominant nature of Lr13 and Lr28. However, in concurrent studies conducted on F2 populations Strzelecki/WAWHT2454 and EGA Gregory/Ajana where the resistant parents Strzelecki and EGA Gregory are known to carry Lr21, Lr23, Lr28 and Sr33 (Cakir et al. 1997) it appears recessive with a 1R:3S reaction observed in both populations. For 196 F2 individuals of Strzelecki/WAWHT2454 chi square was 1.9 and p value 0.17 while for 196 F3 individuals of EGA Gregory/Ajana chi square was 0.5 and p value 0.5. Although, Lr23 is not effective against 104-1,2,3,(6),(7),11 +Lr37 it appears that it has some sort of an epistatic effect on +Lr37 it appears recessive with a 1R:3S reaction observed in both populations. For 196 F2 individuals of Leichardt/WAWHT2071 and Sunland/Arrino showed a 3R:1S segregation ratio ($\chi^2 = 0.1$ and 0.8; $P = 0.8$ and 0.1) (Table 1) and the F3 families showed a segregation of 1:2:1 (TR:seg:TS ) ($\chi^2 = 5.5$ and 1.2; $P = 0.1$ and 0.6) indicating the single dominant nature of Sr32 and Sr33.

Phenotypic leaf rust and stem rust data of the above populations was used to develop closely linked markers to genes Lr13, Lr21, Lr28, Sr32 and Sr33 (Cakir et al. this conference). These markers are currently being implemented in the InterGrain wheat breeding program.

Table 1. Frequency distribution of F2 and F3 generations of various crosses targeting leaf rust and stem rust resistance genes.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Gene</th>
<th>Generation</th>
<th>Segregation Ratio</th>
<th>$\chi^2$</th>
<th>$P$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leichardt/ WAWHT2071</td>
<td>Lr13</td>
<td>F2</td>
<td>3R : 1S</td>
<td>0.3</td>
<td>0.6</td>
</tr>
<tr>
<td>F3</td>
<td>1TR : 2seg : 1TS</td>
<td>1.8</td>
<td>0.4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tincurin+Lr21/ EGA2248</td>
<td>Lr21</td>
<td>F2</td>
<td>13R : 3S</td>
<td>0.3</td>
<td>0.6</td>
</tr>
<tr>
<td>F3</td>
<td>7TR : 6Seg : 3TS</td>
<td>1.4</td>
<td>0.5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sunland/Arrino</td>
<td>Lr28</td>
<td>F2</td>
<td>3R : 1S</td>
<td>1.3</td>
<td>0.3</td>
</tr>
<tr>
<td>F3</td>
<td>1TR : 2seg : 1TS</td>
<td>1.0</td>
<td>0.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C77.19/3*77W:549-163658</td>
<td>Sr32</td>
<td>F2</td>
<td>3R : 1S</td>
<td>0.1</td>
<td>0.8</td>
</tr>
<tr>
<td>F3</td>
<td>1TR : 2seg : 1TS</td>
<td>5.5</td>
<td>0.1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sr33(R.L.5405)/ 2*Shortim</td>
<td>Sr33</td>
<td>F3</td>
<td>3R : 1S</td>
<td>3.3</td>
<td>0.1</td>
</tr>
<tr>
<td>F3</td>
<td>1TR : 2seg : 1TS</td>
<td>1.2</td>
<td>0.6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

1R = resistant; 5S = susceptible; TR = true breeding resistant; seg = segregating; TS = true breeding susceptible

ACKNOWLEDGEMENTS

Funding for this research was provided by GRDC (Grains Research and Development Corporation) through Australian Winter Cereal Molecular Marker Program, and Molecular Plant Breeding CRC.

REFERENCES


