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Short Communication

Inheritance of resistance to leaf rust (*Puccinia recondita* f. sp. *tritici*) in two *durum* wheat lines

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Durum wheat (*Triticum durum* desf.) in India is grown in large area under rainfed as well as irrigated conditions. Brown rust (*Puccinia recondita* Rob.Erikss. & E. Henn. ex. Desm. f. sp. *tritici*) of wheat is widely distributed and pathotype 77 group is considered as the most virulent knocking down the resistance of several bread wheat genotypes. Greater proportion of durum wheat varieties have been found resistant to race 77 [1-2]. The present study was to investigate the inheritance of resistance to most virulent pathotype 77-5 (121 R63-1) in two durum wheat varieties *viz.* CPAN 6051 and Malavika (HD 4502).

Two durum wheat varieties resistant to leaf rust *viz.*, CPAN 6051 and HD 4502 (Malavika) were selected. Of these, Malavika is a released variety and CPAN 6051 is a genetic stock from the CIMMYT programme with good resistance to leaf rust. These were crossed to Gulab, a susceptible variety to raise F_1, F_2 and F_3 populations for study. The parents, F_1, F_2 and F_3 populations were tested with highly virulent pathotype 77-5 (121 R 63-1) at seedling stage. Leaf rust pathotype was obtained from DWR Research station, Shimla. A set of isogenic lines for specific *Lr* genes and standard differentials was also tested to know the virulence pattern on leaf rust resistance genes identified so far.

All tests were carried in a controlled chamber maintained at 20°C±1°C with a 18 hr. day length supplied by Fluorescent lamps and a relative humidity of 70-80 per cent. Primary leaves were inoculated with spore suspension 7 days after planting and infections were recorded after 12 days as suggested [3] suitably modified for leaf rust. Infection types 0, ;, 1 and 2 were considered as resistant and 3 and 4 as susceptible. Chi-square test was used to compare the actual segregation with the proposed theoretical ratios.

Results of isogenic lines (differentials) showed following avirulance virulence formulae in seedling stage: PLr9, 18, 19, 21, 24, 25, 28, 29, 32/pLr1, 2, 3, 10, 11, 12, 13, 14, 15, 16, 17, 20, 22, 23, 26, 27 + 31, 30, 33, 34. Reaction of F_1s obtained from crosses Gulab × HD 4502 and Gulab × CPAN 6051 showed susceptibility and moderate resistance against pathotype 77-5 (121R 63-1), respectively suggesting that resistance of HD 4502 was recessive and CPAN 6051 was partially dominant.

The segregation of plants in F_1, F_2 and F_3 families of two crosses when tested with highly virulent pathotype 77-5 (121 R 63-1) is given in Table 1. Resistance of Malavika (HD 4502) was recessive for race 77-5 (121 R 63-1) whereas that of CPAN 6051 F_1 at seedling stage was partially dominant for race 77-5.

The F_2 plants from the cross Gulab/HD 4502 (Malavika) segregated 138 resistant and 457 susceptible seedlings. The segregation is a good fit to a 1:3 ratio (χ^2 = 1.028, P = 0.30-0.20) suggesting one recessive gene for resistance in Malavika.

Table 1. Reaction of F_1, F_2 plants and F_3 generations against leaf rust pathotype 77-5 (121 R63-1)

Combinations	Generation	No. of Plants/families			Total	Ratio	χ^2	P value
		Resistant	Segregating	Susceptible				
Gulab/HD 4502	F_1	0	0	10	10			
	F_2	138	0	457	595	1:3	1.028	0.30-0.20
(Malavika)	F_3	15	46	19	80	1:2:1	1.66	0.30-0.20
Gulab/	F_1	10	0	0	10			
CPAN 6051	F_2	395	0	76	471	13:3	2.10	0.20-0.10
	F_3	36	44	5	85	7:6:2:1	0.608	0.70-0.50

The F_3 families from this cross segregated 15 homozygous resistant (HR), families 46 segregating (Seg.) and 19 homozygous susceptible (HS) which appear to segregate 1 (HR) = 2 (Seg.):l (HS). (χ^2 = 1.66, P = 0.30-0.20). Of the segregating families, the segregations fit a (1:3) ratio (543 R : 1529 S, χ^2 = 1.60, P = 0.20-0.10) suggesting that HD 4502 carries a single recessive gene.

The F_2 population from the cross Gulab/CPAN 6051 segregated 395 resistant and 76 susceptible seedlings. The segregation is a good fit to a 13:3 ratio (χ^2 = 2:10, P = 0.10-0.20) suggesting one dominant and one recessive gene for resistance in CPAN 6051. Testing of F_3 families indicated a second gene for resistance in CPAN 6051 that was recessive. The F_3 families segregated into four classes. Out of eighty-five F_3 families from F_2 plants were segregated 36 were homozygous resistant (HR), 44 segregating (Seg.) (3R:1S or 13R:3S and 1R:3S) and 5 homozygous susceptible (HS) families. Of the 44 these segregating families, the segregation of 31 families fit a 3R:1S ratio (918R:345S, χ^2 = 3.62, P = 0.10-0.5) and 13 families the segregation fit a ratio 1 R : 3S ratio (120 R:312 S, χ^2 = 1.77, P = 0.200.10). Chi-square test indicated that the F3 families satisfactorily fit a 7:6:2:1 [7HR : 6 Seg. (3R: 1 S) and : 2 Seg. (1 R : 3S), : 1 (HS) digenic ratio for one dominant and one recessive gene. Thus, CPAN 6051 suggests to carry one dominant and one recessive gene.

Similar results ere demonstrated in earlier studies [4] where three genes out of nine were dominant and six found to be recessive. This is different from the situation in bread wheat where most of the genes are dominant. Gene *Lr23* present in the donor parent CPAN 6051 gives adult plant resistance against race 77A [5]. Malavika carried one dominant and one recessive gene for resistance to race 77 [6].

As such genes from durum wheat posses a great value, both for improvement of durum wheat as well as bread wheat, Though transfer of resistance genes from durum to bread wheat met with limited success [7-8] due to supressor genes on D genome, if a large number of sources were tested, it may be possible to identify genes that are effective at hexaploid level.

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