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Short Communication

Inheritance of stripe rust (*Puccinia striiformis* Westend) resistance in wheat (*Triticum aestivum* L.) against pathotype 46S119 from the Indian sub-continent

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Stripe rust (*Puccinia striiformis* Westend) is one of the most devastating diseases of wheat (*Triticum aestivum* L.) world wide. The disease is more destructive in temperate and cooler regions and it can cause severe damage resulting into poor tillering and shriveled grain [1]. Till 1994-95, 1BL/1RS translocation carrying *Yr9/Lr26/Sr31/Pm8* gene complex provided protection against the losses due to yellow rust in Indian subcontinent. The evolution of new pathotype 46S119 which is virulent on the gene *Yr9* has resulted in susceptibility of large number of wheats to stripe rust [2]. During last three years approximately 600 lines were screened under All India Co-ordinated Wheat Improvement Programme and only two 'Attila' lines PBW 343 and PBW 373 showed resistance against this race. As resistance in the cultivars is neutralized with the evolution of new races, breeding for resistance using diverse sources is the most effective strategy to prolong the life of newly evolved varieties. The present study was therefore, planned to examine the inheritance of stripe rust resistance against pathotype 46S119 in wheat genotype PBW 343, newly registered resistant source FLW 3 [3] and two more identified resistant sources WBM 1587 and WBM 1591.

To determine the nature and number of resistance gene(s) in the resistant cultivar PBW 343 and other three sources FLW 3 (UP 2338/China 84.40022), WBM 1587 (Milan/SHA7) and WBM 1591 (PYN/BAU// Milan), these lines were crossed with a stripe rust susceptible land race 'Kathia Local'. PBW 343 and FLW 3 were also crossed with WBM 1587 and WBM 1591 to examine the allelic relationship of their gene for resistance with those present in PBW 343 and FLW 3. Parents, F_1 and F_2 generations were tested for infection types in seedling stage against stripe rust pathotype 46S119. Seeds of each of these generations were space planted in aluminium tray (29 × 12 × 7 cm.) filled with mixture of loam soil and farm yard manure in the ratio of 3:1. Seedlings were inoculated as per procedure described by Luthra [4]. The infection types were recorded following the scale described by Stakman *et al.*, [5]. The infection types, 0;, ;, 1, 2 and X were regarded resistant and 3 to 3+ as susceptible. Chi square (χ^2) test was used to test the goodness of fit of expected ratio in segregating generations.

The seedlings of standard differential set were used to test the purity of pathotype 46S119 and avirulence/virulence of pathotype 46S119 was confirmed as *Yr1*, *Yr5*, *Yr10* /*Yr2*, *Yr2ks*, *Yr3*, *Yr4*, *Yr6*, *Yr7 Yr8*, *Yr9 Yr11*, *Yr12*, *Yr17* and *Yr18*. Parents, F_1 and F_2 generations were scored for infection types (Table 1). F_1 seedlings of the cross PBW 343 × Kathia Local showed susceptible reactions while all other crosses showed resistant reaction indicating resistance against pathotype 46S119 in PBW 343 is recessive, while resistance in FLW 3, WBM 1587 and WBM 1591 is dominant. The F_2 seedlings of the cross PBW 343 × Kathia Local segregated 46 resistant and 166 susceptible and fitted well in the expected ratio of 1R : 3S suggesting that the resistance of PBW 343 is controlled by a recessive gene. The F_2 from the cross FLW 3 × Kathia Local contained 130 resistant and 7 susceptible seedlings which gave a good fit of 15R : 1S ratio suggesting role of two dominant duplicate genes conditioning resistance in FLW 3 against stripe rust pathotype 46S119.

Crosses involving two newly identified resistant sources WBM 1587 and WBM 1591 with susceptible parent Kathia Local, segregated 134R : 121S and 124R: 108S respectively in F_2, and gave a good fit for the 9:7 ratio, indicating role of two dominant complimentary genes in controlling resistance against pathotype 46S119. Considering similar genetic nature of resistance against 46S119 in both WBM 1587 and WBM 1591, only WBM 1587 was further used for test of allelism. Test of allelism applied to test similarity of genes in

Table 1. Seedling reaction of F_1 and segregation pattern in F_2 for different crosses against stripe rust pathotype 46S119 in wheat

Cross	F_1 reaction	Number of plants in F_2 Generation			Expected ratio (R:S)	χ^2	P
		R	S	Total			
PBW 343 × Kathia Local	S	46	166	212	1 : 3	1.233	.30-.20
FLW 3 × Kathia Local	R	130	7	137	15 : 1	0.476	.50-.30
WBM 1587 × Kathia Local	R	134	121	255	9 : 7	1.289	.30-.20
WBM 1591 × Kathia Local	R	124	108	232	9 : 7	0.629	.50-.30
FLW 3 × WBM 1587	R	136	14	150	15 : 1	2.955	.10-.05
PBW 343 × WBM 1587	R	158	58	216	11 : 5	1.752	.20-.10

R = Resistant, S = Susceptible

FLW 3 and WBM 1587 showed that resistance to pathotype 46S119 in both the stocks was due to different genes. The F_2 seedlings of cross PBW 343 × WBM 1587 segregated 158R : 58S which gave a good fit ratio of 11R : 5S. This ratio further confirms that PBW 343 and WBM 1587 have different genes for resistance against stripe rust pathotype 46S119. Therefore, the present report suggests that the two newly identified resistant sources (WBM 1587 and WBM 1591) against stripe rust pathotype 46S119 carry diverse resistance genes and these may be useful in breeding programs in the Indian sub-continent.

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