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Short Communication

Genetic analysis for spot blotch (*Bipolaris sorokiniana* Sacc. In Borok. Shoem.) reaction in wheat [*Triticum aestivum* (L.) Em. Thell.]

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Wheat is the most important cereal crop after rice. India is one of the major producers of wheat and occupies second place after China in terms of area and production among wheat growing countries of the world. However, wheat crop production is constrained by a number of diseases. Among these diseases, spot blotch (*Bipolaris sorokiniana* Sacc. In Borok. Shoem.) is of increasing concern in India and other countries of South East Asia due to its wide spread prevalence and increasing severities [1]. Spot blotch may yield loss between 20 and 80 per cent [2]. Therefore, in order to stabilize the higher productivity, it is important to develop resistant varieties. The success of the resistance breeding programme lies in the sound knowledge of genetic behaviour of the resistance genes. Hence, the present investigation was carried out to obtain the estimates of gene effects in resistance varieties namely, PBW 343, PBW 373 and WH 581.

Three spot blotch resistant (WH 581, PBW 343 and PBW 373) and three susceptible (UP 2338, PBW 154 and Sonalika) genotypes of bread wheat were used. These six genotypes were crossed in half diallel fashion to develop F_1 crosses during *rabi* crop season 2001-02 and then these F_1 were advanced to F_2, B_1 and B_2 during *rabi* season, 2002-03. All the six generations (Parents, F_1, F_2, B_1 and B_2) were screened under the artificial epiphytotic conditions at Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar during *rabi* crop season, 2003-04. The experiment was laid out in Randomized Block Design (RBD) with three replications. Line to line and plant to plant distance was maintained at 23 cm and 10 cm, respectively.

A pure culture of *B. sorokiniana* was multiplied on sorghum seeds and spores were harvested in distilled water. A spore suspension of fixed concentration (10^4 spores/ml) was sprayed at 2 month old plants. Plots were irrigated immediately after inoculation to maintain relative humidity. Spot blotch severity was measured on individual plant basis and subjected to scaling test [3] to detect the presence of epistasis. In case of significance of scaling tests, data were then subjected to the estimation of various genetic components according to Jinks and Jones [4].

The estimates of A, B, C and D scaling tests and gene effects from six parameter model are presented in Table 1 and 2, respectively. It is clear from the results presented in Table 1 that all the crosses exhibited significant estimates of one or more scales, suggesting inadequacy of simple additive-dominance model. The inadequacy of additive dominance model indicate the presence of non-allelic interaction. The estimate of mean (m) was highly significant in all the crosses except Sonalika/PBW 373 and PBW 373/PBW 343. Both additive (d) and dominance (h) were significant in eight crosses only out of fifteen. This indicated predominance of both additive and dominance gene action in controlling disease reaction in these crosses. However, the remaining crosses *viz.*, UP 2338/WH 581, PBW 154/WH 581, Sonalika/WH 581 and PBW 373/WH 581 exhibited only significant additive type of interaction controlling disease reaction in these crosses. These findings are supported by Joshi *et al.* [5]. While the cross PBW 154/PBW 373 is revealing the involvement of dominance type of gene interaction. On the other hand, cross PBW 343A/VH 581 was non-significant for both additive and dominance gene effects, indicating that disease reaction in the cross does not involve additive/dominance gene effects in this crosses.

Among the non-allelic interactions, a perusal of Table 2 indicates that in the cross UP 2338/PBW 343, additive × additive (i) and additive × dominance (j) gene effects were highly significant. The additive × additive gene effect was significant for spot blotch severity in the crosses, UP 2338/PBW 343, UP 2338/PBW 373, PBW 154/PBW 373, Sonalika/PBW 343, Sonalika/PBW 373 and PBW 373/PBW 343 while it was non-significant in other remaining eight crosses. However, all the crosses exhibited significant additive × dominance gene effect except UP 2338/PBW 373, Sonalika/PBW 154 and Sonalika/PBW 373.

All the crosses showed significant dominance × dominance (l) type of non-allelic interaction excluding,

Table 1. Estimates of scaling test for spot blotch (*Bipolaris sorokiniana*) reaction in wheat

Crosses	Disease reaction to spot blotch			
	A	B	C	D
UP 2338/PBW 343	−10.00*±4.85	16.00**±2.43	38.67**±10.88	16.33**±5.68
UP2338/PBW 373	6.67±4.06	10.00**±1.16	31.33**±6.33	7.33*±3.40
UP2338/WH 581	25.00**±4.51	6.67±3.86	43.00**±9.09	5.67±5.15
PBW154/PBW 343	20.67**±3.27	8.00**±3.69	23.33**±4.01	−2.67±1.49
PBW 154/PBW 373	31.00**±2.77	−6.33*±2.77	44.67**±5.54	10.00±2.75
PBW154/WH 581	20.00**±2.56	12.33**±2.26	41.67**±7.05	4.67±2.98
Sonalika/PBW 343	8.33**±2.75	22.00**±2.24	5.67±4.12	−12.33**±1.33
Sonalika/PBW 373	20.67**±3.93	15.00**±2.56	9.67*±3.83	−13.00**±2.36
Sonalika/WH 581	15.00**±3.15	3.67*±1.49	24.00**±3.99	2.67±1.49
PBW 373/PBW 343	29.67**±2.52	6.33**±2.36	24.00**±4.18	−6.00**±2.21
PBW373/WH 581	25.33**±2.31	3.67±1.97	43.00**±10.04	7.00±4.92
PBW343/WH 581	37.00**±3.77	5.33*±2.16	51.00**±6.04	4.33±3.20
UP 2338/Sonalika	29.00**±3.35	11.33**±3.96	26.33**±7.97	−7.00±3.94
UP 2338/PBW 154	20.33**±4.98	8.33*±4.20	18.67*±8.72	−5.00±3.59
Sonalika/PBW 154	53.00**±3.25	47.96**±2.82	92.00**±5.95	−4.48**±1.59

Significant at 5% and 1% level of probability, respectively

Table 2. Estimates of gene effects along with standard error and type of epistasis in fifteen crosses for spot blotch (*Bipolaris sorokiniana*) reaction in wheat

Crosses	Disease reaction to spot blotch						Type of epistasis
	m	d	h	i	j	l	
UP 2338/PBW 343	63.33**±11.44	17.33**±1.42	−69.33**±25.23	−32.67**±11.35	−13.00**±2.67	26.67±14.15	Duplicate
UP 2338/PBW 373	48.33**±6.88	14.33**±1.05	−35.00*±16.05	−14.67*±6.80	−1.67±2.06	−2.00±9.48	Complementary
UP 2338/WH 581	40.17**±10.36	19.17**±1.09	−12.83±24.18	−11.33±10.31	9.17**±2.94	−20.33±14.20	Complementary
PBW154/PBW 343	23.00**±3.27	15.00**±1.34	23.67*±9.44	5.33±2.98	6.33**±1.89	−34.00**±6.68	Duplicate
PBW154/PBW 373	51.33**±5.58	12.00±0.94	−32.33*±13.22	−20.00**±5.50	18.67**±1.76	−4.67±8.14	Complementary
PBW154/WH 581	35.83**±6.04	16.83**±0.99	1.17±12.76	−9.33±5.96	3.83**±1.19	−23.00**±7.54	Duplicate
Sonalika/PBW 343	9.17**±3.10	20.50**±1.57	59.17**±7.75	24.67**±2.67	−6.83**±1.71	−55.00**±4.91	Duplicate
Sonalika/PBW 373	10.83*±4.88	17.50**±1.25	71.83**±13.37	26.00**±4.71	2.83±2.31	−61.67**±8.67	Duplicate
Sonalika/WH 581	37.33**±3.25	22.33**±1.28	−10.00±8.31	−5.33±2.98	5.67**±1.59	−13.33**±5.49	Complementary
PBW373/PBW 343	4.33±4.55	3.00**±1.07	54.00**±11.14	12.00**±4.42	11.67**±1.71	−48.00**±6.77	Duplicate
PBW 373/WH 581	28.50**±9.86	4.83**±0.55	−4.83±20.35	−14.00±9.84	10.83**±1.19	−15.00±10.89	Complementary
PBW 343/WH 581	20.17**±6.49	1.83±1.11	21.17±15.41	−8.67±6.39	15.83**±2.08	−33.67**±9.29	Duplicate
UP 2338/Sonalika	37.17**±8.04	−3.17*±1.56	72.83**±18.53	14.00±7.89	8.83**±2.45	−54.33**±10.98	Duplicate
UP 2338/PBW 154	35.67**±7.30	2.33±1.38	54.67**±17.89	10.00±7.18	6.00*±2.49	−38.67**±12.13	Duplicate
Sonalika/PBW 154	39.87**±3.51	5.50**±1.49	98.05**±8.33	8.96**±3.17	2.52±1.57	−109.92**±6.26	Duplicate

Significant at 5% and 1% level of probability, respectively

UP 2338/PBW 343, UP 2338/PBW 373, UP 2338/WH 581, PBW 154/PBW 373 and PBW373/WH 581. In most of the crosses both the parameters i.e., h (dominance) and l (dominance × dominance gene effect) have the opposite signs, indicating the presence of duplicate type of gene interaction, while in crosses UP 2338/PBW 373, UP 2338/WH 581, PBW 154/PBW 373, Sonalika/WH 581 and PBW 373/WH 581, h and l sign have the same magnitude, which indicates the presence of complementary gene effects in these crosses.

The resistant parents WH 581, PBW 373 and PBW 343 have two genes for disease resistance and resistance was found to be dominant over susceptibility. The findings of the study reveal that for spot blotch resistance, duplicate and complementary gene effects are contributing significantly along with additive gene effects. Therefore, to inculcate spot blotch resistance in wheat genotypes, the hybridization followed by pedigree selection for exploitation of additive and non-additive variances may be followed.

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