GENETIC ANALYSIS OF RESISTANCE TO RICE WEEVIL *Siltophilus oryzae* L. IN BREAD WHEAT

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ABSTRACT

The present experiment was conducted at GBPUA&T, Pantnagar during 2011-12 to investigate the genetics of rice weevil resistance to wheat. The experimental materials were constituted with 15 cross combinations derived from crosses involving 3 resistant stocks and 3 highly susceptible cultivars. Almost all the scaling tests were found significant which indicated the presence of all 3 types of interactions. Six parameter models indicated the additive as well as dominance effects of genes significant in crosses obtained involving reaction types of resistant × susceptible and resistant × resistant while additive (d), dominance (h) and additive × additive (i); dominance × dominance (l) effects were found significant only in resistant × resistant crosses. In the cross K76 X K50 both the parameters i.e., h (2.383 ± 4.102 and l (-13.700 ± 0.936) gene effect have the opposite signs , indicating the presence of duplicate type of gene interaction, while h and l sign have the same magnitude in the cross K 21 x K 50 (2.00 ± 2.772 and 2.667 ± 1.012 respectively), which indicates the presence of complimentary gene effects. It may be concluded that resistance is dominant over susceptibility and is primarily governed by two genes showing inhibitory and duplicate gene action along with some minor genes.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is widely grown cereal almost all over the world and contributes more calories and protein to the world's diet than any other food crop. India is the second largest producer in the world after China. The other major wheat producing countries are United States of America, Russian Federation and Canada and these 5 countries together contribute more than half of the global wheat production. In 2016-17, India produced 97.44 million tonnes of wheat from an area 30.72 million hectare (Anonymous, 2017). In this continent, it is primarily used for making chapatti, bread and biscuits and a number of other food items which are liked in Indian diet and its uses are enormous from fast food products to industry at global level. Wheat is also used as multiple food and non-food raw material in some industries such as stiffening or surface coating agent in paper industry, as an adhesive in the manufacturing of corrugated boxes, as fermentation substrate in the production of vitamins, antibodies, etc.

The rice weevil (*Sitophilus oryzae* L.) is the most widespread and destructive major insect pest of stored cereals throughout the world. Chemical control of stored-product pests is very hazardous since protected products are used for human food. Now there is an increased concern by consumers over insecticide residues in processed cereal products. Due to increase in occurrence of insecticide resistance and environmental concerns, there is requirement of alternative control methods. The use of resistant varieties of wheat against storage insect pests is a major control measure, a good alternative which is environment friendly and causes no cost to farmers. But unfortunately, wheat varieties are not developed for their ability to resist for storage insects.

Losses of stored grains due to insects and other storage problems are estimated to be greater than US$ 1 billion annually in the United States (Cuperus and Krischik, 1995) and may exceed 30% in developing countries. Most new grain varieties are selected for agronomic traits, such as yield, but not for resistance to pests in storage. One strategy that has been used to find germplasm for developing improved plant varieties is to test ancestral germplasm for the desired traits.

The precise knowledge of nature and magnitude of gene action for characters related to insect resistance is helpful in choice of effective breeding methods to accelerate the pace of genetic improvement of insect resistance. However, epistasis is important in the inheritance of quantitative traits besides additive effects (Singh and Batia, 1978) and non-additive (Kim and Kossou, 2003) effects.

In the present study, an effort has been made to study the genetics of resistance to rice weevil *Sitophilus oryzae* in bread wheat.

MATERIALS AND METHODS

The present study was carried out at N. E. Borlaug Crop Research Center and Wheat Grain Quality Laboratory, G. B. Pant University and Agriculture and Technology, Pantnagar, Uttarakhand. The experimental material of the study consisted of six wheat parental genotypes i.e. 3 resistant (K 20, K 21 and K 50) and 3 susceptible (PBN 51, K 76 and K 77) to *Sitophilus oryzae* L. and their F_1s, F_2s and backcrosses (BC_1s and BC_2s). The F_{1s} were made by crossing the all six parents in half diallel fashion during *Rabi* 2008-09 including intercrossed of three

resistant parents for studying the genetics of rice weevil resistance. . All the F_{1s} were advanced to backcrosses BC_{1s} and BC_{2s} and fresh F_{1s} were generated during rabi season 2009-10. The six generations including parents (P_1 and P_2) F_{1s}, F_{2s}, BC_{1s} and BC_{2s} were evaluated during *rabi* 2010-11. These six generation were used to study the genetics of resistance to weevil under laboratory condition during 2011-12. The experiment was performed in incubator at $27 \pm 1^{\circ}C$ temperature and 70 ± 5 % relative humidity. Twenty seeds from each genotype of P_1, P_2 & F_1, 60 seeds of F_2 and forty seeds from each genotype of BC_1 and BC_2 were filled in plastic vials of 5 x 2.5 cm size and three pairs of unsexed *S. oryzae* aged 0 to 7 days old were released in each vials, then closed with perforated cap and each genotypes replicated three times. The whole experiment was conducted in an incubator for their progeny development. After one month the total number of insects developed from each vials was counted. In the present study, parents, F_1, F_2 and back cross generations of different crosses were scored according to Dobie (1974) and modified by Gudrups *et al.* (2001), Dhliwayo and Pixley (2003) and Derera *et al.* (2010) with the score of 0-3.0 as resistant and 3.1-6.0 as moderate resistant while those with a score of 6.1-8.0, 8.1-10 and >10 were considered as moderate susceptible, susceptible and high susceptible respectively. The 6 generations data were subjected to the joint scaling test (Cavalli 1952), generation mean analysis and perfect fit solution (Hayman, 1958; Jinks and Jones, 1958 and Mather and Jinks, 1971) were used to estimate the gene effects for inheritance studies of rice weevil in bread wheat.

RESULTS AND DISCUSSION

The analysis of variance (Table.1) indicated significant difference among different treatments for weevil infestation. The material under investigation possessed considerable amount of variability with respect to weevil infestation.

Mean weevil infestation from six relevant generations *i.e.* P_1, P_2, F_1, F_2, BC_1 and BC_2 were utilized for computing scaling tests (A, B, C and D) in order to find out the adequacy of additive dominance model. The generation means analysis and estimated A, B, C and D scaling test of different crosses are presented in Table. 2. It is clear from the results presented in the table that all the crosses exhibited significant estimates of one or more scales suggesting inadequacy of simple additive dominance model. Because of the presence of epistatic effect in all the crosses as indicated by the inadequacy of additive dominance model, only six parameters model was applied for the estimation of different components of epistatic effects in all the crosses as suggested by Hayman (1958), Jinks and Jones (1958). In all the 3 cross combinations, almost all the scaling tests were found significant which indicated the presence of all 3 (additive, dominance and epistatic) types of gene effects. Significance of A and B scaling tests will indicate presence of j (additive × dominance) type of epistasis, whereas significance of C and D scaling tests will indicate presence of l dominance x dominance) and i (additive × additive) component of epistasis. The estimates of different types of gene effects and their interactions in the individual cross combination illustrated the variation.

Using the weevil infestation, severity of six relevant generations (P_1, P_2, F_1, F_2, BC_1 and BC_2), six genetic parameters i.e., m (mean), d (additive), h (dominance), i (additive x additive), j (additive x dominance) and l (dominance x dominance effects) were estimated. The estimates of parameters for fifteen crosses are presented in Table. 3.

Table 1: Analysis of variance (ANOVA) for weevil infestation in bread wheat

Source of Variation	Degree of freedom	Sum of Squares	Mean Sum of Square	F-value
Replications	2	98.557	49.2879	0.521
Treatments	65	169526.30	2608.97	27.593**
Error	130	12287.66	94.520	
Total	197	181912.50		

*,**:Significant at 5% and 1% level of probability, respectively.

Table 2: Estimation of scaling test for weevil (*Sitophilus oryzae* L.) infestation in wheat

Crosses	Infestation reaction to weevil			
	A	B	C	D
PBN51 x K20	-5.480** ± 0.399	4.253** ± 0.144	-5.760** ± 0.440	2.733** ± 0.304
PBN51 x K21	-15.680** ± 1.206	4.000** ± 0.462	-10.467** ± 0.716	0.607** ± 0.716
PBN51 x K50	-16.800** ± 1.144	0.333 ± 0.453	-22.467** ± 1.059	-3.000** ± 0.782
K76 x K20	-8.633** ± 0.473	4.867** ± 0.473	-1.767 ± 0.892	1.000** ± 0.258
K76 x K21	-17.500** ± 0.553	6.200** ± 0.650	-12.633** ± 1.140	-0.667 ± 0.502
K76 x K50	-6.100** ± 0.346	7.600** ± 0.913	-3.833* ± 1.584	-2.667** ± 0.885
K77 x K20	-14.533** ± 0.850	-0.200 ± 0.850	-11.933** ± 1.812	1.400* ± 0.572
K77 x K21	-15.000** ± 0.850	-0.333 ± 0.776	-7.333** ± 2.029	4.000** ± 4.859
K77 x K50	-14.333** ± 0.742	2.333* ± 0.973	-9.333** ± 1.931	1.333 ± 1.053
K20 x K21	1.800** ± 0.184	3.467** ± 0.407	12.067** ± 0.905	3.400** ± 0.484
K20 x K50	2.600** ± 0.293	3.467** ± 0.579	16.733** ± 1.279	5.333** ± 0.673
K21 x K50	0.333 ± 0.304	2.333** ± 0.831	5.333** ± 0.681	1.333** ± 0.506
PBN51 x K76	0.800 ± 0.840	-7.367** ± 0.557	-12.167** ± 0.726	-2.80**0 ± 0.560
PBN51 x K77	-8.133** ± 0.726	-3.267** ± 0.836	-12.467** ± 1.079	-0.533 ± 0.613
K76 x K77	-3.233** ± 0.656	-7.933** ± 0.992	-16.900** ± 1.574	-2.867** ± 0.904

*,**:Significant at 5%, and 1% probability level, respectively.

Table 3: Estimation of gene effects with standard error and type of epistasis in fifteen crosses for weevil (*Sitophilus oryzae*) infestation in wheat

Crosses	Infestation reaction to weevil						Types of epistasis
	m	d	h	i	j	l	
PBN51 x K20	15.467**±0.71	9.800**±0.000	-31.947**±2.378	-5.467**±0.609	-19.733**±0.424	16.693**±0.953	Duplicate
PBN51 x K21	11.780**±1.434	9.233**±0.064	-22.007**±4.046	-1.213±1.433	-19.680**±1.280	12.893**±2.645	Duplicate
PBN51 x K50	4.900*±1.567	8.900**±0.110	-9.033±4.131	6.000*±1.563	-17.133**±1.218	10.467**±2.619	Duplicate
K76 x K20	11.950**±0.515	9.750**±0.015	-14.783**±1.354	-2.000*±0.515	-13.500**±0.350	5.767**±1.131	Duplicate
K76 x K21	9.183**±1.006	9.183**±0.064	-16.683**±2.481	1.333±1.004	-23.700**±0.633	9.967**±1.683	Duplicate
K76 x K50	5.517*±1.774	8.850**±0.110	2.383±4.102	5.333*±1.770	-13.700**±0.936	-6.833*±2.413	Duplicate
K77 x K20	12.233**±1.146	9.233**±0.064	-25.233**±2.708	-2.800*±1.144	-14.333**±0.562	17.533**±2.117	Duplicate
K77 x K21	18.000**±1.694	8.667**±0.089	-37.667**±3.658	-8.000**±1.646	-14.667**±0.660	23.333**±2.394	Duplicate
K77 x K50	13.000**±2.109	8.333**±0.126	-24.000**±4.903	-2.667±2.105	-16.667**±1.129	14.667**±2.928	Duplicate
K20 x K21	7.567**±0.969	-0.567**±0.064	-8.567*±2.149	-6.800**±0.967	-1.667*±0.428	1.533±1.218	Duplicate
K20 x K50	11.767**±1.351	-0.900**±0.110	-15.167**±3.00	-10.667**±1.346	-0.867±0.609	4.600±1.712	Duplicate
K21 x K50	4.333**±1.019	0.333**±0.126	2.000±2.772	2.667**±1.012	2.000±0.866	0.000±1.792	Complementary
PBN51 x K76	14.150**±1.121	0.050**±0.015	0.117±3.110	5.600**±1.121	8.167**±0.959	-0.967±2.051	Duplicate
PBN51 x K77	18.167**±1.227	0.567**±0.064	-11.500**±3.287	1.067±1.225	-4.867**±0.970	10.333**±2.205	Duplicate
K76 x K77	13.450**±1.808	0.517**±0.064	-0.283±4.381	5.733*±1.80	4.700**±1.103	5.433±2.697	Duplicate

*, **, :Significant 5% and 1% probability level, respectively.

Further, a perusal of Table. 3 indicates that in the cross PBN51 x K20, additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effects were highly significant. Additive type of gene effects were significant for all the crosses namely PBN51 x K21, PBN51 x K50, K76 x K20, K76 x K21, K76 x K50, K77 x K20, K77 x K21, K77 x K50, K20 x K21, K20 x K50, K21 x K50, PBN51 x K76, PBN51 x K77 and K76 x K77. However, the crosses PBN51 x K20, PBN51 x K21, K76 x K20, K76 x K20, K77 x K20, K77 x K21, K77 x K50 and PBN51 x K77 exhibited significant dominance gene effects.

The additive x additive gene effect was significant for weevil infestation severity in crosses namely, PBN51 x K20, PBN51 x K50, K76 x K20, K76 x K50, K77 x K20, K77 x K21, K20 x K21, K20 x K50, K21 x K50, PBN51 x K76 and K76 x K77 while it was non-significant in other remaining four crosses. However, all the crosses exhibited significant additive x dominance gene effect except K20 x K50 and K21 x K50.

The crosses PBN 51 x K20, PBN 51 x K 21, PBN 51 x K 50, K 76 x K 20, K 76 x K 21, K 76 x K 50, K 77 x K 20, K 77 x K 21, K 77 x K 50 and PBN 51 x K 77 showed significant dominance x dominance type of non-allelic interaction while it was non-significant in the crosses, K 20 x K 21, K 20 x K 50, K 21 x K 50, PBN 51 x K 76 and K 76 x K 77.

In most of the crosses both the parameters i.e., h (dominance) and l (dominance x dominance) gene effect have the opposite signs, indicating the presence of duplicate type of gene interaction, while h and l sign have the same magnitude in the cross K 21 x K 50, which indicates the presence of complimentary gene effects.

It is worth mentioning here that all the crosses exhibited significant additive and non-additive gene effects (Table. 3). However, type of non-additive gene effects were exhibited varied from cross to cross. Dominance gene effects were also significant in majority of the crosses except PBN 51 x K 50, K 76 x K 50, K 21 x K 50, PBN 51 x K 76 and K 76 x K 77.

All the three components i.e., i (additive x additive), j (additive x dominance) and l (dominance x dominance) were significant in case of the crosses PBN 51 x K 20, PBN 51 x K 50, K 76 x K 20, K 76 x K 50, K 77 x K 20 and K 77 x K 21 in addition to

significant additive effects. However, three remaining susceptible x resistant crosses viz., PBN 51 x K 21, K 76 x K 21 and K 77 x K 50 also showed similar type of non-additive gene effects. Similar sign of h an l components in the cross K 21 x K 50 indicated the presence of complementary gene effects.

The results obtained in the present investigation are in partial agreement with Singh and Batia (1978) who reported that rice weevil resistance in wheat was mainly an additive gene effects with duplicate type of epistasis. On the other hand Kim and Kossou (2003) who reported that both additive and non-additive gene actions were responsible for resistance to maize weevil in maize. Dhliwayo and Pixley (2005) confirmed that additive gene action for weevil resistance was important. The importance of additive and non-additive gene action for inheritance of resistance to maize weevil was also reported by Dari *et al.* (2010) while Widstrom *et al.* (1975) reported that additive gene action is important for maize weevil resistance. Derera *et al.* (1999) suggest that development of weevil resistant varieties is a challenging task, as additive, non-additive and maternal effects were important in determining maize weevil resistance for maize. Serratos *et al.* (1994) reported that both additive and dominance gene action were important for conferring resistance to weevil in maize. Garcia-Lara *et al.* (2003) confirmed quantitative inheritance, importance of maternal effect, additive and non-additive gene action for weevil resistance in maize. Similarly Gafishi *et al.* (2010) reported that additive effects were more important than non-additive for most weevil resistance in maize. Kang *et al.* (1995) and Zunjare, *et. al.* (2015) reported significant additive, non-additive, and maternal effects, with additive being more important than non-additive effects. Inheritance of resistance to maize weevil and reported that additive gene action and, to a lesser extent, non-additive gene action were important. Widstrom *et al.* (1975) investigated the inheritance of resistance to maize weevil in maize was dominance effects. Derera *et al.* (2001) reported significant additive, non-additive, and maternal effects.

Based on present investigation it may be concluded that resistance is dominant over susceptibility and is primarily governed by two genes showing inhibitory and duplicate gene action along with some minor genes. Among genetic

interactions, predominantly the dominance type of gene effects governed the rice weevil resistance, while additive, additive × additive and dominance × dominance type of gene interactions also played a partial role in conferring resistance against rice weevil. However, polygenic inheritance of the trait can't be denied considering the ratio obtained in BC$_1$ generations. All the crosses exhibited different types of non-allelic interaction in addition to additive type of gene interaction (Raiyani *et. al.*, 2015; Singh *et. al.*, 2015). In present study, susceptible seeds were obtained in BC$_1$ also which further supported the non-identical nature of the gene(s) conditioning resistant to weevil. The finding of the present study are useful   as all the resistant parents can provide alternative source of resistance, which may be exploited in breeding programme by utilising them in various combination in developing a weevil resistant variety of wheat. There is very negligible information available on inheritance pattern of weevil resistance in wheat; further investigation is to be needed for confirmation of the results of present investigation.

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