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Allelic relationship among genes for resistance to rice weevil (*Sitophilus oryzae* L.) in bread wheat

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Abstract

The present investigation was conducted at G. B. Pant University of Agriculture and technology during 2011-12. Rice weevil resistance to wheat is an important storage pest of wheat in the tropics and sub-tropics. An effort has been made to establish the gene identity for rice weevil resistance in the wheat. F₁ progenies showed resistant type of response towards weevil infestation; however, segregation in the F₂ generations revealed that resistant parents had a different set of genes conferring weevil infestation. All the crosses namely, K20 x K21, K20 x K50 and K21 x K50 segregated in the pattern of 15 (resistant): 1 (susceptible) indicating that resistance to weevil infestation is controlled by two dominant genes and the genes interacted with each other in duplicate manner. Susceptible seeds were obtained in backcrosses also which further supported the non-identical nature of the gene(s) conditioning resistant to weevil.

Keywords: wheat, rice weevil, genetics, allelic relationship

Introduction

Wheat (*Triticum aestivum* L.) is the second most important cereal crop after rice in India. India is the second largest producer of wheat in world. It was grown on 30.72 million hectares with the production of 97.44 million tonnes during 2016-17 (Anonymous, 2017) [1]. Phenomenal increase in wheat production and productivity has been achieved with the advent of high yielding improved varieties.

During harvest season, wheat is procured by public and private agencies for storage and sale as a part of the produce. The wheat grain is retained by the farmers for their own consumption and for seed purpose. Insect infestations in grain cause quantity and quality losses and hence the crop value is lowered. The amount of damage in quality, quantity and health hazards due to insect infestation when converted into monetary concerns may run into millions of rupees to national exchequer annually. Insects not only consume grain but also contaminate it with their metabolic by-products and body parts. Insects produce heat and moisture due to their metabolic activities that could lead to the development of hotspots and growth of microflora in grain. Heavily infested wheat is unfit for seed purposes and its products are unsuited for human consumption.

Wheat is heavily infested by a number of insect pests during storage, among these, rice weevil (*Sitophilus oryzae* L.); granary weevil (*Sitophilus granarius* L.); lesser grain borer (*Rhyzopertha dominica* F.); Khapra beetle (*Trogoderma granarium* Everts); Angoumois grain moth (*Sitotroga cerealella* (Olivier) and red flour beetle (*Tribolium castaneum* Herbst.) are important. (Khattak *et al.* 2000; Toews *et al.* 2000; Ebeling, 2002; Atwal and Dhaliwal, 2005; Shafique *et al.* 2006) [10, 17, 7, 3, 15].

The rice weevil is the most widespread and destructive insect-pest of stored cereals throughout the world. The name is misleading, because it may infest other grains besides rice. The rice weevil is a cosmopolite insect supposedly originated in India and spread all around the world through infested and ship-transported grains (Metcalf and Flint, 1962) [11].

In cereals, there are three important species of weevil namely, *Sitophilus oryzae* L., *Sitophilus granarius* L. and *S. zeamais* Motsch. (Coleoptera: Curculionidae).

Out of these weevils, *Sitophilus granarius* L. is called granary weevil is one of the most harmful pests of stored grain in temperate climate, while the rice weevil (*Sitophilus oryzae*) is considered a primary stored-grain insect pest in warm climate areas including India. Both species are often known as "snout weevils" and they penetrate and feed on the internal portions of whole grains in wheat.

One way to increase the quantity and quality of food grains is to reduce damage from insects and diseases that attack stored grain. Such damage is commonly responsible for losses of more than 20% of the grain harvested in LDCs, where tropical conditions allow insects and disease agents to reproduce rapidly and to colonize unprotected grains (Meikle *et al.* 1999) [12].

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Several attempts have been made to control rice weevil but no single control measure has been successful. Hence, an integrated approach with host resistance as a major component has been advocated. If it is incomplete, any degree of resistance will complement chemical and other control measures. It is generally accepted that weevil resistance of stored wheat grain is not yet satisfactory.

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. Wheat varieties behave differently to stored grain pests, resulting in the increase of research to develop grain varieties resistant to stored grain insects (Seifelnasr and Mills, 1985)^[14].

Due to increasing threat of insect-pests in storage particularly rice weevil, there is a need for understanding the various dimensions of its resistance to breed the resistant genotypes. However, the major hindrance in utilizing the resistance against the pest is that resistant source is scanty. Also the nature of resistance is still not very clear because there are negligible studies on the inheritance of weevil resistance.

Therefore, the success of the breeding programme lies in the identification of source of resistant genes and sound knowledge of genetic behaviour of the resistant genes. Keeping the usefulness of resistant genes in view, efforts have been made to establish the gene identity for rice weevil resistance in the present investigation.

Materials and Methods

The present study was conducted at the N. E. Borlaug Crop Research Centre of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar located in Udham Singh Nagar (Uttarakhand). The experimental material of the study consisted of six wheat parental genotypes *i.e.* 3 susceptible (PBN 51, K 76 and K 77) and 3 resistant (K 20, K 21 and K 50) depicted in Table-1 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. 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 (P₁ and P₂) F_{1s}, F_{2s}, BC_{1s} and BC_{2s} were evaluated during *rabi* 2010-11 and were used to study the genetics of resistance to weevil.

Table 1: Pedigree of Parentage used in the study

| Parentage | Pedigree |
|-----------|------------------------|
| PBN 51 | BUC'S/FLK'S' |
| K 76 | VL 616/HD 2857 |
| K 77 | UP2467/HD 2590/UP 2556 |
| K 20 | HD 2857/UP 2556 |
| K 21 | HPW 89/PBW 343 |
| K 50 | K 9107/GW 9909 |

Table 2: Segregation pattern among resistance genes for resistance to *Sitophilus oryzae* L. in bread wheat

| Generations | Observed frequency | | Expected frequency | | Expected segregation ratio (R:S) | χ^2 value | P value |
|------------------------------------|--------------------|------|--------------------|------|----------------------------------|----------------|-----------|
| | R | S | R | S | | | |
| Cross (K 20/K 21) | | | | | | | |
| P ₁ (K20) | 20.00 | - | All | - | - | - | - |
| P ₁ (K21) | 18.67 | 1.33 | All | - | - | - | - |
| F ₁ (K20 x K21) | 20.00 | - | All | - | - | - | - |
| F ₂ | 54.67 | 5.33 | 54.43 | 3.82 | 15 : 1 | 0.268 | 0.50-0.70 |
| BC ₁ (K 20/K 21// K20) | 37.47 | 2.53 | All | - | - | - | - |
| BC ₂ (K 20/K 21// K21)) | 38.33 | 1.67 | All | - | - | - | - |
| Cross (K 20/K 50) | | | | | | | |

The experiment was conducted for screening of resistance in wheat genotypes/lines against *Sitophilus oryzae* under laboratory condition. The experiment was performed in incubator at 27±1°C temperature and 70 ± 5 % relative humidity. Twenty seeds from each genotype of P₁, P₂ & F₁, 60 seeds of F₂ and forty seeds from each genotype of BC₁ and BC₂ 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, F₁, F₂ and back cross generations of different crosses were scored according to Dobie (1974)^[5] and modified by Gudrups *et al.* (2001)^[9], Dhliwayo *et al.* (2003)^[6] and Derera *et al.* (2010)^[4] 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 information on the allelic relationship obtained from the present investigation is based on Chi-square test with Yates correction for continuity proposed by Yates (Panse and Sukhatme, 1957)^[13].

$$\chi^2_{\text{(Corrected)}} = \sum \frac{(O - E - 0.5)^2}{E}$$

This χ^2 value was tested against table value of χ^2 at n-1 degree of freedom.

Where;

Σ = summation

O = observed frequency in a phenotypic class

E = expected frequency in a phenotypic class

n = number of phenotypic class

d. f. = degree of freedom

Results and Discussion

The experimental material was consisted from six generations including parents (P₁, P₂), F_{1s}, F_{2s}, BC_{1s} and BC_{2s} of three families which confers resistance reaction against *sitophilus oryzae* L. for studies of allelic relationship as follows:

K20/K21

In F₁ generation of this combination, all the 20 observed seeds in F₁ were resistant to weevil infestation (Table-2). In F₂ out of 60 seeds, 54.67 showed resistant response and only 5.33 exhibited susceptibility. This gave a good fit to expect 15 resistant: 1 susceptible ratio ($\chi^2 = 0.268$, P= 0.50-0.70). The segregation pattern observed in BC₁ verified the observed F₂ ratio. In BC₂ generation, 38.33 observed seeds were resistant to weevil.

| | | | | | | | |
|-----------------------------------|-------|------|-------|------|--------|-------|-----------|
| P ₁ (K20) | 20.00 | - | All | - | - | - | - |
| P ₁ (K50) | 18.00 | 2.00 | All | - | - | - | - |
| F ₁ (K20 x K50) | 19.33 | 0.67 | All | - | - | - | - |
| F ₂ | 53.67 | 6.33 | 53.44 | 5.22 | 15 : 1 | 0.073 | 0.70-0.80 |
| BC ₁ (K 20/K50//K 20) | 37.00 | 3.00 | All | - | - | - | - |
| BC ₂ (K 20/K50//K 50)) | 37.67 | 2.33 | All | - | - | - | - |
| Cross (K 21/K 50) | | | | | | | |
| P ₁ (K21) | 18.67 | 1.33 | All | - | - | - | - |
| P ₁ (K50) | 18.00 | 2.00 | All | - | - | - | - |
| F ₁ (K21 x K50) | 19.00 | 1.00 | All | - | - | - | - |
| F ₂ | 53.33 | 6.67 | 53.44 | 4.56 | 15 : 1 | 0.574 | 0.30-0.50 |
| BC ₁ (K 21/K50//K 21) | 36.33 | 3.67 | All | - | - | - | - |
| BC ₂ (K 21/K50//K 50) | 37.33 | 2.67 | All | - | - | - | - |

K20/K50

Similarly in the F₁ of this cross, 19.33 seeds were resistant (Table-2). In F₂ population comprised of 60 seeds, out of which 53.67 were resistant and the remaining 6.33 susceptible. The segregation pattern observed in F₂ generation provides a good fit to expected 15 resistant: 1 susceptible ratio ($\chi^2 = 0.073$, P = 0.70-0.80). In BC₁ generation, out of 40 observed seeds 37.00 were resistant and 3 susceptible while in BC₂ 37.67 seeds were found resistant.

K21/K50

Perusals of Table-2 confirm that 19.0 out of 20 observed seeds in F₁ generation of this cross were resistant. In F₂ generation out of 60 observed seeds, resistant and susceptible seeds were 53.33 and 6.67 respectively. This provides a good fit to expected 15 resistant: 1 susceptible ratio ($\chi^2 = 0.571$, P= 0.30-0.50). In BC₁ generation, out of 40 evaluated seeds, 36.33 were resistant and 3.67 susceptible, while in BC₂ generation, out of 40 screened seeds 37.33 were found resistant.

This clearly indicates that two dominant genes govern resistance and the resistant parents have dissimilar gene constellation. Thus showing non allelic interaction among each other resistant genes of K20 showed dominant duplicate gene interaction with genes of K21 and K50 while the resistant genes of K21 have complimentary type of interaction with gene(s) of K50.

The information on allelic interaction among genes for resistance to weevil is negligible in wheat. However, the present findings are in partial agreement with Singh and Batia (1978) [16] who reported that in the resistant x resistant crosses all the seeds in F₁, reciprocal F₁ and back crosses were almost free from weevil infestation, however in F₂ generation seed showed weevil infestation in these crosses, which was indication of the presence of non-allelic interaction among them. Dissimilar genes for resistance in the parental lines have also been suggested, on the basis of appearance of susceptible plants in F₂s of resistant x resistant crosses. Some aspects on allelic relation in Russian Wheat Aphid (RWA) has been covered by Aasad and Dorry (2001) [2] and Estakhr and Assad (2002) [8] who observed that two different genes conditioning resistance to RWA in two wheat resistant lines and segregated independently while in maize Zunjare (2015) [18] reported similar type of findings.

In present study, susceptible seeds were obtained in BC₁ 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.

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