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## Gene Action for Resistance to Sunn Pest (*Eurygaster integriceps* Put.) in Bread Wheat

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**Abstract:** Sunn pest *Eurygaster integriceps* Put. (Heteroptera: Scutelleridae) is well known as a serious limiting factor for production of wheat grain with strong gluten in the wide area of the Near and Middle East, Eastern and South Europe and North Africa. To study the genetics of resistance to sunn pest in bread wheat, two susceptible (Falat and Line 14) and a resistant (Line 30) lines were crossed to each other as follow: Line 14/Line 30 and Falat/Line 30. The six basic generations (parent cultivars (P1, P2), first and second filial generations (F1, F2), first and second backcrosses (BC1, BC2)) of crossings were planted in a randomized block design in three replicate plots. In early seed development stage, six sunn pest (nymph3) were introduced in each cage having a wheat plant. after 40 days percent damaged seed along with their genetic characteristics were assessed through generation mean analysis method. Gene effects including mean effect, additive, dominance, epistasis effects of additive×additive, additive×dominance and dominance×dominance were observed. The broad sense heritability for the Line 14/Line 30 cross and the Falat/Line 30 cross were estimated 0.78 and 0.84 while narrow sense heritability were 0.51 and 0.67, respectively.

**Key words:** Generation mean analysis, sunn pest (*Eurygaster integriceps* Put.), wheat (*Triticum aestivum*), gene effects

### INTRODUCTION

Wheat, *Triticum aestivum* L. and barley, *Hordeum vulgare* L., are very important food crops in the near East, Middle East and South-Western Asian countries. They are very strategic crops for Iran as well as many other countries. Wheat is grown on approximately 6.4 million ha in Iran. Total production of wheat is 14.308 million ton and the yield is 23437 Hg ha<sup>-1</sup> in average (FAO, 2007).

The crops are attacked by several species of bugs. Sunn pest, is the most important pest constitutes a major threat to wheat production and, to a lesser extent, barley production. Sunn pests are a complex of true bugs which belong to the genera *Eurygaster* (Scutelleridae), *Aelia*, *Carpocoris* and *Dolycoris* (Pentatomidae). *Eurygaster integriceps* is probably the most important species in Afghanistan, Iran, Iraq, Jordan, Pakistan, Syria, Lebanon, Germany, Spain, Hungary and Turkey (Aykut *et al.*, 2006).

There are two economically important species of *E. integriceps*, *E. maura* L. and *E. austriaca* Schrk (Aykut *et al.*, 2006). Over 15 million ha can be affected annually and during outbreaks, infestations may result in 100% crop loss. Damage commonly results in yield losses of 20-30% in barley and 50-90% in wheat. This pest also injects chemicals into the grain that destroy the gluten and greatly reduce the baking quality of the flour (Hariri *et al.*, 2000).

As a consequence a deterioration of pasta quality due to alteration of gluten occurs, worsening the cooking

and sensory pasta properties (Ozderen *et al.*, 2008). Bug damage not only negatively affects the baking properties of *aestivum* wheat but also the cooking potential of durum wheat, especially in varieties with weak gluten quality (Petrova, 2002).

The study of Wheat sunn pest, blackpoint, kernel smudge and quality factors in Spanish durum wheat showed that the average Sunn pest damaged kernels was 2.5% both in 2006 and 2007. The blackpoint (including kernel smudge) was detected very often (9.8% in 2006 and 6.4% in 2007, as an average) (Gordún *et al.*, 2008).

Generation mean analysis provides information on the relative importance of average effects of the genes (additive effects), dominance deviations and effects due to non allelic genic interactions, in determining genotypic values of the individuals and, consequently, mean genotypic values of families and generations (Viana, 2000). Generation mean analysis is a simple but useful technique for estimating gene effects for a polygenic trait, its greatest merit lying in the ability to estimate epistatic gene effects such as additive×additive (aa), dominance×dominance (dd) and additive×dominance (ad) effects (Singh and Singh, 1992).

Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic and to what extent this variation is heritable, because efficiency of selection mainly depends on additive genetic variance, influence of the environment and interaction between genotype and environment.

The research reported in this study was carried out to provide information about gene effects and available genetic variability for the resistance to sunn pest (*Eurygaster integriceps* Put.) in Bread Wheat (*Triticum aestivum* L.).

**MATERIALS AND METHODS**

To study the genetics of resistance to sunn pest in bread wheat, two susceptible (Falat and Line 14) and a resistant (Line 30) lines were crossed to each other as follow: Line 14/Line 30 and Falat/Line 30. The six basic generations (parent cultivars (P1, P2), first and second filial generations (F1, F2), first and second backcrosses (BC1, BC2) of crossings were planted in a randomized block design in three replicate plots at Research Farm of University of Tehran in Karaj during the autumn season of 2006/2007. The plots were 2 m long with a between-row spacing of 20 cm and a within-row spacing of 10 cm. Aluminum cages (25×100 cm) were placed on wheat plants at head initiation. In early seed development stage, six sunn pest (nymph 3) were introduced in each cage having a wheat plant. The nymphs fed on wheat seed for 40 days. After seed maturity the cages were collected and transferred to the lab and then the spikes of each cage were grinded separately. And the number of damaged seed was counted then the percent damaged seed for each generation was determined.

The means and variances of parental, F1, F2, F3, BC1 and BC2 generations were used to estimate the components of gene action by the weighted least squares method (Mather and Jinks, 1982). The accuracy of the additive-dominance model was tested using the following equations:

$$A = 2 BC1-P1-F1$$

$$B = 2 BC2-P2-F1$$

$$C = 4 F2-2F1-P2-P2$$

Additionally, a joint scaling test was performed for verifying the adequacy of all the models studied. The epistatic model describing non-allelic interactions between pairs of loci was tested by following the statistical model described by Mather and Jinks (1982):

$$Y = m + \alpha[d] + \beta[h] + \alpha^2[i] + 2\alpha\beta[j] + \beta^2[l]$$

where, Y is generation mean, m is mean of all possible homozygous lines deriving from the cross, [d], [h], [i], [j] and [l] are net directional effects of loci contributing to additive, dominance, additive×additive, additive×dominance and dominance×dominance components, respectively and  $\alpha$  and  $\beta$  are coefficient of genetic parameters.

Due to the different sizes and variances of generations, the weighted least square method was used to predict the genetic parameters (Kearsey and Pooni, 1996). The genetic model that best fit the data was found by the mean of joint scaling test (Mather and Jinks, 1982) and the accuracy of the models was verified by Chi-square test. Components within each model were evaluated for significance by t-test.

Estimates of dominance ratio, broad-sense heritability ( $h^2b$ ) (Kearsey and Pooni, 1996) and narrow-sense heritability ( $h^2n$ ) for percent damaged seed were obtained using the following equations:

$$\text{Broad-sense heritability} : h^2b = [V_{F2}-V_E]/V_{F2}$$

$$\text{Narrow-sense heritability} : h^2n = [2V_{F2}-(V_{BC1}+V_{BC2})]/V_{F2}$$

$$\text{Additive variance} : VA = 2V_{F2}-(V_{BC1}+V_{BC2})$$

$$\text{Dominance variance} : VD = V_{BC1}+V_{BC2}-V_{F2}-V_E$$

$$\text{Environmental variance} : VE = (V_{p1}+V_{p2}+2V_{f1})/4$$

All statistical analyses were carried out using the SAS and Minitab software.

**RESULTS AND DISCUSSION**

The result showed that the covariate was statistically significant and the means of generation corrected (Table 1).

The results showed that Line 30 had significantly lower percent damaged seed than Falat and Line 14 and the parents differed in respect to the percent damaged seed, although for the F1 generation only the means were between the tow parents. Backcrossing to the two parents resulted in convergence of gene for higher susceptibility in the Falat/line 30 cross and higher resistance in the Line 14/Line 30 cross (Table 2).

In the Line 14/Line 30 cross complementary epistasis was found, only the Additive×Additive component [I] of

Table 1: Corrected mean square from analysis of covariance for percent damaged seed in tow crosses

SOV	Line 14/Line 30	Falat/Line 30
Rep	152.00	49.55
Generation	508.67**	1110.13**
Covariate	1020.18**	1975.13**
Error	108.92	160.99

\*\* : Highly significant

Table 2: Mean±SD of percent damaged seed in six generations of tow crosses

Generation	Line 14/Line 30	Generation	Falat/Line 30
Line 14	72.28±1.33a	Falat	64.37±10.82ab
Line 30	51.90±3.7d	Line 30	44.89±9.89c
F1	67.13±6.55ab	F1	60.33±8.24ab
F2	64.07±17.97abc	F2	71.18±19.4a
BC1	57.98±14.05cd	BC1	59.80±16.12ab
BC2	58.07±15.19bcd	BC2	55.97±18.03bc

Mean with different letter(s) are significantly different

Table 3: Six parameter model for estimation of various genetic components for percent damaged seed

Cross	Mean (m)	Additive (d)	Dominance (h)	Additive× additive (I)	Additive× dominance (j)	Dominance× dominance (l)	Chi-square
Line 14/Line 30	86.26±15.69**	10.19±1.73**	-69.65±39.73*	-24.17±15.60	-20.55±11.23*	50.52±25.03*	0.00ns
Falat/Line 30	108.78±17.88**	8.89±2.40**	101.94±46.07*	-53.17±17.71	-	53.49±29.39*	0.74ns

\*, \*\*Statistically significant at  $p = 0.95$  and  $p = 0.99$ , respectively, ns: Not significant

Table 4: Estimates of variance components and heritability of percent damaged seed

Parameters	Line 14/Line 30	Falat/Line 30
Genetic variance (VG)	650.19	817.75
Additive variance (VA)	434.51	406.40
Dominance variance (VD)	215.68	411.35
Environmental variance (VE)	51.59	87.75
Broad sense (h <sub>2b</sub> )%	78.00	84.00
Narrow sense (h <sub>2n</sub> )%	51.00	67.00

the digenic interaction terms was not significant (Table 3). In the Falat/Line 30 cross a digenic epistatic model was adequate, only the Additive×Additive component [i] of the digenic interaction terms was not significant. Significant digenic interaction terms in tow crosses indicated that epistasis was responsible for the departure from simple additive-dominance model with respect to percent damaged seed in tow crosses. The negative sign of additive×dominance [j] interaction in the Line 14/Line 30 cross also suggested dispersion of genes in the parents (Table 3).

Estimates of variance components as shown in Table 4 revealed that the Additive Variance (VA) was smaller than Dominance Variance (VD) for the Falat/Line30 cross but larger than VD for the Line 14/Line 30 cross. Narrow-sense heritability broad-sense heritability estimates were relatively high for tow crosses.

The F1 values were significantly different from those of the parents on one hand and the mid-parent values on the other hand suggesting positive heterosis for the percent damaged seed. Partial dominance of alleles for high percent damaged seed was observed.

Although, the two backcrosses in tow crosses were not statistically different, the backcross breeding method could provide a profitable means of improving resistance to sunn pest. Transgressive segregation for increased susceptibility was also observed in the F2 generation in the Falat/Line 30 cross.

Observed presence of nonadditive effects (dominance and epistasis) in the current study could lower the expected progress from selection during early segregating generation and thus, lower the gain anticipated from continued inbreeding. Using the current study as a yardstick, selection for resistance to sunn pest may not be profitable and feasible in the early segregating populations, the relatively high heritability estimate notwithstanding. The backcross breeding method would be an effective means of transferring the genes for resistance to sunn pest.

To identify whether a cause of the model failure is the presence of higher order interactions or linkage effects there further analyses needs to be carried out with enough generations to fit a full trigenic interaction and linkage model. In respect of epistatic effects, additive×additive effects were more important than dominant×dominant effects and only complementary epistasis was observed. This situation is more favorable than the presence of dominant×dominant effects and/or duplicate epistasis due to a greater chance of breeding success and partially explains why heterosis was not as frequent as might be expected from the fact that dominance effects were more important than additive effects.

Estimates of additive effects can be small due to a high degree of dispersion of increasing alleles between parents and dominance can be small due to its bi-directional nature. This might explain why additive genetic component of variance (VA) varied greatly, although a clear-cut relationship between additive effects and additive genetic variance could not be detected.

Narrow-sense heritability estimate was relatively high for tow crosses. John and Thangavelu (1997) have reported that heritability estimates could not solely provide sufficient information for the genetic improvement that would result from selection of best plant genotypes. However, heritability estimates is more important than just knowing the number of genes involved because heritability provides a realistic means of measuring progress in plant improvement by indicating how easy or difficult it would be to provide changes in a given trait by applying selection (Graham and Welch, 1996). According to the authors, the closer heritability estimates is to 100%, the less environmental influence a trait is subjected to and the easier it is to make progress through selection. Thus, predominance of dominance effects coupled with relatively high heritability estimates for percent damaged seed in this study tends to suggest that resistance to sunn pest could not be readily selected for in the early segregating generations.

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