

# Genetics of resistance to sunn pest (*Eurygaster integriceps* Put) in bread wheat

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## 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 6.41 million ha in Iran. Total production of wheat is 13.44 million t and the yield is 2355 kg/ha in average (FAO, 2005).

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 (Moore, 1998).

There are two economically important species of *E. integriceps*, *E. maura* L. and *E. austriaca* Schrk. (Aydemir, 1998; Simsek, 1998). 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 (Moore, 1998; Hariri et al., 2000).

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 x additive (aa), dominance x dominance (dd) and additive x 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 paper 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.).

## MATERIAL AND METHODS

To study the genetics of resistance to sunn pest in bread wheat, two susceptible ( Falat and Line14) and a resistant ( Line 30) lines were crossed to each other as follow: Line14/Line30 and Falat/Line30. 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 2004/2005. 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 by 100 cm) were placed on wheat plants at head initiation. In early seed development stage, six sunn pest (nymph3) were introduced in each cage having a wheat plant. The nymphs fed on wheat seed for 40 d. After seed maturity the cages were collected and transferred to the lab, and then the spikes of each cage were threshed separately. The number of damaged seed were counted then the percent damaged seed for each generation was determined.

The mean values standard errors and variances of the different generations were subjected to weighted least squares analysis using the joint scaling test (Mather and Jinks, 1982) to estimate gene effects and the maximum likelihood method (Hayman, 1960) to estimate variance components to fit models of increasing complexity until an adequate description of the observed means were found as shown by non-significance in the Chi-square test. The significance of genetic parameters was tested by t-test. The type of epistasis was determined only when dominance (d) and dominance x dominance (dd) effects were significant, when these effects had the same sign the effects were complementary while different signs indicated duplicate epistasis (Kearsey and Pooni, 1996).

Additive, dominance and environmental variance components were estimated using the maximum likelihood method with the observed variances of the six basic generations being used as the initial weights ( $df/2*s^2 + 2$ ) until the Chi-square test values reached a minimum (Lynch and Walsh, 1998).

Broad sense heritability ( $h^2b$ ) and narrow-sense heritability ( $h^2n$ ) were calculated as follows:

$$h^2b = V_{F2} - ((V_{P1} * V_{P2})^{0.5} / V_{F2})$$

$$h^2n = 2V_{F2} - ((V_{BC1} + V_{BC2}) / V_{F2})$$

All statistical analyses were carried out using the STAT module and PROC REG procedure of the SAS software (SAS Institute, 1996).

### Results and Discussion

Because of the different number of sunn pest in each cage (covariate), the analysis of covariance was carried out and the result is presented in Table 1. The result showed that the covariate was statistically significant and the means of generation corrected.

Table 1. Corrected mean square from analysis of covariance for percent damaged seed in two crosses

S.O.V	Line14/Line30	Falat/Line30
Rep	152.00	49.55
Generation	508.67**	1110.13**
Covariate	1020.18**	1975.13**
Error	108.92	160.99

Means and standard deviation of percent damaged seed in the six generations are presented in Table 2. The results showed that Line30 had significantly lower percent damaged seed than Falat and Line14 and the parents differed in respect to the percent damaged seed, although for the F1 generation only the means were between the two parents. 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.

Backcrossing to the two parents resulted in convergence of gene for higher susceptibility in the Falat/line30 cross and higher resistance in the Line14/Line30 cross. Although, the two backcrosses in two 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/Line30 cross.

Table 2- Means and standard deviation of percent damaged seed in six generations of two crosses.

Generation	Line14/Line30	Generation	Falat/Line30
Line 14	72.28 ± 1.33 a	Falat	64.37 ± 10.82 ab
Line 30	51.9 ± 3.7 d	Line 30	44.89 ± 9.89 c
F1	67.13 ± 6.55 ab	F1	60.33 ± 8.24 ab
F2	64.07 ± 17.97abc	F2	71.18 ± 19.4 a
BC1	57.98 ± 14.05 cd	BC1	59.8 ± 16.12 ab
BC2	58.07 ± 15.19bcd	BC2	55.97 ± 18.03 bc

The estimates of the main and first order interaction gene effects and chi-square values are presented in Table 3. In the Line14/Line30 cross complementary epistasis was found, only the Additive x Additive component [i] of the digenic interaction terms was not significant. In the Falat/Line30 cross a digenic epistatic model was adequate, only the Additive x Additive component [i] of the digenic interaction terms was not significant.

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

Significant digenic interaction terms in two crosses indicated that epistasis was responsible for the departure from simple additive-dominance model with respect to percent damaged seed in two crosses. The negative sign of additive x dominance [j] interaction in the Line14/Line30 cross also suggested dispersion of genes in the parents.

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 Line14/Line30 cross. Narrow-sense heritability estimate was relatively high for two 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.

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, 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 x additive effects were more important than dominant x dominant effects and only complementary epistasis was observed. This situation is more favorable than the presence of dominant x 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.

cross	Mean [m]	Additive [d]	Dominance [h]	Additive x Additive [i]	Additive x Dominance [j]	Dominance x Dominance [l]	Chi-square [X2]
Line14/Line30	86.26 $\bar{\pm}$ 15.69**	10.19 $\bar{\pm}$ 1.73**	-69.65 $\bar{\pm}$ 39.73*	-24.17 $\bar{\pm}$ 15.6	-20.552 $\bar{\pm}$ 11.23*	50.52 $\bar{\pm}$ 25.03*	0.00 <sup>ns</sup>
Falat/Line30	108.78 $\bar{\pm}$ 17.88**	8.89 $\bar{\pm}$ 2.4**	101.94 $\bar{\pm}$ 46.07 <sup>†</sup>	-53.17 $\bar{\pm}$ 17.71	-	53.49 $\bar{\pm}$ 29.39*	0.74 <sup>ns</sup>

\* and \*\* = statistically significant at p = 0.95 and p = 0.99 respectively

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

	Line14/Line30	Falat/Line30
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 [HB]%	78	84
Narrow sense [HN]%	51	67

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.

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