

*Full Length Research Paper*

## **Estimation of the heritability of agro-morphological traits in rice (*Oryza sativa* L.) using F<sub>2:3</sub> families**

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**Heritability is an important genetic parameter of the trait under selection. 193 F<sub>2:3</sub> families of a cross between 'MousaTarom' and '304' were evaluated under field conditions. The studied traits were seedling height, plant height, culm length, panicle length, penultimate leaf length and width, brown rice length, width, and shape. The parameter *m*, was highly significant for all traits. The additive component of means and variance were highly significant for all the traits except for the additive component of means of seedling height, panicle length, and leaf length. Special environmental component of variance was not significant only for brown rice shape. Culm number and panicle length showed the lowest (<0.19), and brown rice characters showed the highest (>0.78) narrow sense heritability. Common environmental component was not statistically significant for any of the corresponding traits even for those with low heritability estimates and hence means of variances of 'between replication of each non-segregating genotype', including parents and checks used to estimate the common environmental component instead of its deletion, and to estimate heritability with more confidence. Thus, for generations with high environmental component of variance, such as F<sub>2s</sub>, this method could be used to find good information about environmental variation components.**

**Key words:** Rice (*Oryza sativa* L.), F<sub>2:3</sub> families, heritability, environmental variance.

### **INTRODUCTION**

Improving the productivity of rice systems would contribute to hunger eradication, poverty alleviation, national food security and economic development (Khurram et al., 2007). The considered characters in rice breeding may include reduced plant height, strong culms; moderate tillering, short and erect leaves, large and compact panicles, and earliness of maturation (Miller et al., 1993; Nemoto et al., 1995; Mackill and Lei, 1997; Wayne and Dilday, 2003; Paterson et al., 2005). Under field conditions, cultivars have a maximum tiller number and have a termination point for effective tillering also (Hoshikawa, 1989; Moldenhauer et al., 1994; Gravois and Helms, 1996). The prime characters among the various grain

quality characters in deciding the overall grain quality in rice are grain length, breadth, shape, and its weight (Chang and Somrith, 1979; Gravois and Helms, 1996; Tan et al., 1999). Rice grain characteristics such as length, breadth and shape have a direct effect on the marketability, and therefore the commercial success of modern rice cultivars (Redona and MacKill, 1998). Most of the grain quality characters of rice are controlled by quantitative trait loci (QTLs) showing continuous phenotypic variation (Yano and Sasaki, 1997). Genetic postulates on grain length vary from monogenic, digenic, trigenic to essentially polygenic inheritance. Grain breadth showed polygenic inheritance (Lin, 1978; Govindaraj et al., 2005).

Successfully changing the characters of the population using hybridization is predictable only from knowledge of the degree of correspondence between phenotypic values and breeding values. An important function of the

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heritability parameter is expression of the degree of correspondence between the phenotypic and genotypic values. Narrow sense heritability (NSH), expresses the extent to which phenotypes are determined by the genes transmitted from the parents and the proportion of the total variance that can be attributed to the average gene effects (Falconer, 1989; Falconer and Mackay, 1997). Heritability estimates for agro-morphological traits in rice are sparse and contradictory, depending on the genetic materials and used methods (Falconer, 1989). Using parent-offspring correlation based on  $F_2$  populations, narrow sense heritability of grain length and grain width are 0.8 and 0.55, respectively and the estimates do not fluctuate drastically with generation advancement from  $F_2$  to  $F_4$ . Therefore, the authors postulate that selection for grain size of rice is effective even in early segregating generations after crossing (Kato, 1990). Based on analysis of variance of 56 high yielding diverse rice genotypes, broad sense heritability (BSH) is 96.9% for grain length, 92.1% for grain breadth, and 96.4% for length/breadth ratio (Vanaja and Babu, 2006). Narrow and broad sense heritability for plant height is 0.75 and 0.98, respectively, based on diallel crosses analysis (Boonhong, 1997). Using an  $F_2$  population, broad sense heritability is 0.74 for grain length, 0.74 for grain breadth, and 0.89 for grain shape (Rabiei et al., 2004). Panicle length has shown NSH of 9.5 - 82.5% (Horie et al., 1964) and BSH of 4.0% (Sabu et al., 2009). Seedling height and tiller per plant have shown BSH of 76.8 (Lu et al., 2007) and 35.0% (Sabu et al., 2009), respectively.

Environmental variance could be partitioned into general,  $V_{Eg}$  (Falconer, 1989), or common,  $V_{Ec}$  (Kearsey and Pooni, 1996), component of environmental variance, and special,  $V_{Es}$  (Falconer, 1989), or environmental component,  $V_E$  (Kearsey and Pooni, 1996), of environmental variance (Mather and Jinks, 1982; Kearsey and Pooni, 1996). The  $V_{Es}$  or  $V_E$  refers to the within-individuals variance arising from temporary or localized circumstances, and the  $V_{Eg}$  or  $V_{Ec}$ , refers to the environmental variance contributing to the between-individuals component and arising from permanent or non-localized circumstances (Falconer, 1989).

The objectives of this study were estimation and evaluation of means and variance parameters in order to discuss about the gene effects for corresponding traits, and estimation of narrow sense heritability of agro-morphological traits using  $F_{2:3}$  families' analysis with more details and emphasis on components of environmental variation as part of phenotypic variance, with the assumption that having more detailed information of the environmental variance is better to aiding the planning of effective experimental design to improve the plants.

## MATERIALS AND METHODS

### Population development

A cross was made between MousaTarom (the most popular rice

cultivar in Iran due to its favourite grain quality) and 304 (a high-yielding cultivar improved from Huri 302, Hungarian origin) in 2006. A population of 193  $F_{2:3}$  families, parents, and 3 check cultivars named Lenjan Askari, DomSia, and 304 were transplanted at 5-leaf growth stage using an augmented design with 6 replications in June 2008. Preparing of the transplants was conducted in May 2008. Field experiment was conducted at Khanmirza region, (Altitude 1564 m, longitude 50.49, latitude 31.31, mean annual temperature 15.4°C, mean annual precipitation 569.4 mm, with clay-loam soil type), Lordegun, Shahrekord province, Iran. Each plot consisted of 4 rows with 60 plants per plot. The plants were at 25 cm distances both within and between rows. The plants in each plot were the progeny of individual plants, in both segregating ( $F_2$ ) and non-segregating (parents and checks) genotypes. Evaluation of the traits was conducted according to the 'Standard Evaluation System for rice (SES) manual' provided by International Rice Research Institute (IRRI) (IRRI, 2002). The evaluated traits comprised seedling height, plant height, culm length, panicle length, penultimate leaf length, penultimate leaf width, brown rice length, brown rice width, and brown rice shape (brown rice length/width ratio).

### Statistical analysis

The data collected from check cultivars were subjected to analysis of variance (ANOVA) using a randomized complete block design.  $F_3$  generation analysis for all corresponding traits was conducted using one way ANOVA also. Weighted least squares (WLS) were used in multiple variable regression method to estimate the parameters of means and variance, and their standard errors (SE). For computing the  $h^2$ , only statistically significant components of variance were used. The full model matrix was used for means analysis as:  $w_i y_i = w_i (m + [a] X_{1i} + [d] X_{2i})$ , where  $w_i$  was weight of  $i$ th generation, equal to the ratio of family size in the  $i$ th generation ( $n_i$ ) per variance ( $s_i^2$ ). The parameter  $m$  was average phenotype of the two parents, and  $[a]$  was the net balance of additive genetic effects over all the genes. The parameter  $[d]$  was the net balance of the dominance effects, which indicated the direction of dominance of the majority, and  $X_{1i}$  and  $X_{2i}$  are the coefficients of additive and dominance effects for (Table 1)  $i$ th generation according to the previous authors (Mather and Jinks, 1982; Kearsey and Pooni, 1996).

The MSs in the ANOVA are independent, that is, orthogonal, but  $\sigma^2$ s are not. Thus, models are fitted to MSs (Kearsey and Pooni, 1996). Therefore, in ANOVA table of  $F_3$  generation the 'between families' and 'within families' sources of variation family mean squares had expectations  $\sigma_W^2 + r \sigma_B^2$  and  $\sigma_W^2$ , respectively, in which  $r$  was equal to the number of individuals per family. Using the expectations of  $\sigma_W^2$  and  $\sigma_B^2$  given for  $F_3$  generation (Kearsey and Pooni, 1996), then:

$$\begin{aligned} \text{EMS}_B &= \left( \frac{1}{2} V_A + \frac{1}{2} V_D + V_E \right) + r \left( V_A + \frac{1}{4} V_D + V_{Ec} \right) \\ &= \frac{2r+1}{2} V_A + \frac{r+2}{4} V_D + V_E + r V_{Ec}, \text{ and} \end{aligned}$$

$$\text{EMS}_W = \frac{1}{2} V_A + \frac{1}{2} V_D + V_E$$

Where  $V_A$  is the additive component of genetic variance,  $V_D$  is the dominant component of genetic variance, and  $V_E$  is environmental

**Table 1.** The generations, their additive-dominance model, and the coefficients were used in the model.

Parameters			
Generation	<i>m</i>	[ <i>a</i> ]	[ <i>d</i> ]
P <sub>1</sub>	1	1	0
P <sub>2</sub>	1	-1	0
F <sub>3</sub>	1	0	0.25

**Table 2.** Expectation of sources of variation in terms of the additive genetic and environmental components, and the coefficients of variance components used in regression.

Parameters			
Sources	V <sub>E</sub>	V <sub>EC</sub>	V <sub>A</sub>
MS <sub>B</sub>	1	<i>r</i>	(2 <i>r</i> + 1)/2
MS <sub>W</sub>	1	0	0.5
MS <sub>BCs</sub>	1	<i>r</i>	0

variance resulted from differences between individuals within families, and  $V_{EC} = V_{Eg}$  is equal to environmental variance arising from differences between replications of each non-segregating genotype, parents and checks.

Estimation of all the genetical and environmental components of variation was not possible for conducting goodness of fit test; also because there were 4 parameters  $V_A$ ,  $V_D$ ,  $V_{EC}$ , and  $V_E$  and only 4 statistics,  $\sigma_W^2$ ,  $\sigma_B^2$ ,  $\sigma_{BCs}^2$  and  $\sigma_{WCs}^2$ , in which  $\sigma_{BCs}^2$  computed

based on means of variances of 'between replications' and  $\sigma_{WCs}^2$  computed based on means of 'within replications' of parents and controls. It is therefore necessary to ignore one parameter and, because there is bound to be environmental variation ( $V_E$  and  $V_{EC}$ ),  $V_D$  is set to zero (Kearsey and Pooni, 1996).

The computing of  $\sigma_{BCs}^2$  and  $\sigma_{WCs}^2$  was based on interpretation derived from  $EMS_B$ , and  $EMS_W$  when there was not any genetic segregation or in other words using pure lines as parents and control varieties. Therefore, for non-segregating families in which the individuals within each family were derived from single plants, it could be interpreted that:

$$EMS_{BCs} = \sigma_{WCs}^2 + r \sigma_{BCs}^2 = V_E + r V_{EC}, \text{ and}$$

$$EMS_{WCs} = \sigma_{WCs}^2 = V_E$$

Thus, to estimate components of variance of existing generations the full model:  $w_i V_i = w_{1i} (V_A X_{1i} + V_E X_{2i} + V_{EC} X_{3i})$  was used, where  $w_i$  is weight of the *i*th division which is equal to degrees of freedom of the corresponding division  $i / 2(V_i)^2$ , and  $V_i$  is the variance of *i*th division.  $X_{is}$  are coefficients of corresponding variance components as shown in Table 2.

Histograms and kernel density estimations for the distribution of progeny values, the Shapiro-Wilks statistic to study each empirical

distribution, and means and standard deviations were computed for each trait using the STATISTICA7 software (STATISTICA, 2004). ANOVA and matrix operations and other statistical calculations were conducted using EXCEL software (Microsoft office, 2003). Test of goodness of fit was conducted for full model of variance analysis using  $\chi^2$  distribution (df = 1, and  $\alpha=0.05$ ); three parameters based on 4 Statistics or sources. As there were just 3 different generation means including  $F_{2:3}$  families and the parents, so test of goodness of fit for means analysis was conducted for 2-parameter model.

## RESULTS AND DISCUSSION

There were no significant effect of blocks in the ANOVA (data not shown) and thus, it was unnecessary to adjust the data obtained from  $F_{2:3}$  families.

Analysis of means of generations showed that the parameter *m* was highly significant for all evaluated traits. The parameter [*a*] was not significant statistically for panicle length, seedling height, and leaf length (Table 3). The parameter [*d*] was not significant for all of the evaluated traits when 3-parameter model analysis was used (data not shown). Test of goodness of fit showed that using 2-parameter model based on *m* and [*a*], was adequate for all the traits (Table 3). In fact, according to previously cited literature, there was no reason to expect other genetical effects affecting the traits (Kearsey and Pooni, 1996) based on our information.

Variance components analysis showed that additive component of variance ( $V_A$ ) was highly significant for all of the evaluated traits based on all three different computations, 2 (Tables 4, 7) and 3-parameter (Table 6) models and ANOVA method. The amount of  $V_E$  was not significant just for brown rice shape based on all three different computational methods (Tables 4, 6, and 7). There were six replications for each check cultivar and parents, and the differences among blocks were not statistically significant based on the results derived from augmented design as mentioned before. The geometric means of variances resulted from the source of variations of 'between groups or between replication' of each check or parent variety in ANOVA table using one-way ANOVA procedure, was considered to estimate common environmental component ( $V_{EC}$ ) of environmental variation. The  $V_{EC}$  component is negligible for  $F_3$  generation (Kearsey and Pooni, 1996), but ignoring it, is doubtfully.

Using the mentioned procedure,  $V_{EC}$  was not significant statistically using 3-parameter model in analysis of variances (Table 7) and therefore it was possible to ignore the  $V_{EC}$ , reasonably. Two-parameter model based on  $V_A$  and  $V_E$ , was adequate for our obtained information in variance analysis (Table 7). Negative  $V_E$  for grain shape could be due to experimental errors and it could be assumed to be zero (Kearsey and Pooni, 1996). Magnitude of narrow sense heritability for a highly heritable trait is more than 0.5 and for a medium heritable it is between 0.2 and 0.5 (Singh, 2005). The heritability of corresponding traits cited by other authors are shown in

**Table 3.** Means analysis of two-parameter model for the evaluated traits and their  $\pm$  standard errors in  $F_{2:3}$  rice families.

	Culm length (cm)	Plant height (cm)	Panicle length (cm)	Seedling height (cm)	Culm number	Leaf length (cm)	Leaf width (mm)	Brown rice length (mm)	Brown rice width (mm)	Brown rice shape†
<i>M</i>	77.996**	97.994**	21.347**	29.777**	19.094**	65.768**	11.998**	6.2724**	2.281**	2.783**
	$\pm 0.912$	$\pm 0.290$	$\pm 0.087$	$\pm 0.170$	$\pm .240$	$\pm 0.214$	$\pm 0.037$	$\pm 0.0121$	$\pm 0.004$	$\pm 0.010$
[ <i>a</i> ]	9.284**	8.604**	0.557 n.s.	1.057	5.634**	1.084	0.971**	0.6449**	0.212**	0.537**
	$\pm 0.912$	$\pm 0.676$	$\pm 0.415$	$\pm 0.849$	$\pm 0.460$	$\pm 0.687$	$\pm 0.096$	$\pm 0.0458$	$\pm 0.020$	$\pm 0.026$
$X^2_{(df=1)}$	0.0255	0.0379	0.0080	0.0026	2.6795	1.5016	0.0173	0.0175	0.0003	0.0069

† Grain length/width, \*\*  $P < 0.01$ . n.s., not significant.

**Table 4.** Coefficient of variation of evaluated traits, variance components, their  $\pm$  Standard error, and narrow sense heritability resulting from ANOVA of  $F_3$  families based on Kearsley method (Kearsley and Pooni, 1996).

	Culm length (cm)	Plant height (cm)	Panicle length (cm)	Seedling height (cm)	Culm number	Leaf length (cm)	Leaf width (mm)	Brown rice length (mm)	Brown rice width (mm)	Brown rice shape†
CV %	9.27	8.69	13.96	16.79	27.23	10.18	9.48	5.61	5.46	8.30
$V_A$	41.851**	48.280**	1.579**	18.012**	4.683**	19.863**	0.779**	0.180**	0.025**	0.137**
	$\pm 5.743$	$\pm 6.769$	$\pm 0.303$	$\pm 2.460$	$\pm 0.864$	$\pm 2.958$	$\pm 0.109$	$\pm 0.023$	$\pm 0.003$	$\pm 0.017$
$V_E$	29.361**	48.306**	8.083**	15.970**	21.496**	34.649**	0.898**	0.034**	0.003*†	- 0.015 n.s.
	$\pm 3.581$	$\pm 4.562$	$\pm 0.404$	$\pm 1.612$	$\pm 1.092$	$\pm 2.387$	$\pm 0.076$	$\pm 0.012$	$\pm 0.002$	$\pm 0.009$
$h^2$ (Narrow)	0.5877	0.4999	0.1634	0.5300	0.1789	0.3644	0.4643	0.8419	0.8840	1.0000

† Grain length/width, \*\*  $P < 0.01$ . n.s., not significant.

in Table 5. Narrow sense heritability ( $h^2$ ) of studied traits is given in Tables 4, 6 and 7. Similar to previous report (Totiyama and Futsuhara, 1958; Sabu et al., 2009) and in contrast to Rabiei and his colleagues' report (2004), Panicle length and culm number showed the lowest heritability ( $<0.19$ ). Narrow sense heritability of brown rice characteristics was high ( $>0.77$ ) based on the information derived from 3 methods of variance analysis and this was in agreement with previous reports for both grain length and grain breadth (Rabiei et al., 2004; Vanaja and Babu, 2006), but for grain breadth was not in agreement with the results reported by Kato (1990) (Tables 4, 6 and 7).

Based on the presented information, plant height, culm length, seedling height, and brown rice characters, had high heritability and so breeding for these traits is easy to operate. High narrow sense heritability of seedling height showed different explanation from the sentence 'During seedling growth stage, rice seedlings exhibit great morphological plasticity in response to changes in aeration, light, and temperature' as acclaimed by Takashi (Takahashi, 1984) at least for new improved rice cultivars. Leaf characters had medium heritability, and the heritability of culm number and panicle length was low. Therefore, breeding for these traits is difficult because low heritability means that the phenotype is not highly correlated with the genotype. In other words, for these

traits the contribution of environmental conditions is relatively high (Singh, 2005). The low heritability of Panicle length is in agreement with the previous results reported earlier (Toriyama and Futsuhara, 1958; Wells and Faw, 1978; Jennings et al., 1979; Wayne and Dilday, 2003; Sabu, 2009).

The  $V_E$  of brown rice shape was negative in all 3 used methods of variance analysis, and as the variance cannot be negative, it could be said that such unusual event takes place because of experimental errors and should be assumed to be zero. Low heritability of culm number and panicle length showed that environmental factors strongly influence these characters. This was in agreement with previous reports (Hoshikawa, 1989; Moldenhauer et al., 1994; Gravois and Helms, 1996).

Comprising the gained results from 3 used different methods of variance, component analysis showed that the results derived from ANOVA method of Kearsley and Pooni (Kearsley and Pooni, 1996) based on ignoring dominance and  $V_{EC}$  components of variance was completely similar to the 2-parameter model of regression method (Tables 4 and 7). This was not out of suspense because the 2-parameter model was similar to ANOVA method with ignoring the dominance and  $V_{EC}$  components. The results derived from 3-parameter model of variance analysis showed some differences with the

**Table 5.** Reported heritability of corresponding traits cited by different authors.

Trait	Heritability		Reference
	Narrow sense	Broad sense	
Culm height	24.1	-	Toriyama and Futsuhara, 1958
	16.8 - 80.6	-	Horie et al., 1964
	-	72.0	Sabu et al., 2009
Grain breadth	55.5	-	Kato, 1990
	-	92.1	Vanaja and Babu, 2006
	-	74.0	Rabiei et al., 2004
Grain length	-	96.9	Vanaja and Babu, 2006
	-	74.0	Rabiei et al., 2004
	80.0	-	Kato, 1990
Grain shape	-	96.4	Vanaja and Babu, 2006
	-	89.0	Rabiei et al., 2004
Panicle length	-	52.0	Rabiei et al., 2004
	6.0	-	Toriyama and Futsuhara, 1958
	9.5 – 82.5	-	Horie et al. 1964
	-	4.0	Sabu et al., 2009
Penultimate leaf breadth	-	79.0	Mohapatra and Mohanty, 1985
Penultimate leaf length	-	88.0	Mohapatra and Mohanty, 1985
Plant height	75.0	98.0	Boonhong, 1997
	-	93.0	Rabiei et al., 2004
Panicle per plant	-	41.0	Sabu et al., 2009
	-	45.0	Rabiei et al., 2004
	20.4	-	Toriyama and Futsuhara, 1958
	-3.3 – 41.5	-	Horie et al. 1964
	45.0	-	Gravais and McNew, 1993
	16.0	-	Kato, 1997
	< 20.0	-	Surek and Korkut 1998
	< 20.0	-	Surek and Beser, 2005
Seedling height	-	76.8	Lu et al. 2007
Tiller per plant	-	35.0	Sabu et al., 2009

other 2 mentioned method of analysis of variance (Table 7). The results of all methods showed almost no differences among the estimated amounts of narrow sense heritability of evaluated characters for the most characters.

The estimated narrow sense heritability by 3-parameter model for some characters such as plant height and leaf width was higher than their estimations based on other 2 methods. Some characters, on the other hand, such as brown rice length and panicle length had lower heritability

than their estimations based on other 2 methods.

The definition of  $V_A$  shows that gene dispersion does not affect the magnitude of  $V_A$ . Furthermore, being a component of variance,  $V_A$  is orthogonal to  $[a]$  and therefore should not be correlated with  $[a]$ . Consequently, no systematic relationship between  $[a]$  and  $V_A$  will be expected. Small or statistically zero magnitudes of  $[a]$  could be seen due to gene dispersion while  $V_A$  could be large (Kearsey and Pooni, 1996).

Considering the results of means and variances

**Table 6.** Variance components for 3-parameter model and their  $\pm$  standard error, and narrow sense heritability for evaluated traits.

	Culm Length (cm)	Plant Height (cm)	Panicle Length (cm)	Seedling HEIGHT (cm)	Culm number	Leaf length (cm)	Leaf width (mm)	Brown rice length (mm)	Brown rice width (mm)	Brown rice Shape <sup>†</sup>
V <sub>A</sub>	36.896**	48.081**	1.398**	17.808**	4.840**	19.361**	0.994**	0.158**	0.021**	0.113**
	$\pm 5.265$	$\pm 6.130$	$\pm 0.414$	$\pm 3.625$	$\pm 1.161$	$\pm 3.166$	$\pm 0.090$	$\pm 0.024$	$\pm 0.003$	$\pm 0.016$
V <sub>E</sub>	30.982**	34.718**	8.330**	16.009**	20.746**	33.954**	0.694**	0.046**	0.005**	- 0.003 n.s.
	$\pm 2.545$	$\pm 3.514$	$\pm 0.389$	$\pm 1.994$	$\pm .986$	$\pm 2.015$	$\pm 0.048$	$\pm 0.012$	$\pm 0.002$	$\pm 0.008$
V <sub>EC</sub>	8.258	0.746	0.114	0.391	0.166	1.811	0.004	0.007	0.001	0.004
	$\pm 4.403$	$\pm 2.597$	$\pm 0.310$	$\pm 2.994$	$\pm 0.880$	$\pm 2.010$	$\pm 0.033$	$\pm 0.009$	$\pm 0.001$	$\pm 0.004$
$\chi^2$ (df=1, 0.05)	1.28	0.04	0.60	0.70	1.79	3.32	0.39	0.40	0.03	0.02
h <sup>2</sup> (Narrow)	0.5436	0.5807	0.1437	0.5266	0.1892	0.3631	0.5889	0.7763	0.7973	1.000

† Grain length/width, \*\* P < 0.01. n.s., not significant.

**Table 7.** Variance components for 2-parameter model and their  $\pm$  standard error, goodness of fit and narrow sense heritability for evaluated traits.

	Culm Length (cm)	Plant height (cm)	Panicle length (cm)	Seedling Height (cm)	Culm Number	Leaf length (cm)	Leaf Width (mm)	Brown Rice Length (mm)	Brown Rice Width (mm)	Brown Rice Shape <sup>†</sup>
V <sub>A</sub>	41.131**	47.403**	1.575**	17.991**	4.662**	19.619**	0.778**	0.179**	0.024**	0.134**
	$\pm 5.743$	$\pm 6.769$	$\pm 0.303$	$\pm 2.460$	$\pm 0.864$	$\pm 2.958$	$\pm 0.109$	$\pm 0.023$	$\pm 0.003$	$\pm 0.017$
V <sub>E</sub>	29.908**	49.077**	8.096**	15.987**	21.550**	34.947**	0.900**	0.034**	0.003*	-0.014
	$\pm 3.581$	$\pm 4.562$	$\pm 0.404$	$\pm 1.612$	$\pm 1.092$	$\pm 2.387$	$\pm 0.076$	$\pm 0.012$	$\pm 0.002$	$\pm 0.009$ n.s.
$\chi^2$ (df=1)	0.0133	0.0178	0.0000	0.0000	0.0000	0.0000	0.0000	0.2338	0.0364	0.0029
H <sup>2</sup> (Narrow)	0.5790	0.4913	0.1628	0.5295	0.1779	0.3596	0.4636	0.8393	0.8811	1.0000

† Grain length/width, \* P < 0.05, \*\* P < 0.01. n.s., not significant.

expected. Small or statistically zero magnitudes of [a] could be seen due to gene dispersion while V<sub>A</sub> could be large (Kearsey and Pooni, 1996).

Considering the results of means and variances analysis, it could be interpreted that genes with low association control panicle length, seedling height, and leaf length traits, because they had non-significant [a] and significant V<sub>A</sub>.

On the other hand, it could be interpreted that for the expression of these 3 mentioned traits more than one gene are affected. Other-wise, with one affected gene, when [a] is zero it could be expected statistically to be zero magnitude of V<sub>A</sub>. The remaining traits had higher gene association as they had significant values of [a] and V<sub>A</sub>.

Using the computed common environment component of environmental variance in the 3-parameter model, showed that this part of environmental variance, V<sub>EC</sub>, is not statistically significant for any of the studied characters, even for those with low heritability, and this is in agreement with the earlier findings (Kearsey and

Pooni, 1996).

## Conclusions

As in the 3-parameter model, the proportion of V<sub>EC</sub> separated from the total variance and having close result to other 2 methods; it could be said that the recommended method for estimation of components of environmental variance was practical. In order to have correct estimation of environmental components of variation the necessary conditions were having non-segregating genotypes and the individuals of each non-segregating family must be derived from single plants. This method could be used in generations with high proportion of environmental variation in phenotypic variance such as F<sub>2</sub> generations in order to estimate the component of variance with more confidence and reality. The better prediction of the environmental component of phenotypic variance, helps the more reliable estimation of both broad and narrow sense heritability, and so the better planning

program for cross and self pollinated plants improvement.

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