

# Genetic Parameters of Some Wheat (*Triticum aestivum* L.) Genotypes Using Factorial Mating Design

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## Abstract

Using parents and mating designs appropriate in the field of conventional plant breeding are the beginning to successful plant breeding program. However, there are many factors that influence their choices of mating designs, such as genetic parameters, experimental conditions and other biological constraints used in the evaluation process. In this study, Two wheat (*Triticum aestivum* L.) genotypes used as males while, fifteen used as females were assessed for yield and yield associated traits using North Carolina Design II (factorial mating design). The seventeen parents and their 30 F1 progenies were planted in randomized complete block design with three replications in three sets, during the growing season 2009/2010 and 2010/2011 in Ras-Sudr Regoin, South of Sinai, Egypt. Highly significant differences among males, females and hybrids between them were observed for all traits except No. of tillers and weight of grains /spike for females and the hybrids between males and females. The dominance genetic variance was higher than additive genetic variance for all studied traits except grain and straw yield per plant. Both heritability in narrow sense and expected genetic advance as percent were relatively high for spike weight grain yield and straw yield per plant. Depending on the previous genetic parameters we can achieve a quick and easy insight to a successful assessment.

**Keywords:** wheat, additive, dominance, heritability, genetic variance

## 1. Introduction

Wheat (*Triticum aestivum* L.) is the main staple food in Egypt and it occupies a prominent position in the cropping pattern of the country. So, there is a great deal of research work in the field of wheat breeding through genetic variability. However increasing population and climate changes in the country require the breeders for further breakthrough in this food crops. For achieving an improvement in the heritable traits and estimation of genetic parameters is paramount importance in any breeding programme. In plant breeding, various mating designs and arrangements are used by breeders and geneticists to generate improved plants. The selection of suitable parents and good mating designs are keys to a successful plant breeding schemes (Khan et al., 2009). However, there are several factors affecting the choices of mating designs. Mating design refers to the procedure of producing the progenies, in plant breeding, plant breeders and geneticists, theoretically and practically, they use different forms of mating designs and arrangements for targeted purpose. The choice of a mating design for estimating genetic variances should be dictated by the objectives of the study, time, space, cost and other biological limitations. The analysis of variance can be adopted to estimate the components of variances. Therefore, this review aimed at highlighting the most used mating design in plant breeding and genetics studies. It provides easy and quick insight of the different form of mating designs and some statistical components for successful plant breeding (Hallauer et al., 2010). The North Carolina mating design II (factorial mating design) is one of the most widely used genetic designs in plant breeding programs to identify the best parents for hybrid formation, identify superior hybrids, and to assign lines to new heterotic groups (Hallauer & Miranda, 1988). Genetic variability is essential in order to realize response to selection pressure as the estimation of genetic parameters of variation are specific for a particular population and the phenotypic expression of the quantitative character may be altered by environmental stress that affect plant growth and development. In a population under selection for a quantitative character, genotypic frequencies and hence gene frequencies are altered and these changes are further modified by the mating systems that may be employed to advance the selected individuals to the next generation(s) (Chopra, 2000). Thus, the utilization of any criterion for selection is linked with high

genetic coefficient of variation and estimates of heritability as the magnitudes of heritability and other genetic parameters for a character would vary from location to location and the importance of estimation heritability with genetic advance to predict the resulting effect of selecting Johnson et al. (1955) and Ramachandran et al. (1982).

## 2. Material and Methods

Genotypes used in this study were seventeen wheat genotypes, two wheat (*Triticum aestivum* L.) genotypes used as males while fifteen genotypes used as females. The pedigree of these wheat genotypes are shown in Table 1 were assessed for grain and straw yield and yield associated traits using factorial mating design (North Carolina mating design II). In 2009/2010 and 2010/2011 growing seasons, each of fifteen wheat genotypes were crossed to low performing one i.e., (Azeghar-2/3/Mrf2//Bcr/Gro1) and high performing parent (Gemiza 7) to produce the F1 seeds. The seventeen parents (two males and fifteen female) and their 30 F1 progenies were planted in randomized complete block design with three replicates in three sets in Ras-Sudr, South of Sinai, Egypt, (electrical conductivity of soil was 3.8 and water 7.6 mmhos/cm and pH 7.1 during the growing seasons 2009/2010 and 2010/2011) according to Comstock and Robinson, 1952 and Singh and Narayanan 1993. Each replicates consists of 2 rows (beside that 2 rows as a guard), one row for each genotype; 15.0 m long and the distance maintained between rows and between plants were 75 cm and 25 cm, respectively. Data were recorded on various parameters, viz; plant height (cm), No of tillers/plant, spike length, No. of spikelet's/spike, weight of grains/spike, 1000-grain weight (g), No. of grains/ spike and both grain and straw yield/plant (g).

Table 1. Pedigree of seventeen investigated genotypes and the gender of parents used in hybridization

Code	Gender	Pedigree name
V1	♀	(Mrb5/T.dicds600545//Mrb5)903/3/Stj3//Bcr/Lks4/4/Icasyr-1
V2	♀	Azeghar-2//Wdz6/Gil4
V3	♀	Ouasbar-3/3/Topdy-18/Focha-1//Altar 84
V4	♂	Azeghar-2/3/Mrf2//Bcr/Gro1
V5	♀	Azeghar-2/Murlagost-1
V6	♀	ICAMOR-TA04-63/Arislahn-5
V7	♀	319-ADDO/5/D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn
V8	♀	Icasyr-1/4/Assassa/Waha/Brch/3/Bicredera1
V9	♀	MORL-F38//Berch1/Kund1149/3/Bicredera1/Miki
V10	♀	Mrf1/Stj2/3/1718/BT24//Karim
V11	♀	Bcr/Gro1//Mgn1
V12	♀	Geromtel-1/Icasyr-1
V13	♀	Azeghar-2/Murlagost-2
V14	♀	1364-OTDO//Lgt3/Bcrch1/3/Quasnima-1
V15	♀	MORL-F38//Berch1/Kund1149/3/Bicredera1/Miki
V16	♀	Msb11//Awl2/Bit/3/1718/BT24//Karim/4/Assassa//Waha/Brch/3/Bicredera1
V17	♂	CMH74 A. 630/5x//Seri 82/3/Agent (Gemiza 7)

♀: female; ♂: male; code: serial number of genotypes from v1:v17.

### 2.1 Estimation of Genetic Variance

The analysis of variance, the variance components and expected mean square were estimated in Table 2 using software of SAS program. The factorial mating design allowed estimation of some genetic variance components (additive and dominance variance) according to Singh and Narayanan (1993) design. Where, we assumed that epistasis variance was negligible and that the inbreeding coefficient of the parents was zero. The formulas for estimation of genetic variation components calculated according to Foster and Shaw (1988), Lynch and Walsh (1998) and Gilmour et al. (2006) as follows: additive variance within female population:  $VA_f = 4\sigma^2_f$ , additive variance within male population:  $VA_m = 4\sigma^2_m$ , additive variance estimated for the hybrid population is average of  $\sigma^2_A f$  and  $\sigma^2_A m$ :  $VA = 2(\sigma^2_m + \sigma^2_f)$  and the variance of dominance effects will be defined as:  $VD = 4(\sigma^2_m f)$ .

Table 2. Analysis of variance and expected mean squares

S.O.V	d.f	M.S	E.M.S
Set (S)	(s-1)		
Replication within sets	S(r-1)		
Male (M) within sets	s(m-1)	M4	$\sigma^2 e + r \sigma^2 f m + r f \sigma^2 m$
Female (F) within sets	s(f-1)	M3	$\sigma^2 e + r \sigma^2 f m + r m \sigma^2 f$
(M* F) within sets	s(m-1) (f-1)	M2	$\sigma^2 e + r \sigma^2 f m$
Error	s(mf-1)(r-1)	M1	$\sigma^2 e$

S.O.V: source of variance; d.f: degree of freedom; M.S: mean square; E.M.S: expected mean square.

### 2.2 Estimation of Heritability and Expected Genetic Advance

- Total genetic variance (VG) of the hybrid population can be calculated by the following equation:  $VG = VA + VD$  and Phenotypic variance (VP) can be calculated by the following equation:  $VP = VG + VE = (VA + VD) + VE$
- Heritability in the narrow sense  $H^2$  (ns) was estimated by using the following equations:  $H^2 ns = VA / VP$  where, VA = additive variance, VP = Phenotypic variance, and Expected genetic advance (EGA) =  $(H^2 ns) (\sigma P)$  (i) where,  $\sigma P$  = Phenotypic standard deviation,  $i$  = Coefficient of selection which is 2.06 at 5% selection intensity and expected genetic advance as a percent of mean:  $(EGA\%) = (EGA / \bar{x}) \times 100$  where,  $\bar{x}$  = grand mean of each trait.

## 3. Results and Discussion

### 3.1 Mean Performance

The analysis of variance showed that the mean squares for all traits are presented in Table 3. Means sum of squares due to males (M) within sets were high significant for all studied characters. Also, the means sum squares for females (F) were significant for all traits except No. of tillers and weight of grains/spike and the same content for hybrids between males and females (M \* F) in addition to spike weight. That indicated the existence of a high degree of genetic variability to be exploited in breeding program, and it reflected the broad ranges observed for each trait. These findings are in accordance with Asif et al. (2004) who also observed significant variability in wheat germplasm. Hence, it could be noted that, indicates selection for different quantitative characters could be selected for improvement in wheat yield.

Table 3. Mean square of parents and hybrids for the studied characters

S.O.V	d.f	M.S.									
		Plant height	No.of tillers	Spike length	No.of spikelet's /spike	Spike weight	Weight of grains /spike	1000 grain weight	No.of grains /spike	Grain yield	Straw yield
Set(S)	2	4.97	4.40	0.95	3.94	0.23	0.04	6.52	3.63	57.40	682.11
S(r-1)	6	0.43	0.06	0.04	0.04	0.01	0.01	0.17	0.03	0.27	0.82
Male (M)	3	788.56**	20.91**	47.91**	21.38**	37.18**	13.13**	403.13**	2282.11**	583.87**	4963.24**
Female(F)	42	146.29**	0.95ns	2.20**	6.07**	2.06**	0.80ns	17.06**	272.99**	29.44**	252.14**
M* F	42	122.49**	0.88ns	2.07**	7.21**	1.47ns	0.57ns	17.77**	176.73**	16.68**	152.92**
Error	174	0.11	0.20	0.02	0.05	0.01	0.01	0.09	0.04	0.30	0.57

\*, \*\*, ns: significant at 5% and 1% probability level and not significant respectively.

### 3.2 Gene Action and Other Genetic Parameters

Estimates of environmental (VE), additive (VA), dominance (VD), and variances for studied traits are presented in Table 4. The values of dominance genetic variance were greater than additive genetic variance for all studied characters except grain and straw yield per plant and these results depicts the importance of dominant gene effect for controlling these traits. Such results were also reported by Kage et al. (2013). At the same time, the lowest values of narrow sense heritability (0.195 and 0.029) were obtained for plant height and number of spikelet's /

spike respectively and these results indicated that these traits were affected by over-dominance effects of some genes controlling the characters under study which is reflected in the low narrow-sense heritability. Similar results were recorded by Shahrokhi et al. (2013) whom also showed the importance of dominance relative to additive genetic effects by using generation mean analysis method. On the other hand, both grain and straw yield per plant recorded the highest values of additive genetic variance (31.26 and 262.14) respectively and the highest values of narrow sense heritability (0.585 and 0.563) which indicated greater proportion of additive genetic variation suggesting possible improvement in early generations depending on these traits using selection for these traits (Hayman, 1958). In the same manner, Sardana et al. (2007), suggested that high heritability may not necessarily lead to increased genetic gain, unless sufficient genetic variability existed in the germplasm.

### 3.3 Heritability and Genetic Advance

It has been stressed that without expected genetic advance, the Heritability values would not be of practical importance in selection based on phenotypic appearance. According to Ansari et al. (2004) who reported that, high heritability percentage reflects the large heritable variance which may offer the possibility of improvement through selection. However, the estimation of heritability and genetic advance as percentage mean considered together will no doubt help in drawing conclusion about the nature of gene action governing a particular character (Johnson et al., 1955). That was due to the fact that combined study of heritability and genetic advance is more reliable in forecasting the effect of selection. So, genetic advance should be considered along with heritability in coherent selection breeding program. Estimation of heritability in narrow sense ( $H^2_{ns}$ ) and expected genetic advance (EGA%) as percentage of each trait mean are shown in Table 4. In the present investigation, moderate to high heritability values relative in narrow sense (0.585, 0.563 and 0.493) coupled with high expected genetic advance (108.94, 107.44 and 42.05%) were recorded for Grain yield per plant, straw yield per plant and spike weight respectively (Table 4). In the same manner, low heritability values in narrow sense (0.029 and 0.195) was accompanied by low expected genetic advance as a percentage of each trait mean (0.97 and 5.64%) for the number of spikelet's per spike and plant height, respectively. That gives promises for selection of progenies with high heritability values in narrow sense and expected genetic advance values depending on selection for grain yield per plant, straw yield per plant and spike weight traits in early segregating generations. While, number of spikelet's per spike and plant height that showed low  $H^2_{ns}$  and low EGA% showing preference of heterosis for improvement of this trait. Similar findings were also reported by Waqar et al. (2008) who reported that grain yield per plant displayed high heritability estimates with relatively high value of genetic advance. While, Pawar et al. (2002) reported that, plant height, number of tillers exhibited higher heritability.

Table 4. Estimation of components of variance and genetic parameters for different traits in wheat

Character	(VE)	(VA)	(VD)	(Vph)	$H^2$ (n.s)	EGA(%)
Plant height	0.107	39.65	163.18	202.94	0.195	5.64
No. of tillers	0.192	0.98	0.92	2.08	0.468	41.14
Spike length	0.025	2.23	2.72	4.97	0.448	17.11
No. of spikelet's/spike	0.049	0.29	9.55	9.89	0.029	0.97
Spike weight	0.008	1.90	1.94	3.85	0.493	42.05
Weight of grains/spike	0.005	0.67	0.75	1.43	0.471	32.97
1000 grain weight	0.087	18.12	23.57	41.78	0.434	10.68
No. of grains/spike	0.039	132.35	235.58	367.97	0.359	22.97
Grain yield/plant	0.300	31.26	21.84	53.41	0.585	108.94
Straw yield/plant	0.574	262.14	203.12	465.83	0.563	107.44

VE: environmental variance; VA: additive variance; VD: dominance variance; VP: Phenotypic variance;  $H^2$  (n.s): Heritability narrow sense; EGA: expected genetic advance.

## 4. Conclusion

The present study indicated that we can depend on additive variance through grain yield per plant and straw yield per plant in early generations selection for improvement in wheat yield and these finding are consistent with results of both heritability and expected genetic advance. On the other hand, we can use dominance

variance through No. of grains/spike, plant height and No. of spikelet's/spike in hybrid vigor in F1 generation.

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