



Scholars Research Library

Annals of Biological Research, 2012, 3 (5):2464-2468  
(<http://scholarsresearchlibrary.com/archive.html>)



## Combining ability analysis of bread quality in wheat

Ehsan Khodadadi<sup>1\*</sup>, Saeed Aharizad<sup>2</sup>, Mohsen Sabzi<sup>1\*</sup>, Hossein Shahbazi<sup>3</sup> and Ehsaneh Khodadadi<sup>1</sup>

<sup>1</sup>Young Researchers Club, Tabriz Branch, Islamic Azad University, Tabriz, Iran

<sup>2</sup>Plant Breeding and Biotechnology Department of Tabriz University, Iran

<sup>3</sup>Plant Breeding Department of Ardabil Branch, Islamic Azad University, Ardabil, Iran

---

### ABSTRACT

To evaluate the inheritance traits of bread making quality of bread wheat, the  $F_1$  seeds of a  $5 \times 5$  half diallel along with their parents were grown in watered and terminal drought conditions in randomized complete block design with two replications at Islamic Azad University, Ardabil, Iran in 2009. The grain protein content, Zeleny sedimentation volume, loaf volume, grain moisture content, grain hardness, water absorption, SDS-sedimentation volume, wet gluten content, thousand kernel mass and hectoliter mass were measured. The result of combined analysis of variance (in two environments) showed that there are significant differences among genotypes for all of the traits excepts for Zeleny sedimentation volume, grain moisture content and wet gluten content, indicating the presence of enough genetic availability among genotypes and as a result genotype mean square can be further separated to general and specific combining ability mean squares. Furthermore, it was concluded that the conditions of drought stress has significance on the grain protein content, SDS-sedimentation volume, wet gluten content, thousand kernel mass and hectoliter mass. A signification GCA and SCA for some traits also observed additive and non additive gene affects in this traits.

**Keywords:** Bread wheat, Combining Ability, Specific Combining Ability, Diallel cross, Grain quality.

---

### INTRODUCTION

Bread wheat (*Triticumaestivum*L.) is the major staple food source for a large part of world population and is used to produce a wide diversity of baked food products. Therefore, wheat and its production is the main food sources for human. Grain morphology and texture are important quality traits because they influence the market value of wheat [1]. Identification of the basic components determining quality and explaining their modes of function and interrelationships has perplexed scientists for decades [2].

Among the various diallel techniques, combining ability analysis outlined by Griffing[3] is being considered to be more useful to the wheat breeders. Earlier workers revealed that both general and specific combining abilities were involved for yield and yield components [4, 5, and 6]. For effective improvement of quality and yield of wheat, a plant breeder must have knowledge of inheritance of quality and agronomic traits. Until now, many wheat breeders studied heterosis and combining ability of  $F_1$  generation of different agronomic and quality characters in wheat [7, 8]. Wheat quality is influenced by both the genotype and environment and because of the polygenic nature of the characteristics involved [9]; the inheritance of the components of quality is complex [10]. The negative correlations which often exist between quality and yield are a further constraint in breeding [11].

The first aim of this study was to determine the general combining ability (GCA) and specific combining ability (SCA). Knowledge of the genetic systems controlling the quantitative and qualitative characters is essential to choose the most effective and efficient breeding strategy [12]. The second aim was to determine degree of

dominance for the quality characteristics and the third aim was to determine broad sense and narrow sense heritability of the quality characteristics as successful selection and rapid progress is dependent on high heritability.

## MATERIALS AND METHODS

Five bread wheat varieties were crossed in half diallel fashion at the experimental farm of Islamic Azad University, Ardabil, Iran, in 2008. A  $F_2$  diallel was used in order to generate enough seed for a replicated planting. The  $F_2$  progeny, together with the parents, were planted on October 2009, according to randomized complete block design with two replications in normal and drought conditions. These five parents were selected because of the diversity of their SDS-sedimentation volume characteristics. The parents, Sabalan, Pishtaz, Gascogen, Alvand and Soisson have been widely used as commercial cultivars. Plots consisted of 3 rows 1m length that and seeds were spaced 5 cm apart within the rows. Spaces between rows were 20 cm. Nitrogen and potassium were applied based on results of a soil analysis that performed for optimum yield. Normal irrigation applied according to the regional conditions. However, under the drought stress condition, the irrigation is stopped before the flowering stage to prevent the rain to plants, the plastic sealing is utilized. Rust, aphid (*Duraphisnoxia*) infections, and weeds were chemically controlled. In addition, characters related to bread quality of wheat, have been tested in the Seed and plant improvement institute, Karaj, Iran. Near-infrared reflectance spectroscopy (NIR), if calibrated properly, can provide estimates of characters related to Bread quality of wheat [13]. The quantity of grain protein content, Zeleny sedimentation volume, loaf volume, grain moisture content, grain hardness and water absorption were determined by a near infrared reflectance spectrophotometer calibrated against Kjeldahl data. The Zeleny [14] and SDS sedimentation [15] tests can be used to obtain a semi quantitative estimation of the amount of glutenin (or indirectly, of general gluten strength). Heritability of SDS-sedimentation volume is intermediate to high [11]. In this study, SDS-sedimentation volume was performed manually in a 100 ml cylinder filled with 50 ml water at 22 °C in a water bath. A 4g sample of flour was mixed with water and shaken three times at regular intervals. A lactic acid mixture (containing SDS) was added to the mixture, and inverted at regular intervals. Six minutes after the third inversion, a reading was taken [16]. Hectoliter mass is considered an important prediction of flour yield and represents the mass of wheat per volume. The principle of this test is the packing of kernels in a container. Plump kernels pack more uniformly, giving rise to a higher hectoliter mass, whereas smaller kernels usually more elongated, pack more randomly giving a lower mass [17]. Kernel size is usually reported as the actual mass per thousand kernels. In smaller kernels the ratio of endosperm to bran is smaller resulting in low thousand kernel mass and consequently a lower hectoliter mass [17].

**Statistical analysis:** The harvested  $F_2$  seed, together with the parental lines planted at University experimental farm, were analyzed as a  $F_2$  diallel. All statistical analyses performed by SAS 9.1 (Statistical Analysis System software) and EXCEL. An ANOVA was done on the  $F_2$  generation for each characteristic evaluated. The GCA and SCA, as well as the relationship between these two values, were evaluated. GCA is used to designate the average performance of a line in hybrid combination. SCA is used to identify cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved [18]. Degree of dominance indicates whether a character is mainly under the control of additive or non-additive (dominant) gene action [19]. The closer this ratio is to unity, the greater the predictability based on general combining ability alone [20]. Heritability is in fact a regression coefficient of genotypic values (G) on phenotypic values (P). It is defined as the ratio of genotypic to phenotypic variance [21], and is thus the portion of phenotypic variation among individuals due to genetic differences among them. Broad sense and narrow sense heritability's were determined.

## RESULTS AND DISCUSSION

The Combined analysis of variance is given in Table 1. As expected, a significant genotype effect was found for all of the traits except for Zeleny sedimentation volume, Grain moisture content and wet gluten content indicating the presence of enough genetic availability among genotypes and as a result genotype mean square can be further separated to general and specific combining ability mean squares. A significant environment effect was shown for grain protein content, SDS-sedimentation volume, wet gluten content, thousand kernel mass and hectoliter mass.

An ANOVA combining ability of the different quality traits is also given in Table 2. GCA was significant for all the traits except Zeleny sedimentation volume and wet gluten content. This is in agreement with data presented by Barnard *et al.* [17] showing a highly significant GCA for grain protein content, Sing *et al.* [19] and Jain & Sing [12] who reported a significant GCA for thousand kernel mass. This indicates that these various traits are controlled mainly through additive gene action.

SCA was significant for thousand kernel mass and hectoliter mass. Paroda& Joshi [22] reported a significant SCA for thousand kernel mass. The SCA could be an indication of non additive gene action in these traits.

**Table 1. Combined Analysis of Variance for traits**

Source	DF	Means square									
		Grain protein content	Zeleny sedimentation volume	loaf volume	Grain moisture content	Grain hardness	Water absorption	SDS-sedimentation volume	Wet gluten content	Thousand kernel mass	Hectoliter mass
Environment	1	0.541**	0.816 <sup>ns</sup>	814.016 <sup>ns</sup>	0.037 <sup>ns</sup>	0.6 <sup>ns</sup>	0.00016 <sup>ns</sup>	66.15*	18.150**	159.740**	12.096*
Replication(Environment)	2	0.084	3.75	2004.083	0.12	2.83	1.3228	0.016	4.283	7.782	6.699
Hybrid	14	0.086**	2.173 <sup>ns</sup>	1249.757*	0.096 <sup>ns</sup>	5.78**	1.9045**	56.88**	1.214 <sup>ns</sup>	72.031**	19.619**
Environment× Hybrid	14	0.049 <sup>ns</sup>	1.745 <sup>ns</sup>	1222.838**	0.029 <sup>ns</sup>	1.24 <sup>ns</sup>	0.3026 <sup>ns</sup>	6.828 <sup>ns</sup>	1.543 <sup>ns</sup>	13.887 <sup>ns</sup>	9.072**
Error	28	0.027	1.535	510.44	0.056	1.79	0.3989	11.94	0.783	7.388	2.970

\*, \*\* and <sup>ns</sup> significant at  $p \leq 0.05$ ,  $p \leq 0.01$  and non-significant, respectively

**Table 2 Analysis of variance of general combining ability (GCA) and specific combining ability (SCA) for measured traits**

Source	DF	Grain protein content	Zeleny sedimentation volume	loaf volume	Grain moisture content	Grain hardness	Water absorption	SDS-sedimentation volume	Wet gluten content	Thousand kernel mass	Hectoliter mass
GCA	4	0.0425**	0.6475 <sup>ns</sup>	612.595**	0.06**	3.1125**	1.3825**	40.38**	0.235 <sup>ns</sup>	40.847**	8.4125**
SCA	10	0.012 <sup>ns</sup>	0.501 <sup>ns</sup>	192.375 <sup>ns</sup>	0.0075 <sup>ns</sup>	0.7775 <sup>ns</sup>	0.1125 <sup>ns</sup>	3.752 <sup>ns</sup>	0.33 <sup>ns</sup>	8.87**	3.5125**

\*, \*\* and <sup>ns</sup> significant at  $p \leq 0.05$ ,  $p \leq 0.01$  and non-significant, respectively

In Table 3 the GCA effects of the quality traits are listed. To produce the best progeny, parental lines with the highest GCA for a specific trait should be used. Sabalan proved to be the best general combiner for thousand kernel mass, SDS-sedimentation volume, and second best for Grain moisture content. To improve any of these characteristics, Sabalan should be one of the parental lines. Pishtaz was the best combiner for water absorption and second best for grain protein content. Gascogen was the best combiner for loaf volume and second best for grain hardness, Zeleny sedimentation volume and grain protein content. Alvand was the best combiner for hectoliter mass and thousand kernel mass. Sisson proved to be the best general combiner for loaf volume and SDS-sedimentation volume.

**Table 3 GCA effects of measured traits**

Source	Grain protein content	Zeleny sedimentation volume	loaf volume	Grain moisture content	Grain hardness	Water absorption	SDS-sedimentation volume	Wet gluten content	Thousand kernel mass	Hectoliter mass
Sabalan	-0.123**	-0.18 <sup>ns</sup>	-1.42 <sup>ns</sup>	0.12**	-1.15**	-0.72**	3.17**	-0.03 <sup>ns</sup>	3.45**	0.41 <sup>ns</sup>
Pishtaz	0.055*	0.1 <sup>ns</sup>	-8.45*	-0.12**	0.38 <sup>ns</sup>	0.49**	-1.25*	0.03 <sup>ns</sup>	-0.29 <sup>ns</sup>	-0.03 <sup>ns</sup>
Gascogen	0.076**	0.49*	10.82**	0.013 <sup>ns</sup>	0.52*	0.13 <sup>ns</sup>	-1.57*	0.21 <sup>ns</sup>	-1.14*	-1.77**
Alvand	-0.027 <sup>ns</sup>	-0.18 <sup>ns</sup>	-9.38*	-0.029 <sup>ns</sup>	0.13 <sup>ns</sup>	0.06 <sup>ns</sup>	-2.28**	-0.28 <sup>ns</sup>	0.99*	1.21**
Soisson	0.019 <sup>ns</sup>	-0.22 <sup>ns</sup>	8.43*	0.017 <sup>ns</sup>	0.1 <sup>ns</sup>	0.03 <sup>ns</sup>	1.92**	0.07 <sup>ns</sup>	-3.01**	0.17 <sup>ns</sup>
S.E.	0.0277	0.209	3.81	0.04	0.226	0.106	0.58	0.14	0.45	0.29

\*, \*\* and <sup>ns</sup> significant at  $p \leq 0.05$ ,  $p \leq 0.01$  and non-significant, respectively

Table 4 gives the SCA effects of the quality traits for all the crosses. The SCA effect is an indication of the heterosis (interaction) for a specific trait. Although Paroda and Joshi [22] stated that marked decrease in the magnitude of the SCA in the F<sub>2</sub> population were found, good results could still be obtained. Pishtaz×Sabalan proved to be the best specific combination to improve thousand kernel mass characteristics. The combination Gascogen×Sabalan can be used to develop desirable progenies for grain hardness. Soisson×Gascogen proved to be the best cross to improve Zeleny sedimentation volume. Soisson×Alvand proved to be the best cross to improve water absorption, wet gluten content, thousand kernel mass and hectoliter mass.

The calculated values for the degree of dominance are listed in Table 5. This value reveals whether the different characters show an additive or non-additive gene action. In descending order, the following characteristics showed degree of dominance for water gluten content, hectoliter mass, Zeleny sedimentation volume, thousand kernel mass, grain moisture content, loaf volume grain protein content, Grain hardness, SDS-sedimentation volume and Water absorption. Barnard *et al.* [17] also found non-additive gene action for grain protein content, Zeleny sedimentation volume, thousand kernel mass and hectoliter mass. Souza and *et al.* [23] found Zeleny sedimentation volume and hectoliter mass to have equal effects of additive and non-additive gene action.

**Table 4.SCA effects of measured traits**

Crosses	Grain protein content	Zeleny sedimentation volume	loaf volume	Grain moisture content	Grain hardness	Water absorption	SDS-sedimentation volume	Wet gluten content	Thousand kernel mass	Hectoliter mass
Pishtaz×Sabalan	-0.038 <sup>ns</sup>	0.36 <sup>ns</sup>	3.67 <sup>ns</sup>	-0.07 <sup>ns</sup>	0.38 <sup>ns</sup>	-0.11 <sup>ns</sup>	-0.34 <sup>ns</sup>	-0.25 <sup>ns</sup>	2.48*	1.18 <sup>ns</sup>
Gascogen×Sabalan	-0.009 <sup>ns</sup>	-1.02 <sup>ns</sup>	-6.60 <sup>ns</sup>	-0.04 <sup>ns</sup>	1.32*	0.103 <sup>ns</sup>	-1.27 <sup>ns</sup>	0.07 <sup>ns</sup>	0.98 <sup>ns</sup>	-1.01 <sup>ns</sup>
Alvand×Sabalan	-0.006 <sup>ns</sup>	-0.09 <sup>ns</sup>	17.10 <sup>ns</sup>	0.1 <sup>ns</sup>	-0.11 <sup>ns</sup>	-0.33 <sup>ns</sup>	-1.05 <sup>ns</sup>	0.32 <sup>ns</sup>	0.69 <sup>ns</sup>	0.14 <sup>ns</sup>
Gascogen×Pishtaz	-0.086 <sup>ns</sup>	0.19 <sup>ns</sup>	10.17 <sup>ns</sup>	-0.03 <sup>ns</sup>	0.2 <sup>ns</sup>	-0.08 <sup>ns</sup>	-0.09 <sup>ns</sup>	0.5 <sup>ns</sup>	0.7 <sup>ns</sup>	-0.81 <sup>ns</sup>
Alvand×Pishtaz	0.14 <sup>ns</sup>	-0.13 <sup>ns</sup>	-26.61*	-0.18 <sup>ns</sup>	-1.40*	0.17 <sup>ns</sup>	2.36 <sup>ns</sup>	-0.25 <sup>ns</sup>	-5.26**	-3.41**
Alvand×Gascogen	-0.106 <sup>ns</sup>	-0.77 <sup>ns</sup>	-13.14 <sup>ns</sup>	-0.005 <sup>ns</sup>	-0.04 <sup>ns</sup>	-0.53 <sup>ns</sup>	1.44 <sup>ns</sup>	-1.17**	-0.65 <sup>ns</sup>	1.15 <sup>ns</sup>
Sisson×Sabalan	0.138 <sup>ns</sup>	0.84 <sup>ns</sup>	-4.82 <sup>ns</sup>	0.005 <sup>ns</sup>	-0.41 <sup>ns</sup>	0.207 <sup>ns</sup>	1.95 <sup>ns</sup>	0.03 <sup>ns</sup>	-1.94 <sup>ns</sup>	-0.54 <sup>ns</sup>
Sisson×Pishtaz	-0.147 <sup>ns</sup>	-0.51 <sup>ns</sup>	14.03 <sup>ns</sup>	0.12 <sup>ns</sup>	-0.02 <sup>ns</sup>	-0.02 <sup>ns</sup>	-3.01*	-0.42 <sup>ns</sup>	1.14 <sup>ns</sup>	0.16 <sup>ns</sup>
Sisson×Gascogen	0.012 <sup>ns</sup>	1.31*	4.17 <sup>ns</sup>	-0.001 <sup>ns</sup>	-0.95 <sup>ns</sup>	0.07 <sup>ns</sup>	0.2 <sup>ns</sup>	0.28 <sup>ns</sup>	-0.99 <sup>ns</sup>	0.65 <sup>ns</sup>
Sisson×Alvand	0.24 <sup>ns</sup>	0.34 <sup>ns</sup>	11.82 <sup>ns</sup>	0.07 <sup>ns</sup>	0.97 <sup>ns</sup>	0.61*	-2.15 <sup>ns</sup>	0.78*	5.67**	1.41*
S.E	0.071	0.54	9.86	0.103	0.58	0.27	1.5	0.38	1.18	0.75

**Table 5 Dominance and additive variances and degree of dominance for measured characteristics**

Traits	Dominance variance	Additive variance	Degree of dominance
Grain protein content	0.01	0.013	1.24
Zeleny sedimentation volume	0.019	0.01	1.95
loaf volume	115.12	184.74	1.25
Grain moisture content	0.011	0.017	1.29
Grain hardness	0.21	0.936	0.66
Waterabsorption	0.023	0.488	0.31
SDS-sedimentation volume	1.56	14.28	0.47
Wet gluten content	0.238	0.015	5.63
Thousand kernel mass	12.48	14.85	1.30
Hectoliter mass	4.92	2.12	2.15

The broad and narrow sense heritability are tabulated in Table 6. Heritability of a trait is important to a plant breeder, because it reflects its response to selection. The narrow sense heritability (phenotypic variance due to additive genetic variability) differed from as high as 0.82 for water absorption to 0.03 for wet gluten content. Bhatt & Derera[24] reported that for thousand kernel mass heritability, the additive component was higher than the dominance component. This indicates that selection for higher thousand kernel mass should give a good response. Narrow sense heritability for water absorption, SDS-sedimentation volume, was higher than other traits. Selections for these traits to produce superior progeny are much easier because the environmental effects are non-significant. The broad sense heritability's (phenotypic responses for which genetic differences are responsible) were relatively high for most of the characteristics. Thousand kernel mass had the highest value, followed by hectoliter mass, SDS-sedimentation volume, water absorption, grain protein content, loaf volume, grain hardness, wet gluten content, Zeleny sedimentation volume and Grain moisture content. In broad sense heritability the environment plays a significant role in the expression of the phenotype. Bhatt & Derera[24] also found that hectoliter mass, thousand kernel mass, flour protein content and grain protein content had high heritability.

**Table 6. Broad and narrow sense heritability estimates for characteristics**

Traits	Narrow sense heritability	Broad Sense heritability
Grain protein content	0.44	0.79
Zeleny sedimentation volume	0.19	0.23
loaf volume	0.43	0.71
Grain moisture content	0.11	0.16
Grain hardness	0.51	0.63
Water absorption	0.82	0.83
SDS-sedimentation volume	0.76	0.84
Wet gluten content	0.03	0.56
Thousand kernel mass	0.51	0.93
Hectoliter mass	0.27	0.91

## CONCLUSION

Highly significant GCA effects were evident for the grain protein content, loaf volume, grain moisture content, grain hardness, water absorption, SDS-sedimentation volume, thousand kernel mass and hectoliter mass. Therefore good selection responses should be possible for these characteristics highly significant SCA for thousand kernel mass and hectoliter mass effects in these traits.

High narrow sense heritability was also found for water absorption, SDS-sedimentation volume, Grain moisture content and thousand kernels mass. Selections for these traits to produce superior progeny are much easier because the environmental effects are non-significant. The broad sense heritability were relatively high for thousand kernel mass, SDS-sedimentation volume, water absorption, grain protein content, hectoliter mass and grain hardness. In broad sense heritability the environment plays a significant role in the expression of the phenotype.

However, most quality traits are under polygenic control, it is possible to improve quality characteristics through traditional breeding and selection techniques. The results from this study indicate that, by using the correct breeding parents and selection procedures, grain quality can be improved. Selection for the correct quality characteristics will ensure progress and because of the genetic correlations, more than one characteristic can be improved simultaneously.

#### REFERENCES

- [1] C. Lyford, W. Kidd, P.R. Duarte, C. Deyoe, *Journal of Food Quality*, **2005**, 28, 279-288.
- [2] D.B. Fowler, I.A. Delaroche, *Can. J. Plant Sci.*, **1975**, 55, 251-262.
- [3] B. Griffing, *Aust. J. Biol. Sci.* **1956**, 9, 463-493.
- [4] M.A. Chaudhry, M.S. Akhtar, M.T. Ahmad, *J. Agric. Res.*, **1992**, 30, 17-22.
- [5] M.A. Chowdhary, M. Sajad, M.I. Ashraf, *J. Agric. Res.*, **2007**, 45, 11-18.
- [6] Z. Hasnain, G. Abbas, A. Saeed, A. Shakeel, A. Muhammad, M.A. Rahim, *J. Agric. Res.* **2006**, 44, 167-173.
- [7] R.M. Kamaluddin, L.C. Singh, M.Z. Prasad, A.K. Joshi, *Genetics and Molecular Biology*, **2007**, 30, 411-416.
- [8] S.N. Sharma, U. Meno, R.S. Sain, *Acta Agronomica Hungarica*, **2005**, 52, 63-68.
- [9] C.S. Gaines, P.L. Finney, G. Raubenthaler, *Cereal Chem.*, **1996**, 73, 521-525.
- [10] E.R. Ausemus, F.H. Mcneal, J.W. Schmidt, Genetics and inheritance. In: Quisenberry KS, Reitz LP. (ed) *Wheat and Wheat Improvement*, American Society of Agronomy, Publisher Madison, **1967**, Wisconsin, USA.
- [11] J.M. Clarke, F.R. Clarke, N.P. Ames, T.N. Mccaig, R.E. Knox, Evaluation of predictors of quality for use in early generation selection. In: Royo C, Nachit MM, Fonzo ND, Araus JL, Serie A (ed) *Durum wheat improvement in the Mediterranean region*, *Instituto Agronomico Mediterraneo*, **2000**, Zaragoza España.
- [12] K.B. Jain, G. Singh, Estimates of additive, dominance and additive  $\times$  additive genetic variances in common wheat. In: Ramanujam S (ed), *Fifth Int Wheat Genetics Symp.* New Delhi, India. **1978**.
- [13] P.M. Burrridge, G.A. Palmer, G.J. Hollamby, Developing a strategy for rapid wheat quality screening. In: Paull J, Dundas IS, Shepherd KJ, Hollamby GJ (ed) *Proceedings of the 7th Assembly of the Wheat Breeding Society of Australia*, **1994**, Adelaide.
- [14] L. Zeleny, *Cereal Chemistry*, **1947**, 24, 465-475.
- [15] D.W. Axford, E.E. Mcdermott, D.G. Redman, *Cereal Chemistry*, **1979**, 56, 582-584.
- [16] Anonymous. American Association of Cereal Chemists (AACC), USA. *Approved methods of the American Association of Cereal Chemists Inc.*, St. Paul. **1995**.
- [17] A.D. Barnard, M.T. Labuschagne, H.A. Vanniekerk, *Euphytica*, **2002**, 127, 115-122.
- [18] G.F. Sprague, L.A. Tatum, *J. Am. Soc. Agron.*, **1942**, 34, 923-932.
- [19] I. Sing, R.S. Paroda, R.K. Behl, *Wheat Information Service*, **1986**, 62, 74-76.
- [20] R.J. Baker, *Crop Sci.*, **1978**, 18, 533-536.
- [21] G. Wricke, W.E. Weber, *Quantitative Genetics and Selection in Plant Breeding*, Walter de Gruyter & Co, **1986**, Berlin.
- [22] R.S. Paroda, Joshi, A.B. *Ind J Genet & Plant Breed.* **1970**, 30, 630-637.
- [23] E.J. Souza, R.A. Graybosch, M.J. Guttieri, *Haworth Press*, **2002**, 1, 39-74.
- [24] G.M. Bhatt, N.F. Derera, *Euphytica*, **1975**, 24: 597-604.