The Bioscan 8(2): 503-507, 2013
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES
www.thebioscan.in

ESTIMATION OF COMPONENTS OF GENETIC VARIANCE IN MAIZE (*ZEA MAYS* L.)

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KEYWORDS
Additive variance
Dominance variance
Dominance ratio
Full sib and Half sib family

Received on :
06.12.2012

Accepted on :
04.03.2013

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ABSTRACT

A total 256 full sib progenies (64 half sib families) of a large random mating heterozygous population of maize composite Mahidhawal were evaluated in two environments consisting of two different levels of fertility *viz*., (i) high N (E_1) and (ii) low N (E_2). The estimate of additive variance for grain yield per plant was positive and significant in E_2 and pooled analysis while it was positive but non-significant in E_1. This suggested additive variance is more important in determining grain yield under low N. Dominance variance for grain yield per plant was positive significant in E_1, E_2 and pooled analysis but higher magnitude under high N. This indicated that both additive variance and dominance variance contribute significant role in expression of total genetic variability for seed yield and other traits. Additive x environments interaction components were non-significant for all the traits In contrast, dominance x environments interaction components were positive significant for days to 50% tasseling, days to 50% silking, 100 - grain weight, grain yield per plant and stover yield per plant. Study of dominance ratio revealed that the genes responsible for expression of majority of traits including grain yield per plant showed complete dominance to over dominance.

INTRODUCTION

Maize (*Zea mays* L.) is tropical C_4 plant and photo-insensitive nature grown in all seasons. It has highest yield potential than any of cereal crops, that's why, it is also known as 'Queen of cereals'. It is an allogamous plant has been widely use for fundamental and applied genetic studies. Maize cultivars present different behavior when grown in low levels of N and show different N partition and biomass inside the plant, especially in terms of N removed from the vegetative tissues (Ta and Wieland, 1992). Nitrogen affects cell and tissue growth, thereby influencing leaf area and photosynthetic capacity (Settini and Maranville, 1998). With respect to genetics parameters related to N use efficiency, dominance effects had the great contribution to the observed genetic variance (Clark and Duncan, 1991). Estimation of genetic variance components in maize population is of prime importance for breeder to select the best breeding programs. The choice of the most efficient breeding scheme for improving maize population is dependent upon the relative amount and type of genetic variability involved. It has been well established that most of the broad based and relatively unselected composite varieties built from genetically diverse source materials have a preponderance of additive genetic variance for most of the agronomic traits of economic importance (Singh, 1980). Estimates of additive and dominance genetic variance help to choose the most effective breeding procedure for a crop species. Selection within populations would be advisable only when the gene action is mainly additive. On the other hand, existence of dominance or epistasis justifies the use of hybrid programme (Gulzaffar *et al*., 2001). North Carolina Design-I mating scheme which was suggested by Comstock and Robinson (1948, 1952) has been extensively used for estimating genetic variations for quantitative characters in maize populations. In the present investigation genetic analysis of a large random mating heterozygous maize population, Mahidhawal was undertaken to study its genetic architecture using North Carolina Design-I to derive information on relative magnitude of additive and dominance variance, their interaction with environments and dominance ratio (average level of dominance) at 5 per cent selection intensity through full sib family selection and mass selection methods.

MATERIALS AND METHODS

The experimental material consisted of 256 full sib families (64 half sib families) developed as per North Carolina Design-I in heterozygous, large random mating Mahidhawal population of maize at the Research Farm of the Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Udaipur. To develop full sib and half sib families, each 64 randomly chosen male plants were crossed with five randomly chosen female plants. After harvest, out of the five female plants, four successfully pollinated female plants that had sufficient seed for field evaluation were retained to constitute a male group (a group of four families involving the same male parent). Sixty four such male groups (half sib families) or a total of 256 full sib families were obtained in Mahidhawal population. The 256 full sib families were

Table 1: Analysis of variance (NC Design-I) for different characters in population Mahidhawal

S.No.	Source of variation	d.f.	Mean square Days to 50% tasseling E_1	 E_2	 Days to 50% silking E_1	 E_2	 ASI E_1	 E_2	 Ear length E_1	 E_2	 Ear girth E_1	 E_2	 Kernel rows per ear E_1	 E_2
1.	Sets	15	11.98**	14.44**	10.31**	13.09**	0.59	0.37	9.51**	10.63**	0.64**	0.98**	2.88**	1.42**
2.	Replication in sets	16	10.01**	10.82**	9.25**	13.67**	0.17	0.35	4.33**	4.13**	0.82**	0.65*	0.43	0.76
3.	Males in sets	48	6.79**	10.34**	7.50**	11.34**	0.36	0.27	2.91**	3.10**	0.70**	0.62**	2.09**	2.06**
4.	Females in males in sets	192	3.20**	4.34**	3.81**	4.91**	0.34	0.31	1.97*	1.79**	0.40**	0.33	0.73**	0.94**
5.	Error	240	1.00	0.91	1.39	1.15	0.35	0.25	1.45	1.28	0.23	0.32	0.51	0.49

*Significant at 5% level; ** Significant at 1% level

Table 1: Cont.....

S.No.	Source of variation	d.f.	Mean square 100-grain weight E_1	 E_2	 Number of cobs per plant E_1	 E_2	 Grain yield per plant E_1	 E_2	 Stover yield per plant E_1	 E_2	 Harvest index E_1	 E_2
1.	Sets	15	15.26**	20.10**	0.011	0.010	1659.73**	1237.19**	2662.60**	2027.07**	24.75**	16.29**
2.	Replication in sets	16	7.10**	2.64	0.011	0.008	517.54**	452.10**	412.64**	325.08**	5.75	7.23**
3.	Males in sets	48	14.21**	21.16**	0.020**	0.007	539.97**	431.77**	416.41**	362.48**	12.38**	4.83**
4.	Females in males in sets	192	10.47**	11.26**	0.025**	0.013**	340.27**	246.18**	318.26**	254.60**	6.95**	4.73**
5.	Error	240	1.85	2.63	0.011	0.009	92.25	85.75	72.51	67.59	4.31	2.01

evaluated in two different environments created by two different levels of fertility *viz.*, (i) High N, 120: 60:00 NPK kg per hectare (E_1 or HN) and (ii) Low N, 60: 60: 00 NPK kg per hectare (E_2or LN) in incomplete block design with two replication. The mean values were used to compute the analysis of variance for individual environment by Comstock and Robinson (1948) and pooled analysis over the environments by Robinson *et al.,* (1955). Estimation of additive and dominance components by Comstock and Robinson (1948, 1952) and dominance ratio by Robinson *et al.* (1955).

RESULTS AND DISCUSSION

The mean squares due to sets were significant for all the characters in both environments except due to anthesis silking interval and number of cobs per plant in E_1 and E_2 (Table 1). Further, the mean square due to partitioning of genotypic variance into males in sets and females in males in sets were also significant for all the characters in both environments except due to males in sets for anthesis silking interval in E_1 and E_2 and number of cobs per plant in environment E_2 and due to females in males in sets for anthesis silking interval in both environments (E_1 and E_2) and ear girth in E_2 environment. This suggested that experiment materials were variable for all the characters. In the pooled analysis of variance, the mean squares due to environments, sets, males in sets and females in males in sets were found significant for all the traits except number of cobs per plant due to environments and for ASI due to males in sets and for kernel rows per ear due to females in males in sets (Table 2). Further, the mean squares due to sets x environments and males in sets x environments were found non-significant for most of the traits under study except due to sets x environments for 100-grain weight, grain yield per plant, stover yield per plant and harvest index and due to males in sets x environments for grain yield per plant, stover yield per plant and harvest index. The mean squares due to female in males in sets x environments were significant for most of the traits under study except ASI, ear length, ear girth, kernel rows per ear and number of cobs per plant. This suggested that were considerable variability was present in experimental materials for most of the characters. Similar trend of variance and its components for different traits were reported by Wolf *et al.* (2000) and Vasic *et al.* (2001) and significant estimates of interaction components of variance for different traits were also reported by Pacheco *et al.* (1998) and Gulzaffar *et al.* (2000).

Estimates of additive genetic variance (σ^2_A) were positive and significant for days to 50% tasseling, days to 50% silking, ear girth and kernel row per ear in environment E_1, E_2 and in pooled analysis (Table 3). This indicated the scope for manipulation of different characters in desired direction through selection in population Mahidhawal. Estimates of additive genetic variance were also found significant for ear length in E_2, for 100 grain weight and grain yield per plant in E_2 and pooled analysis. This indicated that additive genetic variance is important in determining the inheritance of grain yield of maize under low N. Whereas σ^2_A was positive but non-significant for anthesis silking interval (ASI) and ear length in E_1 and pooled analysis, 100-grain weight and grain yield per plant in environment E_1, harvest index in E_2 and in pooled

Table 2: Pooled analysis of variance (NC Design-I) for different characters in population Mahidhawal

S.No.	Source of variation	d.f.	Mean square					
			Days to 50% tasseling	Days to 50 % silking	ASI	Ear length	Ear girth	Kernel rows per ear
1.	Environments	1	58.14**	100.00**	5.64**	48.08**	20.70**	43.50**
2.	Sets	15	24.98**	21.92**	0.85**	18.14**	1.40**	3.70**
3.	Sets x Environments	15	1.44	1.48	0.11	2.00	0.23	0.605
4.	Replication in sets in environments	32	10.42**	11.46**	0.26	4.23**	0.73**	0.60**
5.	Males in sets	48	15.88**	17.35**	0.42	4.77**	1.14**	3.77**
6.	Females in males in sets	192	5.72**	6.41**	0.38*	3.00**	0.54**	1.34
7.	Males in sets x Environments	48	1.25	1.49	0.21	1.24	0.18	0.38
8.	Females in males in sets x Environments	192	1.82**	2.31**	0.27	0.76	0.18	0.33
9.	Pooled error	480	0.96	1.27	0.30	1.36	0.28	0.50

* Significant at 5% level; ** Significant at 1% level

Table 2: Cont.....

S.No.	Source of variation	d.f.	Mean square				
			100-grain weight	Number of cobs per plant	Grain yield per plant	Stover yield per plant	Harvest index
1.	Environments	1	162.79**	0.02	15551.64**	11302.34**	110.76**
2.	Sets	15	30.94**	0.01*	2407.77**	4213.31**	33.43**
3.	Sets x Environments	15	4.43**	0.002	489.15**	476.36**	7.61**
4.	Replication in sets in environments	32	4.87**	0.009	484.82**	368.86**	6.49**
5.	Males in sets	48	32.83**	0.022**	809.38**	648.59**	12.43**
6.	Females in males in sets	192	18.10**	0.032**	429.84**	419.89**	7.44**
7.	Males in sets x Environments	48	2.55	0.006	162.36**	130.29**	4.77*
8.	Females in males in sets x Environments	192	3.63**	0.006	156.61**	152.97**	4.24**
9.	Pooled error	480	2.24	0.010	89.009	70.05	3.16

analysis and for stover yield per plant in E_1, E_2 and pooled analysis. On the other hand, negative estimates of σ^2_A were observed for anthesis silking interval in E_2 and number of cobs per plant in E_1, E_2 and pooled analysis (Table 3). However, information on gene action conditioning grain yield under low N has been limited and contradictory. Beck and Betran (1997) reported that both additive and non-additive genetic effects were important in determining the inheritance of grain yield of maize under low N. On the other hand, Betran *et al.* (2003) reported that non-additive genetic effects condition grain yield of maize hybrids under low N while additive genetic effects govern grain yield under high N. Kling *et al.* (1997) found that additive genetic effects condition grain yield of maize under low N while non-additive genetic effects control yield under high N conditions. Guedes *et al.* (2011) showed that additive genetic effects are more important under conditions of average and low availability of N.

The estimates of dominance variance (σ^2_D) showed in Table 3 revealed that positive significant for 100-grain weight, number of cobs per plant, grain yield per plant and stover yield per plant under high N (E_1), low N (E_2) and pooled analysis but their magnitude was higher under high N (E_1). It indicated that high nitrogen (E_1) was more favourable for the manifestation of genetic worth of the genotypes than low N (E_2). Dominance variance was also positive significant for days to 50% tasseling, days to 50% silking and harvest index in environment E_1 and E_2, ear length and ear girth in pooled analysis. Thus dominance variance played significant role in the expression of these traits under both the environment for total genetic variability. However, dominance variance estimates were positive but non-significant for days to 50% silking, days to 50% tasseling and harvest index in pooled analysis, anthesis silking interval and kernel rows per ear in E_2 and in pooled analysis, for ear length in E_1 and E_2 and for ear girth in E_1, while negative estimates of dominance variance were observed for anthesis silking interval and kernel rows per ear in environment E_1 and ear girth in E_2. These results are in agreement with the findings of earlier workers (Gulzaffar *et al.*, 2001 and EL-Badawy, 2011). Interaction components (σ^2_{AL} and σ^2_{DL}) in Table 3 revealed that the estimates of additive x environments interaction components (σ^2_{AL}) were non-significant for all the traits but positive estimates for ear length, kernel rows per ear, grain yield per plant and harvest index, while remaining traits showed negative estimates of additive x environments interaction components. In contrast, dominance x environments interaction component (σ^2_{DL}) estimates were positive and significant for days to 50% tasseling, days to 50% silking, 100-grain weight, grain yield per plant and stover yield per plant. While non-significant but positive estimates observed for harvest index and negative estimates of σ^2_{DL} were observed for anthesis silking interval, ear length, ear girth, kernel rows per ear and number of cobs per plant. These results suggested that dominance x environments interaction component played greater role in determining the total genetic variability in Mahidhawal population than additive x environments interaction component. But Silva *et al.* (2004) reported that additive x environments interaction components (σ^2_{AL}) were significantly greater than dominance x environments interaction component (σ^2_{DL}) for grain yield and other traits. Dominance ratio (σ^2_D/σ^2_A) aids in deciding the most efficient selection methodology for obtaining significant genetic advance as it is an indicator of comparative magnitude of dominance and additive variance. Dominance ratio revealed that out of 33 estimates, in 21 estimates were showed complete dominance to over dominance, as values ranged from one to more than one, thereby indicated that dominance variance

Table 3: Estimates of genetic components of variance for eleven characters in maize composite Mahidhawal

Character	Environment	σ^2_A	σ^2_D	σ^2_{AL}	σ^2_{DL}	σ^2_D/σ^2_A
Days to 50% tasseling	E_1	1.80**	2.59**			1.44
	E_2	2.99**	3.84**			1.28
	Pooled	2.68**	1.22	-0.28	1.99**	0.45
Days to 50% silking	E_1	1.84*	2.99**			1.62
	E_2	3.21**	4.31**			1.34
	Pooled	2.94**	1.15	-0.41	2.49**	0.39
Anthesis silking interval	E_1	0.009	-0.032			-
	E_2	-0.02	0.14			-
	Pooled	0.02	0.09	-0.031	-0.036	3.68
Ear length (cm)	E_1	0.47	0.54			1.21
	E_2	0.65*	0.37			0.57
	Pooled	0.32	1.91**	0.23	-1.44	5.90
Ear girth (cm)	E_1	0.15*	0.17			1.14
	E_2	0.14*	-0.14			-
	Pooled	0.15*	0.20*	-0.0007	-0.18	1.36
Kernel rows per ear	E_1	0.67**	-0.22			-
	E_2	0.56**	0.33			0.60
	Pooled	0.59**	0.41	0.02	-0.35	0.68
100-grain weight (g)	E_1	1.86	15.38**			8.22
	E_2	4.95**	12.29**			2.48
	Pooled	3.95**	10.51**	-0.54	3.32**	2.65
Number of cobs per plant	E_1	-0.0025	0.031**			-
	E_2	-0.0028	0.010**			-
	Pooled	-0.0025	0.028**	-0.0001	-0.0074	-
Grain yield per plant (g)	E_1	99.85	396.17**			3.96
	E_2	92.79*	228.05**			2.45
	Pooled	93.44*	179.77**	2.87	132.33**	1.92
Stover yield per plant (g)	E_1	49.07	442.41**			9.01
	E_2	53.93	320.07**			5.93
	Pooled	62.84	204.07**	-11.33	177.17**	3.24
Harvest index (%)	E_1	2.71*	2.57**			0.94
	E_2	0.049	5.37**			107.72
	Pooled	1.11	2.08	0.26	1.89	1.86

* Significant at 5% level; ** Significant at 1% level; — One of the component of ratio was absent.

was main contributor to total genetic variability for most of the traits (Table 3). Estimates of dominance ratio showed over dominance for grain yield per plant and stover yield per plant but higher in magnitude under high N (E_1) than low N (E_2). This showed that high nitrogen was more favorable for expression of over dominance for mostly traits. Silva *et al.* (2004) also reported over dominance for grain yield. Similar findings of results for dominance ratio in maize were also reported (Umakanth, *et al.,* 2000; Gulzaffar *et al.,* 2001 and EL-Badawy, 2011). Non-additive gene effects were played an important role in the inheritance of yield and other traits (Soliman *et al.,* 2005; El-Hosary *et al.,* 2006; Sedhom *et al.,* 2007 and El-Badawy, 2013). Meseka *et al.* (2006) also reported non-additive gene action was slightly higher than additive gene action for grain yield under low N. From the foregoing discussion, it is clear that there is preponderance of non-additive genetic variance for yield and other traits in this population. The population Mahidhawal at this stage is fit for the exploitation of non-additive gene effects, which can be mobilized in specific hybrid combinations to ensure development of superior hybrids in maize breeding programme.

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