

## GENERATION MEAN ANALYSIS IN MAIZE (*Zea mays* L.)

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### ABSTRACT

The present investigation on generation mean analysis in maize was carried out during the year 2016-17 in RBD replicated thrice and data were recorded for grain yield and its contributing traits for six generations of two crosses viz., NMI-3 × NMI-7 and NAUM-26 × NAUM-21. ANOVA showed significant variation among generations. The data were subjected to test epistasis and different gene action by using scaling test and six parameter model of generation mean analysis. It was observed that all types of gene action i.e. additive, dominance and epistatic components were playing important role in the inheritance of different characters but their degree differed with their crosses. Generation mean analysis revealed the presence of both additive and dominance type of gene action observed in the cross NMI-3 × NMI-7 for all yield and its contributing characters except dominance gene effect for cob girth. The cross NAUM-26 × NAUM-21 showed both additive and dominance type of gene effects for yield attributing characters except cob length, cob girth and number of grains cob<sup>-1</sup>. The magnitude of dominance gene action was more than additive in both the crosses. Regarding inter-allelic interactions i.e. dominance × dominance type was more pronounced than additive × additive and additive × dominance interaction for yield and its components in both the crosses. The opposite sign of dominance (h) and dominance × dominance (l) components indicated duplicate type of epistasis. Non applicability of simple additive-dominance model revealed importance of epistasis components in yield contributing traits can be exploited through reciprocal recurrent selection.

(Key words: Maize, additive, dominance, epistasis, generation mean analysis, gene action, quantitative traits)

### INTRODUCTION

Maize (*Zea mays* L.) is the third most important cereal crop in the world belongs to family Poaceae. Maize is one of the versatile crop with wider genetic variability and able to grow successfully throughout the world covering tropical, subtropical and temperate agroclimatic conditions. It can grown throughout the year for different purposes including grain, fodder, green cobs, sweet corn, baby corn and pop corn. In any breeding program, it is essential to have an idea of the nature and magnitude of variability in respect of breeding material at hand. The simple scaling test (Mather, 1949) followed by generation mean analysis (Hayman, 1958) provide a more precise assessment of additive, dominance and epistatic gene effects in respect of individual cross.

Since nature and magnitude of gene effects tend to change with cross, more studied based on generation mean analysis in diverse crosses are warranted for getting deeper understanding of gene actions involved in inheritance of various traits in maize.

Generation mean analysis is a simple but useful technique for estimating gene effects for polygenic traits and its greatest lying in the ability to estimate gene effects such as additive × additive, additive × dominance and dominance × dominance effects (Novoselovic *et al.*, 2004). The knowledge of genetic architecture and inheritance pattern of yield and yield contributing components is very essential for breeder to plan breeding program for getting efficient results in succeeding generations. Hence, present investigation was undertaken with the objective of studying genetic nature of yield attributing traits by applying simple scaling test for detection of non-allelic interaction and estimate gene effects by generation mean analysis.

### MATERIALS AND METHODS

The present investigation was carried out at Agricultural research farm of College of Agriculture, Nagpur during 2017-18. Four homozygous and genetically diverse strains of maize viz., NMI-3, NMI-7, NAUM-26 and NAUM-21 were selected for building up the experimental materials.

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During *kharif* 2016-17, all four parental lines were crossed to produce two  $F_1$  hybrids. The  $F_1$  hybrids were selfed to obtain  $F_2$  and backcrossed for setting  $BC_1$  and  $BC_2$  in *rabi* 2016-17. The experimental materials for the present investigation comprised of the six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) of each of the two crosses i.e. NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21. All six generations of above crosses were grown in randomised block design with three replications. In each of replication non segregating parents  $P_1$ ,  $P_2$  and  $F_1$ 's generations were represented by two rows,  $BC_1$  and  $BC_2$  by three rows and  $F_2$ 's by five rows. The rows 5 m long with row spacing 60 cm and 20 cm between plants and within row. The data were recorded on 20 plants in parents and  $F_1$ 's, 30 plants in backcrosses and 50 plants in  $F_2$  replication wise for days to 50% tasseling, days to 50% silking, days to maturity, cob length, cob girth, number of grains  $\text{cob}^{-1}$ , 100 grain weight and grain yield  $\text{plant}^{-1}$ . The data were analyzed by using Indostat advanced breeding package for testing epistasis and six generations mean analysis.

## RESULTS AND DISCUSSION

Mean performance of two crosses in six generations for various characters are presented in table 1. The estimates of scaling tests are presented in table 2 and 3.

### Days to 50% tasseling

Significant differences among different generations under study for days to 50% tasseling indicated the presence of sufficient variability. Significant values of scaling tests in both the crosses i.e. NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21 showed presence of non-allelic genetic interactions. The estimates of m, d, h, i, j and l were significant in both the crosses, which indicated predominant role of additive, dominance and epistatic gene effects. But the magnitude of dominance (h) component was higher than additive (d) component but in negative direction which indicated dominance of decrease alleles.

Among the epistatic dominance  $\times$  dominance (l) was higher in magnitude than additive  $\times$  additive (i) and additive  $\times$  dominance (j). Opposite sign of dominance (h) and dominance  $\times$  dominance (l) components indicated duplicate type of gene action. Therefore, reciprocal recurrent selection can be utilized the fixable and non-fixable genetic components of variation for the trait in both the crosses i.e. NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21. Haq *et al.* (2010) and Ishfaq (2011) reported that both additive and non-additive gene action are important in controlling this trait while Moradi (2014) also reported additive gene effects for this trait.

### Days to 50% silking

After obtaining significant differences from analysis of variance, six parameter model was used to find out the genetic effects as well as contribution of genetic interactions for the expression of days to 50% silking attitude. Results of scaling test revealed that non-allelic interactions played their role significantly in the inheritance

of said character because the entire scaling test i.e. A, B, C and D were significant in both the crosses i.e. NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21. It is evident from table 2 and 3 that both additive and dominance genetic components were significant in both the crosses.

Among the epistatic gene effects, all the three types of digenic interactions were found in the inheritance of this trait in both the crosses expect additive  $\times$  additive (i) in cross NAUM-26  $\times$  NAUM-21. Duplicate type of epistasis was found for this trait in both the crosses. Thus, reciprocal recurrent selection can be feasible breeding strategy for both NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21 crosses. Wannows *et al.* (2015) observed non-additive gene effect was responsible in the inheritance of this trait, while Singh and Roy (2007) stated that additive gene effect was responsible in controlling this trait.

### Days to maturity

Parental lines showed significant differences for days to maturity. Both additive and dominance gene action was significant for this trait in both the crosses but later was greater in magnitude indicating preponderance of dominance gene effects in the expression of days to maturity. Among epistasis gene interaction, dominance  $\times$  dominance (l) gene effect was common in the inheritance of this trait in both the crosses. Opposite sign of dominance (h) and dominance  $\times$  dominance (l) components indicated the presence of duplicate type of gene action for this trait in both NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21 crosses. Thus, reciprocal recurrent selection can be feasible breeding strategy for both the crosses. Similar results have been reported by Ishfaq (2011) and Iqbal *et al.* (2010), who demonstrated that the days to maturity was under the control of non-additive gene action.

### Plant height

The genotype exhibited variation in plant height where in NMI-7 was tallest and NMI-3 was dwarf among parents. The significance of both additive and non-additive gene effects were important in controlling the inheritance of plant height in both NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21 crosses. All three types of digenic interactions were found in the inheritance of this character in both the crosses. The opposite sign of dominance (h) and dominance  $\times$  dominance (l) in both the crosses indicated the presence of duplicate type of epistasis. Thus, reciprocal recurrent selection would be most beneficial for exploitation of plant height in both the crosses. These results are in accordance with the findings of Sofi *et al.* (2006) and EI-Badawy (2012), who reported that plant height was under the control of duplicate type of gene action in maize.

### Cob length

Sufficient variability for ear length was observed in parents and it varied from 16.48 cm to 15.52 cm. The additive (d) gene effect was common in both the crosses studied for governing the inheritance of this trait. However, in cross NMI-3  $\times$  NMI-7 both additive and dominance gene effects were found to be significant. All the epistatic interactions were found to be significant in both the crosses

whereas additive  $\times$  dominance (j) type of non-allelic interaction was non-significant in cross NAUM-26  $\times$  NAUM-21. Duplicate type of epistasis was found for this trait in both the crosses i.e. NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21. Presence of this type of epistasis is likely to cause hindrance in selection response. Umar *et al.* (2015) and Wannows *et al.* (2015) found predominant of non-additive type of gene action in governance of cob length in maize.

#### **Cob girth**

Variability was observed for this trait in parental lines and it ranges from 14.25 cm to 13.20 cm. The additive gene effect was common in both the crosses studied for governing the inheritance of cob girth. However, in cross NMI-3  $\times$  NMI-7 both additive and dominance gene effects were found to be significant. Among epistasis gene interaction, all three types of digenic interactions were found to be significant in the inheritance of this trait in both the crosses *viz.*, NMI-3  $\times$  NMI-7 and NAUM-26  $\times$  NAUM-21. Duplicate type of epistasis was found for this trait in both the crosses. Therefore, reciprocal recurrent selection can be utilized the fixable and non-fixable genetic components of variation for the trait in both the crosses. The result corroborated with the findings of Azizi *et al.* (2006) and Sofi *et al.* (2006). They found that cob girth of maize was controlled by dominance and dominance  $\times$  dominance type of gene action.

#### **Number of grains cob<sup>-1</sup>**

The parents were diverse for this trait. The significance of both additive and non-additive gene actions were important in controlling the inheritance of this trait in cross NMI-3  $\times$  NMI-7. Therefore, efficient utilization of fixable and non-fixable components of genetic variation, reciprocal recurrent selection would be suggested for cross NMI-3  $\times$  NMI-7. All the epistatic interactions were found to be significant in this cross. Whereas only dominance  $\times$  dominance (l) type of interaction was observed in cross NAUM-26  $\times$  NAUM-21. Duplicate type of epistasis was found for this trait in cross NMI-3  $\times$  NMI-7. Presence of this type of epistasis is likely to cause hindrance in selection response. Sher *et al.* (2012) and Azizi *et al.* (2006) have also reported that, the duplicate type of epistasis was found for this character.

#### **100 grain weight**

100 grain weight among parents varied from 22.81 g to 17.56 g. The significant of both additive and non-additive gene effects were important in controlling the inheritance of this in both the crosses. But the magnitude of dominance

gene effect was higher than additive gene effect in negative direction which indicated dominance of decrease alleles. All three types of digenic interactions were found to be significant in the inheritance of this trait in both the crosses expect additive  $\times$  dominance (j) in cross NAUM-26  $\times$  NAUM-21. The opposite sign of [h] and [l] gene effects confirmed existence of duplicate type of epistasis for 100 grain weight in both the crosses. Thus, reciprocal recurrent selection can be a feasible breeding strategy for both the crosses. Moradi (2014) and Hussein *et al.* (2017) reported both additive and non-additive gene action with predominant of non-additive genetic effects govern in the inheritance of 100 grain weight.

#### **Grain yield plant<sup>-1</sup>**

Significant differences among different generations under study for grain yield plant<sup>-1</sup> indicated the presence of sufficient genetic variability. Significant values of scaling tests in both the crosses showed presence of non-allelic genetic interactions. Results revealed that both additive and non-additive genetic components were significant in both the crosses. Epistasis resulting from dominance  $\times$  dominance (l) component was significant and larger in magnitude than additive  $\times$  additive and additive  $\times$  dominance component, opposite sign of [h] and [l] component in most of the yield and its contributing traits indicated duplicate type of gene interaction. Thus, reciprocal recurrent selection can be suggested in both the crosses for the enlisted trait which will facilitated selection of best recombinations. The non-additive gene effects with dominance  $\times$  dominance epistatic effects is responsible for controlling the inheritance of grain yield plant<sup>-1</sup> in maize are in agreement with the results obtained by Wannows *et al.* (2015) and Hussein *et al.* (2017).

It is concluded from this study that for characters like days to 50% tasseling, days to 50% silking, days to maturity, plant height, cob length, cob girth, number of grains cob<sup>-1</sup>, 100 grain weight and grain yield plant<sup>-1</sup> both additive and non-additive gene effects were important in cross NMI-3  $\times$  NMI-7. In cross NAUM-26  $\times$  NAUM-21, most of the characters were controlled by both additive and non-additive gene effects except cob length, cob girth and number of grains cob<sup>-1</sup>. The dominant gene effects were predominantly significant for most of the characters in both the crosses. Reciprocal recurrent selection will be effective in improvement of all traits that were governed by both additive and non-additive gene effects.

**Table 1. Mean for various attributes in six generations of two different crosses**

Generations		Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Cob length (cm)	Cob girth (cm)	No. of grains cob <sup>-1</sup>	100 grain weight (g)	Grain yield plant <sup>-1</sup> (g)
Cross	P <sub>1</sub>	52.00	56.33	99.33	146.63	15.52	13.56	288.93	17.56	49.87
		± 0.28	± 0.32	± 0.34	± 1.07	± 0.11	± 0.09	± 3.00	± 0.11	± 0.53
NMI-3 × NMI-7	P <sub>2</sub>	55.00	59.67	94.33	177.53	16.48	14.25	318.73	22.81	61.96
		± 0.18	± 0.06	± 0.26	± 0.96	± 0.09	± 0.06	± 2.93	± 0.11	± 0.49
	F <sub>1</sub>	56.67	60.00	106.00	190.28	19.64	15.21	353.41	24.16	82.81
		± 0.12	± 0.10	± 0.38	± 0.43	± 0.10	± 0.05	± 1.52	± 0.07	± 0.53
	F <sub>2</sub>	53.67	57.33	100.67	181.28	16.22	14.83	320.13	22.32	69.04
		± 0.10	± 0.13	± 0.20	± 0.53	± 0.03	± 0.04	± 1.58	± 0.04	± 0.38
	BC <sub>1</sub>	52.00	55.67	94.33	167.48	16.63	14.94	297.09	20.79	57.29
		± 0.08	± 0.18	± 0.05	± 0.61	± 0.06	± 0.05	± 2.51	± 0.07	± 0.58
	BC <sub>2</sub>	51.67	55.67	95.00	169.73	15.60	13.75	287.89	21.53	62.27
		± 0.05	± 0.13	± 0.17	± 0.50	± 0.10	± 0.04	± 1.93	± 0.09	± 0.91
Cross	P <sub>1</sub>	48.33	53.67	93.00	157.24	16.31	13.20	308.68	20.61	57.44
		± 0.42	± 0.22	± 0.38	± 0.78	± 0.12	± 0.08	± 2.39	± 0.16	± 0.53
NAUM-26 × NAUM-21	P <sub>2</sub>	55.67	59.00	97.33	153.88	15.57	13.85	316.94	19.91	58.72
		± 0.54	± 0.48	± 0.74	± 0.95	± 0.09	± 0.05	± 3.51	± 0.11	± 0.49
	F <sub>1</sub>	53.67	57.00	108.67	184.72	18.20	14.04	341.46	23.17	78.15
		± 0.12	± 0.10	± 0.12	± 1.09	± 0.11	± 0.08	± 4.36	± 0.08	± 0.58
	F <sub>2</sub>	51.00	54.67	99.00	169.12	14.95	13.00	298.81	21.11	63.53
		± 0.06	± 0.13	± 0.11	± 0.71	± 0.02	± 0.005	± 2.78	± 0.02	± 0.22
	BC <sub>1</sub>	48.00	53.67	91.33	164.79	15.56	12.73	303.56	20.93	58.80
		± 0.08	± 0.13	± 0.18	± 0.60	± 0.08	± 0.07	± 3.19	± 0.10	± 0.47
	BC <sub>2</sub>	51.67	56.33	93.00	165.52	15.12	13.53	299.52	20.25	59.80
		± 0.13	± 0.05	± 0.14	± 0.73	± 0.11	± 0.07	± 2.98	± 0.08	± 0.32

**Table 2. Scaling test, gene effects and gene action for different yield attributing characters in crosses NMI-3 × NMI-7****Cross NMI-3 × NMI-7**

Characters Scaling test	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Cob length (cm)	Cob girth (cm)	No. of grains cob <sup>-1</sup>	100 grain weight (g)	Grain yield plant <sup>-1</sup> (g)
A	-4.66**	-5.00**	-16.66**	-1.96	-1.96**	1.11**	-48.2**	-0.13	-6.22**
	± 0.35	± 0.49	± 0.52	± 1.68	± 1.68	± 0.15	± 6.05	± 0.19	± 1.39
B	-8.33**	-8.33**	-10.33**	-28.34**	-28.34**	-1.96**	-96.35**	-3.9**	-16.13**
	± 0.24	± 0.29	± 0.58	± 1.46	± 1.46	± 0.15	± 5.09	± 0.23	± 1.97
C	-5.66**	-6.66**	-3.00*	20.39**	20.39**	1.10**	-34.02**	0.58**	11.34**
	± 0.58	± 0.68	± 1.20	± 2.73	± 2.73	± 0.24	± 8.18	± 0.28	± 2.00
D	3.66**	3.33**	12.00**	25.35**	0.20	0.97**	55.26**	2.31**	16.85**
	± 0.22	± 0.35	± 0.44	± 1.33	± 1.33	± 0.11	± 4.47	± 0.15	± 1.32
Genetic effects	60.83**	64.66**	120.83**	212.78**	16.41**	15.84**	414.38**	24.80**	86.85**
m	± 0.48	± 0.73	± 0.91	± 2.78	± 0.28	± 0.24	± 9.19	± 0.31	± 2.68
d	-1.5**	-1.66**	2.5**	-15.45**	-0.47**	-0.34**	-14.87**	-2.62**	-3.27**
	± 0.16	± 0.16	± 0.21	± 1.67	± 0.07	± 0.05	± 2.10	± 0.08	± 0.36
h	-24.5**	-24.66**	-65.83**	-103.51**	-4.01**	-3.42	-316.06**	-9.29**	-71.96**
	± 1.13	± 1.81	± 2.10	± 6.78	± 0.82	± 0.58	± 23.73	± 0.84	± 7.30
i	-7.33**	-6.66**	-24.00**	-50.7**	-0.41	-1.94**	-110.53**	-4.29**	-33.7**
	± 0.45	± 0.71	± 0.89	± 2.67	± 0.27	± 0.23	± 8.95	± 0.3	± 2.65
j	3.66**	3.33**	-6.33**	26.38**	3.00**	3.07**	48.15**	3.76**	9.90**
	± 0.39	± 0.55	± 0.56	± 2.14	± 0.28	± 0.18	± 7.6	± 0.29	± 2.29
l	20.33**	20.00**	51.00**	81.00**	7.24**	2.79**	255.0**	8.65**	56.05**
	± 0.70	± 1.12	± 0.40	± 4.18	± 0.57	± 0.37	± 15.0	± 0.55	± 4.79
Type of epistasis	D	D	D	D	D	D	D	D	D

\*, \*\* = Significant at 5% and 1% level respectively

**Table 3. Scaling test, gene effects and gene action for different yield attributing characters in crosses NAUM-26 × NAUMI-21****Cross NAUM-26 × NAUMI-21**

Characters Scaling test	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Cob length (cm)	Cob girth (cm)	No. of grains cob <sup>-1</sup>	100 grain weight (g)	Grain yield plant <sup>-1</sup> (g)
A	-6.00** ± 0.47	-3.33** ± 0.36	-19.00** ± 0.54	-12.38** ± 1.81	-3.39** ± 0.24	-1.78** ± 0.19	-43.02** ± 8.10	-1.92** ± 0.27	4.3** ± 1.24
B	-6.00** ± 0.61	-3.33** ± 0.50	-20.00** ± 0.81	-7.56** ± 2.06	-3.54** ± 0.27	-0.82** ± 0.18	-59.36** ± 8.18	-2.58** ± 0.22	-4.22** ± 1.00
C	-7.33** ± 0.78	-8.00** ± 0.80	-11.66** ± 0.99	-4.09 ± 3.81	-8.48** ± 0.29	-3.11** ± 0.20	-113.31** ± 14.77	-2.41** ± 0.28	11.36** ± 1.65
D	2.33** ± 0.20	-0.66* ± 0.31	13.66** ± 0.33	-7.92** ± 1.72	-77.00** ± 0.15	-0.25* ± 0.10	-5.46 ± 7.07	1.05** ± 0.14	5.64** ± 0.73
Genetic effects									
m	56.66** ± 0.54	55.00** ± 0.67	122.5** ± 0.78	171.41** ± 3.49	14.39** ± 0.32	13.02** ± 0.21	301.89** ± 14.31	22.35** ± 0.30	61.92** ± 1.51
d	-3.66** ± 0.34	-2.66** ± 0.26	-2.16** ± 0.42	1.67** ± 0.61	0.36** ± 0.07	-0.32** ± 0.05	-4.13 ± 2.12	0.35** ± 0.10	-2.08** ± 0.36
h	-19.66** ± 1.51	-3.33* ± 1.61	-80.16** ± 2.10	-22.49** ± 8.37	-1.57 ± 0.93	-1.08 ± 0.66	-51.91 ± 35.26	-5.79** ± 0.89	-8.38* ± 4.09
i	-4.66** ± 0.41	1.33* ± 0.62	-27.33** ± 0.65	-15.85** ± 3.44	1.54** ± 0.31	0.50* ± 0.21	10.92 ± 14.15	-2.1** ± 0.28	-11.28** ± 1.46
j	0.00 ± 0.76	0.00 ± 0.60	1.00 ± 0.96	-4.82* ± 2.26	0.14 ± 0.32	-0.96** ± 0.23	16.34 ± 9.72	0.66 ± 0.33	8.52** ± 1.36
l	16.66** ± 1.00	5.33** ± 0.98	66.33** ± 0.36	35.80** ± 5.38	5.39** ± 0.64	2.10** ± 0.47	91.47** ± 22.8	6.61** ± 0.60	11.21** ± 2.83
Type of epistasis	D	D	D	D	-	-	-	D	D

\*,\*\* = Significant at 5% and 1% level respectively

## REFERENCES

- Azizi, F., A. M. Reazi and G. Saedi, 2006. Generation mean analysis to estimate genetic parameters for different traits in two crosses of corn inbred lines at three planting densities. *J. Agric. Sci. Technol.* **8**: 153-169.
- El-Badawy, M. El. M., 2012. Estimation of genetic parameters in three maize crosses for yield and its attributes. *Asian J. Crop Sci.* **4**(4): 127-138.
- Hayman, B. I. 1958. The separation of epistatic from additive and dominance variation in generation means. *Heredity*, **12**: 371-390.
- Haq, Muhammad, H. I. Ul., S. U. Ajmal, M. Munir and M. Gulfaraz, 2010. Gene action studies of different quantitative traits in maize. *Pak. J. Bot.* **42**(2): 1021-1030.
- Hussein, M. A., M. Othman and F. H. Mourad, 2017. Generation mean analysis using generation variance in maize traits. *Iraqi J. Agric. Sci.*, **48**: 24-29.
- Ishfaq, A. 2011. Generation mean analysis of reproductive and yield traits in maize (*Zea mays* L.). *SAARC. J. Agric.* **9**(2): 37-44.
- Iqbal, M., K. Khan, H. Rahman and H. Sher, 2010. Detection of epistasis for plant height and leaf area per plant in maize from generation mean analysis. *Maydica*, **55**(1): 33-39.
- Mather, K. 1949. *Biometrical Genetics*. Diverse publication. Inc., New York.
- Moradi, M. 2014. Genetic analysis to determine the nature and magnitude of genetic variances and heritability estimates in maize. *Int. J. Agron. Agric. Res.* **5**(9): 183-188.
- Novoselovic, D., M. Baric, G. Drezner, J. Gunjaca and A. Lalic, 2004. Quantitative inheritance of some wheat plant traits. *Genet. Moi. Bio.* **27**: 92-98.
- Sofi, P., A. G. Rather and S. Venkatesh, 2006. Detection of epistasis by generation means analysis in maize hybrids. *Pak. J. Biol. Sci.* **9**(10): 1983-1986.
- Singh, P. K. and A. K. Roy, 2007. Diallel analysis of inbred lines in maize (*Zea mays* L.). *Int. J. Agric. Sci.* **3**(1): 213-216.
- Sher, H., M. Iqbal, K. Khan, M. Yasir and H. Ur-Rahman, 2012. Genetic analysis of maturity and flowering characteristics in maize (*Zea mays* L.). *Asian Pac. J. Trop. Bio.* **2**(8): 621-626.
- Umar, U. U., S. G. Ado, D. A. Aba and S. M. Bugaje, 2015. Combining ability, gene action and heterosis in maize (*Zea mays* L.) under drought stress. *Int. J. Agric. Innov. and Res.* **3**(3):2319-1473.
- Wannows, A. A., M. Y. Sabbouh and AL- Ahmad, 2015. Generation mean analysis technique for determining genetic parameters for some agronomic traits in two maize hybrids. *Jordan J. Agric. Sci.* **11**(1): 59-73.

Rec. on 10.09.2018 & Acc. on 10.10.2018