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Generation Mean Analysis in Maize (*Zea mays* L.)

Bishwajyoti Pradhan, J. P. Shahi

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Abstract The present experiment on generation mean analysis in maize were carried out during the year 2015-2016. The characters studied were plant height, ear height, ear length, ear diameter, number of kernel rows per ear, number of kernels per row and 100-grain weight for six generation of two crosses. ANOVA showed significant variation among generations. The data were then 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 type 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 dominance type of gene action observed in the cross HKI–162 × HUZM–329 for all yield attributing traits except for number of kernel rows per ear and number of kernels per row. The cross HKI–162 × HKI–586 showed dominance type of gene actions for yield attributing characters. Regarding inter-allelic interaction dominance × dominance types were more pronounced than additive × additive and additive × dominance interaction for yield attributing traits except for ear diameter and ear length in both the crosses. The opposite sign of h (dominance gene action) and (dominance × dominance) indicated the presence of duplicate type of epistasis and same sign indicated presence of complementary epistasis. Non applicability of simple additive-dominance model revealed importance of epistasis components in yield attributing traits can be exploited through heterosis breeding or recurrent selection.

Keywords Additive, Dominance, Epistasis, Gene action, Generation mean analysis.

Introduction

Maize (2n = 20) is the third most important cereal crop in the world belong to family poaceae. It is one of the most versatile crop having wider adaptability under varied agroclimatic condition. It can be grown throughout the year for different purposes including grain, fodder, green cobs, sweet corn, baby corn, popcorn. 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 [1] followed by generation mean analysis [2] 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 crosses, more studied based on generation mean analysis in diverse crosses are warranted for getting deeper understanding of gene actions in-

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B. Pradhan*
PhD Scholar, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, India

J. P. Shahi
Professor, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, India
e-mail: pradhan.biswajyoti@gmail.com
*Correspondence

Table 1. Mean ± SE for various attributes in six generation of two different crosses.

Generations		Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of kernel rows per ear	Number of kernels per row	100-grain weight (g)
Parents	HKI-162	78.33 ±3.47	47.33 ±2.57	8.76 ± 0.17	3.32 ± 0.04	10.93 ± 0.22	14.00 ± 0.25	14.84 ±0.10
	HUZM-329	79.33 ±2.00	30.66 ±1.18	9.72 ± 0.23	3.49 ± 0.04	12.93 ± 0.46	15.40 ± 0.54	17.41 ±0.27
	HKI-586	61.33 ±2.82	31.00 ±1.00	7.40 ± 0.15	2.96 ± 0.03	8.80 ± 0.26	11.20 ± 0.22	13.42 ±0.18
Cross HKI-162× HUZM-329	F_1	149.33 ±2.28	72.00 ±2.32	15.12 ± 0.26	4.62 ± 0.04	12.53 ± 0.23	26.40 ± 0.75	28.82 ±0.17
	F_2	135.55 ±2.37	53.33 ±0.94	12.70 ± 0.31	4.06 ± 0.05	12.42 ± 0.18	22.28 ± 0.68	25.89 ±0.14
	B_1	123.33 ±3.72	53.00 ±1.47	12.20 ± 0.22	4.02 ± 0.05	12.63 ± 0.22	17.23 ± 0.72	27.46 ±0.31
	B_2	113.16 ±2.09	48.66 ±1.31	12.24 ± 0.28	3.95 ± 0.07	12.86 ± 0.18	22.66 ± 0.66	22.66 ±0.20
Cross HKI-162× HKI-586	F_1	163.00 ±2.91	51.44 ±1.60	15.64 ± 0.38	4.23 ± 0.07	15.06 ± 0.26	22.53 ± 0.63	22.47 ±0.14
	F_2	114.88 ±2.15	46.44 ±1.16	12.04 ± 0.36	3.62 ± 0.08	11.46 ± 0.30	19.82 ± 0.41	22.10 ±0.24
	B_1	110.83 ±3.25	49.83 ±1.52	12.09 ± 0.37	3.86 ± 0.05	12.70 ± 0.18	16.26 ± 0.63	21.32 ±0.08
	B_2	104.66 ±4.49	46.50 ±1.16	10.76 ± 0.33	3.46 ± 0.08	13.20 ± 0.22	15.92 ± 0.54	18.72 ±0.15

volved 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 [3]. 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 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 investigations were carried out at Agricultural research farm of BHU, Varanasi, UP during 2015-2016. Three homozygous and genetically diverse strains of maize i.e. HKI-162, HUZM-329, HKI-586 were selected for building up the experimental materials. The parental materials and F_1 of these crosses were obtained from the maize breeding program of IAS, BHU The F_1 hybrids were selfed to obtained F_2 and back croseed for setting B_1 and B_2. The experimental materials for the present investigation comprised of the six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of each of the two crosses i.e. HKI-162 × HUZM-329 and HKI-162 × HKI-586. All six generations of above two crosses were grown in randomized block design with three replications. In each of replication non segregating parents P_1, P_2 and F_1's generation were represented by one row, B_1 and B_2 by three rows and F_2's by eight rows. The rows 3 m long with row spacing of 60 cm and 25 cm between plants within row. The data were recorded on 5 plants in parents and F_1's, 20 plants in back crosses and 30 plants in F_2 replication wise for plant height, ear height, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, 100-grain weight. The data were analyzed by

Table 2. Scaling test, gene effects and gene action for different yield attributing characters in crosses HKI–162×HUZM–329. * Significant at 5%, ** Significant at 1%.

Cross HKI-162×HUZM-329

Characters	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of kernel rows per ear	Number of kernels per row	100-grain weight (g)
Scaling test							
A	19.00**	– 13.33**	0.52	0.10	1.80**	– 5.93**	11.26*
	± 1.53	± 4.55	± 0.54	±0.12	± 0.56	±1.65	± 0.66
B	–1.46	– 5.33	– 0.35	– 0.20	0.26	5.53*	– 0.91
	±0.17	± 3.70	± 0.67	±0.15	± 0.63	±1.61	± 0.52
C	85.88**	– 8.66	2.08	0.20	0.75**	6.95*	13.68**
	± 3.29	± 6.62	± 1.40	± 0.23	± 1.03	±3.18	± 0.73
D	– 34.61*	5.00	0.95	0.15	– 0.65	4.67**	1.67**
	± 1.39	± 2.72	± 0.73	±0.13	± 0.47	±1.68	± 0.47
Genetic effects							
(m)	135.55**	53.33**	12.70**	4.06**	12.42**	22.28**	25.89**
	± 2.38	± 0.94	± 0.31	±0.05	± 0.18	±0.68	± 0.14
(d)	10.17**	4.33*	– 0.04	0.06	– 0.23	– 5.43**	4.80**
	±0.27	± 1.97	± 0.36	±0.09	± 0.29	±0.98	± 0.37
(h)	1.28**	23.00**	3.96**	0.91**	1.91	2.34	9.35**
	±0.15	± 6.09	± 1.49	±0.27	± 1.01	±3.47	± 0.97
(i)	– 69.22**	– 10.00	– 1.91	–0.30	1.31	– 9.35**	– 3.34**
	± 2.79	± 5.44	± 1.46	±0.27	± 0.95	±3.37	± 0.94
(j)	10.17**	– 4.00	0.43	0.15	0.76	– 4.73**	6.08**
	±0.72	± 2.42	± 0.39	±0.009	± 0.39	±11.02	± 0.40
(l)	52.56**	28.66*	1.75	0.39	– 3.37*	11.75*	– 7.00**
	± 2.50	± 10.29	± 2.02	±0.42	± 1.55	±5.06	± 1.66
Type of epistasis	Complementary	Complementary	–	–	–	–	Duplicate

using indostat advanced plant breeding package for testing epistasis and six generation mean analysis (Table 1).

Results and Discussion

Plant height

The genotypes exhibited variation in plant height wherein HUZM-329 was tallest and HKI-586 was dwarf among parent. Non-additive (h) gene effect was controlling the inheritance of this trait in cross HKI-162×HKI-586 but additive gene effect was equally important as non-additive gene effect in cross HKI-162 × HUZM-329 (Tables 2 and 3). Therefore for efficient utilization of fixable and non-fixable components of genetic variation, reciprocal recurrent selection would be suggested for cross HKI-162×HUZM-329. The estimates of (d), (h), (i), (j) and (l) were significant in the cross HKI-162×HUZM-329, which indicated predominant role of additive, dominance and epistatic gene effect. The significant of (h) and (l) component with same sign in both the crosses indicated the presence of complementary type of epistasis. So heterosis breeding would be appropriate method to improve the trait. Mosa [4] observed non-additive gene action was responsible in the inheritance of this trait while Singh and Roy [5] found additive gene effect was responsible in controlling this trait.

Ear height

Parental lines showed significant differences for ear height. Both additive and dominant gene action was

Table 3. Scaling test, gene effects and gene action for different yield attributing characters in crosses HKI–162×HKI–586. * Significant at 5%, ** Significant at 1%.

Cross HKI-162×HKI-586

Characters	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of kernel rows per ear	Number of kernels per row	100-grain weight
Scaling test							
A	– 19.66* ±7.93	–28.89** ±4.30	–0.21 ±0.85	0.16 ±0.14	–0.60 ±0.51	–4.01** ±1.44	5.34** ±0.24
B	–15.00 ±9.86	–10.5** ±3.48	–1.52 ±0.79	– 0.26 ±0.18	2.53** ±0.58	– 1.89** ±1.27	1.55** ±0.39
C	– 6.11 ±11.34	–4.55** ±2.29	0.73 ±1.67	– 0.25 ± 0.38	–4.00** ±1.36	9.02** ±2.12	15.21** ±1.03
D	– 14.27* ±7.03	–3.44 ±3.14	1.23 ±0.89	– 0.08 ±0.20	–2.96** ±0.67	7.46** ±1.18	4.15** ±0.51
Genetic effects							
(m)	114.88** ±2.15	46.44** ±1.16	12.04** ±0.36	3.62** ±0.08	11.46** ±0.30	19.82** ±0.42	22.10** ±0.24
(d)	6.16 ±5.55	3.33 ±2.11	1.33** ±0.50	0.39** ±0.10	–0.50 ±0.29	– 0.34** ±0.83	2.60** ±0.18
(h)	64.61** ± 14.53	19.72** ±6.63	5.09** ±1.82	1.25** ± 0.41	11.13** ±1.37	– 4.99** ±2.45	27.10** ±1.05
(i)	– 28.55* ± 14.06	6.88 ±6.28	–2.47 ±1.78	0.16 ±0.40	5.93** ±1.33	– 14.9** ±2.36	– 8.32 ±1.03
(j)	– 2.33 ±5.98	–4.83 ±2.52	0.65 ±0.51	0.21 ± 0.10	– 1.56** ±0.34	– 1.06** ±0.85	1.89** ±0.21
(l)	63.22* ±24.93	–18.55** ±5.53	4.21 ±2.61	– 0.07 ±0.56	–7.86** ±1.79	20.82* ±3.95	1.43** ±1.26
Type of epistasis	Complementary	Duplicate	–	–	Duplicate	Duplicate	Complementary

significant for this trait in cross HK162 ×HUZM-329 but later was greater in magnitude indicating preponderance of dominance gene effects in the experession of this trait. Dominance gene effect was found significant in governing this trait in other cross. Dominance × dominance gene interaction was common in inheritance of this trait in both crosses. Same sign (h) and (l) component indicates the presence of complementary type of gene action for this trait in cross HKI-162 ×HUZM-329. Thus this trait can be exploited through heterosis breeding in this cross while duplicate type of epistasis govern this trait in other cross. Irshad-Ul-Haq et al. [6] found inheritance of this trait was primarily governed by dominance gene effect than additive gene action. While Prakash and Ganguli [7] found additive type of gene action was important for inheritance of this trait.

Ear length

Sufficient variablility for ear length was observed in parents and it varied from 7.40 cm to 9.72. The dominance gene effect (h) was common in both the crosses studied for governing the inheritance of this trait. However in cross HKI-162 ×HK-586 both additive and dominance gene effect were found significant. Therefore reciprocal recurrent selection can be used for the utilisation of the fixable and non-fixable genetic components of variation in this cross. Epistasis had no role in inheritance of this trait in both the crosses. In case of cross HKI-162×HUZM-329, this trait could be successfully utilized in the formation of hybrids and promoting earliness in the materials. Kanagarasu et al. [8] found predominance of non-additive type of gene action in governance of this character while

Muraya et al. [9] observed preponderance of additive gene effects for inheritance of this trait.

Ear diameter

Variability was observed for this trait in parental lines and it ranges from 2.96 to 3.49. The significance of non-additive (h) gene effects was responsible for inheritance of this trait in cross HKI-162×HUZM-329. The preponderance of dominance gene action indicated that this trait could be utilized successfully in the formation of hybrids in this cross. While both (d) and (h) gene action plays an important role in governing inheritance of this trait in cross HKI-162×HKI-586. So reciprocal recurrent selection method can be used for this cross. No epistatic interactions were found for this trait in both the crosses. Similar finding was reported by Kanagarasu et al. [8].

Number of kernel rows per ear

The parents were diverse for this trait. Non-additive gene effect was controlling the inheritance of this trait in cross HKI-162×HKI-586. Preponderance of dominance gene action indicated this trait could be successfully utilized in the formation of hybrid in this cross. All the epistatic interactions were found to be significant in this cross whereas only dominance × dominance type of interaction were observed in HKI-162×HUZM-329 cross. Duplicate type of epistasis was found for this trait in cross HKI-162×HKI-586. Presence of this type of epistasis is likely to cause hindrance in selection response. Mahto and Ganguli [10] and Vijayabharathi et al. [11] also reported non-additive gene effects for this trait.

Number of kernels per row

Lots of variation noticed among the parental genotype for this trait. The additive gene effect was significant for this trait in cross HKI-162×HUZM-329 indicating exploitation of additive gene action can occur through selection. While both additive and dominance gene actions were significant for this trait in the cross HKI-162×HKI-586 indicating both (d) and (h) effects were important in the inheritance of this trait. Therefore reciprocal recurrent selection can be utilized the fixable and non-fixable genetic components of variation for the trait in this cross. All the epistatic interactions were found significant in both the crosses. Opposite sign of (h) and (l) components indicated presence of duplicate type of gene action for this trait in cross HKI-162×HKI-586. Subramanian and Subbaraman [12] reported that both and non-additive gene actionare important in controlling this trait while Moradi [13] also reported additive gene effects for this trait.

100-grain weight

100-grain weight among parents varied from 13.42 to 17.41 gm. The significance of both additive and non-additive gene effects were equally important in controlling the inheritance of this trait in both the crosses. All three types digenic interactions were found in the inheritance of this trait in cross HKI-162×HUZM-329. Duplicate type of epistasis was found for this trait in this cross. Thus reciprocal recurrent selection can be a feasible breeding strategy for this cross. While (j) and (l) type of gene interactions were found significant in cross HKI-162×HKI-586. Same sign of (h) and (l) showed complementary type of epistasis was governing the inheritance of this trait in this cross. Thus this trait can be exploited through heterosis breeding for this cross. Hussain [14] reported both additive and non-additive genetic effects govern in the inheritance of 100-grain weight.

Conclusion

For characters like plant height, ear height, 100-grain weight both additive and non-additive gene effects were important in cross HKI-162×HUZM-329. The dominance gene effects were predominantly significant for all characters in cross HKI-162×HKI-586. Reciprocal recurrent selection will be effective in improvement of all traits that were governed by both additive and non-additive gene effects. Heterosis breeding will be effective in improvement of traits in cross HKI-162×HKI-586.

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