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Detection of Epistasis for Reproductive and Maturity Traits in Maize (*Zea mays* L.) from Generation Mean Analysis

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ABSTRACT: The experimental material comprised of six generations of the crosses IC-328883 x IC-541068, IC-328953 x GPM-210, IC-326865 x GPM-470, GPM-470 x GPM-405 and IC-274556 x GPM-210 in maize. The role of gene action and interactions in the inheritance of reproductive and maturity traits in maize was examined through generation's means analysis. Significant differences among generation means were indicated. Chi square values were significant for all the crosses for all traits according to a joint scaling test except in the cross IC-274556 x GPM-210 for days to 50% tasseling and days to maturity. Six parameters model was applied to accommodate the digenic epistatic interactions. The crosses *viz* IC-328883 x IC-541068, IC-328953 x GPM-210 and GPM-470 x GPM-405 exhibited positive significant additive x additive type of interaction was observed in the inheritance of the trait days to 50% tasseling. The crosses *viz* IC-328883 x IC-541068, IC-328953 x GPM-210 exhibited positively significant additive x additive type of interaction was present in the inheritance of days to 50% silking and maturity traits. Duplicate type of epistasis was observed in all the crosses and traits, except GPM-470 x GPM-405 for days to maturity, and IC-274556 x GPM-210 for 50% tasseling and maturity traits exhibited complementary type of epistasis. Complementary and duplicate gene interactions appeared operative in the inheritance of silking and maturity traits. Duplicate gene interactions were seen functioning in controlling 50 % tasseling in most of the crosses. These traits can be selected and utilizing selection purpose for the crop improvement because these traits are fixable due to additive x additive type of gene interaction. These traits were utilized for the selection of elite genotypes/ segregants for the development of variety. While several studies in maize have demonstrated the important role of epistasis plays in trait expression, there are currently no precise genetic models to test and estimate it. Epistasis plays a major role in both the growth and development of plants as well as the inheritance of quantitative traits, as demonstrated by recent studies using molecular markers. Therefore, it would make more sense to look for epistasis and maximize its application in the creation of promising cultivars for target environments than to attribute it to residual variance after dominance and additive effects have been taken into consideration.

Keywords: Generation mean analysis, Reproductive, Maturity traits, Gene action, Maize.

INTRODUCTION

One of the biometrical procedures that involve estimating the magnitude of different additive, dominant, and epistatic effects is generation mean analysis (GMA). Plant breeders might choose breeding techniques that are more appropriate for improving the qualities under study by using estimates of genetic effects (Gamble, 1962a). Generation mean analysis, a biometrical method developed, greatly helps in the estimation of various components of genetic variance. Estimation of the types of gene action involved in the expression of traits, the level of additive effects and the degree of dominance are very important in designing a breeding method for improving the trait of interest (Mather and Jinks 1971). Understanding how genes function and interact can assist clarify the role of breeding systems in agricultural plant evolution and identify which breeding system can maximize gene action most effectively (Hallauer and Miranda 1988). Anthesis to silking interval depicted the duplicate gene action under normal condition (Shankar *et al*., 2022).

The complex loci help scientists conducting maize research and breeders of corn understand the concentration of zeaxanthin content maize kernel (Dong *et al*., 2020). According to Patil Krantikumar *et al.* (2016), dominance gene action and dominance x dominance type of epistatic gene action control yield contributing traits in maize crosses. Additionally, Patil Krantikumar *et al.* (2020) reported that heterosis breeding or recurrent selection can be used to take advantage of epistatic/inter allelic components for quantitative traits in maize.

It may be possible to increase maize production by comprehending the genetic foundation of maturity and reproductive features (*Zea mays* L.). Before beginning a successful hybrid development program, it is imperative to understand the blooming habit, type of gene action, and mode of inheritance of maize inbreds (Sher *et al.*, 2012).

There have been observed days to silk gene dominance effects. After analyzing a few populations of maize, researchers found that additive effects were more significant for silking, but additive x dominance effects were more significant for tasselling. In order to clarify the kind of gene action and interaction that controlled the inheritance of maturity and flowering traits in maize (Sher *et al.*, 2012). The current study is designed for determining type of gene action responsible for the inheritance of the reproductive and maturity traits in maize.

MATERIALS AND METHODS

Six generations of the crosses of maize, IC-328883 x IC-541068, IC-328953 x GPM-210, IC-326865 x GPM-470, GPM-470 x GPM-405, and IC-274556 x GPM-210, made up the experimental material. During the 2010–11 Kharif, the parents were crossed to create single cross hybrids. In order to produce the BC_1, BC_2, and F_2 generations, the crosses were sown in the summer of 2012 together with the parents. The Commercial variety "Maharaja" (Hybrid) as a check and the six generations of each cross were assessed during the 2012–13 Kharif season at the Experimental Farm, Department of Agricultural Botany, College of Agriculture, Latur. The experimental unit was made up of six row plots, each measuring five meters in length, for the F_2, BC_1, and BC_2 (segregating) generations and four row plots, each measuring five meters for the non-segregating P_1, P_2, and F_1 generations. The rows were spaced 60 by 25 centimetres apart in a separate RBD for the cross. At the five leaf stage, the plots were divided and thinned to 20 plants per row. The experiment's specifics are as follows:

Experimental Design: RBD
1. Number of replications: Two (each)
2. Number of treatments: 7 (P_1, P_2, F_1, F_2, BC_1, BC_2 and check)
(In each of the five crosses)
3. Spacing: 60 x 25 cm
4. Fertilizer Dose: 120:60:60 NPK kg/ha

The details of population raised and selected for observation is as follow:

Name of generation	Total No. of plants raised in each generation	Plants chosen per replication	Total plants chosen per generation for observation
P_1, P_2, F_1	80	10	20
BC_1, BC_2, F_2	120	40	80
Check Maharaja	80	20	40

Statistical and Genetic analysis. The data collected in the experiment was subjected to analysis of variance (Panse and Sukhatme 1985) for testing significance of differences. The mean values, standard errors and variances of different generations were subjected to weighted list square analysis using scaling test (Mather, 1949) and the joint scaling test to estimate gene effects. Genetic effects were estimated using the model suggested by Mather and Jinks (1971) and Jinks and Jones (1958). The significance of scales and gene effects were tested using t-test (Singh and Chaudhary 1985).

RESULTS AND DISCUSSION

The mean performance of six generations in five crosses for reproductive and maturity traits are presented in Table 1. Generation means calculated for days to 50% tasseling in five crosses. The mean values for days to 50% tasseling among parents varied from 52.20 (IC-328953) to 56.90 days (IC-326865), while, in the crosses it ranged from 51.60 (IC-328883 x IC-541068) to 55.55 days (IC-274556 x GPM-210). The Mean values of F_2 generations of all crosses ranged from 53.77 (IC-328953 x GPM-210 selfed) to 56.10 days (IC-274556 x GPM-210selfed). The back cross generation ranged in between F_1 and their respective parent. The mean values of BC_1 and BC_2 generations differed among themselves. The mean values of BC_1 were at par with the P_1 parent, except in the crosses IC-326865 x GPM-470 and GPM-470 x GPM-405. The earliest tasseling was observed in the cross IC-328883 x IC-541068 (51.60 days), while the most late tasseling was observed in the cross IC-274556 x GPM-210 (55.55 days). Variability results for this trait were reported by Bhalla *et al.* (1988) and Muhammad Akbar *et al.* (2008).

The data revealed significant difference for days to 50% silking for all the crosses. The mean values of parents ranged from 54.65 (IC-328953) to 60.55 days (IC-326865) and their F_1 ranged from 53.60 (IC-328883 x IC-541068) to 59.00 days (IC-274556 x GPM-210) and segregating F_2 generation varied between 56.00 (IC-328953 x GPM-210) to 59.95 days (IC-326865 x GPM-470). The mean values of BC_1 and BC_2 generations differed among parents P_1 and P_2 respectively, except the cross IC-326865 x GPM-470. The earliest silking was recorded in the cross IC-328883 x IC-541068 (53.60 days), while the hybrid cross IC-274556 x GPM-210 (59.00 days) was found to be the latest in silking. Variability results for this trait were reported by Muhammad Akbar *et al.* (2008). The mean performance of parents for days to maturity ranged from 86.50 (IC-328883) to 98.050 days (IC-326865). The F_1 generation varied from 85.20 (IC328883 x IC-541068) to 96.10 days (IC-274556 x GPM -210). The most early maturing cross was observed to be IC-328883 x IC-541068 (85.20 days) followed by cross IC-328953 x GPM-210 (86.95 days), whereas, the hybrid IC-274556 x GPM-210 (96.10 days) was found to be late for days to maturity and segregating F_2

generation varied from 88.32 (IC-328883 x IC-541068) to 97.10 days (GPM-470 x GPM-405). The mean values of BC_1 and BC_2 generations differed among parents P_1 and P_2 respectively, except in the crosses GPM-470 x GPM-405 and IC-274556 x GPM-210. Variability results for this trait were reported by Shaw and Thom (1951); Hallauer and Russel (1962).

Analysis of variance for the experimental design: The analysis of variance for randomized block design was carried out for reproductive and maturity traits. Analysis of variance given in Table 2 showed highly significant differences were present among the crosses studied for the characters. This indicated the existence of sufficient variation for effective selection for the characters in the material under study.

Scaling test and joint scaling test and Gene effects

Days to 50 % tasseling: It is observed that the results of scaling test in all the crosses were significant except for the cross IC-326865 x GPM-470 for scaling test B and IC-274556 x GPM-210 for scaling test A, C and D scale. This indicated the presence of non-allelic gene interaction for days to 50 *per cent* tasseling in this population.

Table 1: Mean performance of six generation in five crosses for reproductive and maturity traits in maize (*Zea mays* L.)

Generations	$\overline{P}_1$	$\overline{P}_2$	$\overline{F}_1$	$\overline{F}_2$	$\overline{BC}_1$	$\overline{BC}_2$
Crosses/ Characters	Days to 50% tasseling					
IC-328883 x IC-541068	54.65 ± 0.3420	55.35± 0.2986	51.60 ± 0.371	54.55 ± 0.2203	55.425 ± 0.394	57.15± 0.3639
IC-328953 x GPM-210	52.20 ± 0.8762	56.05± 0.4113	51.60 ±0.2963	53.77 ± 0.3002	55.35±0.3101	57.27± 0.2702
IC-326865 x GPM-470	56.90 ± 0.2867	55.90 ± 0.3712	53.65±0.3948	56.025 ± 0.4112	53.65±0.2993	55.10± 0.2705
GPM-470 x GPM-405	55.80 ± 0.3887	53.25 ± 0.5336	52.55 ±0.3452	55.15 ± 0.3346	56.22±0.2913	56.75± 0.2751
IC-274556 x GPM-210	55.70 ± 0.3590	56.05 ± 0.3287	55.55 ±0.4180	56.10 ± 0.2847	55.60±0.2705	56.75± 0.2628
Days to 50% silking						
IC-328883 x IC-541068	56.75 ± 0.4099	57.15 ± 0.2478	53.60±0.4137	56.65 ± 0.2489	57.87±0.3837	59.20± 0.3352
IC-328953 x GPM-210	54.65 ± 0.7381	58.10 ± 0.2560	54.10 ±0.5099	56.00 ± 0.2590	57.60±0.2753	60.10 ± 0.2680
IC-326865 x GPM-470	60.55 ± 0.1893	59.70± 0.2809	57.50 ±0.3162	59.95 ± 0.3750	57.62±0.3282	59.05 ± 0.3097
GPM-470 x GPM-405	59.50 ± 0.444	57.25 ± 0.6203	56.55±0.5795	59.27 ± 0.2913	60.025±0.2980	59.90 ± 0.3434
IC-274556 x GPM-210	59.30 ± 0.3432	59.50 + 0.4014	59.00 ±0.4216	58.92 ± 0.2816	57.97±0.2336	59.15 ± 0.2239
Days to maturity						
IC-328883 x IC-541068	86.50 ± 0.2236	88.05 ±0.2630	85.20 ±0.4485	88.32± 0.2826	90.67±0.4847	91.52 ± 0.6214
IC-328953 x GPM-210	86.60 ± 0.40	93.60 ± 0.4989	86.95 ±0.6030	94.67 ± 0.3844	97.0250±0.2221	97.60 ± 0.1906
IC-326865 x GPM-470	98.050 ± 0.174	96.75± 0.3354	94.70 ±1.0493	96.42 ± 0.5082	95.00±0.7487	92.42 ± 0.6642
GPM-470 x GPM-405	96.85± 0.4833	95.60 ± 0.6944	92.30 ±1.3948	97.10 ± 0.3866	97.30±0.2550	97.87 ± 1.1845
IC-274556 x GPM-210	95.85 ± 0.4349	95.80 ± 2.0578	96.10 ±0.3786	97.00 ± 0.4368	95.80±0.6761	97.62± 0.2347

Table 2: Analysis of variance (Mean sum of squares) of generation means for reproductive and maturity traits in five crosses of maize (*Zea mays* L.).

Source of variance	d.f.	Days to 50% tassling	Days to 50% silking	Days to maturity
IC-328883 x IC-541068				
Replication	1	0.00	0.68	0.18
Treatment	6	5.58**	5.87*	8.93**
Error	6	0.5742	0.71	0.95
IC-328953 x GPM-210				
Replication	1	1.71	4.51	1.89
Treatment	6	8.53*	9.74*	42.30**
Error	6	1.41	2.056	3.10
IC-326865 x GPM-470				
Replication	1	1.2007	1.54	1.68
Treatment	6	3.7168*	3.058*	7.65**
Error	6	0.5470	0.46	0.71
GPM-470 x GPM-405				
Replication	1	0.900	0.078	0.85
Treatment	6	4.67*	3.67*	7.24**
Error	6	0.62	0.72	0.73
IC-274556 x GPM-210				
Replication	1	0.0016	0.27	0.37
Treatment	6	0.51*	1.24**	2.17**
Error	6	0.092	0.10	0.73

*, ** significant at 5% and 1 % respectively

The chi square (x^2) values were significant according to joint scaling test for all the traits in all four crosses studied, except for days to 50% tasseling in the cross IC 274556 x GPM- 210, which was found to be non-significant so, showing the inadequacy of three parameter model. The significant value of chi square for all the plant traits in all the crosses indicated that the three parameter model did not adequately explain the genetic variability for these traits. The inadequacy of the model also indicated the presence of epistasis (non-allelic gene interaction), which is also inferred from the generation means. As the three parameter models did not satisfactorily explain the genetic variability for all these traits, therefore, a six parameter model was applied to accommodate epistatic interactions.

In all the crosses, highly significant values of 'm' showed that six generations differed from each other with respect to mean values of days to 50 *per cent* tasseling from the generation mean analysis. The estimates of epistatic gene effects were also similar to results observed in six parameter model. Estimates of gene effects showed that additive component was negatively significant in four crosses *viz*. IC-328883 x IC-541068, IC-328953 x GPM-210, IC-326865 x GPM-470 and IC-274556 x GPM-210. Dominance components and additive x additive (i) component was positive and significant in three crosses *viz.* IC-328883 x IC-541068, IC-328953 x GPM-210 and GPM-470 x GPM- 405 and negatively significant in the cross IC-326865 x GPM -470. The Additive x Dominance interaction was found to be negatively significant in four crosses, except cross IC-328953 x GPM-210. The Dominance x Dominance type of gene interaction was observed to be significant in four crosses but with negative magnitude and non-significant in the cross IC-274556 x GPM 210 and positively significant in the cross IC-326865 x GPM-470.

The scaling test indicated the presence of non-allelic gene interaction in all the crosses. The character, days to 50 *per cent* tasseling is important for earliness on the basis of generation mean analysis. Inheritance of days to 50 *per cent* tasseling was under the control of additive (d) effect. This effect was negatively significant in the four crosses IC-328883 x IC-541068, IC-328953 x GPM-210, IC-326865 x GPM-470 and IC-274556 x GPM-210, whereas, the cross IC-328953 x GPM-210 showed highly significant additive effect than any other parameter. Dominance (h) effects were significant in the crosses IC-328883 x IC-541068, IC-328953 x GPM-210 and GPM-470 x GPM-405, whereas, it was negatively significant in the cross IC-326865 x GPM-470. It indicates that these hybrids can perform well and can be developed for cultivar. Among epistatis, additive x additive interaction were important in the crosses IC-328953 x GPM-210, GPM-470 x GPM-405 and IC-326865 x GPM- 470. This indicates that there is a scope for selection of plants. Additive x dominance interaction was observed to be significant in four crosses IC-328883 x IC-541068, GPM-470 x GPM-405, IC-326865 x GPM-470 and IC-274556 x GPM-210 in desirable directions, similar reports were given by Sher *et al.*, 2012. Dominance x dominance interaction was observed to be significant in the crosses IC-328883 x IC-541068, IC-328953 x GPM-210, IC-326865 x GPM-470 and GPM-470 x GPM-405 indicating scope for development of hybrids of these crosses. Generally contribution of epistatic gene effects where greater than main effects. Duplicate type of interaction was observed to be present in four crosses due to opposite signs of (h) and (l) components. The complimentary type of interaction was observed to be present in the cross IC-274556 x GPM-210 as (h) and (l) components have same signs. Varying role of gene actions for controlling this trait have been reported by Darrah and Hallauer (1972); Wolf and Hallauer (1977); Kassem *et al.* (1978a and 1978b); Hema *et al*. (2001).

Days to 50 % silking: It is observed that the results of scaling test (Table 3) in all the crosses were significant except for the crosses IC-326865 x GPM-470 and IC-274556 x GPM-210 for scaling test B and the crosses IC-274556 x GPM-210 and IC-328953 x GPM-210 for scaling test C, while non-significant scale D was observed for the crosses GPM-470 x GPM-405 and IC-274556 x GPM-210. This indicated the presence of non-allelic gene interaction for days to 50 % silking in this population. The chi square (x^2) values were significant according to joint scaling test for all the traits in all the crosses studied, except the cross IC-274556 x GPM-210 for which it had a non-significant value, showing the inadequacy of three parameter model for this trait (Table 5). The significant value of chi square for all the plant traits in all crosses indicated that the three parameter model did not adequately explain the genetic variability for these traits. The inadequacy of the model also indicated the presence of epistasis (non-allelic gene interaction), which is also inferred from the generation means. As the three parameter model did not satisfactorily explain the genetic variability for all these traits, a six parameter model was applied to accommodate epistatic interactions.

In all the crosses, highly significant values of 'm' showed that six generations differed from each other with respect to mean for days to 50% silking from the generation mean analysis. The genetic effects for d (additive) (Table 6), were negatively significant in all the crosses for silking character, except the cross GPM-470 x GPM-405 which was observed to be non-significant. The genetic effects for h (dominance), indicated the involvement of dominance gene action in the inheritance of days to silking and were observed to be positively significant in two crosses IC-328883 x IC-541068 and IC-328953 x GPM-210, whereas, negatively significant in the cross IC-326865 x GPM-470. Further, it was non-significant for the crosses GPM -470 x GPM-405 and IC-274556 x GPM-210. The additive x additive type of interaction were positively significant in two crosses IC-328883 x IC-541068 and IC-328953 x GPM-210 with higher magnitude and negatively significant in the cross IC-326865 x GPM-470. Additives x dominance type of non-allelic gene interaction were negatively significant in two crosses *viz.*, IC-326865 x GPM-470 and IC-274556 x GPM-210, whereas, the same was non-significant in remaining three crosses. Dominance x dominance type of non-allelic gene interaction was negatively significant in all the crosses except IC-326865 x GPM-470 and IC-274556 x GPM-210. Additive x additive type of gene interaction play an important role in the inheritance of days to 50 *per cent* silking and was controlled by additive gene action. The significant values for genetic components, dominance (h) and dominance x dominance (l), with opposite signs were indicative of duplicate type of epistasis in the inheritance of this trait in all the five crosses studied. The scaling test indicated the presence of non-allelic gene interaction in all the crosses. The character, days to 50 *per cent* silking is important for earliness on the basis of generation mean analysis. Inheritance of days to 50 *per cent* silking was under the control of additive (d) effect; similar results were reported for days to 50% flowering in soybean crosses by Sher *et al.* (2012); Singh *et al.* (2023). This effect was negatively significant in the four crosses *viz.* IC-328883 x IC-541068, IC-328953 x GPM-210, IC-326865 x GPM-470 and IC-274556 x GPM-210. The dominance gene effect were positively significant in two crosses viz., IC-328883 x IC-541068, IC-328953 x GPM-210 and negatively significant in the cross IC-326865 x GPM-470. The dominance x dominance gene interaction was negatively significant in two crosses, whereas, positively significant in the two crosses *viz.* IC-326865 x GPM-470 and IC-274556 x GPM-210. Among epistatis, additive x additive interaction were important in the crosses IC-328883 x IC-541068, IC-328953 x GPM-210 and IC-326865 x GPM-470. Additive x dominance interaction was observed to be significant in two crosses *viz.* IC-326865 x GPM-470 and IC-274556 x GPM-210 in desirable direction.

Dominance x dominance gene interaction are of primary importance among the digenic non-allelic interactions for controlling the inheritance of days to silking. The non-allelic interaction of additive x additive was also observed to be important and positively significant contributor in the expression of days to 50 *per cent* silking in the crosses IC-328883 x IC-541068 and IC-328953 x GPM-210. Dominance component having major importance in the trait could be successfully utilized in the formation of hybrids and promoting earliness in the material. The presence of epistasis was mostly indicative of greater genetic diversity in the parents. The significant values for genetic components, dominance (h) and dominance x dominance (l), with opposite signs are indicative of duplicate type of epistasis in the inheritance of this trait for all the crosses. These results are in agreement with results reported by Darrah and Hallauer (1972); Wolf and Hallauer (1977); Kassem *et al.* (1978a and 1978b); Hema *et al*. (2001).

Days to maturity: It is observed that the results of scaling test (Table 3) in all the crosses were significant, except the crosses IC-326865 x GPM-470 and GPM-470 x GPM-405 for scaling test A, C and D scales respectively. Presence of any scale indicated the presence of non-allelic gene interaction for days to maturity in this population. The cross IC-274556 x GPM-210 depicts the absence of all scales there by indicates the absence of non-allelic gene interaction (i.e. epistatic) in that particular cross in the three parameter model. Chi square (x^2) values were significant according to joint scaling test for all the traits in all the crosses studied, except in the cross-IC-274556 x GPM-210 which was observed to be non-significant (Table 4 and 5). The significant value of chi square for all the plant traits in all the crosses indicated that the three parameter model did not adequately explain the genetic variability for these traits. The inadequacy of the model also indicated the presence of epistasis (non-allelic interaction), which is also inferred from the generation means. As the three parameter model did not satisfactorily explain the genetic variability for all these traits, therefore, a six parameter model was applied to accommodate epistatic gene interactions.

In all the five crosses studied, highly significant values of 'm' showed that six generations differed from each other with respect to mean of days to maturity from the generation mean analysis. The estimates of epistatic gene effects studied were also similar to results observed in six parameter model. Estimates of gene effects showed that, additive component was negatively significant in cross IC-274556 x GPM-210 and positively significant in the cross IC-326865 x GPM-470.

A dominance component was positive and significant in the two crosses *viz.* IC-328883 x IC-541068, IC-328953 x GPM-210 and negatively significant in the cross IC-326865 x GPM-210. Additive x Additive type of interaction was positively significant in the crosses IC-328883 x IC-541068, IC-328953 x GPM-210. The same were non-significant in the crosses GPM-470 x GPM-405 and IC-274556 x GPM-210.

The additive x Dominance component was negatively significant in the cross GPM-470 x GPM-405 and non-significant in the crosses IC-328883 x IC-541068, IC-326865 x GPM-470 and IC-274556 x GPM-210. The Dominance x Dominance type of interaction was observed to be present in four crosses but it was negatively significant in three crosses *viz.* IC-328883 x IC-541068, IC-328953 x GPM-210 and GPM-470 x GPM-405 and positively significant in the cross IC-326865 x GPM-470, whereas, non-significant in the cross IC-274556 x GPM-210.

The scaling test indicated the absence of non-allelic gene interaction in the cross IC-274556 x GPM-210. The character day to maturity is important for earliness. On the basis of generation mean analysis, inheritances of days to maturity was predominantly under the control of additive (d) gene effects and were negatively significant in the cross IC-274556 x GPM-210. Among epistatis, Dominance x dominance effect for days to maturity in two crosses were negatively significant *viz* IC-328883 x IC-541068, IC-328953 x GPM-210, and GPM-470 x GPM-405. The cross IC-328953 x GPM-210 exhibited dominance effect and was observed to be more important than additive effects in governing the inheritance of this trait. Moreover, additive x additive gene interaction also played paramount role in controlling this character in three crosses. Prevalence of epistasis is indicative of greater genetic diversity in the parental lines.

Table 3: Scaling test for different character in five crosses in maize (*Zea mays* L.).

Cross/Scales	A	B	C	D
Days to 50% tasseling				
IC-328883 x IC-541068	4.60**±0.93	7.35**±0.86	5.00**±1.23	-3.47**±0.69
IC-328953 x GPM-210	6.90**±1.11	6.90**±0.74	3.65*±1.65	-5.075**±0.72
IC-326865 x GPM-470	-3.25**±0.77	0.65±0.76	4.00*±1.88	3.30**±0.91
GPM-470 x GPM405	4.10**±0.78	7.70**±0.84	6.45**±1.64	-2.67**±0.78
IC-274556 x GPM-210	-0.050±0.77	1.90*±0.74	1.55±1.49	-0.150±0.68
Days to 50% silking				
IC-328883 x IC-541068	5.40**±0.96	7.65**±0.82	5.50**±1.38	-3.77**±0.71
IC-328953 x GPM-210	6.45**±1.052	8.00**±0.78	3.050±1.65	-5.70**±0.64
IC-326865 x GPM-470	-2.80**±0.75	0.90±0.75	4.55**±1.66	3.22**±0.87
GPM-470 x GPM405	4.00**±0.94	6.00**±1.091	7.25**±1.81	-1.375±0.73
IC-274556 x GPM-210	-2.35**±0.71	-0.20±073	-1.10±1.50	0.725±0.65
Days to maturity				
IC-328883 x IC-541068	9.65**±1.095	9.80**±1.34	8.35**±1.50	-5.55**±0.97
IC-328953 x GPM-210	20.50**±0.84	14.65**±0.87	24.60**±2.056	-5.27**±0.82
IC-326865 x GPM-470	-2.75±1.83	-6.60**±1.72	1.50±2.94	5.42**±1.42
GPM-470 x GPM405	5.45**±1.56	7.85**±1.60	11.35**±3.29	-40.250±2.94
IC-274556 x GPM-210	0.35±1.47	3.35±2.14	4.15±2.83	0.575±1.12

*, ** significant at 5% and 1 % respectively

Table 4: Result of Joint scaling test in five crosses in maize (*Zea mays* L.).

Character	Cross	m	d	h	Degree of Dominance	X^2 values
Days to 50% tasseling	IC-274556 x GPM-210	56.013 **± 0.221	0.454*± 0.204	0.020 ± 0.440	- 0.2085	7.318
Days to 50% silking	IC-274556 x GPM-210	59.224**± 0.233	-0.499*±0.204	-0.846±0.459	1.3017	15.173**
Days to maturity	IC-274556 x GPM-210	97.39**±0.35	-1.54**±0.34	-1.87±0.62	0.87	6.333

Table 5: Three parameter model (Jinks and Jones, 1958) in the absence of epistasis in maize (*Zea mays* L.).

Cross/Parameter	m	D	h
Days to 50 % tasseling			
IC-274556 x GPM-210	55.5750**±1.3875	0.1750±0.2434	2.1250±3.3190
Days to 50 % silking			
IC-274556 x GPM-210	60.85**±1.3257	-0.1000±0.2640	-5.85±3.1065
Days to maturity			
IC-274556 x GPM-210	96.9750**±2.4915	0.0250±1.0516	0.9750±6.3833

*, ** significant at 5% and 1 % respectively

Table 6: Estimates of gene effects in five crosses for three traits in maize (*Zea mays* L.).

Cross / Gene effects	M	d	h	i	j	l	Types of epistasis	X^2 values
Character 1. Days to 50% tassling								
IC-328883 x IC-541068	54.55**± 0.22	-1.7250**± 0.53	3.55*+ 1.45	6.950**±1.38	-1.37*± 0.58	-18.90**± 2.4	Duplicate	84.14**
IC-328953 x GPM-210	53.77**+ 179.1	-1.9250**±0.41	7.62**±1.5+6	10.15**±1.45	-0.00±0.63	-23.95**±2.33	Duplicate	126.86**
IC-326865 x GPM-470	56.02**±0.41	-1.45**±0.40	-9.35**±1.88	-6.60**±1.83	-1.95**±0.46	9.20**±2.48	Duplicate	30.68**
GPM-470 x GPM-405	55.15**±0.33	-0.52±0.40	3.37*±1.63	5.35**±1.56	-1.80**±0.51	-17.15**±2.29	Duplicate	98.07**
IC-274556 x GPM-210	56.10**±0.28	-1.15**±0.37	-0.02±1.44	0.30±1.36	-0.97*±0.44	-2.15±2.12	Complimentary	7.318
Character 2. Days to 50% silking								
IC-328883 x IC-541068	56.65**+0.24	-1.32*+0.50	4.20**+1.50	7.55**+1.42	-1.12+0.56	-20.60**+2.46	Duplicate	100.60**
IC-328953 x GPM-210	56.00**±0.25	-2.50**±0.38	9.12**±1.44	11.44**±1.29	-0.77±0.54	-25.85**±2.25	Duplicate	147.42**
IC-326865 x GPM-470	56.025**±0.41	-1.45**+0.40	-9.35**±1.88	-6.60**±1.83	-1.95**±0.46	9.20**±2.48	Duplicate	29.30**
GPM-470 x GPM-405	59.27**±0.29	0.12±0.45	0.92±1.63	2.75±1.47	-1.00±0.59	-12.75**±2.56	Duplicate	37.61**
IC-274556 x GPM-210	58.92**±0.28	-1.17**±0.32	-1.85±1.39	-1.45±1.29	-1.075*±0.41	4.00*±1.98	Duplicate	15.17**
Character 3. Days to maturity								
IC-328883 x IC-541068	86.32**±0.28	-0.85±0.78	9.025**±2.01	11.10**±1.95	-0.07±0.80	-30.55**±3.49	Duplicate	120.042**
IC328953 x GPM-210	94.678**±0.38	-0.57±0.29	7.40**±1.78	10.55**±1.64	2.92**±0.43	-45.70**±2.36	Duplicate	623.326**
IC-326865 x GPM-	96.42**±0.50	2.57*±1.008	-13.55**±3.04	-10.85**±2.85	1.92±1.018	20.20**±4.97	Duplicate	22.009**
GPM-470 x GPM405	97.10**±0.38	-0.57±0.31	-1.97±2.21	1.95±1.66	-1.20*±0.52	-15.25**±3.53	Complimentary	28.717**
IC-274556 x GPM-210	97.00**±0.43	-1.82*±0.71	-0.87±2.52	-1.15±2.25	-1.85±1.27	-1.85±4.03	Complimentary	6.333

*, **significant at 5% and 1 % respectively

Duplicate type of interaction was observed to be present in three crosses due to opposite signs of (h) and (l) components. Complimentary type of interaction was observed to be present in the crosses IC-274556 x GPM-210 and GPM-470 x GPM-405 as (h) and (l) components have same signs. Similar result was reported by Sofi *et al*., (2006).

CONCLUSIONS

Duplicate type of epistasis was observed in all the crosses and traits, except GPM-470 x GPM-405 for days to maturity, and IC-274556 x GPM-210 for 50% tasseling and maturity traits exhibited complementary type of epistasis. Especially duplicate type of epistasis observed in days to 50% silking trait inheritance. Complementary and duplicate gene interactions appeared operative in the inheritance of silking and maturity traits. Duplicate gene interactions were seen functioning in controlling 50 % tasseling in most of the crosses.

FUTURE SCOPE

Breeder can be utilizing these traits such as days to 50 % tasseling, silking and maturity in the selection purpose for the crop improvement because these traits are fixable due to Additive x Additive type of gene interaction.

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REFERENCES

Bhalla, S. K., Bali, S., Sharma, S. and Sharma, B. K. (1988). Assessment of genetic variability and correlations in indigenous maize (*Zea mays* L.) germplasm of Himachal Pradesh. *Himachal Journal of Agricultural Research, 12*(2), 75-81.

Darrah, L. L. and Hallauer, A R. (1972). Genetic effects estimated from generation means in four diallel sets of maize inbreds. *Crop Science*, *12*(5), 615-621.

Dong, E., Bai, Y., Qin, L., Liang, Q., Liu, C., Cai, Y. (2020). Identification and epistasis analysis of quantitative trait loci for zeaxanthin concentration in maize kernel across different generations and environments. *Breeding Science*, *70*(2), 212-220.

Gamble, E. E. (1962a). Gene effects in corn (*Zea mays* L.). I. Separation and relative importance of gene effects for yield. *Canadian Journal Plant Science, 42*, 339–348.

Hallauer, A. R and Russel, W A. (1962). Estimates of maturity and its inheritance in maize. *Crop Science, 2* (4), 289-294.

Hallauer, A. R. and Miranda, J. B. (1988). Quantitative genetics in maize breeding *2nd ed. Iowa State Univ. Press. Ames. IA (USA).*

Hema, D. K., Soonkwon, F., Mondeil, B. B., Tiotoure, A., Tapsoba, and Kim, S. K. (2001). Anthesis silking interval in maize: importance in breeding for drought tolerance. *Cahiers Agricultures, 10*(4), 255-260.

Jinks, J. L. and Jones, R. M. (1958). The analysis of diallel crosses. Maize Genetics co-operative *News Letter, 27*, 48-54.

Kassem, E. S., El-Marshidy, M. A., Hassaballa, E. A. and Khalifa, M. A. (1978 b). Relative importance of effects in the inheritance of: II. Yield and yield components in maize. *Egyptian Journal of Agronomy, 3*(2), 213-225.

Kassem, E. S., Hassaballa, E. A., El-Marshidy, M. A and Khalifa, M. A. (1978a). Relative importance of effects in the inheritance of: I. plant height, ear height and flowering of maize plants *Egyptian Journal of Agronomy, 3*(2), 203-212.

Mather, K. (1949). Biometrical genetics. Methuen and Co. Ltd. London.

Mather, K. and Jinks, J. L. (1971). Introduction to Biometrical Genetics. *Cornell University Press. Ithaca, NY.* PP.382.

Muhammad, A., Shabbir, S. M., Amer, H. and Muhammad, S. (2008). Evaluation of Maize 3-way Crosses through Genetic Variability, Broad Sense Heritability, Characters Association and Path Analysis. *Journal of Agricultural Research, Pakistan, 46*, 32.

Panse, V. C. and Sukhatme, P. V. (1985). *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research, New Delhi, pp. 152-161.

Patil Krantikumar, H., Mahajan, R. C. and Nagargoje, V. T. (2020). Generation mean analysis in Maize (*Zea mays* L.) paper publishing in National conference. *Journal of Oilseeds Research,* p79.

Patil Krantikumar, H., Mahajan, R. C. and Lekha Rani, C. (2016). Generation mean analysis for grain yield attributing traits in Maize (*Zea mays* L.).*Green Farming, 7*(2), 277-282.

Shankar, M., Singh, R., Shahi, J. P., Devesh, P. and Singh, P. (2022). Generation mean analysis for yield and drought related traits in Maize (*Zea mays* L.). *Current Journal of Applied Science and Technology*, *41*(22), 30–45.

Shaw, R. H. and Thom, H. C. H. (1951). On the phenology of field corn, silking to maturity. *Agronomy Journal, 43*, 546-548.

Sher, H., Iqbal, M., Khan, K., Yasir, M., and Rahman, H. U. (2012). Genetic analysis of maturity and flowering characteristics in maize (*Zea mays* L.). *Asian Pacific Journal of Tropical Biomedicine, 2*(8), 621–626.

Singh R. K. and Chaudhary, B. D. (1985). *Biometrical Methods in Quantitative Genetic Analysis.* Kalyani publishers, New Delhi, pp. 178-185.

Singh, M., Nag, S. K. and Yadav, R. K. (2023). Determination of Gene Effects and Inheritance of genes for various Generations of Soybean Crosses (*Glycine max* L. *Merrill*). *Biological Forum – An International Journal*, *15*(4), 243-245.

Sofi, P., Rather, A. G. and Venkatesh, S. (2006). Detection of epistasis by generation means analysis in maize hybrids. *Pakistan Journal of Biological Sciences, 9* (10), 1983-1986.

Wolf, D. P. and Hallauer, A R. (1977). Triple test cross analysis to detect epistasis in maize. *Crop Science, 37*, 763-770.

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