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ESTIMATE OF COMPONENTS OF GENETIC VARIATION FOR GRAIN YIELD AND ITS ATTRIBUTING TRAITS IN MAIZE (*ZEA MAYS* L.)

Bhushan Umesh Jadhao[1], Sanjeev Kumar[2], Kshitij Sanjay Shahare[1], Satyam Sanjay Ingle[1], Amrita Sharma[1], Arpita Atul Chaudhari[1], R.K. Patel[3], Vishwanath[1]*, Upasana Singh[4] and Lokesh Pratap Narayan Chandel[1]

[1]Lakshmi Narain College of Technology University, Bhopal, (M.P.), India
[2]Technical Assistant, Govt. of Uttar Pradesh, Lucknow, (U.P.), India
[3]SAM Global University, Bhopal, (M.P.), India
[4]Department of Botany, Om Degree College, Shikohabad, Firozabad, U.P., India
*Corresponding author e-mail: vishwa8159@gmail.com

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ABSTRACT

The investigation material for the experiment consisted of 14 lines *viz.*, CML 439, CML 359, CML 326, DMR N-21, CML 338, CML 139, HKI 34(H2)-1, HKI 26-24(1-2), CML 470-B×15, CML 358, CML 411, CML 41, HKI 164-4(1-3)-2 and CM 500 was sown at main research farm of LNCTU, Bhopal, (M.P.) during *Kharif* 2024-25. Analysis of variance indicated highly significant differences for days to 50% tasseling, silking, anthesis-silking interval (ASI), plant height, ear height, ear diameter, kernels per row, and grain yield, while ear length was non-significant. Additive genetic variance was significant for all traits except shelling percentage and test weight, whereas dominance variance (H1, H2) was highly significant for most traits. The covariance between additive and dominance effects (F) was significant for several yield traits, and the average degree of dominance ($\sqrt{H1/D}$) exceeded unity, suggesting over-dominance for most characters. Environmental variance was largely non-significant, highlighting genetic control. Ratios such as H2/4H1 and h2/H2 indicated unequal distribution of positive and negative alleles and fewer dominant genes for traits like ASI, ear height, kernel rows per ear, and grain yield. Narrow-sense heritability estimates were generally low, ranging from -0.82 to 0.15, suggesting limited scope for direct selection. Correlation analysis showed positive association of parental order of dominance

***Keywords*:** Genetic Variation; Grain Yield; Maize (*Zea mays* L.)

Introduction

Maize (*Zea mays* L.) is a globally significant cereal crop that plays a central role in the agricultural economy. Ranking third in production after wheat and rice, it is valued not only as a staple food but also as a source of animal feed and a raw material for numerous industries. Rich in starch, protein, oil, vitamins, and minerals, maize contributes to both nutrition and industrial processing. It noticed significant GCA and SCA variances for most of the traits studied Mandal *et al.* (2001). Here observed that both additive and non-additive genetic components for 100-grain weight and shelling percentage in CML 85 and CML 79. The crosses showed positive and highly significant specific combining ability effect for grain yield Mahto and Ganguly (2001). Roughly one-third of global output is consumed directly by humans or used in industrial applications, while the remaining two-thirds serve as feed for livestock. One of maize's greatest strengths lies in its adaptability. It thrives across a wide range of environments, from latitudes of 58°N to 40°S, elevations up to 3000 meters, and rainfall zones spanning 250 to 5000 mm annually. This ecological flexibility has enabled its expansion worldwide, making it one of the most productive tropical crops.

They suggested that early testing was effective for predicting the combining abilities expressed at later inbreeding generations. In addition, the additive effects of inbred lines may be a main contributor and the relationships between the S2 and S5 generation hybrids for ear dry weight and grain dry weight Shieh GuangJauh and Thseng-Fusheng (2001). Global maize production stands at about 590 million tonnes, covering 139 million hectares with an average yield of 4.3 tonnes per hectare. India is the fourth largest producer, contributing over 21 million tonnes from 8.55 million hectares, though productivity remains lower than the global average. Major maize-growing states include Andhra Pradesh, Karnataka, Bihar, Madhya Pradesh, Rajasthan, Uttar Pradesh, and Punjab. Karnataka, in particular, leads national production, with rapid expansion driven by modern cultivation practices and profitability. The crop's importance continues to rise due to its diverse applications. In Africa and Asia, maize is a primary food grain, while in the United States nearly 85% is directed toward cattle feed. In India, consumption patterns are more varied: about half is eaten as food, one-third goes into poultry and livestock feed, around 12% supports starch and oil industries, and a small fraction is reserved for seed.

It evaluated six sweet corn inbreeds, three each of sugary and shrunken types derived from different source populations and developed hybrids following half dialled mating design. They reported that of both GCA and SCA variances for most of the characters and implied that both additive as well as non-additive components are important Jyoti Kumari *et al.* (2007).

The aim of identifying the relative importance of additive, dominance, and environmental effects. This was help in understanding the heritability of yield-related traits, guiding effective selection strategies, and improving breeding efficiency for higher productivity**.**

Material and Method

The present investigation was carried out during *Kharif* 2024-25 at Main Experiment Station Farm of LNCTU, Bhopal, (M.P.). The material for the experiment consisted of 14 lines *viz*., CML 439, CML 359, CML 326, DMR N-21, CML 338, CML 139, HKI 34(H2)-1, HKI 26-24(1-2), CML 470-B×15, CML 358, CML 411, CML 41, HKI 164-4(1-3)-2 and CM 500 the selected lines crossed with testers (broad/narrow genetic base) identifies superior parents and hybrids in three replications. The recommended plant spacing was 60 cm × 20 cm under normal conditions, and fertilizer dose varies by maturity applied for 200:60:60 kg NPK/ha. The statistical analysis of the data was carried out using 'Genres' and 'SPAR2' software packages at the Department of Genetics and Plant Breeding, for various parameters were estimated as genetical and physiological characters. The observation was recorded Days to 50 % tasseling, Days to 50 % silking, ASI, Plant height (cm), Ear height (cm), Ear length (cm), Ear diameter (cm), Kernel rows per ear, kernels per row, Grain yield per five plants (kg), Shelling percentage, and 100-seed weight. Estimating the components of variance, analysis of variance (ANOVA) was carried out according to Panse and Sukhatme (1967). If the variance due to genotypes (Parents) was significant, then the genetic components of variance were estimated. Significance of t^2 value at (n-2) degrees of freedom indicate the fulfilment of assumptions. The value of t^2 was obtained by the following formula (Panse and Sukhatme, 1967).

Results and Discussion

Analysis of variance revealed significant differences among the parents and crosses for most of the characters studied significantly for days to 50 percent tasseling, days to 50 percent silking, ASI, plant height, ear height, ear diameter, kernel per row, grain yield except ear length (cm)The estimates of components of variation and genetic variations are presented in table 1. The result revealed that the estimate of additive genetic variation was significant with respect to all characters except shelling percentage and test weight. The estimates of H_1 (variance due and dominance effects of gene) and H_2 (proportion of dominance variance due to the positive and negative effects of genes) were highly significant for all the traits under study except shelling percentage and yield in table 2.

The estimate of F, which is a measure of covariance between additive and dominance gene effects at different loci, was significant for days to 50 percent tasselling, days to 50 percent silking, Anthesis-silking interval, ear length, ear diameter (cm), kernel rows per ear, kernel per row, grain yield per five plants (kg).The estimate of h^2dominance effect, expressed over all loci in heterozygous phase in all crosses (h^2) was significant for all characters under study except ASI, grain yield for per five plant, shelling percentage and test weight in table 2.

The ratio $(H_1/D)1/2$ which is the measure of the degree of dominance was more than unity for all the characters estimated. It was found highest for plant height (2.18) followed by grain yield per plants (1.79) and ASI (1.66). The average degree of dominance $(H_1/D)^{½}$ most of the value were observed greater than 1, it indicates most of characters, days to 50 % tasselling, days to 50 % silking, ASI, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), kernel rows per ear, kernels per row, grain yield per plants (kg), 100 seed weight were over dominance governed except shelling percentage. The environmental component of variation (E) was non-significant for kernel rows per ear, grain yield, shelling percentage trait in table 2.

The ratio $H_2/4H_1$ (proportion of positive and negative alleles in plant) was less than 0.25 for all the characters. Another ratio which expresses the proportion of dominant and recessive genes in the parents was more than unity for all the character the characters studied. The number of dominant (h^2/H_2) genes governing the characters was less than unity for ASI (0.15), ear height (0.74), kernel rows per ear (-0.1), test weight (0.18), grain yield (0.21), shelling percentage (0.004). The narrow sense heritability ranged from -0.82 (ear diameter) and 0.15 (days and 50 per cent silking) in table 2.

The correlation coefficient between mean of the common parent of an array and parental order of dominance for each array was negative for most of the traits except for characters viz., days to 50 percent tasselling (0.67), days to 50 percent silking (0.42), ASI (0.52) and shelling per cent (0.31). The highest correlation was found in trait days to 50 per cent tasselling (0.67), while lowest correlation was found in ear length (-0.87). The t-test was performed for testing the validity of the hypothesis. The t test was found highly significant at P=0.01 for ASI, ear height, ear diameter and grain yield while for plant height and kernel per row it was significant at P=0.05 in table 2.

Table 3, The following Bar Graphs (Trait-wise comparison) Plot D, H1, H2, F, h², E values for each trait as grouped bars. This was clearly showing which genetic components dominate for traits like plant height, grain yield, or tasseling. Line Graph (Degree of dominance) Plot $(H1/D)^{1/2}$ values across traits. Traits above 1 indicate over-dominance, so the line graph will highlight which traits are strongly influenced by dominance. Scatter Plot (Heritability vs Grain Yield) X-axis: Narrow-sense heritability, Y-axis: Grain yield per plant. This shows whether traits with higher heritability correspond to better yield performance. Heatmap (Component significance) Rows equals to Traits, Columns equals to Genetic components (D, H1, H2, F, h², E). Colour intensity equals to magnitude of values. This gives a quick visual of which traits are controlled more by additive vs dominance variance.

Conclusion

The study demonstrated that maize possesses substantial genetic variability for most yield-contributing traits, with both additive and dominance components playing important roles. Additive genetic variance was significant for several traits, while dominance effects (H1, H2) were particularly influential in plant height, grain yield, and kernel traits. The average degree of dominance exceeded unity for most characters, indicating over-dominance as a governing factor. Environmental variance was largely non-significant, underscoring the genetic basis of trait expression. Ratios such as H2/4H1 and h2/H2 highlighted unequal distribution of alleles and fewer dominant genes for traits like ASI, ear height, kernel rows per ear, and grain yield. Narrow-sense heritability estimates were generally low, suggesting limited scope for direct selection, but the presence of significant variability and dominance effects points to the potential of exploiting heterosis in breeding programs. Overall, the findings emphasize the importance of both additive and non-additive genetic components in maize improvement and provide valuable insights for designing effective breeding strategies.

Table 1 : ANOVA for grain yield and its components among parent in maize

Source	df	Days to 50 % tasseling	Days to 50% silking	ASI	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Kernel rows per ear	kernels per row	Grain yield per five plants (kg)	Shelling percentage	100-seed weight
Replication	1	6.03	0.035	0.15	95.09	-238335	6.82*	0.57*	0.63	3.43	0.0006	1.85	0.32
Parent	13	17.81**	18.65**	6.32*	602.1**	2239.67	23.50**	0.76**	8.36**	52.03**	0.060**	29.85*	24.70**
Error	13	1.42	1.11	0.22	57.93	18413.77	0.86	0.122	0.611	7.47	0.001	10.16	1.63

*Significant @ P= 0.05 ** Significant @ P=0.01

Table 2 : Estimate of components of genetic variation for grain yield and its attributing traits in maize

Component	Days to 50 % tasseling	Days to 50% silking	ASI	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Kernel rows per ear	kernels per row	Grain yield per five plants (kg)	Shelling percentage	100-seed weight
D	8.31**	8.20**	2.74**	229.32**	337.64**	10.87**	0.32**	3.73**	21.47**	0.028**	3.68	3.21
H_1	13.90**	21.42**	7.57**	1096.47**	764.02**	17.82**	0.65**	5.95**	56.74**	0.09**	109.01	25.08**
H_2	8.02**	13.95**	4.76**	966.97**	470.53**	8.69**	0.34**	2.65**	34.23**	0.06	95.68**	22.92**

F	13.32**	13.93**	5.11**	284.16	572.60**	19.51**	0.61**	7.00**	43.07**	-0.5**	5.76	3.43
h^2	28.26**	26.83**	0.93	3968.38**	351.12**	7.15**	0.40**	-0.5**	98.12**	0.013	0.40	4.16
E	0.59**	1.12**	0.41**	71.70**	73.06**	0.87**	0.05**	0.39	1.33**	0.001	18.59	9.13**
$(H_1/D)^{½}$	1.29	1.61	1.66	2.18	1.50	1.28	1.40	1.25	1.62**	1.79	-5.42	2.79
$H_2/4H_1$	0.14	0.16	0.15	0.22	0.15	0.12	0.13	0.11	0.15	0.16	0.21	0.22
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$	4.25	3.21	3.56	1.79	3.58	5.68	5.013	6.64	4.22	3.37	1.33	1.47
Heritability(ns)	0.14	0.15	0.11	0.10	0.13	0.07	-0.82	0.03	0.03	0.10	0.04	0.06
r (Wr +Vr),Yr	0.67	0.42	0.52	-0.76	0.75	-0.87	-0.82	-0.55	-0.78	-0.55	0.31	-0.10
h^2/H_2	3.52	1.92	0.15	4.10	o.74	0.82	1.18	-0.1	2.86	0.21	0.004	0.18
t^2	0.08	0.04	5.60**	1.95	6.13**	0.42	3.68**	1.08	1.91	2.10	1.33	0.74

*Significant at P = 0.05 ** Significant at P=0.01

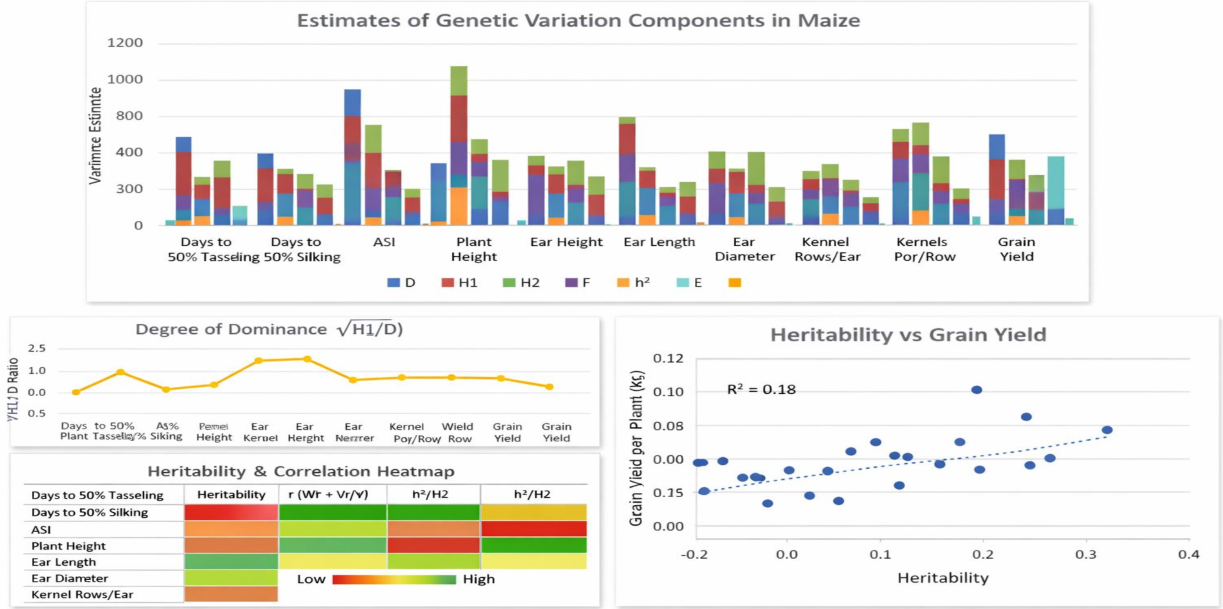

Fig. 1 : Bar Graphs (Trait-wise comparison), Line Graph (Degree of dominance), Scatter Plot (Heritability vs Grain Yield) and Heatmap (Component significance)

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