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Genetic variability, correlation and path coefficient analysis of yield attributing traits in maize (*Zea mays* L.) inbred lines

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Abstract
The present study was conducted at the AICRP on Maize, Maize Improvement Project, Ambikapur (C.G.), during the *Rabi* 2024 season. The experiment aimed to investigate the genetic variability, correlation and path coefficient analysis of yield attributing traits in twenty-nine maize inbred lines. The experimental layout was a Randomized Complete Block Design (RCBD) with three replications. Analysis of variance revealed highly significant genetic divergence among genotypes for all traits, indicating substantial genetic diversity. Genetic variability analysis demonstrated moderate to high genotypic and phenotypic coefficients of variation, with plant height exhibiting highest genotypic coefficient of variation (17.00%) and heritability (90.53%), alongside greatest genetic advance (33.31%). Initial Plant Population (IPP) showed moderate genetic variability (GCV: 6.85%, PCV: 7.97%) with high heritability (73.81%) and genetic advance (12.13%), indicating effective selection potential. Yield-related traits including grain yield (GY) and 100-kernel weight (KW) demonstrated high heritability (91.27% and 98.32%) with genetic advance (22.31% and 30.55%), confirming suitability for improvement. Correlation analysis revealed grain yield exhibited highest positive correlations with initial plant population (IPP) (r = 0.606**), followed by days to maturity (DM) (r = 0.516**), number of leaves per plant (NLP) (r = 0.379*), ear height (EH) (r = 0.455*) and ear weight (EW) (r = 0.377*) showed significant correlations. Path coefficient analysis identified ear height (EH) with highest positive direct effect (1.268*), followed by number of leaves per plant (NLP) (0.686*) and initial plant population (IPP) (0.500**). These findings provide valuable insights for effective breeding programs, highlighting the complexity of maize breeding and the importance of comprehensive trait selection for genetic optimization.

Keywords: Genotypic, phenotypic, coefficient of variation, genetic variability, heritability, genetic advance, inbred lines, correlation coefficient and path coefficient

Introduction
Maize (*Zea mays* L.) is one of the most important staple cereal crop globally, valued for its high yield potential, nutritional composition. As a cross-pollinated crop with abundant genetic variability, maize breeding seeks to harness this diversity to develop high-yielding, stress-tolerant and nutritionally superior hybrids. Maize grains have approximately 9.9 % protein, 4 % oil, 70 % starch and 2.7 % crude fiber. Given its versatility for use in food, animal feed and various industrial applications, maize is a highly sought-after crop globally (Bisen *et al.*, 2017) [6]. Maize as a C4 species, shows high photosynthetic efficiency, yield potential and adaptability to diverse conditions. Modern breeding strategies focus on developing inbred lines and hybrids with superior grain yield, which remains the core agronomic goal (Pandey *et al.*, 2017) [13]. Its rich grains include approximately 70% starch, 10% protein and 8.5% dietary fiber. This nutritional profile underscores maize grains wide spread utility, ranging from edible oil and human consumption to animal feed and biofuel production (Galal *et al.*, 2025) [7]. The global maize production in a few major countries is the United States remained the leading global producer of maize, accounting for 31% of world production with 377.63 million metric tons, followed by China with 24% (294.92 million metric tons) and Brazil with 11% (135 million metric tons). The European Union 5% (59.31 million), Argentina 4% (50 million) and India contributed 3% (42.28 million)

respectively (Foreign Agricultural Service, U. S. DEPARTMENT OF AGRICULTURE 2024-25). In India, during this year 2023-2024 despite an expansion of maize cultivation area to 108.87 lakh hectares from 105.24 lakh hectares in the previous year, estimated production decreased from 380.85 to 356.73 lakh tonnes by the Government of India (ANGRAU and CARP report 2023-24). In maize Chhattisgarh, grown on 193.60 thousand hectares of land, yielding 598.03 thousand million tonnes and 3.019 tonnes per hectare of productivity in 2023-24 (Dept. of statistics, C.G. Govt., 2024).

In maize genetic variability corroborates that heritability, genetic advance, GCV and PCV gaps together determine genetic potential in maize breeding populations. This suggests that traits with high GCV, PCV, and heritability offer a strong genetic base for improving yield stability through direct selection or through heterotic combinations (Kumar *et al.*, 2024) [10]. Variability is the foundation for the success of any crop improvement program. It provides the raw material upon which selection acts to develop superior genotypes with enhanced yield potential and adaptability to diverse agro-climatic conditions (Hasan *et al.*, 2024) [9]. Its indicates that moderate heritability with high genetic advance reflects the combined effect of additive and non-additive gene actions, which can be effectively exploited in hybrid development (Saritha *et al.*, 2024) [17]. GCV and PCV are valuable tools for quantifying the extent of variability present in specific traits (Ghorpade *et al.*, 2025) [8]. High broad-sense heritability coupled with high genetic advance is especially for plant height, leaf area and seedling fresh weight suggests the predominance of additive genes, which favor direct selection (Singh and Singh 2025) [18].

Correlation coefficient analysis is essential in identifying the degree and direction of association between different quantitative traits in maize. It helps plant breeders to understand how traits influence one another and facilitates indirect selection when traits are positively correlated with yield (Kumar *et al.*, 2024) [10]. Both phenotypic and genotypic correlations are used to dissect genetic relationships among traits, where phenotypic correlations reflect both genetic and environmental effects, while genotypic correlations indicate inherent genetic associations (Reddy and Rao 2023) [16]. The significant positive genotypic correlations of grain yield with related traits such as support the use of these yield-contributing traits for indirect yield improvement. Such information is vital for designing efficient selection strategies in maize breeding programs (Singh and Singh 2025) [18].

Path analysis enhances trait association studies by quantifying the magnitude of each trait's influence, thereby helping breeders to prioritize traits for selection and hybrid development in maize (Reddy and Rao 2023) [16]. This analysis separates correlation coefficients into direct and indirect effects, helping identify traits that most influence yield. It clarifies that some highly correlated traits may have low direct effects, preventing misinterpretation in selection. This analysis precisely pinpoints traits with the greatest impact on yield improvement (Kumar *et al.* 2024 and Hasan *et al.* 2024) [10, 9]. Stress that considering both direct and indirect effects through path analysis improves selection efficiency in breeding programs (Singh and Singh 2025) [18]. Thus, knowledge of genetic variability, correlation and path coefficient is essential for a breeder to choose the best genotypes and decide the correct methodology for crop improvement.

Materials and Methods

In this experiment genetic variability, correlation and path analysis of yield attributing traits was performed on a total of 29 inbred lines (Table 1), representing collections from AICRP on Maize, Ambikapur (Chhattisgarh), with under the supervision of Department of Genetics and Plant Breeding during *Rabi* 2024-25, located at a latitude of 20^{0}8'N, longitude of 83^{0}15'E and altitude of 592.62 m MSL (Mean Sea Level). The experimental layout was a Randomized Complete Block Design (RCBD) with three replications.

Statistical analysis

The data for all traits from the two experiments in this study were averaged from five randomly taken plants per plot per replication. These mean values were subjected to statistical analysis, including analysis of variance (ANOVA) following the Randomized Block Design procedure as described by Panse and Sukhatme 1967 and association analysis (correlation and path coefficient analysis) was calculated for all possible combination of grain yield and its component parameters by using the standard procedure given by (Uppal *et al.*, 2024) [21].

Table 1: List of 29 diverse inbred lines

S. No.	Inbred	S. No.	Inbred	S. No.	Inbred
1.	AMI-118	11.	AMI-106	21.	VL-1342-95
2.	AMI-125	12.	AMI-124	22.	VL-171522
3.	AMI-101	13.	AMI-111	23.	VL-18941
4.	AMI-120	14.	AMI114	24.	VL-19204
5.	AMI-107	15.	AMI-116	25.	LM-13
6.	AMI-122	16.	AMI-103	26.	LM-14
7.	AMI-119	17.	IAMI-43-1	27.	CML-151
8.	AMI-104	18.	IAMI-83-2	28.	HKI-163
9.	AMI-115	19.	IAMI-57	29	BML-06
10	AMI-113	20.	VL-131204		

Results and Discussion

Analysis of variance (Table 2) indicated highly significant genetic divergence among genotypes for all 15 yield and agronomic traits studied. The genetic variability analysis (Table 3) and diagrammatic representation (Figure 1.) revealed moderate to high genotypic and phenotypic coefficients of variation (GCV and PCV) across evaluated traits. Initial Plant Population showed moderate GCV (6.85%) and PCV (7.97%) with high heritability (73.81%) and genetic advance as percent of mean (12.13%), indicating effective selection potential. Traits like Leaf Width and Ear Length exhibited relatively high GCV (10.24%, 20.79%) and corresponding PCV with moderate to high heritability (70.68%, 53.48%) and genetic advance (17.73%, 31.32%), suggesting good genetic control despite environmental influence. Plant Height displayed very high GCV (17.00%) and heritability (90.53%), alongside the highest genetic advance (33.31%), signifying strong additive gene effects suitable for breeding. Yield-related traits such as Grain Yield and 100-Kernel Weight had high heritability (91.27%, 98.32%) and substantial genetic advance (22.31%, 30.55%), confirming their potential for improvement through selection. Conversely, traits related to flowering time and maturity had high heritability but low genetic advance, reflecting limited variability for rapid gains. Overall, these findings emphasize the genetic basis and breeding value of key agronomic traits for crop improvement.

Similar observations have been reported by different workers *i.e*., Bello *et al.* (2012) [5] reported high GCV, PCV, heritability (>70%), and genetic advance ford specific traits, indicating additive gene action and effective selection. Sravanti *et al.* (2017) [20] assessed 42 inbreds and found highest GCV (26.42) and PCV (27.52) for ear weight, and lowest for days to maturity (GCV 3.07, PCV 3.45) with high heritability and genetic advance for ear height and grain yield per plant. These findings suggest strong genetic control on these key traits to guide maize breeding. Singh *et al.* (2019) [19] reported genetic variation and high heritability in traits closely associated with yield, such as ear height and kernel rows, supporting their use in indirect selection. Ahmed *et al.* (2020) [2] reported phenotypic coefficients of variation from 2.27% to 13.25% and genotypic coefficients from 1.72% to 11.48%, with heritability ranging between 19.21% and 86.79%, indicating moderate to high genetic advance suitable for selection. Kumar *et al.* (2024) [10] found significant variance for 12 maize traits, with high heritability but low genetic advance for some traits, suggesting non-additive gene action limiting selection gains. Singh and Singh (2025) [18] reported high PCV and GCV above 20% for seedling weight and grain yield. Heritability was high for days to tasseling (85%), plant height (88%), leaf area (80%), and grain yield (75%). Genetic advance exceeded 30% for traits like plant height, leaf area and seedling weight, indicating strong potential for improvement through selection. Hybrid vigor was evident in superior F_1 performances, emphasizing hybridization's role in enhancing maize yield.

Table 2: Analysis of Variance (ANOVA) for fifteen traits in inbred lines.

Characteristics	Mean Sum of Sqaures		
	Replication	**Genotypes**	**Error**
Df	**2**	**28**	**56**
IPP	8.32	63.88**	6.76
NLP	0.85	1.32**	0.39
LL	3.57	45.84**	11.55
LW	0.12	2.70**	0.33
EH	4.14	13.39**	2.34
PH	216.60	1489.03**	50.19
TSL	2.84	42.42**	0.65
SLK	1.98	48.20**	0.68
DM	6.12	73.04**	3.19
EL	17.73	23.78**	5.34
ED	0.28	1.21**	0.14
NKR	0.01	12.26**	2.80
EW	7.24	174.53**	16.97
KW	0.10	42.07**	0.24
GY	0.93	33.57**	1.04

Table 3: Genetic parameters of variability for grain yield and ancillary 15 traits in maize inbred lines

Characters	Mean	GV	PV	GCV	PCV	h^2(bs)	GA	GAM (%)
IPP	64	19.04	25.80	6.85	7.97	73.81	7.72	12.13
NLP	8.7	0.31	0.70	6.41	9.62	44.36	0.77	8.79
LL	61.2	11.43	22.98	5.52	7.83	49.74	4.91	8.02
LW	8.7	0.79	1.12	10.24	12.18	70.68	1.54	17.73
EH	24.9	3.68	6.02	7.71	9.86	61.13	3.09	12.42
PH	128.9	479.61	529.80	17.00	17.86	90.53	42.92	33.31
TSL	113	13.92	14.57	3.31	3.38	95.55	7.51	6.66
SLK	117	15.84	16.52	3.41	3.48	95.89	8.03	6.87
DM	148	23.28	26.47	3.25	3.47	87.96	9.32	6.28
EL	11.9	6.14	11.49	20.79	28.43	53.48	3.73	31.32
ED	4.0	0.36	0.50	14.85	17.54	71.63	1.04	25.89
NKR	12.2	3.15	5.95	14.59	20.04	53.00	2.66	21.88
EW	57.22	52.52	69.49	12.67	14.57	75.58	12.98	22.68
KW	25.0	13.94	14.18	14.95	15.08	98.32	7.63	30.55
GY	24.97	10.84	11.88	11.33	11.86	91.27	6.48	22.31

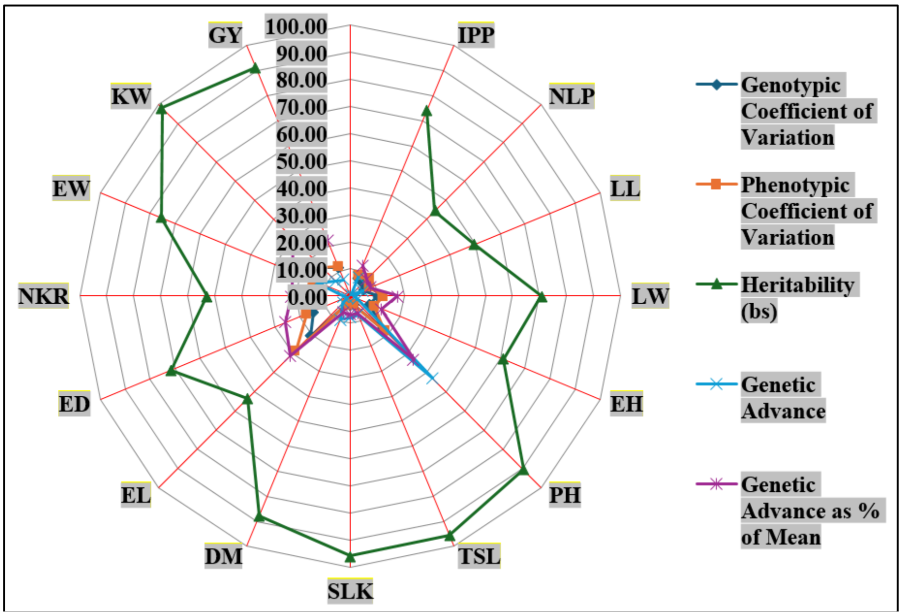


Fig 1: Genetic parameters of variability for grain yield and ancillary agro-economic traits in maize inbred lines

Genotypic Correlation Result

Genotypic correlation (Table 4) found the grain yield exhibited high positive genotypic correlations with initial plant population (IPP) (r = 0.606**), followed by days to maturity (DM) (r = 0.516**) indicating these traits strongly drive yield improvements in maize. Number of leaves per plant (NLP) also showed a significant positive correlation with grain yield (r = 0.379*), reflecting its role in vegetative growth supporting reproductive success. Moderate correlations were observed between grain yield and ear height (EH) (r = 0.455*), ear weight (EW) (r = 0.377*), tasseling (TSL) (r = 0.437*), silking (SLK) (r = 0.447*) and leaf length (LL) (r = 0.267 NS). These traits contribute indirectly to grain yield by influencing factors like canopy structure and reproductive timing. Traits such as plant height (PH) (r = 0.081 NS), kernel weight (KW) (r = 0.093 NS) and leaf width (LW) (r = −0.010 NS) had nonsignificant correlations with grain yield, suggesting limited direct genetic influence in this set of genotypes. This categorization emphasizes selecting for high and moderately correlated traits like IPP, NLP, EH and EW for indirect genetic gain in maize yield.

Table 4: Genotypic correlation coefficient among yield and yield component traits

	IPP	NLP	LL	LW	EH	PH	TSL	SLK	DM	EL	ED	NKR	EW	KW	GY
IPP	1.000														
NLP	0.1021 NS	1.000													
LL	0.5135 **	0.3674 *	1.000												
LW	0.048 NS	-0.1222 NS	0.011 NS	1.000											
EH	0.2998 NS	0.3051 NS	0.4807 **	-0.1593 NS	1.000										
PH	0.3574 NS	-0.1148 NS	0.3777 *	0.381 *	0.2667 NS	1.000									
TSL	-0.3974 *	0.4073 *	0.1007 NS	-0.0444 NS	0.4372 *	-0.0749 NS	1.000								
SLK	-0.2755 NS	0.4621 *	0.2034 NS	-0.0478 NS	0.4477 *	-0.0557 NS	0.9889 **	1.000							
DM	-0.1972 NS	0.5549 **	0.1243 NS	-0.0198 NS	0.5162 **	-0.0698 NS	0.8786 **	0.8743 **	1.000						
EL	0.2661 NS	0.2386 NS	0.4297 *	0.1104 NS	0.5736 **	0.372 *	0.2825 NS	0.3651 NS	0.3687 *	1.000					
ED	-0.0568 NS	0.0957 NS	-0.0017 N	S 0.3883 *	0.2643 NS	0.3038 NS	0.4314 *	0.4412 *	0.4686 *	0.9659 **	1.000				
NKR	0.2105 NS	0.3324 NS	0.1464 NS	0.0491 NS	0.1111 NS	0.217 NS	0.0631 NS	0.0803 NS	0.1953 NS	0.7288 **	0.6839 **	1.000			
EW	0.1337 NS	0.4633 *	0.3557 NS	0.1676 NS	0.3499 NS	0.2037 NS	0.3835 *	0.3954 *	0.4074 *	0.6661 **	0.4282 *	0.5635 **	1.000		
KW	0.1945 NS	-0.1587 NS	0.3093 NS	0.2679 NS	-0.0434 NS	0.2545 NS	0.092 NS	0.163 NS	0.1519 NS	0.3346 NS	0.3944 *	0.2135 NS	0.2611 NS	1.000	
GY	0.606 **	0.3793 *	0.2669 NS	-0.0098 NS	0.4548 *	0.0814 NS	-0.0112 NS	0.0219 NS	0.0904 NS	0.2113 NS	-0.0775 NS	0.2178 NS	0.3769 *	0.0936 NS	1.000

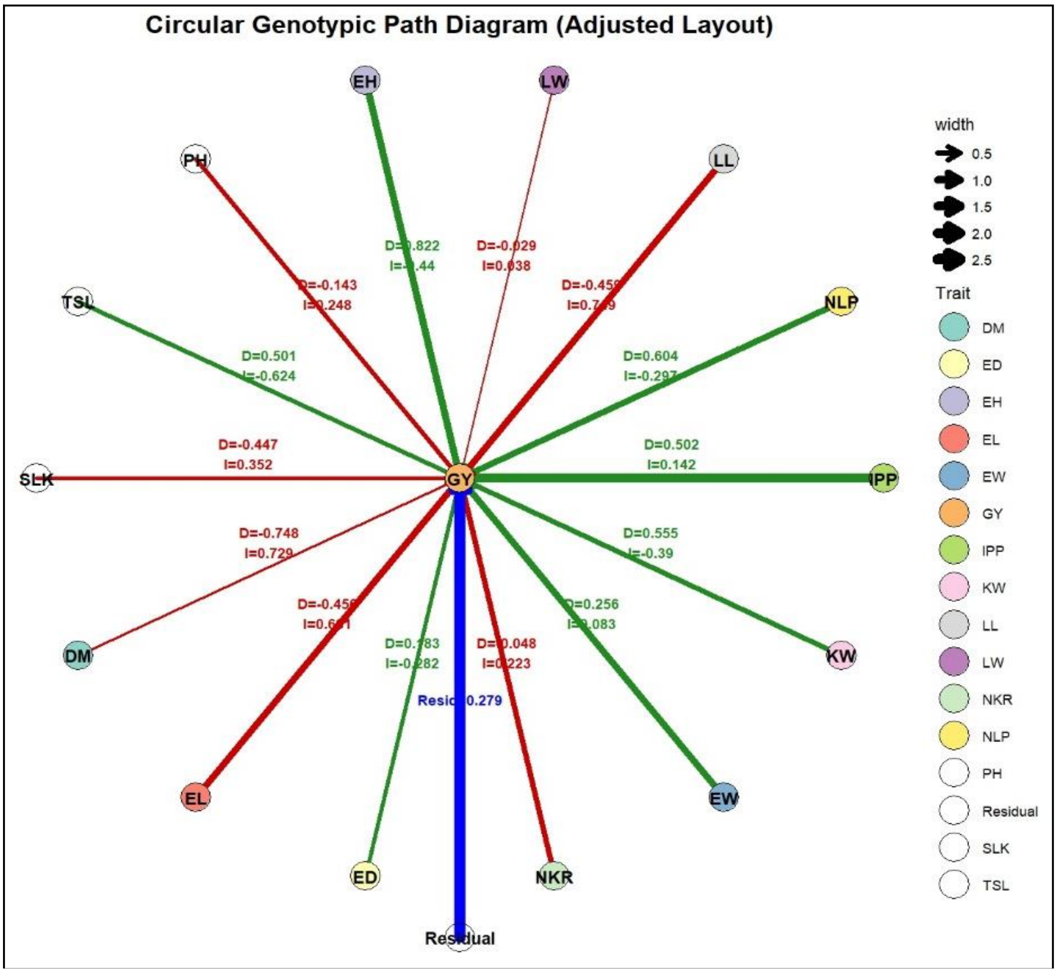
Note: DF = Degree of freedom, IPP = Initial plant population, NLP = No. of leaves, LL = Leaf length, LW = Leaf width, EH = Ear height, PH = Plant height, TSL = Tasseling 50%, SLK = silking 50%, DM = Days of maturity, EL = Ear length, ED = Ear diameter, NKR = No. of kernel row, EW = Ear weight, KW = 100 kernel weight, GY = Grain yield(q/ha.), "* Significant at 5% level of significance and ** Significant at 1% level of significance"

Path coefficient analysis at genotypic level (Table 5) revealed ear height with highest positive direct effect (1.268*) but negative indirect effect (-0.813), indicating complex trait interactions. Number of leaves per plant showed second highest direct effect (0.686*) with negative indirect effect (-0.307), emphasizing genetic significance for photosynthetic capacity. Initial plant population demonstrated substantial direct effect (0.500**), positive indirect effect (0.106) and strongest yield correlation (r = 0.606**) establishing it as most reliable genotypic selection criterion. Ear weight exhibited significant direct effect (0.160*) with positive indirect effect (0.217) and strong yield correlation (r = 0.3769*), indicating consistent yield contribution. Among non-significant traits, 100-kernel weight displayed notable direct effect (0.641) despite negative indirect effect (-0.547) while days to maturity showed highest negative direct effect (-1.250) but largest positive indirect effect (1.340) suggesting complex genetic interactions requiring careful management. Leaf length demonstrated substantial negative direct effect (-0.759) but second highest positive indirect effect (1.026) indicating contribution through correlated mechanisms. Additional traits including number of kernel rows (0.478), tasseling 50% (0.348), silking 50% (0.304), ear length (-0.658, 0.869), plant height (-0.213, 0.294) and ear diameter (-0.206, 0.129) exhibited varying contributions.

Similar observations of correlation and path coefficient analysis have been reported by *i.e*., Rajwade *et al.* (2018) [15] evaluated grain yield per plant showed strong positive correlations with traits including ear height (0.640), plant height (0.565), kernels per row (0.917) and ear weight (0.996) among others. Path analysis highlighted cob weight (0.960) and shelling percentage (0.098) as key direct contributors to yield. Prakash *et al.* (2019) found grain yield correlated positively with cob weight (0.974), cob girth (0.764), kernels per row (0.703), plant height (0.594) and ear height (0.562). Tassel length negatively correlated with days to tasseling and silking useful for selecting early maturing varieties. Aman *et al.* (2020) [1] studied traits had positive direct effects on grain yield, with ear height having the highest direct positive effect (0.6514), indicating its predominant influence on yield increase. Magar *et al.* (2021) [11] studied grain yield showed positive and significant phenotypic correlation with number of rows per cob (r = 0.539). Mohanapriya *et al.* (2023) [12] the correlation studies revealed that yield is harmonized positively with all the yield attributes and negatively associated with Anthesis silking interval (ASI). Uppal *et al.* (2024) [21] studied grain yield per plant showed significant positive phenotypic and genotypic correlations with number of kernel rows per cob, kernels per row, kernels per cob, 100-kernel weight, and shelling percentage. Path coefficient analysis confirmed these traits had the highest direct and indirect positive effects on grain yield, making them critical selection criteria for improving maize yield. Yogitha *et al.* (2025) [22] correlation analysis revealed significant positive associations between grain yield per plant and traits including plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100-kernel weight, and SPAD chlorophyll meter reading. These consistently strong correlations indicate the importance of these traits for indirect selection in maize yield improvement.

Table 5: Path coefficient analysis indicating direct (diagonal) and indirect effect of various characters on grain yield at genotypicaly

	IPP	NLP	LL	LW	EH	PH	TSL	SLK	DM	EL	ED	NKR	EW	KW	GY
IPP	0.500	0.070	-0.390	0.013	0.380	-0.076	-0.138	-0.084	0.247	-0.175	0.012	0.101	0.021	0.125	0.606 **
NLP	0.051	0.686	-0.279	-0.034	0.387	0.024	0.142	0.140	-0.694	-0.157	-0.020	0.159	0.074	-0.102	0.3793 *
LL	0.257	0.252	-0.759	0.003	0.610	-0.080	0.035	0.062	-0.155	-0.283	0.000	0.070	0.057	0.198	0.2669 NS
LW	0.024	-0.084	-0.008	0.277	-0.202	-0.081	-0.015	-0.015	0.025	-0.073	-0.080	0.023	0.027	0.172	-0.0098 NS
EH	0.150	0.209	-0.365	-0.044	1.268	-0.057	0.152	0.136	-0.645	-0.377	-0.054	0.053	0.056	-0.028	0.4548 *
PH	0.179	-0.079	-0.287	0.106	0.338	-0.213	-0.026	-0.017	0.087	-0.245	-0.062	0.104	0.033	0.163	0.0814 NS
TSL	-0.199	0.280	-0.076	-0.012	0.555	0.016	0.348	0.300	-1.098	-0.186	-0.089	0.030	0.061	0.059	-0.0112 NS
SLK	-0.138	0.317	-0.154	-0.013	0.568	0.012	0.344	0.304	-1.093	-0.240	-0.091	0.038	0.063	0.104	0.0219 NS
DM	-0.099	0.381	-0.094	-0.005	0.655	0.015	0.306	0.266	-1.250	-0.242	-0.096	0.093	0.065	0.097	0.0904 NS
EL	0.133	0.164	-0.326	0.031	0.728	-0.079	0.098	0.111	-0.461	-0.658	-0.199	0.348	0.107	0.214	0.2113 NS
ED	-0.028	0.066	0.001	0.108	0.335	-0.065	0.150	0.134	-0.586	-0.635	-0.206	0.327	0.069	0.253	-0.0775 NS
NKR	0.105	0.228	-0.111	0.014	0.141	-0.046	0.022	0.024	-0.244	-0.479	-0.141	0.478	0.090	0.137	0.2178 NS
EW	0.067	0.318	-0.270	0.046	0.444	-0.043	0.134	0.120	-0.509	-0.438	-0.088	0.269	0.160	0.167	0.3769 *
KW	0.097	-0.109	-0.235	0.074	-0.055	-0.054	0.032	0.050	-0.190	-0.220	-0.081	0.102	0.042	0.641	0.0936 NS



Note: DF = Degree of freedom, IPP = Initial plant population, NLP = No. of leaves, LL = Leaf length, LW = Leaf width, EH = Ear height, PH = Plant height, TSL = Tasseling 50%, SLK = Silking 50%, DM = Days of maturity, EL = Ear length, ED = Ear diameter, NKR = No. kernel row, EW = Ear weight, KW = 100 GY = Grain yield, "* Significant at 5% level of significance and ** Significant at 1% level of significance"

Fig 2: Path coefficient analysis of various characters on grain yield at genotypicaly

Conclusion

Analysis of variance indicated highly significant genetic divergence among genotypes for all 15 yield and agronomic traits studied. Grain yield varied from 22.83 to 35.44 q/ha with a grand mean of 24.97 q/ha. High heritability (>70%) and genetic advance were recorded for key traits such as plant height (90.5% heritability), 100-kernel weight (98.3%) and grain yield (91.3%) indicating additive gene action and potential for effective selection. Genotypic correlation analysis revealed significant positive associations of grain yield with initial plant population (r = 0.606**), ear height (r = 0.455*), number of leaves per plant (r = 0.379*) and ear weight (r = 0.377*) suggesting that these traits play vital roles in yield improvement. Conversely, traits such as leaf width and phenological parameters showed nonsignificant or weak correlations with grain yield. Path coefficient analysis is direct and indirect effects on grain yield. The analysis identified ear height (1.268), number of leaves (0.686), kernel weight (direct effect = 0.641), initial plant population (0.500) and number of kernel rows per ear (0.478) as key traits exerting strong positive direct influences on grain yield. Notably, certain traits like leaf length and days to maturity exhibited negative direct effects but positive indirect contributions via other yield components, indicating complex inter-trait dynamics. These findings emphasize the importance of selecting for key morphological and yield-associated traits, particularly ear height and kernel weight, to achieve effective genetic improvement in maize grain yield. The combined use of correlation and path analyses provides a robust framework for indirect selection strategies targeting enhanced maize productivity.

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