EVALUATION OF MAIZE (*ZEA MAYS* L.) GERMPLASM FOR YIELD AND RELATED TRAITS IN MID HILLS OF HIMACHAL PRADESH

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Abstract: Maize (*Zea mays* L.) productivity in mid-hill agroecosystems is frequently constrained by suboptimal genotype–environment interactions. This study evaluated genetic variability and identified promising germplasm among 51 diverse maize accessions under mid-hill conditions of Himachal Pradesh, India. Field trials were conducted during the Kharif 2024 season at Chamelti Farm, Shoolini University, using a randomized complete block design with three replications. Eleven agronomic and phenological traits including plant height, cob height, cob girth, cob weight, leaf count per plant, cob count per plant, days to anthesis, days to silking, anthesis–silking interval, leaf area, grain yield per plant, and shelling percentage were recorded. Analysis of variance revealed highly significant genotypic differences across all traits, indicating substantial genetic diversity. The highest genotypic and phenotypic coefficients of variation were observed for cob weight, grain yield per plant, and leaf area, suggesting strong additive genetic control. Grain yield per plant exhibited moderate-to-high heritability (55%) and high genetic advance (185.06 g), affirming its potential as a reliable selection index. Correlation and path coefficient analyses identified cob weight and cob girth as the most influential traits contributing positively to grain yield, while leaf count per plant and anthesis–silking interval exerted negative direct effects. Cluster analysis grouped the accessions into ten genetically distinct clusters, with clusters 4 and 7 exhibiting maximum inter-cluster divergence, thereby representing ideal candidates for hybridization to exploit heterosis.

Keywords: genetic variability, heritability, genetic advance, correlation, path coefficient, cluster analysis, grain yield.

INTRODUCTION

Maize (*Zea mays* L.) is a diploid (2n = 2x = 20) C_4 grass of the Poaceae family that traces its domestication to teosinte in Mesoamerica and now ranks among the most widely cultivated cereals worldwide. [1,2]. Its photosynthetic efficiency and water-use advantage under high light and temperature permit vigorous biomass accumulation, while a fibrous root network—comprising seminal, crown, and brace roots—optimizes soil exploration, nutrient uptake, and anchorage. [3]. As a monoecious cross-pollinator, maize bears protandrous male inflorescences (tassels) atop the canopy and pistillate ears along the stem, a spatial separation that underlies heterozygosity and enables exploitation of heterosis in hybrid breeding. Kernel anatomy—dominated by a starchy endosperm (≈72 %), with protein (≈10 %) and oil (≈4 %) fractions—delivers an energy density of ~365 kcal 100 g^{-1}, making maize a key caloric source in human diets and a staple feedstock in poultry production. [1].

In the mid-hill agroecosystems of Himachal Pradesh, altitude-driven thermal variation, soil heterogeneity, and intermittent moisture stress create a complex genotype–environment matrix that can mask genetic potential for yield and quality. Under these conditions, targeted evaluation of germplasm—including phenological markers such as anthesis-silking interval, morphological traits like plant and ear height, and yield components such as cob girth and weight—becomes critical. Precise quantification of genetic variability, heritability, and trait interrelationships informs indirect selection strategies, while multivariate analyses (e.g., Mahalanobis's D^2) guide the assembly of genetically divergent parental pools. Together, these approaches accelerate the development of high-yielding, climate-resilient maize hybrids tailored to the unique challenges of mid-hill cultivation.

Kernel composition in maize confers a high energy density of approximately 365 Kcal per 100 g, attributable to starch levels of around 72 %, accompanied by 10 % protein and 4 % fat content. While this energy yield surpasses that of staple cereals like rice and wheat, maize protein content remains comparatively lower, compelling breeders to consider both quality and quantity parameters in selection schemes [4]. Nutritional optimization through breeding can thus augment maize's role as a dual-purpose crop, balancing caloric provision with essential amino acid profiles for human consumption and protein requirements in poultry diets.

Fundamental to any genetic improvement endeavor is the accurate assessment of variability within breeding populations. Plant breeders rely on statistical estimates—such as genotypic and phenotypic coefficients of variation, heritability, and genetic advance—to dissect the underlying gene action of quantitative traits and predict selection responses. The direction and strength of trait associations further guide indirect selection efforts, enabling breeders to target component characters that exert the greatest influence on grain yield .Such a multifaceted approach ensures that genetic gains are both rapid and sustainable, particularly when additive genetic variance predominates. [5].

Given the polygenic inheritance of grain yield per plant and its pronounced sensitivity to environmental fluctuations, direct phenotypic selection often exhibits low efficiency due to reduced heritability and high genotype–environment interaction. To overcome these constraints, maize breeders employ highly heritable, genetically correlated secondary traits as indirect selection criteria. Phenological parameters—days to 50 % anthesis and silking, along with the anthesis-silking interval (ASI)—serve as indicators of reproductive synchrony and drought tolerance, with shorter ASI values typically enhancing pollen-silk contact and kernel set under moisture stress. Architectural traits, including plant height and ear height, modulate canopy structure, light interception, and assimilate partitioning, while cob girth and cob weight quantify sink capacity, reflecting potential kernel number and biomass allocation. These secondary traits often display moderate-to-high heritability, enabling more reliable early-generation screening than yield itself. By incorporating precise phenotypic measurements into selection indices and applying path coefficient analysis to partition direct versus indirect effects, breeders can identify genotypes that optimize source–sink relationships, accelerate the fixation of favorable alleles, and streamline hybrid development across diverse agro-climatic regimes. [6].

Genetic diversity among parental lines is the cornerstone of successful hybrid breeding, as greater divergence often translates into higher heterotic potential. Mahalanobis's D^2 statistic provides a rigorous framework to quantify genetic distances among genotypes and to partition germplasm into clusters with shared trait profiles. By evaluating intra- and intercluster divergence, breeders can pinpoint clusters that contribute disproportionately to total genetic variability and prioritize them for hybridization. Moreover, trait-wise contributions to divergence inform targeted parental selection, ensuring that key yield-related attributes are introgressed effectively. [7].

Building on these principles, the present investigation was designed to elucidate the genetic architecture of 51 diverse maize genotypes under mid-hill conditions. Specifically, our objectives were to (i) quantify the extent of genetic variability and divergence using D^2 analysis, (ii) estimate phenotypic and genotypic correlation coefficients among agronomic and phenological traits, and (iii) partition direct and indirect effects of component characters on grain yield through path coefficient analysis. The insights gained are expected to guide breeders in selecting superior parental combinations and refining indirect selection criteria to develop high-yielding maize hybrids adapted to mid-hill agroecosystems.

MATERIALS AND METHODS

A total of fifty-one maize genotypes were collected from K.D. Farm, S.K. University of Agricultural Sciences &Technology of Kashmir. These were evaluated in randomized block design with row to row and plant-to-plant distance of 50 cm and 20 cm with three replications during *kharif*, 2024 at Chamelti farm, Shoolini University of Biotechnology and Management Sciences, Bajhol, Solan (H.P.). (Altitude of 1,270 m and around latitude of 30°85´67.30 N and longitude of 77°13´20.38 E). Fifty one maize genotypes that were used as experimental material were: G2,G4,G6,G8,G12,G15,G18,G19,G21,G22,G25,G27,G28, G30,G31,G35,G40,G41,G42,G44,G47,G49,G50,G51,G52,G53,G55,G58,G72,G74,G76,G77,G79,G80,G81,G82,G84,G90,G91,G92,G93,G94,G95,G96,G98,G99,G100,G34,G68,G11,G7.All recommended package of practices were followed to raise the healthy crop. Data recorded on eleven yield and yield attributing traits viz., days to 50% pollen shed and silking, plant height (cm), ear height (cm), cob girth (cm), number of leaves per plant, number of cobs per plant, leaf area(cm^2), cob weight(g), grain yield per plant (g) and shelling(%) . Randomly, three competitive plants from each replication were selected for the recording of observations on eleven characters and made average. The mean data of yield and yield attributing traits were used for statistical analysis. Analysis of variance (ANOVA) and correlation analysis were conducted using IBM SPSS software version 2.0. The formula described by Kempthorne *et.al,* (1957) and Hanson *et.al.,* (1963) were used to calculate heritability in broad sense (h^2_b), genetic advance and genetic advance as percent of the mean was estimated using formula suggested by Robinson (1966) , phenotypic and genotypic coefficient of variation were estimated using method suggested by Burton and DeVane(1953), path coefficient analysis and D^2 analysis by Mahanalobis method was computed using WINDOWS R STUDIO 4.5.1 version. The formulas used are detailed below:

i.Phenotypic coefficient of variation (PCV%) $= \frac{\sigma_p}{X} \times 100$

ii.Genotypic coefficient of variation (GCV%) $= \frac{\sigma_g}{X} \times 100$

iii.Heritability (%) $= \frac{\sigma^2 g}{\sigma^2 p} \times 100$

iv.Genetic Advance $= K h^2_b \sigma p$

v.Genetic advance as per cent of mean$= \frac{GA}{\bar{X}} \times 100$

Where,

σp = Phenotypic standard deviation
σg = Genotypic standard deviation
$\bar{X}$ = Grand mean
$\sigma^2 g$ = Genotypic variance
$\sigma^2 e$ = Environmental variance
$\sigma^2 p(\sigma^2 g + \sigma^2 e)$ = Phenotypic variance
h^2_b = heritability co-efficient in broad sense
K = selection differential (2.06) a constant at 5% selection intensity.
GA = genetic advance

RESULTS AND DISCUSSION

The present study was carried out to study the genetic variability and diversity among the fifty-one genotypes of maize.

Analysis of Variance (ANOVA):

The analysis of variance was significant for all the characters among genotypes except shelling percentage thus indicating the presence of adequate genetic differences among them. (Table 1).Similar conclusions drawn in the study of earlier workers [8,9,10].

Parameters of Variability:

The phenotypic variance was higher than the genotypic variance for all the eleven traits under study indicating that phenotypic variability may be considered a reliable indicator of genotypic variability and selection would be effective for these traits(Table 2). High estimates of both PCV and GCV (>20%) were recorded for the traits days to 50% anthesis (DA) , days to 50% silking (DS), leaf area (LA), cob weight (CW)& grain yield per plant (GY). These traits exhibited substantial variability and are promising targets for selection. Moderate estimates (10–20%) of PCV and GCV were observed for Plant height (PH), Number of leaves per plant (NLP) , number of cobs per plant (NCP) & Cob girth (CG). Cob height (CH) showed moderate PCV but low GCV, suggesting a considerable environmental influence on this trait. Low estimates (<10%) of both PCV and GCV were recorded for shelling percentage, indicating a narrow genetic base and limited scope for improvement through selection. High broad-sense heritability was recorded for leaf area (0.93), plant height (0.92), and the days to reach 50% anthesis (0.744). The greatest genetic advance as a percentage of the mean was observed for leaf area (79.31%), followed by cob weight (78.2%), and grain yield per plant (69.97%) indicating that additive gene action is dominant and there is potential for effective selection in these traits. Conversely, low heritability and genetic advance were found for shelling percentage (0.046 and 0.14%) and the number of cobs per plant (0.21 and 14.86%) implying minimal potential for improvement through direct selection. These results are in conformation with earlier workers [11,12,13,14,15,16,17,18] for medium to low range of genetic parameters in maize for the most of yield traits.

Correlation Coefficient:

In the current research, grain yield per plant demonstrated a highly significant and positive correlation with cob weight marking it as a key contributor to yield (Table 3). Cob height and the number of cobs per plant also showed significant positive correlations with grain yield. A highly significant positive relationship was found between days to 50% anthesis and days to 50% silking indicating a close timing in flowering. However, both traits were significantly and negatively correlated with plant height suggesting that taller plants are inclined to flower earlier. Other correlations were noted as positive but non-significant. These results are in conformation with earlier workers [19,20].

Path coefficient analysis:

The path analysis revealed that cob weight demonstrated the strongest positive direct influence on grain yield, with cob girth following closely behind, highlighting their significance in improving yield. The number of days to 50% anthesis and silking exhibited considerable negative direct effects, implying that earlier flowering leads to increased yields. Although DA and DS displayed negative direct effects, they still positively impacted cob traits indirectly. To conclude, cob weight and cob girth emerged as the most dependable traits for selection aimed at boosting grain yield (Table 3).

D^2 Analysis:

Based on D^2 analysis 51 maize genotypes were categorized into ten clusters (Table 4, Fig. 1). Clusters I, II, and III each included the most genotypes (10 each), followed by cluster V (8 genotypes) and cluster IV (4 genotypes), while clusters VI, VII, VIII, and IX each contained 2 genotypes. Cluster X contained only one genotype (G44). The highest intra-cluster distance was found in cluster IX (640.55), cluster V (546.33), followed by cluster III (498.48), cluster I (475.96), cluster II (343.37), and cluster VIII (260.01). (Table 5) The lowest intra-cluster distance was noted in cluster X (0.00). The largest inter-cluster distance was noted between cluster IV and cluster VII (230573.39), followed by the distance between cluster I and VII (188650.70), as well as between cluster VII and VII (142543.83). The smallest inter-cluster distance was recorded between clusters II and VIII (1895.29). This research will be beneficial in determining the genotypes that may be tried to achieve the desired results in the breeding programme. The attributes, viz., leaf area (30.9%), plant height (25.6%), and grain yield (12.5%) contributed most to the total genetic divergence. These characteristics could be valuable in selection criteria for identifying diverse parent lines in maize to effectively utilize heterosis.(Fig.2) Earlier workers [21,22,23,24] reported similar findings for different clustering patterns and selection of parents in hybridization programme for yield improvement in maize.

CONCLUSIONS

From the above investigation it can be concluded that days to 50% anthesis (DA) , days to 50% silking (DS), leaf area (LA), cob weight (CW) grain yield per plant (GY), plant height (PH), number of leaves per plant (NLP) , number of cobs per plant (NCP) & cob girth (CG) are the important traits for selection of genotypes for improvement of yield in maize as they recorded medium to high range of PCV and GCV estimates, heritability and genetic advance as per cent of mean. Selection of parental lines from cluster IV and from Cluster VII would yield large number of segregants and can be exploited for the identification of genotypes with the desirable traits in maize.

Table 1 Analysis of variance for 11 characters in maize

	Mean Squares											
Source of Variance	**df**	**Days to anthesis (50%)**	**Days to silking (50%)**	**Plant Height**	**Cob Height**	**Number of leaves per plant**	**Leaf area**	**Number of cobs per plant**	**Cob weight**	**Cob girth**	**Grain yield**	**Shelling**
Replication	2	32.176	34.536	835.9710	349.182	3.630	41054.237	1.553	244130.196*	432.347	165570.529	3.029
Genotypes	50	227.232*	226.476*	1684.310*	183.859*	4.477*	88600.151*	.385**	83320.863*	119.425*	55942.871*	1.693
Error	102	91.284	91.276	581.733	115.123	2.384	30782.777	.270	39669.307	54.262	26624.555	1.548
Total	154											

***Significant<0.05 **Significant<0.01**

Table 2 Estimates of genetic parameters in 51 genotypes of maize

Traits	Range	Mean	GCV (%)	PCV (%)	Heritability in broad sense(%)	Genetic advance	Genetic advance as percentage of mean(%)
DA(50%)	15-63	34.02	24.23	28.08	0.74	14.65	43.08
DS(50%)	22-69	39.22	20.96	24.35	0.74	14.57	37.16
PH(cm)	106.66-221.33	162.83	14.35	14.93	0.92	46.26	28.41
CH(cm)	41-90	62.33	9.40	17.21	0.29	6.60	10.59
NLP	5-13	8.99	11.38	17.18	0.43	1.39	15.55
LA(cm^2)	102-850	427.96	39.72	40.99	0.93	339.42	79.31
NCP	1-4	4.24	15.55	33.54	0.21	0.22	14.86
CG(cm)	10.24-46.99	28.72	19.87	25.64	0.60	9.11	31.72
CW(g)	100-950	323.73	48.35	61.58	0.61	0.24	78.20
GY(g)	8-780	264.49	45.77	61.69	0.55	185.06	69.97
Shelling (%)	78.57-90.00	81.63	0.32	1.52	0.04	0.11	0.14

Table 3 Estimates of simple correlation coefficients between 11 characters in maize genotypes

Traits	**DA(50%)**	**DS(50%)**	**PH(cm)**	**CH(cm)**	**NLP**	**LA(cm^2)**	**NCP**	**CG(cm)**	**CW(g)**	**GY(g)**	**SP(%)**
DA(50%)	**1.000**	0.996*	-0.288*	0.198	-0.176	0.049	0.168	0.075	0.158	0.157	-0.170
DS(50%)		**1.000**	-0.296*	0.171	-0.166	0.009	0.157	0.093	0.147	0.146	-0.146
PH(cm)			**1.000**	0.034	0.131	0.247	0.002	-0.003	-0.068	-0.066	0.149
CH(cm)				**1.000**	0.186	0.156	0.441*	0.025	0.079	0.077	-0.120
NLP					**1.000**	0.041	0.347*	-0.038	0.076	0.075	0.064
LA(cm^2)						**1.000**	-0.079	-0.223	0.069	0.070	-0.074
NCP							**1.000**	-0.089	0.024	0.023	-0.140
CG(cm)								**1.000**	0.177	0.177	0.089
CW(g)									**1.000**	1.000*	0.048
GY(g)										**1.000**	0.057
SP(%)											**1.000**

***Correlation is significant at 0.05 level.**

Table 4 Distribution of genotypes into clusters based on Mahalanobis D^2 statistic

Cluster number	Number of genotypes	Genotypes
1	10	G25,G49,G19,G28,G53,G72,G68,G52,G93,G99
2	10	G41,G42,G58,G7,G74,G4,G90,G82,G34,G98
3	10	G2,G6,G100,G31,G47,G12,G15,G55,G30,G95
4	4	G27,G51,G80,G40
5	8	G84,G11,G81,G35,G22,G79,G21,G8
6	2	G77,G94
7	2	G18,G50
8	2	G91,G96
9	2	G76,G92
10	1	G44

Table 5 Estimates of average intra and inter cluster distance for 10 clusters in maize

Cluster No.	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
Cluster 1	**475.96**	38390.95	3686.02	2435.14	11448.30	78873.92	188650.70	55914.85	21905.46	99515.91
Cluster 2		**343.37**	19471.88	58327.58	8536.81	7490.48	57347.07	1895.29	2664.28	14607.25
Cluster 3			**498.48**	10900.37	2763.38	50225.32	142543.83	32349.41	8461.98	66905.56
Cluster 4				**205.57**	23082.32	106656.69	230573.39	79602.65	37365.77	130484.99
Cluster 5					**546.33**	31105.86	108688.56	17496.21	2167.60	44460.58
Cluster 6						**84.14**	23681.59	2084.54	18078.83	1249.61
Cluster 7							**171.39**	39389.69	82792.95	14225.31
Cluster 8								**260.01**	8196.23	6384.58
Cluster 9									**640.55**	28538.94
Cluster 10										**0.00**

Bold figures represent intra cluster distance.

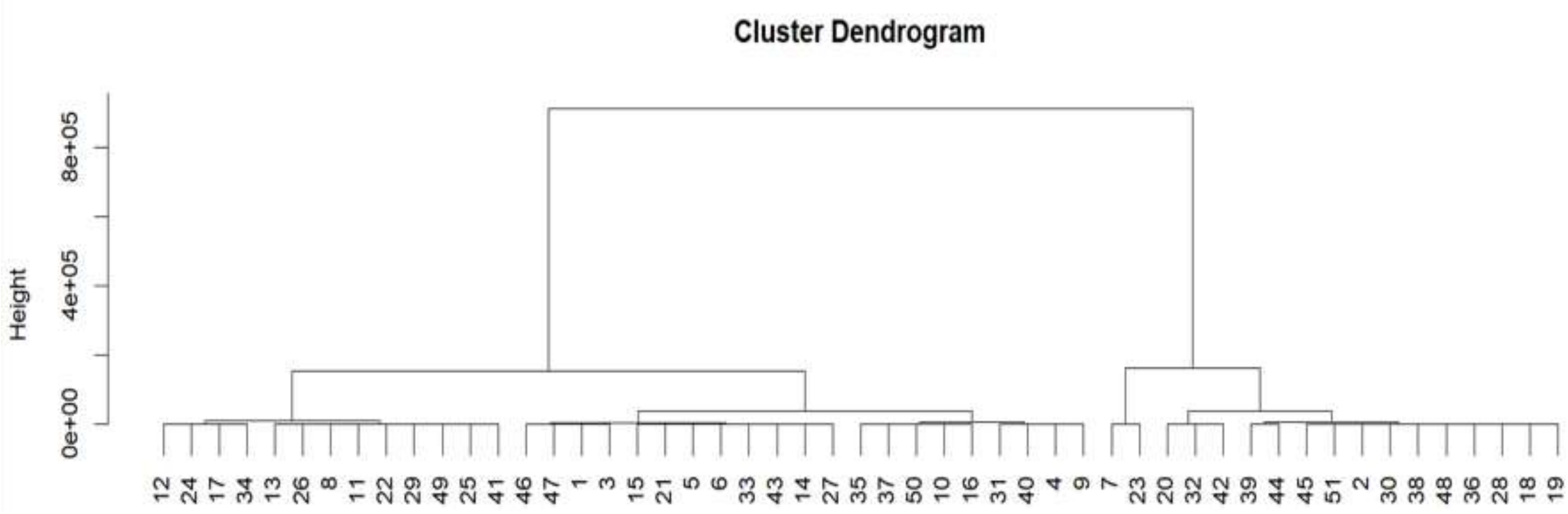

Figure 1 Dendogram showing grouping of 51 maize genotypes based on D^2 statistic using Tocher's method

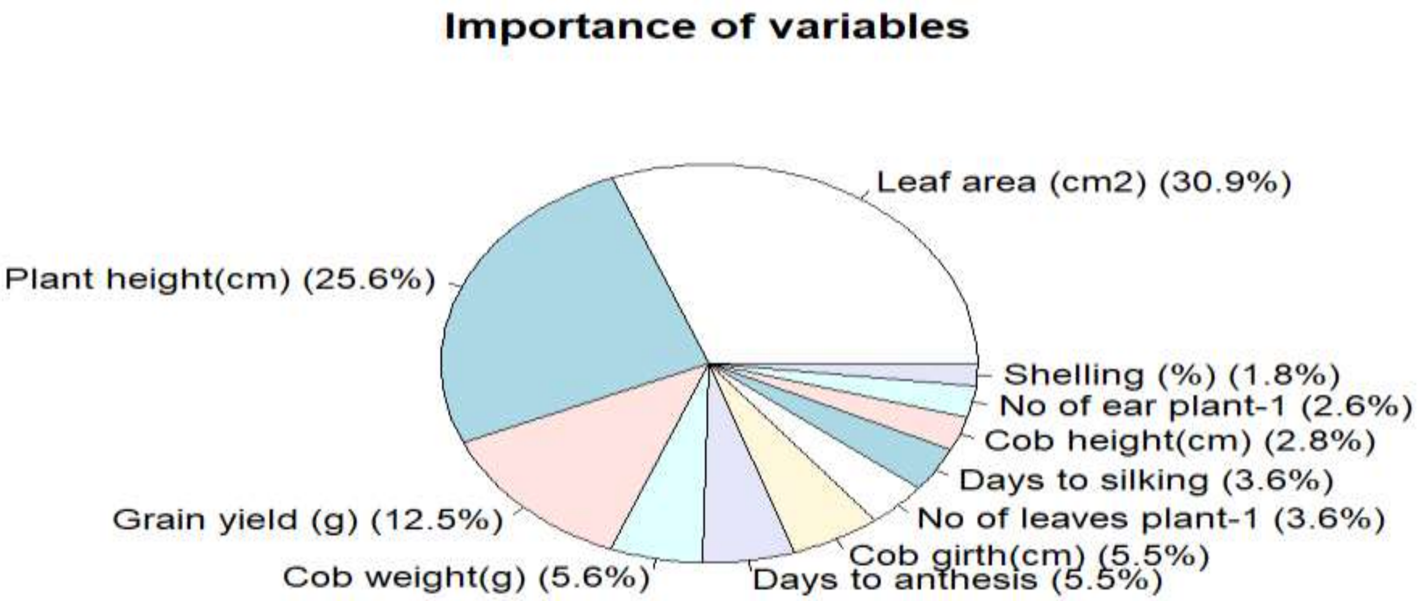

Figure 2 Relative contribution of 11 quantitative characters towards divergence

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REFERENCES

1) Vincent, P.L.D. 2001. *Zea mays* (maize, corn). *e LS.*

2) Aguirre-Liguori, J.A., Aguirre-Planter, E. and Eguiarte, L.E. 2016. Genetics and ecology of wild and cultivated maize: domestication and introgression. In Ethnobotany of Mexico: interactions of people and plants in Mesoameric : 403-416. New York, NY: Springer New York.

3) Crafts-Brandner, S.J. and Salvucci, M.E. 2002. Sensitivity of photosynthesis in a C4 plant maize to heat stress. Plant physiology, 129(4):1773-1780.

4) Erenstein, O., Jaleta, M., Sonder, K., Mottaleb, K. and Prasanna, B.M. 2022. Global maize production, consumption and trade - trends and R&D implications. Food security, 14(5):1295-1319.

5) Fisher, M., Abate, T., Lunduka, R.W., Asnake, W., Alemayehu, Y. and Madulu, R.B. 2015. Drought tolerant maize for farmer adaptation to drought in sub-Saharan Africa: Determinants of adoption in eastern and southern Africa. Climatic Change, 133(2): 283-299.

6) Tadesse Ertiro, B., Olsen, M., Das, B., Gowda, M. and Labuschagne, M. 2020. Genetic dissection of grain yield and agronomic traits in maize under optimum and low-nitrogen stressed environments. International journal of molecular sciences, 21(2):543.

7) Murty, B.R. and Arunachalam, V. 1966. The nature of divergence in relation to breeding system in some crop plants.

8) Rawal, S., Thapa, S., Singh, R.B. and Tripathi, M.P. 2023. Agromorphological Characterization of Maize Hybrids and Estimation of Genetic Parameters in Mid-Hills of Far-West Nepal. Advances in Agriculture, (1): 6138682.

9) Maruthi, R.T. and Rani, K.J. 2015. Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. Journal of Applied and Natural Science, 7(1):149-154.

10) Belay, N. 2018. Genetic variability, heritability, correlation and path coefficient analysis for grain yield and yield component in maize (*Zea mays* L.) hybrids. Advances in Crop Science and Technology, *6*(5): 399.

11) Pradhan, P., Thapa, B., Ghosh, A., Subba, V., Sahu, C.R. and Kundagrami, S. 2022. Genetic variability assessment on yield attributing traits in maize (*Zea mays* L.) inbred lines. The Pharma Innovation Journal, 11(5):1642-1645.

12) Peiffer, J.A., Romay, M.C., Gore, M.A., Flint-Garcia, S.A., Zhang, Z., Millard, M.J., Gardner, C.A., McMullen, M.D., Holland, J.B., Bradbury, P.J. and Buckler, E.S. 2014. The genetic architecture of maize height. Genetics, 196(4):1337-1356.

13) Sharma, H.P., Shrestha, J., Karki, S., Upadhyay, J. and Dhakal, Y.R. 2017. Agro-morphological performance of maize inbreds. Nepalese Journal of Agricultural Sciences, 15:112.

14) Rajwade, J.K., Jagdev, P.N., Lenka, D., Pamirelli Ranjith, P.R. and Gupta Shimla, G.S. 2017. Studies on genetic variability, heritability, genetic advance of maize inbred lines.

15) Reddy, S.G.M., Lal, G.M., Krishna, T.V., Reddy, Y.V.S. and Sandeep, N. 2022. Correlation and path coefficient analysis for grain yield components in maize (*Zea mays* L.). International Journal of Plant & Soil Science, 34(23): 24-36.

16) Chand R, Meena BL, Sharma RK, Jatav RK, Meena R, Sahu RK. 2023. Genetic variability, heritability and genetic advance studies in maize (*Zea mays* L.) lines. The Pharma Innovation Journal,12(6):2165–70.

17) Lal, K., Kumar, S., Singh, S.K., Singh, M., Singh, H.C. and Singh, Y. 2020. Heritability and genetic advance estimates for certain quantitative traits in maize (*Zea mays* L.). Journal of Pharmacognosy and Phytochemistry, 9(3):571-573.

18) Bartaula, S., Panthi, U., Timilsena, K., Acharya, S.S. and Shrestha, J. 2019. Variability, heritability and genetic advance of maize (*Zea mays* L.) genotypes. Research in Agriculture Livestock and Fisheries, 6(2):163-169.

19) Aminu, D., Dawud, M.A. and Modu, A. 2014. Combining ability and heterosis for different agronomic traits in maize (*Zea mays* L.) under drought stress in the Sudan Savanna of Borno State, Nigeria. Plant Breeding Crop Sci, 6(10):128-134.

20) Rafiq, C.M., Rafique, M., Hussain, A. and Altaf, M. 2010. Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). Journal of Agricultural Research, 48(1).

21) More AW, Thakur RS, Manivannan N. 2006. Genetic divergence in maize (*Zea mays* L.). Madras Agricultural Journal, 93: 1–5.

22) Pavan, R., Lohithaswa, H.C., Wali, M.C., Gangashetty Prakash, G.P. and Shekara, B.G. 2011. Correlation and path coefficient analysis of grain yield and yield contributing traits in single cross hybrids of maize (*Zea mays* L.).

23) Rigon, G., Paulo, J., Gonsiorkiewicz Rigon, C.A. and Capuani, S. 2014. Quantitative descriptors and their direct and indirect effects on corn yield.

24) Magar, B.T., Acharya, S., Gyawali, B., Timilsena, K., Upadhayaya, J. and Shrestha, J. 2021. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. Heliyon, 7(9).