GENETIC VARIABILITY FOR *PER SE* GRAIN YIELD POTENTIAL AND ITS ATTRIBUTING TRAITS AMONG INBRED LINES OF MAIZE (*ZEA MAYS* L.)

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ABSTRACT

The magnitude and nature of genetic variability among the genotypes significantly influence the breeding strategies employed. Hence, the present study was carried out to assess the genetic variability among the recently developed 40 inbred lines of maize. These genotypes were evaluated across two locations for grain yield (g) and its attributing traits. The significance of mean sum of squares due to genotype and genotype × environment interaction indicated the presence of substantial amount of variability among the genotypes considered and the influence of environment on trait expression. The estimates of PCV for all the traits were higher than GCV estimates. Moderate to high PCV and GCV along with moderate to high GAM was recoded for all the traits except days to 50% flowering and kernel rows cob[-1]. All the traits under concern displayed high heritability. The genotypes were grouped into four clusters using *k*-means algorithm. The genotypes from cluster I had high cluster mean for grain yield plant[-1] (g) along with plant height (cm), ear height (cm) and kernel rows cob[-1] highlighting the importance of utilizing them in breeding programme for trait improvement.

Key words : Maize, *per se* performance, Genetic variability, Diversity, *k*-means.

Introduction

Maize (*Zea mays* L.), also known as corn, is an important cereal crop in the Poaceae family. It is a highly cross-pollinated crop and has a chromosome number of 2n=2x=20 (Haberer *et al.*, 2005). This crop is often referred to as the 'queen of cereals' due to its significant role in global agriculture and its versatile applications. Maize ranks as the third most important cereal crop worldwide, following rice and wheat (Erenstein *et al.*, 2022). Maize's prominence is attributed to its high yield potential, suitability for high-density planting, adaptability to a variety of agro-climatic conditions, and diverse applications, including feed (61%), food (17%) and for industrial starch and fuel (22%) (Erenstein, 2010; IIMR, 2024).

The amount and nature of genetic diversity among

genotypes significantly influence the breeding strategies employed to enhance a crop's genetics (Yali, 2021). Maize is one such crop wherein hybrids are the commercial requirement. To develop high yielding hybrids, understanding and harnessing the genetic variability for the identification of candidate lines and including them in crop improvement for enhancement of existing germplasm is the key strategy (Reif *et al.*, 2005; Hallauer *et al.*, 1988). The success of any breeding program relies on the level of useful variability within the population and the degree to which desirable traits are inherited (Maruti and Rani, 2015). The descriptive statistics *viz.*, mean, range and genetic variability parameters such as phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), broad sense heritability (H) and genetic advance as *per cent* of mean (GAM) can be utilized to assess the magnitude of genetic

variability (Gazala *et al*., 2021). The inbred lines that have high *per se* grain yield can be used as potential female parents as it saves the cost and resource associated with the hybrid seed production (Lopez *et al*., 2014).

Maize breeders consistently highlight the importance of diversity among parental genotypes as a key factor in selecting parents for producing heterotic hybrids (Ahloowalia and Dhawan, 1963). The *k*-means is a non-hierarchical clustering method that can split the data into two or more groups (Mac Queen, 1967). The *k*-means algorithm is widely used to assess the genetic and phenotypic diversity. The present study was carried out with a view to estimate the nature and magnitude of genetic variability and diversity among new set of 40 maize inbred lines developed and to identify the inbred lines that can be utilized for crop improvement or as a female parent in hybrid seed production.

Materials and Methods

Plant material and phenotypic evaluation

A panel of 40 maize inbred lines belonging to female heterotic pool were sown during *kharif* 2021, in randomized complete block design with two replications at two locations *viz*., Kallinayakanahalli (Gauribidanur-Taluk, Chikkaballapura-District, Karnataka) (Loc_1) and Muppadighatta (Doddaballapura-Taluk, Bangalore Rural-District, Karnataka) (Loc_2). Each inbred line was sown in 3m row with spacing of 0.6m between rows and 0.2m between plants within a row. All agronomic practices were carried out according to the package of practices.

The day at which each plant had 50% extruded silk was recorded as days to 50% flowering. From each genotype the data on plant height (cm), ear height (cm), cob length (cm), kernel rows cob^{-1} and grain yield plant^{-1} was recorded on five randomly selected plants.

Statistical analysis

The within and across environment analysis of variance (ANOVA) was carried out using *anova_ind* and *anova_joint* function in the 'metan' R package. For all the traits, best linear unbiased predictors (BLUPs) were calculated using the META-R software version 6.0. The PCV (%), GCV (%), H (%) and GAM (%) were calculated using the variance estimates obtained from META-R. The *k*-means clustering analysis was carried out to characterize the inbred lines using *k*-means() function of 'factoextra' R package. The intra and inter cluster distances were calculated using *cls.scatt.data* function of 'clv' R package.

Results and Discussion

Analysis of variance

The results of ANOVA from individual locations are given in Table 1. Significance of mean sum of squares due to genotypes in both individual and pooled ANOVA, indicated the presence of substantial amount of genetic variability for the various yield and its attributing traits considered in the study. Mean sum of squares due to locations and genotype by environment interactions were significant indicating the effect of environment in trait expression (Patel *et al*., 2024). The mean sum of squares due to genotype by environment interactions was non-significant for the trait kernel rows cob^{-1} (Table 2).

Descriptive statistics and variability parameters

Exploitation of existing or created genetic variability is the main activity to achieve rapid genetic gain. Understanding and improvement of a complex polygenic trait like yield is difficult and it can be improved by understanding the genetic architecture of component traits.

Descriptive statistics and genetic variability parameters for traits under study are given in Table 3. Box whisker plots representing the range for grain yield and various yield attributing traits indicated the presence of substantial genetic variability within the material for the traits considered (Fig. 1). The trait days to 50% flowering ranged from 55 to 64.25 days with a mean value of 59.38 and standardized range of 0.16 when pooled over locations. Estimated PCV and GCV were 4.24 and 3.98 % with a higher broad sense heritability (87.89%). The GAM was 7.64% for days to 50% flowering. Plant height ranged between 138.00 to 218.25 cm with a mean of 176.09 cm and a standardized range of 0.46. Estimated values of PCV, GCV and broad sense heritability were 11.18, 10.54 and 88.80%, respectively. The observed GAM for plant height was 20.35%. The recorded mean ear height was 82.73cm. It ranged between 59.00 to 108.56 cm with the standardized range value of 0.60. The estimated PCV, GCV, broad sense heritability and GAM were 12.92, 11.64, 81.09 and 21.48%, respectively. For the trait cob length, the range of 9.98 to 16.92cm was observed with an average value of 14.51 cm and 0.48 as a standardized range. The genetic variability parameters *viz*., PCV, GCV, heritability and GAM estimates were 10.25, 9.17, 80.10 and 16.83%, respectively. Kernel rows cob^{-1} across locations had a trait mean of 13.91 with a range of 11.45 to 17.70 and standardized range of 0.45. The estimated PCV, GCV, heritability and GAM were 9.00, 8.20, 82.93 and 15.30%, respectively. Grain yield plant^{-1} across locations, recorded
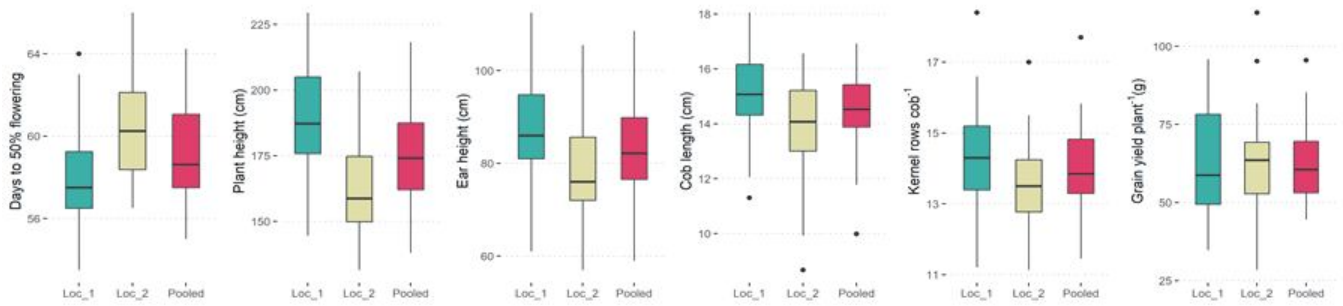
Fig. 1 : Box-Whisker plot representing variation for grain yield and its attributing traits within and across locations in inbred lines of maize.

Table 1 : Analysis of variance for grain yield and its attributing traits in inbred lines of maize in individual locations.

Sources of variation	df	Days to 50% flowering		Plant height (cm)		Ear height (cm)		Cob length (cm)		Kernel rows cob⁻¹		Grain yield plant⁻¹ (g)	
		Loc_1	Loc_2	Loc_1	Loc_2	Loc_1	Loc_2	Loc_1	Loc_2	Loc_1	Loc_2	Loc_1	Loc_2
Replication	1	0.01*	1.80	80	100	57.80	123	0.90	0.02	1.25	0.85	35	72.60*
Genotypes	39	14.6***	13.8***	934***	790***	269***	275***	4.35***	6.26***	4.28***	3.07***	546.00 ***	501.00 ***
Error	39	0.578	2.01	57.3	46.0	25.90	23.10	0.61	0.52	0.85	1.05	0.85	1.05
CV @ 5%		1.3	2.34	4.02	4.14	5.84	6.14	5.14	5.17	6.46	7.53	6.46	7.53

df, CV, *, **, *** represents degrees of freedom, coefficient of variation, significant at 0.05, 0.01 and 0.001 level, respectively.

Table 2 : Analysis of variance for grain yield and its attributing traits in inbred lines of maize pooled across locations.

Sources of variation	df	Days to 50% flowering	Plant height (cm)	Ear height (cm)	Cob length (cm)	Kernel rows cob⁻¹	Grain yield plant⁻¹ (g)
Locations	1	218.55***	24258.08***	3132.90***	62.87***	17.53***	10.17*
Replication (Locations)	2	0.9	50.57	90.15*	0.46	1.04	53.76
Genotypes	39	25.35***	1550.44***	457.23***	8.84***	6.27***	610.42***
Genotypes × Locations	39	3.06***	173.51***	86.45***	1.76***	1.07	436.21***
Residuals	78	1.29	51.61	24.52	0.56	0.94	33.89
CV @ 5%		5.05	4.07	5.98	5.16	6.99	9.39

df, CV, *, **, *** represents degrees of freedom, coefficient of variation, significant at 0.05, 0.01 and 0.001 level, respectively.

a trait mean of 61.99 g with a range of 44.60 to 95.33g with 0.82 as a standardized range. The estimated PCV, GCV and heritability values were 21.62, 15.60 and 58.53%, respectively. The recorded GAM for grain yield plant⁻¹ was 25.94%.

The low PCV and GCV estimates along with high heritability and low to moderate genetic advance as *per cent* mean for days to 50% flowering indicated that the selected genotypes have similar flowering behaviour with little variation. Similarly, the low PCV and GCV estimates for kernel rows cob⁻¹ also indicated the presence of less variability for this trait among the genotypes considered. Moderate estimates of PCV and GCV were observed

for plant height, ear height and cob length with high heritability and moderate to high genetic advance as *per cent* mean indicated the prevalence of additive gene action further suggesting the reward to selection (Reddy *et al.*, 2012). Although, cob length and kernel rows cob⁻¹ had high trait means, they exhibited relatively lower variability as reflected in lower magnitude of PCV and GCV estimates. This could be due to continuous selection for higher grain yield and its strongly associated traits in development of female pool inbred lines (Lauer *et al.*, 2012). Li *et al.* (2022) observed that the mean kernel rows cob⁻¹ and cob length of inbred lines from female heterotic pool were relatively higher the lines from male
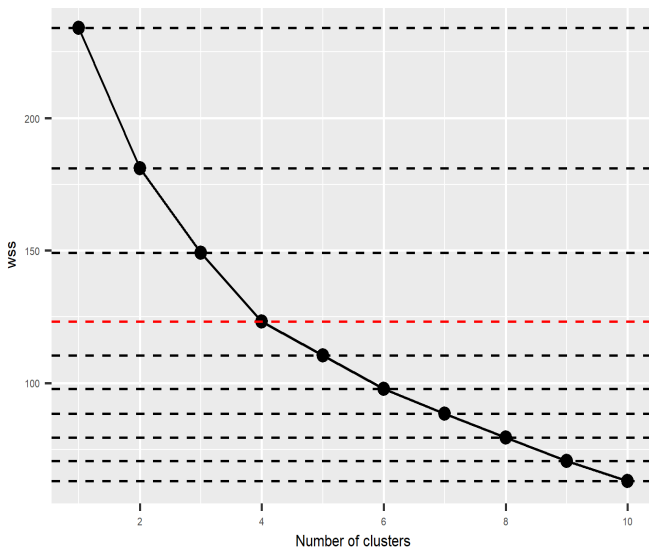
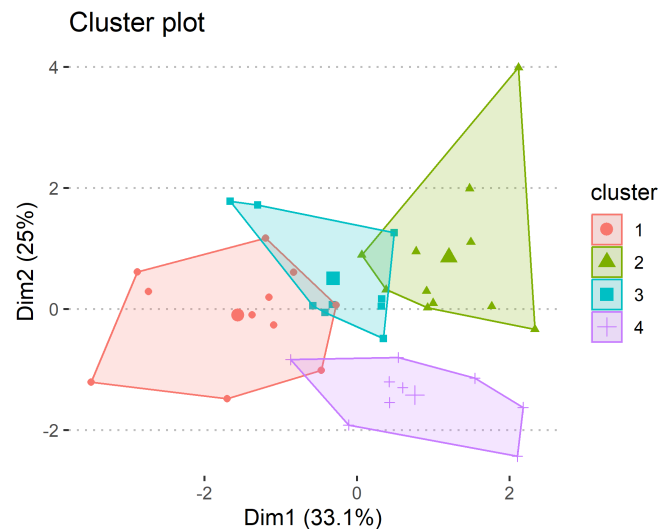**Fig. 2 :** Scree plot illustrating the optimal number of clusters determined using k-means clustering.

Fig. 3 : Cluster plot representing the distribution of genotypes across four clusters.

Table 3 : Descriptive statistics and genetic variability parameters for grain yield and its attributing traits in inbred lines of maize.

Trait	Locations	Mean±SEm	Range	SR	PCV (%)	GCV (%)	H (%)	GAM(%)
Days to 50% flowering	**Loc_1**	58.21±0.41	53.68-63.77	0.17	4.65	4.55	90.06	8.58
	Loc_2	60.55±0.35	57.08-65.20	0.13	4.34	4.01	85.45	7.60
	Pooled	59.38±0.39	55.00-64.25	0.16	4.24	3.98	87.89	7.64
Plant height (cm)	**Loc_1**	188.40±3.20	147.19-226.98	0.42	11.47	11.11	93.86	22.07
	Loc_2	163.78±2.96	133.38-204.49	0.43	12.14	11.78	94.81	23.60
	Pooled	176.09±3.11	138.00-218.25	0.46	11.18	10.54	88.80	20.35
Ear height (cm)	**Loc_1**	87.16±1.65	63.52-110.06	0.53	13.3	12.65	90.36	24.64
	Loc_2	78.31±1.70	58.79-103.21	0.57	14.97	14.32	91.58	28.10
	Pooled	82.73±1.69	59.00-108.56	0.60	12.92	11.64	81.09	21.48
Cob length (cm)	**Loc_1**	15.14±0.20	11.83-17.64	0.38	9.74	9.03	86.04	17.18
	Loc_2	13.89±0.26	9.10-16.38	0.52	12.74	12.20	91.75	23.96
	Pooled	14.51±0.23	9.98-16.92	0.48	10.25	9.17	80.10	16.83
Kernel rows cob^{-1}	**Loc_1**	14.24±0.18	11.08-17.57	0.46	10.27	9.20	80.19	16.88
	Loc_2	13.58±0.13	11.96-15.83	0.28	9.12	7.40	65.93	12.33
	Pooled	13.91±0.19	11.45-17.70	0.45	9.00	8.20	82.93	15.30
Grain yield plant^{-1}(g)	**Loc_1**	61.73±2.41	36.76-93.24	0.91	25.42	24.74	75.74	46.85
	Loc_2	62.24±2.37	30.20-108.22	1.25	26.76	25.72	85.40	39.47
	Pooled	61.99±1.95	44.50-95.53	0.82	21.62	15.60	58.53	25.94

SEm, SR, PCV, GCV, H, GAM represent the standard error of mean, standardized range, phenotypic and genotypic coefficient of variability, broad sense heritability, genetic advance as per cent of mean, respectively.

heterotic pool. The genetic variability parameters estimated for grain yield plant^{-1} were high except the GCV pooled across locations shedding light on presence of genotype by environment interactions. Further moderate heritability coupled with high GAM indicated the scope for genetic improvement through selection. The estimate of PCV was higher than that of the GCV for all the traits, implying the role of environment in total trait variability (Khan and Mahmud, 2021).

Assessment of genetic diversity

Further, genetic diversity present in the material

Table 4 : Inter and intra cluster distance between the four clusters.

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	0.00	7.71	5.89	6.45
Cluster II		0.00	5.95	6.66
Cluster III			0.00	6.18
Cluster IV				0.00

Table 5 : Cluster means for grain yield and its attributing traits.

Traits / Clusters	DFF	PH	EH	CL	KRC	YPP
I	58.86	197.56	92.40	15.31	14.67	72.28
II	57.80	164.40	76.38	13.05	14.32	59.80
III	60.12	177.29	84.77	14.34	13.95	52.15
IV	58.36	162.93	76.64	15.49	12.44	61.92

DFF   Days to 50 % flowering   PH   Plant height (cm)
EH   Ear height (cm)   CL   Cob length (cm)
KRC   Kernel rows cob^{-1} YPP   Grain yield plant^{-1} (g)

considered for the present study was assessed by *k*-means clustering method. Optimum number of clusters to be considered was decided based on the scree plot (Fig. 2). The scree plot represents the decrease in within cluster sum of squares (WSS) with increase in number of clusters. After certain number of clusters, there won't be significant reduction in the magnitude of WSS. Hence, four clusters were considered for further analysis as there was no significant reduction in WSS beyond cluster IV. The distribution pattern of genotypes into four different clusters is given in Fig. 3. The cluster I and II had the highest (11) number of genotypes and cluster III and IV had lowest number of nine genotypes in them. The average intra and inter cluster distances are given in Table 4. The highest average inter cluster distance was recorded between cluster I and cluster II while, the lowest inter cluster distance was recorded between cluster III and cluster II. Cluster means for different traits considered in the current study are given in Table 5. The lowest and highest cluster means for days to fifty per cent flowering was recorded by cluster II (57.80 days) and cluster III (60.12 days), respectively. The highest plant height (197.56 cm), ear height (92.40 cm), kernel rows cob^{-1} (14.67) and grain yield plant^{-1} (72.28 g) was documented in cluster I. Whereas, the lowest plant height (162.93) and kernel rows per ear (12.44) was recorded by cluster IV, ear height (76.38 cm) and cob length by cluster II (13.05cm) and yield plant^{-1} by cluster III (52.15g).

Further based on cluster means, the genotypes belonging to cluster I can be considered as productive since they had high *per se* grain yield potential along with higher kernel rows cob^{-1} and cob length. Assessment of diversity using *k* means was carried out by several research workers and found effective in the quantification of diversity (Kanavi *et al.*, 2020; Jayalakshmi *et al.*, 2022; Banakara *et al.*, 2022). Lopez *et al.* (2014) has reported that the inbred lines with high *per se* grain yield can be exploited as potential female parents in hybrid seed production. Hence, the combining ability of the 11 genotypes grouped in cluster I have to be assessed for utilizing them further as potential female parents in hybrid development.

Conclusion

The present study on assessment of genetic variability in recently developed maize inbred lines underscore the presence of significant genetic diversity for majority of the traits. The in breds grouped in the cluster I could be subjected to combining ability study before they are effectively utilized in hybrid development programme.

Conflict of interest

The authors have declared that no competing or conflict of interest exists.

Acknowledgement

Author contributions

H. C. Lohithaswa, Sunilkumar Biradar and Kalmeshwer Gouda Patil conceived the idea and designed the experiment. Santhoshkumari Banakara conducted the experiments and analysed the data. Sinchana Kashyap G.S., Sowmya M.S., Kalpana P.M., Meenakshi J. and Likhithashree T.R. helped in data collection and data analysis. Santhoshkumari Banakara and Sowmya M.S. drafted the manuscript. Sunilkumar Biradar and H.C. Lohithaswa revised the manuscript. All authors read and approved the final version.

Data availability statement

All data generated or analysed during this study are included in this article.

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