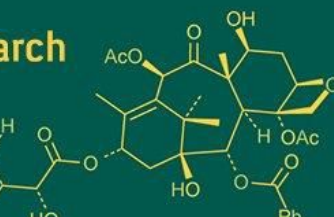
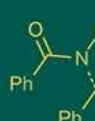


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Pratiksha K
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
College of Agriculture,
KSNUAHS, Shivamogga,
Karnataka, India

Shasikala S Kolakar
Department of Genetics and
Plant Breeding, College of
Agriculture, KSNUAHS,
Shivamogga, Karnataka, India

Santosh Pattanashetti
Department of Genetics and
Plant Breeding, College of
Agriculture, KSNUAHS,
Shivamogga, Karnataka, India

Basavalinghaiah
Department of Agronomy,
ICAR-KVK, V.C. Farm,
Mandya, Karnataka, India

Usha TN
Department of Seed Science
and Technology, PME Cell,
KSNUAHS, Iruvakkki,
Karnataka, India

Shashank MS
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
College of Agriculture,
KSNUAHS, Shivamogga,
Karnataka, India

Corresponding Author:
Pratiksha K
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
College of Agriculture,
KSNUAHS, Shivamogga,
Karnataka, India

Assessment of genetic variability in Maize (*Zea mays* L.) inbred lines for yield and yield related traits

Pratiksha K, Shasikala S Kolakar, Santosh Pattanashetti, Basavalinghaiah, Usha TN and Shashank MS

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Abstract

This study aimed to assess the extent of genetic variability among maize inbred lines for yield and related traits under low nitrogen conditions. Estimating genetic parameters such as GCV, PCV, heritability, and genetic advance helps determine the genetic potential and inheritance of these traits. High heritability combined with high genetic advance indicates additive gene action, suggesting that selection would be effective for improvement. The investigation was conducted during Rabi 2024 at the College of Agriculture, KSNUAHS, Navule, Shivamogga, India, using a factorial design. Forty maize genotypes along with two checks were evaluated for eighteen characters, including days to 50% tasseling, days to 50% silking, anthesis-silking interval, plant height, number of leaves per plant, ear height, leaf length, leaf width, leaf area, stem girth, ear length, ear girth, number of kernel rows per ear, number of kernels per row, test weight, dry fodder yield per plant, grain yield per plant, and harvest index. Data were recorded and analyzed using R software to estimate variance components, PCV, GCV, heritability, and genetic advance as percent of mean (GAM). Analysis of variance revealed significant differences among genotypes, nitrogen levels, and their interactions for all traits except leaf area with respect to genotype. Traits such as ear height (20.97, 26.84, 61.00, 28.06), leaf width (39.47, 42.05, 88.00, 45.28), stem girth (40.74, 42.35, 92.50, 47.66), number of kernel rows per ear (25.66, 28.80, 79.30, 30.06), and grain yield (23.10, 37.54, 95.20, 43.39) exhibited high GCV, PCV, heritability, and GAM values, indicating the predominance of additive gene action.

Keywords: Maize, GCV, PCV, Heritability, Genetic advance per cent of mean

Introduction

Maize (*Zea mays* L.) is the world's most widely cultivated cereal crop and ranks third in importance after rice and wheat. Owing to its high yield potential and versatility (Shiferaw *et al.*, 2011) [24], maize is often regarded as the "Queen of Cereals." It serves as a dual purpose crop, providing nutritious kernels for human consumption and fodder for livestock, it is also being increasingly utilized for bioethanol production to meet growing sustainable energy demands (Borkhatariya *et al.*, 2022) [12]. Compared to other cereals, maize requires less water, and as a C4 and day-neutral plant, it produces higher yields per unit area within a shorter growth period (Borkhatariya *et al.*, 2022) [12]. C4 plants, including maize, utilize water more efficiently and can withstand drought, high temperatures, and low CO₂ conditions, making maize a vital component of climate-resilient agricultural strategies (Crafts-Brandner *et al.*, 2002) [14]. Globally, maize plays a pivotal role in ensuring food and nutritional security (Borkhatariya *et al.*, 2022) [12]. At present, it is cultivated in more than 170 countries, with a total production of about 1147.7 million metric tonnes on 193.7 million hectares, achieving an average productivity of 5.75 t/ha (FAOSTAT). It is the most important food crop in Sub-Saharan Africa and Latin America and holds significant importance in Asia. In India, maize ranks fourth in area and seventh in production, accounting for nearly 4 per cent of global maize acreage and 2 per cent of total production (Borkhatariya *et al.*, 2022) [12]. During 2018-19, the crop covered 9.2 million hectares in the country (DACNET 2020). However, maize productivity in India remains considerably lower than the global average - almost half that of leading maize-producing countries such as the USA and China. This substantial yield gap highlights the urgent need for improved hybrid development to enhance productivity, farmer income and long-term sustainability of maize-based systems (Shiferaw

et al., 2011) [24]. The success of crop improvement largely depends on the extent of genetic variability present within a species. Variability refers to observable differences among individuals, while genetic variability arises from variations in alleles or DNA/RNA sequences within a population, ultimately shaping phenotypic expression (Bhandari *et al.*, 2017) [11]. Since the beginning of systematic plant breeding, natural variability and divergence have been the cornerstones of yield enhancement and adaptation to changing environments. In recent decades, advanced breeding strategies such as marker-assisted selection, genomic selection, and precision phenotyping have further accelerated maize improvement. For effective breeding, it is essential to assess genetic parameters such as genotypic coefficient of variation, heritability, and genetic advance. Heritability estimates the proportion of observable variation attributable to genetic factors, whereas genetic advance indicates the expected progress under selection pressure. Traits that simultaneously exhibit high heritability and high genetic advance are most reliable for direct selection, particularly under diverse environmental conditions (Johnson *et al.*, 1955) [20]. Thus, the present study was undertaken to evaluate genetic variability, heritability, and genetic advance for yield and its contributing traits in maize, providing a basis for future breeding strategies.

Materials and methods

The experiment was conducted during the Rabi season of 2024 at the College of Agriculture, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences (KSNUAHS), Navule, Shivamogga, Karnataka, India. The location is characterized by a humid tropical climate with moderate temperatures and well-distributed rainfall, providing suitable conditions for maize cultivation. The experimental site possesses fertile red loamy soil, which supports good crop growth and facilitates the evaluation of genotypic performance under varying nitrogen levels. The experimental material consisted of forty maize genotypes along with two standard checks, NK6240 and NK6514. These genotypes represented diverse genetic backgrounds and were selected to capture a wide range of variability for yield and related traits. The germplasm lines were procured from the CIMMYT-Asia regional research center, Hyderabad. The experiment was laid out in factorial randomized complete block design. Each genotype was sown in a single row with a row-to-row spacing of 45 cm and a plant-to-plant spacing of 27 cm, maintaining a bed length of 2.7 meters. All standard agronomic practices recommended for maize cultivation were followed to ensure healthy crop growth. These included timely land preparation, nutrient management, irrigation, and pest and disease control measures to achieve uniform crop establishment and reliable experimental results. Observations were recorded on five randomly selected plants from each genotype to ensure accurate and representative data collection. Data were gathered for a total of eighteen yield and yield-contributing traits, which included: days to 50 per cent tasseling, days to 50 per cent silking, anthesis-silking interval (asi), plant height (cm), number of leaves per plant, ear height (cm), leaf length (cm), leaf width (cm), leaf area (cm²), stem girth (mm), ear length (cm), ear girth (mm), number of kernel rows per ear, number of kernels per row, test weight (g), dry fodder per plant (g), grain yield per plant (g), and harvest index (%).

These parameters were selected to comprehensively assess the growth performance, yield potential, and physiological efficiency of the maize genotypes under study.

Methodology

The average values of the observations recorded from five randomly selected plants per genotype were considered for statistical analysis to ensure accuracy and reliability of the data. The experimental data were subjected to analysis using a factorial randomized block design (FRBD) to assess the effects of different treatments and their interactions while minimizing experimental error. Mean values obtained from each germplasm line were used to perform analysis of variance (ANOVA) to determine the presence of significant differences among the genotypes for various traits under study.

Further, variability parameters were estimated to understand the extent of genetic variation among the genotypes. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed using the formulae suggested by Burton and DeVane (1953). Heritability in broad sense (h^2) was estimated following the method proposed by Lush (1949) to evaluate the proportion of total phenotypic variance that is attributable to genetic factors. Additionally, genetic advance (GA) and genetic advance as percent of mean (GAM) were calculated as per the procedure described by Johnson *et al.* (1955) [20] to assess the expected improvement in a trait through selection. All statistical computations and graphical analyses were carried out using R software, ensuring robust and reproducible results.

Results and discussion

Analysis of Variance

The analysis of variance (ANOVA) revealed that the mean squares due to genotype, nitrogen levels, and their interactions (genotype $\times$ nitrogen) were significant for all the eighteen traits studied, indicating the presence of substantial variability and differential genotypic responses under varying nitrogen conditions. The traits that exhibited significant differences included: days to 50 per cent tasseling, days to 50 per cent silking, anthesis-silking interval, plant height (cm), number of leaves per plant, ear height (cm), leaf length (cm), leaf width (cm), ear length (cm), stem girth (mm), ear girth (cm), number of kernel rows per ear, number of kernels per row, test weight (g), dry fodder yield per plant (g), grain yield per plant (g), and harvest index (%).

However, leaf area (cm²) did not show a significant difference with respect to genotypes, suggesting that this particular trait was less influenced by genetic factors and more by environmental conditions or management practices. The significant variation observed among genotypes for most of the traits indicates the presence of ample genetic diversity in the maize germplasm, which can be effectively utilized in future breeding programs aimed at yield and nitrogen use efficiency improvement.

These findings are in close agreement with the results reported by Abdel *et al.* (2013) [1], Kimuti *et al.* (2023) [21], and Badu *et al.* (2011) [7], who also observed significant genotypic variability and genotype $\times$ environment interactions for yield and yield-contributing traits in maize under varying nitrogen regimes. Such consistency with earlier reports further validates the reliability of the present

study's results and highlights the influence of nitrogen management in expressing genetic potential across maize genotypes.

Phenotypic and Genotypic Coefficient of Variation

It was observed that the estimates of the phenotypic coefficient of variation (PCV) were consistently higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied, indicating that the expression of these traits is influenced not only by genetic factors but also by a minor degree of environmental variation. The close proximity between PCV and GCV values for most traits suggests that environmental influence was relatively limited and that the observed variability is largely of genetic origin, which is desirable for effective selection in breeding programs. This trend is consistent with the findings of Alam *et al.* (2022) [5], Singh *et al.* (2019) [23], and Bello *et al.* (2012) [10], who also reported higher PCV than GCV estimates in maize, signifying a similar pattern of genetic and environmental interplay in trait expression. In the present investigation, relatively high estimates of PCV and GCV were recorded for several traits, namely anthesis-silking interval (85.62 and 73.52), number of leaves per plant (84.62 and 77.06), ear height (26.84 and 20.97), leaf width (42.05 and 39.47), stem girth (42.35 and 40.74), ear girth (88.38 and 76.38), number of kernel rows per ear (28.80 and 25.66), test weight (29.79 and 26.99), dry fodder yield per plant (54.37 and 39.84), and grain yield per plant (37.54 and 23.10). The high magnitude of both genotypic and phenotypic variation for these traits indicates the presence of substantial inherent genetic variability, suggesting that these characters are amenable to selection and genetic improvement. Moderate GCV and PCV estimates were observed for ear length (10.52 and 15.87) and harvest index (14.01 and 16.96), indicating a moderate level of genetic control and scope for improvement through selection. Conversely, low GCV and PCV values were recorded for days to 50 per cent tasseling (4.96 and 6.41), days to 50 per cent silking (5.96 and 7.44), plant height (4.60 and 7.31), leaf length (3.08 and 4.27), and leaf area (0.76 and 1.00). The lower values for these traits indicate relatively narrow genetic variability, implying that their improvement through selection may be slow or require a broader genetic base. The overall results are in close agreement with the findings of Abhishek and Mogali (2020) [2], Arunkumar (2013) [6], Arunkumar *et al.* (2020) [7], Gaur (2019) [18], Ajmera *et al.* (2017) [4], and Dar *et al.* (2018) [16], who also reported high to moderate estimates of genotypic and phenotypic coefficients of variation for yield and yield-contributing traits in maize. Such findings reaffirm the existence of considerable genetic diversity among the studied genotypes and underscore the potential for effective selection and genetic enhancement in maize improvement programs.

Heritability (h²) and Genetic Advance as Per cent of Mean (GAM)

The genotypic coefficient of variation (GCV) provides a measure of the extent of genetic variability expressed as a percentage for a given trait; however, it does not indicate how much of this variation is heritable or transmissible to the next generation. Therefore, an understanding of heritability and genetic advance is essential to assess the

potential effectiveness of selection in plant breeding programs.

In the present study, the heritability estimates were found to be high for all the traits studied, indicating that the observed phenotypic differences among genotypes are largely due to genetic factors rather than environmental influences. High heritability suggests that selection based on phenotypic performance would be reliable and effective for genetic improvement. Furthermore, the combined interpretation of heritability and genetic advance as a percent of mean (GAM) provides deeper insight into the nature of gene action governing these traits.

Among the traits studied, ear height (61.00% and 28.06%), leaf width (88.00% and 45.28%), stem girth (92.50% and 47.66%), number of kernel rows per ear (79.30% and 30.06%), and grain yield per plant (95.20% and 43.39%) exhibited high heritability coupled with high genetic advance as percent of mean (Table 2; Fig. 1). This combination indicates that these traits are predominantly governed by additive gene action, and the influence of the environment on their expression is relatively low. Such traits are highly amenable to simple phenotypic selection, and substantial genetic improvement can be achieved through direct selection in early generations.

The results of the present investigation are in close agreement with the findings of Ajmera *et al.* (2017) [4] and Bartula *et al.* (2019) [9], who also reported high heritability estimates along with high genetic advance for yield and yield-contributing traits in maize. This consistency reinforces the conclusion that additive genetic variance plays a major role in the inheritance of these traits, providing valuable opportunities for the development of improved maize genotypes through systematic and efficient selection strategies.

Conclusion

The maize genotypes evaluated in the present study exhibited significant variability for yield and its component traits, indicating the presence of substantial genetic diversity within the germplasm. Such variability is a prerequisite for any successful breeding program, as it provides the foundation for effective selection and genetic improvement. High estimates of both phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for several traits, including anthesis-silking interval, number of leaves per plant, ear height, leaf width, stem girth, ear girth, number of kernel rows per ear, test weight, dry fodder yield, and grain yield per plant. The relatively high magnitude of these parameters indicates a broad range of genetic variability and suggests that the population possesses considerable potential for selection and genetic advancement. The close correspondence between PCV and GCV values for most traits further implies that environmental effects were minimal, and that the observed variation is primarily due to genetic factors. The traits ear height, leaf width, stem girth, number of kernel rows per ear, and grain yield per plant recorded high heritability coupled with high genetic advance as a percent of mean, suggesting that these characters are largely controlled by additive gene action. Additive effects are generally fixable through selection, meaning that improvement achieved through breeding can be retained and transmitted to subsequent generations. Therefore, direct selection for grain yield and its related traits would likely be effective and

rewarding in developing high-yielding maize genotypes. Overall, the combination of high heritability, high genetic advance, and substantial genotypic variability highlights the scope for significant genetic improvement through simple

selection approaches. These findings provide a valuable basis for breeders to identify and utilize promising genotypes in maize improvement programs aimed at enhancing yield potential and stability.

Table 1: Analysis of variance for yield and yield attributing characters in maize

Source of variation	D.f	PH	DFT	DFS	ASI	LL	LW	LA	SG	EH	EL
Replication	1	42.51	15.48	22.72	6.88	13.34	11.50	3.33	10.07	16.15	8.77
Genotype (Factor A)	41	145.29*	42.98*	59.03*	20.33*	16.77*	1.67*	23.48	17.67*	25.39**	20.54*
Nitrogen (Factor B)	1	123.87*	34.72*	39.14*	1.52*	1.68*	0.98*	5.70*	15.51*	3.08*	18.35*
Genotype×Nitrogen (Interaction)	41	100.58*	10.09*	16.81*	9.54*	5.74*	1.93*	6.83**	4.73*	6.51*	10.88**
Residuals	83	5.69	3.28	5.56	0.25	1.33	0.97	1.32	2.64	3.49	1.37

Source of variation	EG	NLP	NKRE	NKR	GY	DF	HI	TW
Replication	7.13	0.03	22.73	37.52	142.69	0.35	2.67	10.37
Genotype (Factor A)	21.44*	30.86*	10.98**	60.60*	293.86**	42.38*	10.50*	36.65*
Nitrogen (Factor B)	23.72*	8.90*	80.75*	38.59*	96.89*	6.070*	3.56*	35.00*
Genotype×Nitrogen (Interaction)	17.13**	14.50*	6.46**	38.20**	79.41*	23.59*	4.80*	16.34*
Residuals	2.63	0.25	3.11	5.58	3.59	0.07	0.82	8.28

Note: * and ** are significance at 5 per cent and 1 per cent levels respectively.

Where D.f: Degrees of freedom, PH: Plant height (cm), DFT: Days to 50 per cent tasseling, DSI: Days to 50 per cent silking, ASI: Anthesis-silking interval, LL: Leaf length (cm), LW: Leaf width (cm), LA: Leaf area (cm²), SG: Stem girth (mm), EH: Ear height (cm), EL: Ear length (cm), EG:

Ear girth (mm), NLP: Number of leaves per plant, NKRE: Number of kernel rows per ear, NKR: Number of kernels per row, GY: Grain yield per plant (g), DF: Dry fodder per plant (g), HI: Harvest index, TW: Test weight (g).

Table 2: Mean, range and genetic variability parameters for yield and yield attributing traits in maize genotypes lines

Character	Nitrogen level	Grand mean	Range	GCV%	PCV%	h ² _{bs} %	GAM
DFT	Optimum	62.11	53.50-68.50	4.96	6.41	59.70	32.18
	Low	64.98	55.00-72.00				
DFS	Optimum	65.06	56.00-71.50	5.96	7.44	54.40	41.35
	Low	68.12	57.50-75.00				
ASI	Optimum	2.98	-3.50 - 8.00	73.52	85.62	50.63	39.06
	Low	3.14	-0.50 - 8.00				
PH (cm)	Optimum	148.16	119.84-173.60	4.60	7.31	39.64	56.00
	Low	108.60	87.94-125.28				
NLP	Optimum	8.99	8.21-9.78	77.06	84.62	82.90	7.13
	Low	6.93	5.99-7.88				
EH (cm)	Optimum	12.19	9.38-15.09	20.97	26.84	61.00	28.06
	Low	10.12	7.20-13.29				
LL (cm)	Optimum	67.66	58.02-85.05	3.08	4.27	52.20	62.48
	Low	59.75	43.90-71.63				
LW (cm)	Optimum	7.14	5.97-9.15	39.47	42.05	88.00	45.28
	Low	6.43	4.78-7.58				
LA (cm ²)	Optimum	341.51	230.02-459.89	0.76	1.00	57.60	23.57
	Low	279.55	165.90-394.13				
SG (mm)	Optimum	17.64	13.72-23.52	40.74	42.35	92.50	47.66
	Low	15.02	9.86-19.71				
EL (cm)	Optimum	13.28	9.25-18.06	10.52	15.87	43.90	47.42
	Low	9.84	7.72-13.29				
EG (mm)	Optimum	22.35	18.59-25.62	76.38	88.38	32.25	40.54
	Low	19.30	13.44-23.54				
NKRE	Optimum	14.18	11.36-17.80	25.66	28.80	79.30	30.06
	Low	12.79	8.76-15.75				
NKR	Optimum	27.51	21.43-35.72	14.67	23.62	38.50	37.10
	Low	23.04	14.71-34.49				
TW(g)	Optimum	26.32	22.09-31.54	26.99	29.79	36.50	57.45
	Low	24.53	16.93-27.92				
DF (g)	Optimum	0.41	19.00-113.00	39.84	54.37	46.20	56.77
	Low	0.37	9.00-78.00				
GY (g)	Optimum	392.48	25.32-58.70	23.10	37.54	95.20	43.39
	Low	296.50	13.40-48.31				
HI (%)	Optimum	0.50	43.00-59.00	14.01	16.96	46.20	11.71
	Low	0.47	30.00-47.00				

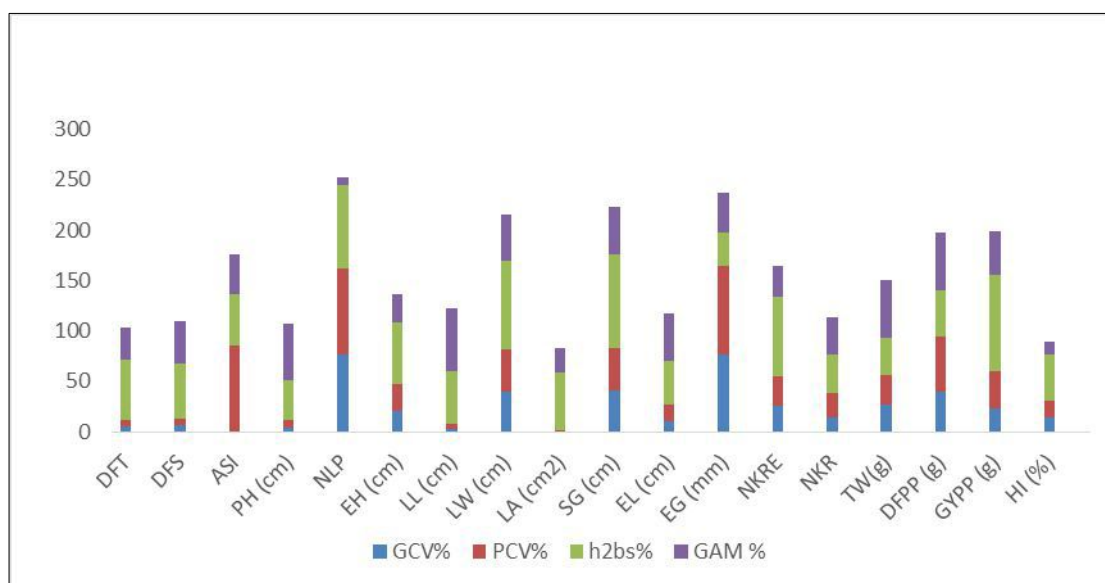


Fig 1: Graphical representation of GCV, PCV, Heritability and GAM.

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