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Estimation of Genetic Parameters of Variability for Yield and Yield-Related Traits in Maize (*Zea mays* L.) Hybrids

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***Abstract*—** *Maize (Zea mays L.; 2n = 20) is a monoecious, cross-pollinated crop with wide scope for the development of hybrids and composites. Composites occupy a major area in India but are poor yielders. Therefore, considering the importance of recently developed single-cross hybrids through superior inbreds, there is a need to promote them. Thus, there is tremendous scope for increasing production and productivity. However, for any breeding programme, germplasm serves as a valuable source material as it provides scope for building genetic variability. Among a series of routine activities in a breeding programme, selection (the effectiveness of which is determined by the selection criteria used) is the most important step for obtaining high-yielding genotypes. Information on genetic parameters such as heritability can be used as a consideration to determine selection criteria. The field experiments were laid out in a randomized block design with three replications and thirty hybrids at IARI-Sipani Krishi Anusandhan Farm, Collaborative Outstation Research Centre, Sitamahu Road, Changli, Mandsaur (M.P.), India. The crop was raised during Kharif 2022–23. Five competitive plants were randomly selected from each replication in a genotype for recording observations on thirteen quantitative characters, viz., days to 50% tasseling, days to 50% silking, plant height, ear height, cob length, cob girth (cob diameter), number of kernel rows per cob, 100-grain weight per cob after shelling, 100-grain weight, number of plant stand per plot, kernel texture (flint/dent), grain yield per plot (kg), and days to maturity (days). The mean squares from the analysis of variance revealed that the mean squares due to genotypes were highly significant for all the characters, indicating the presence of significant genetic variability in the material under study. This provides scope for selection and further subsequent utility of the genotype in the crop improvement programme. High GCV was recorded for grain yield per plot (32.59%), number of plant stand per plot (17.27%), ear height (13.99%), test weight (11.68%), and number of kernel rows per cob (10.90%). Therefore, selection for all these characters would be effective. Heritability (broad sense) estimates were high (>50%) for all the traits except days to maturity (47.36%). Heritability in the broad sense of more than 80% was recorded for plant height, ear height, cob length, number of kernel rows per cob, test weight, number of plant stand per plot, and grain yield per plot. High genetic advance as a percentage of mean (genetic gain), along with estimates of heritability and GCV, was observed for ear height, cob length, number of kernel rows per cob, test weight, number of plant stand per plot, and grain yield per plot, which shows additive gene effects on these characters. Therefore, it appeared from the present study that characters like test weight, ear height, cob length, and number of kernel rows per cob exhibit a predominance of additive gene effects. Hence, simple selection based on phenotypic observations would be effective for these characters to bring genetic improvement in the desired direction.*

***Keywords*— Maize, genetic variability, GCV, PCV, heritability, genetic advance, additive gene effects.**

I. INTRODUCTION

Maize (*Zea mays* L.; 2n = 20) is a monoecious, cross-pollinated C4 plant belonging to the tribe Maydeae of the grass family Poaceae (Matin et al., 2017). The plant is native to South America. *Zea mays* is the only species in the genus *Zea* with chromosome number 2n = 20 (Sharma et al., 2014). It is cultivated under a very diverse agro-climatic zone that extends from tropical and subtropical to cold climates (Muliadi et al., 2021). The suitability of maize to diverse environments is unmatched by any other crop, as the expansion of maize to new areas and environments still continues, as it has a range of plasticity. Maize plays an important role in human and livestock nutrition worldwide. Maize (*Zea mays* L.) is the third most important staple cereal crop in the world after wheat and rice and is the primary staple food in many developing countries (Matin et al., 2017; Erenstein et al., 2022).

Maize, being a cross-pollinated crop, has wide scope for the development of hybrids and composites. In recent years, there has been a perceptible improvement in maize production in India, but the production and productivity of India are much less when compared to countries like the USA. The United States produces almost half of the world's production; other top producing countries are China, Brazil, France, Indonesia, and South Africa. India ranks fourth in maize production, producing 31.51 million tonnes on an area of 9.9 million hectares in 2020–21, whereas in Kharif 2021–22, maize production was 21.24 million tonnes (1st advance estimates) in an area of 8.15 million hectares (MoA&FW, New Delhi; https://agricoop.nic.in). It is mainly grown in Uttar Pradesh, Bihar, Rajasthan, and Madhya Pradesh because of high yield, the ease with which the crop can be cultivated, and the stability of prices. The disparity in average yields at global and national levels is a consequence of environmental, technological, and organizational factors. The productivity of maize in Madhya Pradesh is approximately 20 q/ha, which is less than the national average. Composites occupy a major area in India, but these are poor yielders. Therefore, considering the importance of maize in the state's economy, the study was proposed. Recently, single-cross hybrids developed through superior inbreds need to be promoted. Thus, there is tremendous scope for increasing production and productivity. However, for any breeding programme, germplasm serves as a valuable source material as it provides scope for building genetic variability.

Among a series of routine activities in the breeding programme, selection is the most important step for obtaining high-yielding genotypes. The effectiveness of selection is determined by the selection criteria used. Determining selection criteria can be done in various ways. Information on genetic parameters such as heritability can be used as a consideration to determine selection criteria.

Thus, the present investigation was undertaken with the aim to characterize *Zea mays* L. genotypes at the morphological level with the objective to estimate the genetic parameters of variability for yield and yield-related traits in maize hybrids.

II. MATERIALS AND METHODS

The present investigation was carried out at IARI-Sipani Krishi Anusandhan Farm, Collaborative Outstation Research Centre, Sitamahu Road, Changli, Mandsaur (Madhya Pradesh), India. Field and laboratory experiments were conducted in order to achieve the objectives of the present investigation.

2.1 Experimental Site

The field studies were undertaken at IARI-Sipani Krishi Anusandhan Farm, Collaborative Outstation Research Centre, Sitamahu Road, Changli, Mandsaur (Madhya Pradesh). Mandsaur, situated in the north-eastern part of Madhya Pradesh state, is located at an elevation of 379.50 m above mean sea level at a latitude of 24°07′ N and a longitude of 75°06′ E. The climate of the region is sub-humid type with an average rainfall of about 883 mm, and the soil of the area is sandy loam in nature. The crop was raised during Kharif 2022–23.

2.2 Experimental Material

In the present investigation, seeds of thirty diverse genotypes/varieties of *Zea mays* L. were procured from different geographical sources listed in Table 1.

TABLE 1
NAME OF 30 GENOTYPES OF *ZEA MAYS* L. USED FOR STUDY

S.No.	Name of genotypes	S.No.	Name of genotypes	S.No.	Name of genotypes	S.No.	Name of genotypes	S.No.	Name of genotypes
1	AH-4271	7	AH-4673	13	AH-4680	19	AH-8245	25	BIO-9544 CH
2	AH-4142	8	AH-4674	14	AH-4681	20	AH-8452	26	AH-4164
3	AH-4158	9	AH-4675	15	AH-4682	21	AH-8727	27	AH-4139
4	AH-8181	10	AH-4676	16	AH-8067	22	AH-2038	28	H-2053
5	AH-8106	11	AH-4677	17	AH-8127	23	H-2120	29	H-2110
6	AH-8323	12	AH-4678	18	AH-8178	24	NK-6240 CH	30	H-2142

2.3 Field Studies

2.3.1 Experimental Design

The field experiments were laid out in a randomized block design with three replications. Thirty entries were planted, each in three rows of 15.6 m length, with a row-to-row distance of 70 cm. Fertilizers were applied at 120 kg N: 70 kg P_2O_5 and 70 kg K_2O/ha at the time of sowing, while 40 kg N/ha was top-dressed in three split doses at twenty, thirty, and forty-five days after sowing, respectively. Immediately after sowing, a light irrigation was given, and the remaining irrigations were through rainfall. All the recommended agronomic practices and plant protection measures were adopted to raise a healthy crop during the crop period.

2.3.2 Morphological/Agronomic Characters

Five competitive plants were randomly selected from each replication in a genotype for recording observations. The selected plants were tagged, and data on individual plants were recorded for the following characters, except for days to 50% flowering and days to maturity. The procedure adopted for recording observations on different characters is given below:

1) **Days to 50% Tasseling:** The number of days was counted from the date of sowing to the date on which 50% of plants in a plot completed the opening of the tassel for each genotype.
2) **Days to 50% Silking:** The number of days was counted from the date of sowing to the date on which 50% of plants in a plot completed silking for each genotype.
3) **Plant Height (cm):** Plant height was measured in cm from the base of the plant to the top of the main tassel.
4) **Ear Height (cm):** Ear height was measured in cm from the base of the plant to the node bearing the uppermost ear.
5) **Cob Length (cm):** Cob lengths of twenty plants were taken randomly; length was measured in cm for each cob, and the average was worked out.
6) **Cob Girth (Cob Diameter) (cm):** Cob girth of all randomly selected cobs was measured.
7) **Number of Kernel Rows per Cob:** The number of kernel rows that bear the cob and attained physical maturity was counted on randomly selected plants.
8) **100-Grain Weight per Cob after Shelling (g):** Randomly, 100 seeds were counted for each genotype from each plot and weighed in grams using an electronic single-pan balance.
9) **100-Grain Weight (g):** Randomly, 100 seeds were counted for each genotype from each plot and weighed in grams using an electronic single-pan balance.
10) **Number of Plant Stand per Plot:** The number of plants in a randomly selected plot was manually counted, and the average was estimated.
11) **Kernel Texture (Flint/Dent):** Kernel texture was manually visualized and noted.

12) **Grain Yield per Plot (kg):** Total grains obtained per plot were weighed in kg on an electronic single-pan balance, and the average was worked out.

13) **Days to Maturity (Days):** The number of days was counted from the date of sowing to the date when 100% of the plants in a plot attained physiological maturity or their cobs completely turned brown and leaves started senescence.

2.4 Statistical Analysis

2.4.1 Data Generated from Morphological/Agronomic and Quality Characters

Mean values of five selected plants from each replication were utilized for statistical analysis of all the characters. The data thus obtained were subjected to the following statistical analysis:

(i) Analysis of Variance for the Experimental Design

The analysis of variance for the randomized block design was carried out on the basis of the model described by Panse and Sukhatme (1985) for individual characters for each environment. The statistical model is given below:

$$Y_{ij} = \mu + a_i + b_j + e_{ij}$$

where,

Y_{ij} = an observation of the i-th genotype in the j-th block

μ = general mean

a_i = i-th genotype effect

b_j = j-th replication effect

e_{ij} = random error associated with the i-th genotype in the j-th replication

The assumptions of the model are:

a. Observations are independent.

b. The random errors (e_{ij}) are distributed normally and independently with mean zero and variance σ^2_e.

c. The different effects in the model are additive.

Analysis of variance tables were constructed for each of the studied traits.

TABLE 2
SKELETON ANOVA

Source	Degree of freedom	Mean squares	Expectation of mean square
Replication	$(r-1)$	MS_r	$\sigma^2_e + g\sigma^2_r$
Genotype	$(g-1)$	MS_m	$\sigma^2_e + r\sigma^2_m$
Error	$(r-1)(g-1)$	MS_e	σ^2_e

where,

- r = number of replications
- g = number of genotypes
- MS_r = mean square due to replication
- MS_m = mean square due to genotype
- MS_e = mean square due to error
- σ^2_e = variance due to error
- σ^2_m = variance due to genotype
- σ^2_r = variance due to replication

(ii) Computation of Data Recorded

(a) Mean: The mean value of each character was worked out by dividing the total of the corresponding number of observations under all the replications.

$$\bar{X} = \Sigma x_i / n$$

where,

- x_i = any observation in the i-th genotype
- n = number of observations

(b) Median: The median was computed by arranging the observations in ascending order of magnitude, and the average of the two middle observations was recorded as the median.

(c) Range: Lowest and highest mean values for each character were recorded over the genotypes.

(d) Standard Error (S.E.): It is the dispersion of the family mean around the experimental or estimated population mean. The standard error of the mean was calculated with the help of the error mean square from the analysis of variance.

$$SE(d) = \sqrt{(2MS_e/r)}$$

where,

- MS_e = mean square due to error
- r = number of replications

(e) Critical Differences (C.D.): Critical difference was calculated to compare the treatment means for all the characters. It was computed with the help of S.E.(d) and the tabulated value of 't' at the 5% level of significance at error degrees of freedom.

$$C.D. = S.E.(d) \times t$$

(f) Coefficient of Variation (Experimental Error): The coefficient of variation was estimated by the formula:

$$CV\ (\%) = (\sqrt{\sigma^2_e} / \bar{X}) \times 100$$

where,

- σ^2_e = error variance

(iii) Genotypic Parameters

The parameters were calculated as given hereafter:

a) Genotypic Variance

$$\sigma^2_m = (MS_m - MS_e) / r$$

b) Phenotypic Variance

$$\sigma^2_p = \sigma^2_m + \sigma^2_e$$

where,

- σ^2_m = genotypic variance
- σ^2_p = phenotypic variance
- σ^2_e = mean square due to error/environment (= MS_e)
- r = number of replications

c) Heritability (Broad Sense):

It is the ratio of genotypic variance to phenotypic variance. Heritability in the broad sense was calculated using the formula:

$$h^2B = (\sigma^2_m / \sigma^2_p) \times 100$$

where,

- h^2B = heritability in the broad sense
- σ^2_m = genotypic variance
- σ^2_p = phenotypic variance

(iv) Estimation of Parameters of Variation

The genotypic, phenotypic, and environmental coefficients of variation were estimated as below:

a) Genotypic Coefficient of Variation (GCV):

$$GCV\ (\%) = (\sqrt{\sigma^2_m} / \bar{X}) \times 100$$

b) Phenotypic Coefficient of Variation (PCV):

$$PCV\ (\%) = (\sqrt{\sigma^2_p} / \bar{X}) \times 100$$

c) Environmental Coefficient of Variation (ECV):

$$ECV\ (\%) = (\sqrt{(\sigma^2_e/r)} / \bar{X}) \times 100$$

d) Genetic Advance (% of Mean):

$$GA = K \times \sigma^2_p \times h^2B\ (\text{or } K \times \sqrt{\sigma^2_m})$$

$$GA\ (\%\ \text{of mean}) = (GA / \bar{X}) \times 100$$

where,

- GA = genetic advance
- σ^2_m = genotypic variance
- σ^2_p = phenotypic variance
- K = selection differential; at 5% selection intensity, the value of K is 2.06
- $\bar{X}$ = grand mean

III. RESULTS AND DISCUSSION

Information on genetic diversity and relationships among individuals, populations, plant varieties, and species is important to plant breeders for the improvement of crops, for conservation biology, and for studying the evolutionary ecology of populations. Genetic diversity studies can identify alleles that might affect the ability of the organism to survive in its existing habitat or might enable it to survive in more diverse habitats. This knowledge is valuable for germplasm conservation, individual, population, variety, or breed identification, and genetic improvement (Sumathi et al., 2005; Begna et al., 2022; Salgotra and Chauhan, 2023). Thus, the present investigation was carried out with 30 *Zea mays* genotypes, and the results obtained are presented below.

3.1 Morphological Characterization

Morphological markers are those distinguishable characters that are easily observable to human vision and selected based on the experience of the breeder to correlate a phenotypic trait with a trait of interest (Sharma et al., 2018). Morphological markers differ among species, genera, and varieties of plants. It is the easiest and quickest way to identify or detect the presence of a morphological marker with that of a trait for improvement.

Morphological markers are detected and well established in different members of the Poaceae family, such as different growth, yield, and disease resistance traits related to markers such as purple hull, phenol staining, glabrous leaf and hull, purple node,

awned panicle, lazy growth habit, brown pericarp, and others (Kinoshita, 1990). Cultivar identification mainly has, however, limited usefulness due to variation in morphological traits, which is influenced by environmental factors.

In the present investigation, 11 important morphological/agronomic and quality characters were studied to evaluate the pattern and extent of genetic variability and relatedness among 30 genotypes of *Zea mays* L. (Plate 1). The data recorded on different characters were statistically analyzed using software WINDOSTAT version 7.0 developed by Indostat Services Ltd., Hyderabad, India. The results obtained are discussed under the following headings:

3.1.1 Analysis of Variance

The success of a breeding programme largely depends on the extent of genetic variability present in the material; the greater the diversity in the material, the better the chances for evolving promising and desired types. The mean squares from the ANOVA for different characters (Table 3) revealed that the mean squares due to genotypes were highly significant for all the characters, indicating the presence of significant genetic variability in the material under study. It provides scope for selection and further subsequent utility of the genotype in the crop improvement programme. Hence, the material appeared to be appropriate for further genetic analysis. Ahmad et al. (2011) observed variation for days to 50% pollen shedding, days to 50% silking, plant height, ear height, 100-grain weight, harvest index, and grain yield in *Zea mays* genotypes. Similarly, Turi et al. (2007) and Ali et al., (2007). also reported significant variability for cob length, grains rows cob^{-1}, fresh cob weight, grain moisture content, 300-grain weight, and grain yield.

TABLE 3
ANOVA FOR VARIOUS CHARACTERS IN 30 GENOTYPES OF *ZEA MAYS*

S. No.	Characters	Replications (d.f. = 2)	Treatments (d.f. = 29)	Error (d.f. = 58)	Total (d.f. = 89)
1	Days to 50% tasseling	1.67	28.30**	4.38	12.34
2	Days to 50% silking	1.62	33.50**	5.38	14.46
3	Days to maturity (days)	4.54	27.13**	7.34	14.29
4	Plant height (cm)	0.12	776.65**	56.98	290.19
5	Ear height (cm)	20.68	354.52**	11.06	123.19
6	Cob length (cm)	0.03	7.35**	0.38	2.64
7	Cob girth (cm)	0.17	0.16**	0.03	0.08
8	No. of kernel rows per cob	0.16	7.81**	0.35	2.77
9	100-grain weight (g)	0.02	34.70**	1.65	12.38
10	No. of plant stand per plot	0.48	49.82**	0.99	16.89
11	Grain yield per plot (kg)	0.01	1.48**	0.01	0.49

Significant at 5% probability level; **significant at 1% probability level.

3.1.2 Estimates for Genetic Variability Parameters for Various Characters

The genetic facts are inferred from phenotypic observations, which are the results of the interaction of genotype and environment. Since the environment has a great influence on many quantitative and qualitative characters, the observed variability can be grouped under heritable and non-heritable components, and this can be estimated by parameters such as the genotypic coefficient of variation (GCV), heritability, and genetic gain. This would help the breeder in developing and formulating a selection programme for the genetic improvement of crop plants.

The genetic parameters were worked out separately for all these characters. The components of variance, heritability, and genetic advance as a percentage of mean for various characters are presented in Table 4. The perusal of the table revealed that

the phenotypic coefficient of variation (PCV) was higher than the respective genotypic coefficient of variation (GCV), but the relatively marginal difference between PCV and GCV for ear height, cob length, number of kernel rows per cob, test weight, number of plant stand per plot, and grain yield per plot revealed that variability was due to genotypic differences. On the other hand, environmental influences were predominant for characters like days to 50% tasseling, days to 50% silking, days to maturity, and cob girth. Therefore, selection based on the above characters is expected to be effective, while for other characters, selection must be performed carefully, considering environmental factors. Similar results were also reported by Sesay et al., 2016.

High GCV was recorded for grain yield per plot (32.59%), number of plant stand per plot (17.27%), ear height (13.99%), test weight (11.68%), and number of kernel rows per cob (10.90%). Therefore, selection for all these characters would be effective. Similar results were also reported by Kabdal et al. (2003) for grain yield, ear length, and harvest index in *Zea mays* genotypes. Moderate GCV was recorded for grain yield per plant, cob length, cob girth, days to 50% flowering, leaf number, and days to maturity. However, characters like cob girth, days to maturity, and days to 50% tasseling and silking showed comparatively low estimates of GCV and PCV, indicating that these characters were highly influenced by the environment.

Estimates of GCV and PCV alone do not assess the amount of heritable variation. The genetic contribution to the phenotypic expression of a trait is better reflected by estimates of heritability. A higher estimate of heritability indicates the presence of more fixable variability (Shivakumar et al., 2011). In the present study, heritability (broad sense) estimates were high (>50%) for all the traits except days to maturity (47.36%). The estimates of heritability in the broad sense were moderate to high for most of the characters, with more than 80% recorded for plant height, ear height, cob length, number of kernel rows per cob, test weight, number of plant stand per plot, and grain yield per plot. High heritability for days to 50 % silking, Days to 50% tasseling and number of kernels row in cob was also reported by Shrestha et al., 2021 in single cross maize hybrids. Mahmood et al. (2004) reported low, medium, and high broad-sense heritability for days to tasseling, number of days to silking, plant height, ear length, number of kernel rows ear^{-1}, number of kernels row^{-1}, 100-grain weight, and grain yield plant^{-1} in *Zea mays* genotypes. Similarly, Bello et al. (2012) reported high heritability along with high genetic advance for grain yield, number of grains ear^{-1}, ear weight, and plant and ear heights, providing evidence that these parameters were under the control of additive gene effects, and effective selection could be possible for improvement of these characters.

Burton (1952) suggested that GCV along with heritability estimates would give a better idea about the efficiency of selection, as it simply depicts the amount of genetic variation, while heritability measures the proportion to which the variability of a character is transmitted to its progenies. However, Johnson et al. (1955) suggested that variability and genetic advance, when calculated together, would be more useful in predicting the resultant effect of selection on phenotypic expression.

While assessing the overall position, the present study revealed high genetic advance as a percentage of mean (genetic gain), along with estimates of heritability and GCV, for ear height, cob length, number of kernel rows per cob, test weight, number of plant stand per plot, and grain yield per plot. Kabdal et al. (2003) reported high heritability and genetic advance for grain yield, ear height, plant height, and ear length, while ear diameter, days to 50% tasseling, days to 50% silking, and 100-kernel weight showed low genotypic coefficient of variation combined with low to medium heritability and low genetic advance. However, high heritability with moderate genetic advance was recorded for days to 50% tasseling and silking, cob length, cob girth, and number of kernel rows per cob, indicating the involvement of both additive and non-additive gene action; hence, selection for these characters based on phenotypic observation alone may not be effective.

Based on the per se performance of all genotypes, all traits studied showed a wide range of variation for most of the morphological and yield components (Table 4). However, more variation was found in ear height (57.87–96.70 cm), plant height (160–222.23 cm), test weight (19.74–34.28 g), and number of plant stand per plot (11.00–29.00), indicating sufficient variation in the aforesaid traits and providing a good opportunity for grain yield improvement in maize. Similar to our results, Bhiusal et al. (2017) previously observed huge variation in yield-related traits like anthesis–silking interval (3.00–5.67 days), days to 50% maturity (123.33–146.67 days), seed fill duration (25.67–45.67 days), leaf area index (2.02–5.22), cob weight (31.67–176.67 g), cob length (8.43–20.53 cm), cob girth (9.92–16.91 cm), no. of grain rows/cob (9.33–16.67), no. of grains/row (7.67–32.33), 100-seed weight (17.03–40.00 g), and grain yield/plant (21.74–224.73 g).

Therefore, it appeared from the present study that characters like test weight, ear height, cob length, and number of kernel rows per cob exhibited a predominance of additive gene effects. Hence, simple selection based on phenotypic observations would be effective for these characters to bring genetic improvement in the desired direction.

TABLE 4
GENETIC VARIABILITY PARAMETERS FOR VARIOUS CHARACTERS IN 30 GENOTYPES OF *ZEA MAYS*

Characters	Mean	Range (Min–Max)	σ^2_m	σ^2_p	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)	ECV (%)
Days to 50% tasseling	55.02	49.33–59.00	7.97	12.35	64.54	4.67	8.49	5.13	6.39	13.75
Days to 50% silking	59.93	53.00–64.00	9.38	14.75	63.55	5.03	8.39	5.11	6.41	11.39
Days to maturity (days)	96.89	92.67–102.67	6.6	13.93	47.36	3.64	3.76	2.65	3.85	13.04
Plant height (cm)	195.46	160.00–222.33	239.89	296.87	80.81	28.68	14.67	7.92	8.82	11.2
Ear height (cm)	76.47	57.87–96.70	114.49	125.55	91.19	21.05	27.53	13.99	14.65	8.66
Cob length (cm)	16.6	12.60–19.47	2.32	2.7	85.95	2.91	17.53	9.18	9.9	8.86
Cob girth (cm)	4.3	3.80–4.77	0.05	0.07	56.61	0.32	7.32	4.72	6.28	11.46
No. of kernel rows per cob	14.47	12.00–18.00	2.49	2.83	87.79	3.04	21.04	10.9	11.63	6.02
100-grain weight (g)	28.42	19.74–34.28	11.02	12.66	87	6.38	22.44	11.68	12.52	6.35
No. of plant stand per plot	23.36	11.00–29.00	16.27	17.27	94.26	8.07	34.54	17.27	17.79	5.89
Grain yield per plot (kg)	2.15	0.78–3.54	0.49	0.5	98.44	1.43	66.61	32.59	32.85	3.39

σ^2_m = genotypic variance; σ^2_p = phenotypic variance; GA = genetic advance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; ECV = environmental coefficient of variation.

IV. CONCLUSION

The analysis of variance revealed the presence of significant genetic variability among the genotypes for all eleven characters. Furthermore, the mean and median values for various characters being quite close to their respective values indicates the normal distribution of the genotypes. Estimates of genetic variability parameters showed that the phenotypic coefficient of variation (PCV) was higher than the respective genotypic coefficient of variation (GCV). High GCV was recorded for grain yield per plot, number of plant stand per plot, ear height, test weight, and number of kernel rows per cob. Therefore, selection for all these characters would be effective.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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