International Journal of Agriculture and Nutrition 2025; 7(12): 20-26

ISSN Print: 2664-6064
ISSN Online: 2664-6072
NAAS Rating (2025): 4.69
IJAN 2025; 7(12): 20-26
www.agriculturejournal.net
Received: 17-09-2025
Accepted: 20-10-2025

Assessment of genetic variability among finger-millet (*Eleusine coracana* (L.) Gaertn) genotypes through multivariate analysis

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DOI: https://www.doi.org/10.33545/26646064.2025.v7.i12a.322

Abstract

The Field experiment was conducted to evaluate finger millet genotypes for its variability based on nine important morphological characters and find out the correlation coefficients among them. The experimental material comprised forty genotypes were evaluated in a randomized block design with three replications at the experimental field of the Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS) during the *Kharif* 2024 season. Analysis of variance revealed the statistical significant differences among the genotypes for all nine morphological traits investigated in present study. In the character association study, the seed yield per plant showed significant and positive correlation with plant height, ear head length, total number of tillers, number of productive tillers and 1000 grain weight, indicating their contribution towards yield enhancement. The Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV). The high values of GCV and PCV were observed for grain yield per plant. All the characters studied exhibited the high heritability except for the harvest index. Among the genotypes studied, IC-475301, IC-0475519, IC-474069, IC-012985 and IC-475260 were found promising for grain yield which may be utilized for further improvement program. Whereas, based on principal component analysis, the entire variance was provided by four main components, of which PC-1 and PC-2 contributed 45.8% and 20.4%, respectively, to the total variability. Euclidean distance was used to divide the forty finger millet genotypes into six clusters. The largest number of genotypes (thirteen) in cluster V was followed by Cluster III, with ten genotypes. The maximum inter-cluster distance was exhibited by cluster I and cluster V (31.609), therefore, the genotypes from them may be used as parents for hybridization.

Keywords: Coefficients of variation, correlation, *Eleusine coracana,* finger millet, genetic variability, heritability and multivariate analysis

Introduction

The *Eleusine coracana* L. is one of the oldest millets that serve as a staple food in India. India ranks among the leading countries in millet cultivation worldwide. The most prevalent species include Finger millet (*Eleusine coracana* (L.) Gaertn), Little millet (*Panicum sumatrense* Roth ex Roem. & Schult.), Foxtail millet (*Setaria italica* (L.) P. Beauvois), and Proso millet (*Panicum miliaceum* L.). The finger millet, (*Eleusine coracana* (L.) Gaertn.) sub species *coracana*, is a member of the *Poaceae* family. The cultivated *E. coracana* is a tetraploid (2n = 4X = 36) and has morphological similarities to both *E. indica* (L.) Gaertn. (2n = 18) and *E. africana* (O.) Byrne (2n = 36). This crop is extensively grown in arid and semi-arid regions worldwide. It is referred to as *ragi* in India, *kodo* in Nepal, and *kurakkan* in Sri Lanka. As a tetraploid and self-pollinating species, it likely evolved from its wild relative, *Eleusine africana*, which is indigenous to the highlands of Ethiopia and Uganda. This domesticated nutri-cereal, which has African origins, spread to Asia in prehistoric times having the main commercial component in form of grain, which is highly nutritious and has excellent malting properties. Finger millet plays a vital role in meeting the dietary needs and supporting the incomes of many rural households in Eastern and Southern Africa and South Asia. Its C_4 carbon fixation pathway allows it to thrive at altitudes above 2,000 meters and provides high drought and salt tolerance, along with a long storage life for the grains. (Husain et al., 2018) [13].

In India, finger millet is the most extensively cultivated among the small millets. It stands out from cereals like barley, rye, and oats because of its superior nutritional benefits and exceptional characteristics as a food crop for subsistence. Finger millet can be regarded as a nutria-cereal, being a primary millet crop with nutritional, therapeutic, and commercial significance. Ragi is high in calcium and protein, offering a well-balanced set of essential amino acids. Thus, ragi is an ideal food for conditions such as diabetes, cardiovascular diseases, chronic obstructive pulmonary disease, and cancer. Its high fiber content helps to prevent constipation, high blood pressure, and gluten intolerance. It has also shown the capability to manage blood glucose levels. As a pesticide-free, easy-to-grow, and cost-effective crop, it is a preferred option for commercial success. However, the creation of new finger millet varieties has proven to be a demanding and resource-intensive process, often overlooked due to the global focus on the 'big three' cereals (Ujjainkar et al., 2025) [36].

The productivity of minor millets, especially in finger millet is significantly low due to the lack of high-yielding cultivars and necessary inputs. The main reason for this low productivity is the unavailability of high-yielding cultivars that can thrive in various agro-climatic conditions. Given that the genetic potential of finger millet has not been fully tapped, there is likely a greater opportunity for growth in developing countries. The morphological characterization, estimation of genetic variability present in available germplasm will be helpful to prepare the database to select and include the germplasm lines for further breeding program. Hence the present investigation was carried out with forty germplasm lines to estimate genetic variability, correlation among major nine morphological traits and further to group them into diverse clusters to select parents for hybridization.

Method and Materials

The field investigation was carried out using forty germplasm lines of Finger Millet (*Eleusine coracana* (L.) Gaertn) grown in Randomized Block Design (RBD) with three replications at experimental field of university department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS) during kharif season of 2024 with the objectives to evaluate the performance of finger millet germplasm and to estimate the genetic variability along with correlation among nine major morphological characters viz., plant height (cm), days to 50 per cent flowering, days to maturity, total number of tillers, number of productive tillers, 1000 seed weight (g), harvest index (%) and seed yield per plant (g). Five plants per genotype in each replication were randomly selected for recording the observations on different characters and their averages were used in statistical analysis

Analysis of variance was carried out as per the standard method in order to partition the total variation of different characters under study into its components viz., replication, treatments and error. Analysis of variance for RBD was done based on following linear model as suggested by Panse and Sukhatme (1985) [26]. The Phenotypic (PCV) and Genotypic (GCV) coefficients of variations were calculated by the formula by Burton (1952) [5], heritability in broad sense (h2) by Burton and De Vane (1953) [6] and genetic advance i.e., the expected genetic gain were calculated by using the procedure given by Johnson et al. (1955) [14]. While the correlation coefficients among grain yield and its influencing characters were calculated according to procedure given by Miller and Naismith (1958) [22]. The PCA and cluster analysis were performed using R and R-studio software.

Results and Discussion

Analysis of variance: The analysis of variance was carried out to assess the variation in the genotypes for all morphological traits under study and is presented in Table 1. The significance was tested by applying 'F' test, the analysed data indicated that the treatment mean sum of square were found to be highly significant for all the nine morphological characters, indicating the presence of substantial genetic variation among the genotypes selected for study.

Table 1: Analysis of variance for nine morphological traits of finger millet

Characters	**Sources of variations**		
	Replications	**Treatments**	**Error**
	(Df-2)	***(Df-39)***	***(Df-78)***
Plant height (cm)	7.57	312.70**	12.95
Days to 50% flowering	3.93	89.64**	2.63
Days to maturity	8.78	80.26**	5.89
Ear head length (cm)	0.38	4.59**	0.41
Total number of tillers	0.15	1.74**	0.08
Number of productive tillers	0.01	0.95**	0.06
Test weight (g)	0.03	0.54**	0.02
Harvest index (%)	1.54	6.93**	1.92
Seed yield per plant (g)	0.34	2.43**	0.13

Mean performance of forty genotypes: The mean performance of the forty genotypes of finger millet (Table 2) showed the wide range of variability for all the nine morphological traits studied in present investigation. The variations in respect of mean performance of the characters viz., plant height recorded the range (54.76 cm to 91.02 cm), days to 50 per cent flowering 60.33 days to 76.67 days, days to maturity 91.33 days to 110.33 days (Table 3). The genotype IC-475737 was found early, while the genotype IC-474439 and IC-473716 were found late in maturity as compared to other genotypes. Among ear head related traits wide range observed ear head length (6.09 cm to 10.73 cm), total number of tillers (2.08 to 4.67), number of productive tillers (1.87 to 4.09), test weight in finger millet genotypes were ranged from (2.17 g to 3.69 g). The harvest index (HI) ranged from (11.46% to 17.88%). The grain yield per plant in finger millet genotypes showed the variation for mean values from (3.28 g to 6.70 g). The genotypes IC-475301, IC-0475519, IC-474069, IC-012985 and IC-475260 were identified as promising performers for several morphological traits, including grain yield, 1000 grain weight i.e. test weight, total number of tillers, number of productive tillers. Similar trend of mean performances for various characters was also reported by Rani Jadhav et al. (2015) [28], Goswami et al. (2015) [11], Mahanthesha et al. (2017) [21], Shivangi Negi et al. (2017) [32] and Guntamukla et al. (2024) [12].

Table 2: Mean performance of finger millet genotypes for nine morphological characters

SN	Genotypes	Plant height (cm)	Days to 50% flowering	Days to maturity	Earhead length (cm)	No. of tillers per plant	No of productive tillers	Test weight (g)	Harvest index (%)	Seed yield per plant (g)
1	IC-0476519	88.68	64.67	96.67	8.82	4.57	3.85	3.61	16.06	6.67
2	IC-0475736	62.85	62.33	94.33	7.53	3.47	2.93	2.44	15.94	4.80
3	IC-475301	91.02	61.00	94.33	8.96	4.66	4.09	3.70	16.40	6.70
4	IC-475599	67.29	76.67	106.67	9.77	3.27	2.53	2.70	11.46	4.25
5	IC-475691	61.87	69.00	98.00	7.84	2.53	2.20	3.07	16.77	4.73
6	IC-475712	57.60	65.33	100.33	8.68	2.80	2.27	2.66	15.90	4.12
7	IC-475737	66.42	60.33	91.33	7.06	3.07	2.40	2.78	16.21	4.84
8	IC-474965	61.80	70.00	106.00	6.23	2.53	2.33	2.57	16.34	4.00
9	IC-475260	85.18	62.67	97.00	8.33	4.34	3.28	3.46	17.49	6.55
10	IC-478974	66.97	65.33	104.67	8.09	2.13	2.13	2.97	17.61	5.19
11	IC-0479047	63.47	75.33	106.67	10.73	2.23	1.87	3.08	16.96	4.25
12	IC-0479061	55.69	74.67	104.67	7.15	3.53	2.47	2.38	17.56	4.38
13	IC-053739	62.39	69.33	105.00	7.93	2.40	2.13	2.28	16.12	4.34
14	IC-473572	64.79	70.67	105.67	6.77	3.07	2.33	3.10	14.58	3.84
15	IC-473402	73.83	71.67	104.33	8.00	2.40	1.93	2.77	15.55	4.27
16	IC-473518	72.63	63.00	95.33	7.07	2.53	2.00	2.53	17.09	4.19
17	IC-473535	54.77	76.33	109.33	7.45	2.80	2.20	3.05	16.98	4.47
18	IC-473546	59.97	75.33	109.33	10.34	2.24	2.22	2.24	15.34	3.66
19	IC-473643	74.47	67.33	103.67	7.85	3.07	2.33	3.22	17.54	4.52
20	IC-473716	72.60	72.67	110.33	7.72	2.87	2.20	3.09	17.32	4.20
21	IC-474041	81.53	63.67	98.00	7.49	3.33	2.07	2.89	17.56	4.34
22	IC-474049	58.66	74.33	109.67	6.13	2.15	2.15	2.21	15.63	3.42
23	IC-474069	87.25	62.67	101.33	8.56	4.45	3.47	3.52	16.86	6.65
24	IC-474070	61.56	76.00	109.00	6.09	3.27	2.93	2.56	16.50	4.51
25	IC-474184	54.82	75.33	107.33	9.86	3.73	2.67	2.97	17.88	4.77
26	IC-474196	58.21	73.00	109.67	10.67	3.33	2.93	3.13	17.61	5.03
27	IC-474439	65.37	71.67	110.33	7.23	2.93	2.33	3.02	13.76	3.83
28	IC-012985	85.95	75.00	109.67	8.40	4.40	3.37	3.48	17.52	6.59
29	IC-478822	67.87	71.67	104.00	7.41	4.09	3.07	3.10	15.42	4.41
30	IC-049547	67.21	75.33	109.33	8.41	3.86	3.00	3.29	17.42	4.80
31	IC-478839	61.31	76.00	103.33	7.71	3.78	3.67	2.85	13.76	3.57
32	IC-478798	69.39	76.33	108.33	7.30	3.27	2.60	2.60	16.27	4.69
33	IC-478167	75.73	75.00	106.67	8.79	3.13	2.87	2.56	12.28	4.35
34	IC-478314	84.88	71.67	107.00	8.32	4.31	3.22	3.45	15.52	5.52
35	IC-478415	61.57	76.67	107.67	6.23	2.37	2.35	2.26	15.37	3.75
36	IC-478672	59.15	70.33	107.33	6.40	2.67	2.20	2.56	14.73	4.20
37	IC-096773	57.44	61.33	102.67	6.09	2.08	2.06	2.17	15.14	3.28
38	IC-096820	71.87	60.33	99.33	6.61	2.80	2.67	2.48	13.96	3.89
39	IC-473421	70.52	70.33	108.00	7.44	4.20	3.03	3.39	14.34	4.40
40	GPU-67 (Check)	58.00	73.67	106.67	6.54	3.77	3.27	3.21	14.16	4.53
	SE(M±)	2.08	0.94	1.40	0.37	0.17	0.14	0.09	0.78	0.21
	CD (5%)	5.84	2.63	3.94	1.04	0.46	0.39	0.25	2.25	0.59

Genetic variability studies: The range of Coefficient of Variation (CV) i.e. either GCV or PCV was categorized as per Sivasubramanian and Madhavamenon (1973) [34]: [<10% - Low coefficient of variation; 10-20% - Medium coefficient of variation; > 20% - High coefficient of variation.] While, as suggested by Robinson et al. (1949) [29], the heritability estimates range was classified [< 30% - Low heritability; 30%-60% - Moderate heritability; > 60%- High heritability]. Similarly, the range of genetic advance as per cent of mean (GAM) proposed by Johnson et al., (1955) [14] was grouped as [< 10% - Low GAM; 10%-20% - Medium GAM; > 20%- High GAM].

During the present investigation, for each character under consideration, the range, mean, Genotypic Co-efficient of Variation (GCV), Phenotypic Co-efficient of Variation (PCV), heritability (h2), and genetic advance as a percentage of mean (GAM) were calculated (Table 3). It has shown the extent to which observed variation is caused by genetic factors. Results revealed a minimal difference in GCV and PCV values, suggesting that environmental influences on genotypes were less significant. There was wide range of variability for all the traits studied. The range values were similar to those reported earlier (Lal et al., 1996 and Dinesh et al., 2024) [18, 9] although actual limits were different for some characters in *Ragi*. The genotypic and phenotypic coefficients of variation (GCV and PCV) were found moderate for seed yield per plant (18.96 and 20.53), no of tillers per plant (23.13 and 24.78) and number of productive tillers (20.65 and 22.53), whereas low GCV and PCV were estimated for remaining characters. Heritability estimates were very high for most of the traits studied except that for harvest index (46.56%).

Table 3: Parameters of variability for nine morphological traits in finger millet

Characters	Range	Mean	GCV%	PCV%	Heritability bs (%)	GAM %
Plant Height (cm)	54.76-91.02	68.06	14.69	15.61	88.53	28.47
Days to 50% flowering	60.33-76.67	70.10	7.68	8.02	91.70	15.16
Days to maturity	91.33-110.33	104.22	4.78	5.31	80.81	8.85
Ear head length (cm)	6.09-10.73	7.85	15.03	17.11	77.22	27.21
Total number of tillers	2.08-4.67	3.21	23.13	24.78	87.07	44.45
Number of productive tillers	1.87-4.09	2.64	20.65	22.53	84.03	39.00
Test weight (g)	2.17-3.69	2.88	14.43	15.41	87.60	27.81
Harvest index (%)	11.46-17.88	15.92	8.12	11.89	46.56	11.41
Seed yield per plant (g)	3.28-6.70	4.61	18.96	20.53	85.26	36.06

In the present investigation, the broad sense heritability was computed which includes both additive and non-additive gene effects. Therefore, heritability estimates should be considered in conjunction with genetic advance (Burton and Devane, 1953 and Johnson et al., 1955) [6, 14]. The characters viz., plant height, days to 50 per cent flowering, ear-head length, number of tillers per plant, number of productive tillers and seed yield per plant exhibited the high estimates for heritability and high values for genetic advance as the percent of mean (GAM) indicating significance of both genetic as well as environmental effect on these traits and effectively controlled by additive genes and will be highly responsive for selection. While the trait, days to maturity exhibited high heritability and low GAM values indicates that the character has high heritability, it implies that genetic factors are a major contributor to phenotypic variation. If the GAM is low, it suggests that selection will not effective, which can occur if the genetic control is primarily non-additive i.e. it is due to dominance or epistasis. However, the trait viz., harvest index exhibited low heritability combined with moderate genetic advance as a percentage of mean (GAM) suggesting that a trait is influenced by both genetic and environmental factors, with the moderate GAM indicating that selection for this trait is still somewhat effective. The low heritability shows a smaller proportion of the variation in character is due to genetic factors alone, while the moderate GAM indicates that a portion of the trait have chance to be improved through selective breeding. Similar kind of results were reported by Lal et al. (1996) [18] and Prabhu et al. (2015) [27].

It is evidenced that the selection directly for grain yield in plants is not easy and helpful. Thus, any morphological character that is associated/correlated with higher seed yield· or which makes a significant contribution toward the yielding ability would be more useful and authentic in the improvement of grain yield. In the present study, grain yield per plant was positively correlated with all the traits studied except days for 50 per cent flowering (-0.309) and days to maturity (-0.332) at phenotypic level as depicted in Table 4.

Table 4: Correlation coefficients among nine morphological traits in finger millet

Characters	Plant Height (cm)	Days to 50% flowering	Days to maturity	Ear head length (cm)	Total number of tillers	No. of productive tillers	Test weight (g)	Harvest index (%)	Seed yield per plant (g)
Plant Height (cm)	1.000	-0.407**	-0.364*	0.193	0.600**	0.524**	0.626**	0.102	0.732**
Days to 50% flowering		1.000	0.834**	0.156	-0.088	-0.084	-0.123	-0.168	-0.309
Days to maturity			1.000	0.056	-0.184	-0.185	-0.099	-0.129	-0.332*
Ear head length (cm)				1.000	0.216	0.181	0.363*	0.136	0.362*
Total number of tillers					1.000	0.893**	0.738**	0.066	0.733**
Number of productive tillers						1.000	0.612**	0.082	0.676**
Test weight (g)							1.000	0.251	0.745**
Harvest index (%)								1.000	0.398*
Seed yield per plant (g)									1.000

Seed yield per plant showed positive significant correlation with plant height, ear head length, total number of tillers, productive tillers, test weight and harvest index similar result observed earlier by many researchers (Aradhana Suman et al. 2018, Gohel and Chaudhari, 2018, Chavan et al. 2020, Nikunj et al. 2023 and Lanjewar et al., 2025) [2, 10, 7, 24, 19]. For days to 50 per cent flowering and days to maturity grain yield showed negative correlation while, trait of total number of tillers showed positive significant correlation with number of productive tillers, test weight and yield per plant. The important growth parameters viz., plant height showed negative significant correlation with 50 % flowering and days to maturity, whereas it showed positive significant correlation with total number of tillers, productive tillers 1000 grain weight or test weight, seed yield per plant. Major crop duration indicator trait viz., days to 50 per cent flowering and days to maturity showed negative non-significant correlation with total number of tillers, productive tillers, 1000 grain weight, harvest index and grain yield per plant similar result found earlier by Bothikar et al. (2014) [4], Devaliya et al. (2017) [8], Lad et al. (2020) [17], Soe et al. (2021) [35] and Boddu et al. (2023).

The Principle Component Analysis (PCA) is useful statistical tool to explain the maximum variability of total variables contributing to yield through the identified minimum number of components (Nethra et al., 2014 and

Jyothsna et al., 2016). In present investigation, the data were recovered into four Principal Components (PCs) with eigenvalues greater than unity except in PC 4, which accounted for 87.8 per cent of the overall variation among the forty finger millet genotypes evaluated for nine quantitative parameters (Table 5). The first few PCs have a considerable influence on overall variability, depending on a variety of genotype properties (Anderson, 1984) [1].

Table 5: Principle component analysis in forty finger millet genotypes

Principle components (PCs)	Eigenvalues	Variability (%)	Cumulative variability (%)
PC1	4.12	45.8	45.8
PC2	1.84	20.4	66.2
PC3	1.19	13.2	79.4
PC4	0.76	8.4	87.8

The data shown Table 5 & 6 depicts that the major contributors to PCs were determined from the loading factor values. The PC-1 accounted for approximately 45.8% of the total variation. It can be seen from the plant height (0.969), seed yield per plant (0.724), 1000 seed weight i.e. test weight (0.574), total number of tillers per plant (0.558), number of productive tillers (0.491), earhead length (0.138) and harvest index (0.135) that these quantitative characters had the maximum positive contribution towards divergence, and the days to 50 per cent flowering (-0.610) and days to maturity (-0.570) had a negative contribution towards genetic divergence. PC-1 was therefore regarded as a major component of yield because it included several traits associated with grain yield per plant.

Table 6: Contribution of each principal component towards different characters

Characters	PC1	PC2	PC3	PC4
Plant Height (cm)	0.969	0.247	-0.001	-0.006
Days to 50% flowering	-0.610	0.745	-0.269	0.002
Days to maturity	-0.570	0.763	0.303	0.005
Ear head length (cm)	0.138	0.259	-0.263	0.378
Total number of tillers	0.558	0.262	-0.245	0.086
Number of productive tillers	0.491	0.213	-0.254	-0.050
Test weight (g)	0.574	0.304	-0.038	0.286
Harvest index (%)	0.135	-0.099	0.081	0.950
Seed yield per plant (g)	0.724	0.143	-0.120	0.404

The PC-2 vector accounted for 20.4 % of total variation and the traits contributing positively to these includes days to maturity (0.763), days to 50 per cent flowering (0.745), test weight (0.304), total number of tillers (0.262), ear-head length (0.259), plant height (0.247), number of productive tillers (0.213) and seed/grain yield per plant (0.143). Whereas, the only single character of harvest index (- 0.099) showed the negative contribution towards divergence. However, PC-3 and PC-4 vectors accounted for 13.2 % and 8.4% of total variation respectively. The seed yield per plant contributed negative in PC-3 (-0.120) while found positive for PC-4 (0.404) similar kind of findings were reported by Vaishali Ladumo et al. (2021) [37] in finger millet. Similarly, the author viz., Salini et al. (2010) [30] conducted an experiment and evaluated 368 genotypes of proso-millet based on principal component analysis (PCA) and found that first five Eigen vectors contributed about 93.2 per cent of total variability, which exhibited congruence with that findings noted by Shoba et al. (2019) [33] using PCA and cluster analysis in rice crop.

Based on estimates of genetic distances, the grouping of large number of genotypes is a crucial task to screen and promote them for further utilization in crop improvement projects. Therefore, further in the present investigation, the Euclidean distances were employed to classify the forty finger millet genotypes into different clusters based on the magnitude of genetic diversity among these genotypes. Total six clusters were formed occupying all forty finger millet genotypes; the cluster V comprised of the maximum number of genotypes (thirteen genotypes) followed by cluster III (ten genotypes) as depicted in Table 8. The cluster I and cluster IV comprised of five genotypes each while, the cluster II was having the four genotypes while the minimum number of genotypes (three genotypes) was categorized into cluster VI. The highest inter-cluster distance was recorded among cluster I and V (31.609) followed by cluster I and IV (26.279), cluster IV and VI (23.201) and cluster V and VI (23.143), whereas, the minimum inter-cluster distance was recorded among cluster IV and V (Table 7). Based on the maximum inter cluster distances it may be suggested that the genotypes grouped in cluster I and cluster V may be used as a diverse parents for hybridization program. Similar kind of studies were reported by Sheriff (1992) [31], Mahanthesha et al. (2017) [21], Kandel et al. (2020) [15], Pali et al. (2022) [25] and Kanwer et al. (2025) [16]. The genotypes grouped in these clusters were markedly diverse and may be considered as appropriate parents for evolving superior varieties in subsequent years.

Table 7: Inter cluster distances among six clusters

Cluster	I	II	III	IV	V	VI
I	4.093	18.747	22.204	26.279	31.609	15.838
II		5.215	16.279	11.110	20.142	22.559
III			5.176	11.498	10.410	13.059
IV				5.403	10.114	23.201
V					4.502	23.143
VI						5.389

Table 8: Forty genotypes grouped in clusters

Cluster	No of genotypes	Genotypes included
I	5	IC-476519, IC-475301, IC-475260, IC-474041, IC-474069
II	4	IC-0475736, IC-475737, IC-473518, IC-096820
III	10	IC-475599, IC-473572, IC-473402, IC-473643, IC-473716, IC-474439, IC-478822, IC-049547, IC-478798, IC-473421
IV	5	IC-475691, IC-475712, IC-478974, IC-053739, IC-096773
V	13	IC-474965, IC-0479047, IC-0479061, IC-473535, IC-473546, IC-474049, IC-474070, IC-474184, IC-474196, IC-478839, IC-478415, IC-478672, GPU-67
VI	3	IC-012985, IC-478167, IC-478314

Conclusion

Present investigation suggested that there is substantial degree of variability present in the material studied. The genotypes IC-475301, IC-0475519, IC-474069, IC-012985 and IC-475260 were identified as best genotypes for grain yield potential. Phenotypic coefficient of variation estimate was slightly higher than the genotypic coefficient of variation for all the traits, indicating low environmental influence on the expression of all the traits. The seed yield per plant exhibited the high estimates for heritability and high values for genetic advance as the percent of mean (GAM) indicating significance of both genetic as well as environmental effect on these traits and effectively controlled by additive genes and improvement of these characters is possible through simple selection. Further, it may be suggested that on the basis of mean performance and the characters which were found positively associated viz., test weight, no of tillers and no of productive tillers may be criteria for selection. Whereas, based on diversity estimates and subsequent clustering also useful for selecting diverse parents (cluster I & V) for employing hybridization techniques to get transgressive segregants for desirable traits.

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