IJBSM September 2023, 14(9):1278-1283 Print ISSN 0976-3988 Online ISSN 0976-4038 Article AR3880b

Research Article Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2023.3880b

Genetic Variability of Finger Millet (*Eleusine coracana* (L.) Gaertn) Genotypes on Agro-Morphological Traits

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ABSTRACT

The present study was conducted during *kharif* 2019 (July–October)at the field of All India Coordinated Small Millets Improvement Project, College of Agriculture, Rewa (M.P.), India. Thirty-two (32) genotypes were evaluated for estimation of genetic variability, heritability and genetic advance for yield and yield contributing traits. The finger millet genotypes were sown in randomized block design with three replications. The results revealed that the values of phenotypic coefficients of variability were greater than genotypic coefficients of variability for all the traits studied. Moderate magnitude of PCV and GCV was recorded for number of tillers followed by flag leaf width, flag leaf length, 1000-grain weight, biological yield plant^{-1}, and grain yield plant^{-1}. The analysis of variance revealed that highly significant differences were recorded among the genotypes for all the studied characters, which indicate the presence of wide range of variability among genotypes and scope of selection for improvement. The high heritability coupled with high genetic advance as percentage of mean was recorded for flag leaf length, biological yield plant^{-1}, grain yield plant^{-1}, flag leaf width and 1000-grain weight. It forces to conclude that these characters are governed by additive gene action and phenotypic selection based on these traits in the segregating generations would likely to be more effective. In addition to the genetic variability, knowledge on heritability and expected genetic advance helps the breeder to employ the suitable breeding strategy.

KEYWORDS: Finger millet, genetic variability, heritability, genetic advance, breeding

***Citation* (VANCOUVER):** Yadav et al., Genetic Variability of Finger Millet (*Eleusine coracana* (L.) Gaertn) Genotypes on Agro-Morphological Traits. *International Journal of Bio-resource and Stress Management,* 2023; 14(9), 1278-1283. HTTPS://DOI.ORG/10.23910/1.2023.3880b.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 04th July 2023 RECEIVED in revised form on 03rd August 2023 ACCEPTED in final form on 15th September 2023 PUBLISHED on 24th September 2023

1. INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn) is an annual *kharif* crop and knows as African millet and Ragi. It is self-pollinated tetraploid species (2n=4x=36, AABB), belong to family poaceae and the genus *Eleusine* and plant mainly grown in two major continents, Africa and Asia for both grain and forage purpose (Sood et al., 2017; Sood et al., 2019). The name finger millet was coined from its morphological appearance of fingers/spikes, which look like human fingers. From the cultivation point of view, it is the sixth largest crop mainly among the rural populations of Africa and India and fourth important crop among millets globally (Ceasaret al., 2018). Among the various millets, finger millet ranks fourth on a global scale of production next tosorghum pearl and foxtail millet (Maharajan et al., 2019). It serves as a food-security crop because ofits high nutritional value and excellent storage qualities (Ramashia et al., 2018). Finger millet is being Used as food (grains) in developing countries and as animal Feed (straw) in developed countries indicating that it is considered as a poor man's food (Ceasar et al., 2018; Wambi et al., 2020).

Finger millet is highly nutritious crop as its grain contains 65–75% carbohydrates, 2.5–3.5% minerals, 5–8% protein, 15–20% dietary fiber (Chetan and Malleshi, 2007). The grains of finger millet are rich in fiber, protein, minerals has low glycemic index which helps to manage diabetes and blood pressure. Its calcium (Ca) content (344 mg 100 g^{-1}) is tenfold higher than wheat (*Triticum aestivum*), maize (*Zea mays*), and rice (*Oryza sativa*) and three times higher than milk (Shobana et al., 2013; Kumar et al., 2016). Millets are suitable staples when focusing on the food and nutritional security of the common people (Tiwari et al., 2022, Yadav et al., 2023a)

The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential for any successful plant breeding programmed (Jain et al., 2022; Sharma et al., 2022). The utilization of any species in a breeding programme depends upon its genetic diversity and adaptability in different environments (Rai and Jat, 2022). Genetic improvement through conventional breeding approaches depends mainly on the availability of diverse germplasm and presence of enormous genetic variability. The characterization and evaluation are the important pre-requisites for effective utilization of germplasm and also to identify sources of useful genes and superior genotypes. The genotypic co-efficient of variation estimates the heritable variability, while phenotypic co-efficient measures the role of environment on the Genotype. Hence, selection depends on heritability, selection intensity, and the genetic advance of traits (Barfa et al., 2017, Ningwal et al., 2023a, Ningwal et al., 2023b). Heritability measures the notch of semblance between the phenotypic and breeding worth. Genetic advance is the enhancement in the mean of selection personal over the base populace. Therefore, study of genetic variability of grain yield and its component characters among different varieties provides a strong basis for selection of desirable genotypes for augmentation of yield and other agronomic characters. In recent, mostly conventional breeding programme used with biotechnological methods for crop plant improvement (Asati et al., 2022, Yadav et al., 2023b, Yadav et al., 2023c). The objective of the current study was to identify the best genotypes as parents for further breeding programme based on the genetic variability of various finger millet genotypes based on their agro-morphological characteristics.

2. MATERIALS AND METHODS

The investigation was carried out to know the genetic variability, heritability and genetic advance analysis of 32 finger millet genotypes. The experiment was carried out during *kharif* (July–October) season 2019 at experimental area of All India Coordinated Small Millets Improvement Project, College of Agriculture, Rewa (M.P.). All the 32 genotypes were screened under field conditions by adopting randomized block design with three replications. Each entry was planted in a plot size of 2.25×3.0 m^2 accommodating 10 rows of 3 m length, keeping row-to-row and plant-to-plant distance of 22.5×10 cm^2, respectively. All the recommended package of practices was followed.

Observations were recorded from five randomly selected plants in each accession for 12 characters viz., days to 50% flowering, days to maturity, plant height, number of tillers $plant^{-1}$, flag leaf length, flag leaf width, peduncle length, ear length, biological yield per plant, harvest index, 1000 grain weight and grain yield per plant. The data were subjected to analysis of variance according to the method recommended by Panse and Sukhatme (1985). Phenotypic and genotypic coefficients of variation were computed according to the method suggested by Burton (1952). Heritability on broad sense was calculated as per formula given by Allard (1960). Genetic advance was expressed by using the formula suggested by Johnson et al. (1955) (Table 1).

3. RESULTS AND DISCUSSION

3.1. Genetic parameters of variability

Genetic variability studies provide basic information regarding the genetic parameters of the genotypes based on which breeding methods are constituted for further crop improvement. These studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitivity of crop to environment,

Table 1: List of finger millet genotypes used in the study

Sl. No.	Name of genotype	S.No.	Name of genotype
1.	KWFM-47	17.	RAUF21
2.	KOPN-1112	18.	DPLN-2
3.	GPU-100	19.	DHFM4-9
4.	GPU-101	20.	DHFM9-5
5.	VL-399	21.	OEB-608
6.	VL-400	22.	PPR-1082
7.	TNEc-1302	23.	PPR-1091
8.	TNEc-1311	24.	KMR-703
9.	PR-1643	25.	KMR-704
10.	PR-1506	26.	VR-1112
11.	BR 14-1	27.	VR-1125
12.	BR 14-2	28.	LOCAL CHECK
13.	PRS-38	29.	VL-376
14.	PRSW43	30.	GPU-67
15.	IIMR-R18-5538	31.	GPU-45
16.	IIMR-R18-5725	32.	PR-202

Table 2: Analysis of variance (ANOVA) for 12 characters in Finger millet

Sl. No.	Characters	Replications	Treatments	Error
	Degree of freedom	2	31	62
1.	Days to 50% flowering	5.71	173.50***	10.97
2.	Days to maturity	7.40	182.74***	10.12
3.	Plant height	1.53	260.61***	12.04
4.	No. of tillers plant^{-1}	0.00072	0.12***	0.031
5.	Flag leaf length	3.61	66.15***	4.48
6.	Flag leaf width	0.0020	0.13***	0.011
7.	Peduncle length	0.87	19.41***	3.98
8.	Ear length	0.92	2.89***	0.21
9.	Biological yield	2.32	41.74***	3.07
10.	Harvest index	4.84	26.62***	3.41
11.	1000 grain weight	0.0066	0.28***	0.038
12.	Grain yield plant^{-1}	0.28	2.39***	0.17

***: Significant at (p=0.01) level of significance

heritability of the character, genetic advance and genetic divergence. The analysis of variance showed a wide range of variation and significant differences for all the characters under study, indicating the presence of adequate variability for further improvement. The mean sum of squares due to genotypes was significant for all the characters studied (Table 2). The estimates of mean, range, phenotypic variance, and genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean are presented in table 3.

Mean performance of genotypes in respect of twelve characters under study have been presented in table 3. The higher grain yield per plant was exhibited by GPU-100, BR14-2, TNEc-1311 and VR-1125, while PR-1506 exhibited highest harvest index and lowest ear length and flag leaf length. Highest test weight was recorded by DHFM9-5 and highest biological yield recorded by VR-1125. Similarly higher number of tillers was recorded by

Table 3: Estimation of genetic parameters for different quantitative characters in Finger millet

Sl. No.	Characters	Mean	Range		PCV	GCV	h^2 (bs) %	GA as% of mean
			Minimum	Maximum				
1.	Days to 50% flowering	73.18	59.00	91.33	11.02	10.05	83	18.89
2.	Days to maturity	106.43	92.66	123.33	7.72	7.12	85	13.53
3.	Plant height (cm)	107.28	84.76	127.03	9.08	8.48	87	16.33
4.	No. of tillers plant^{-1}	1.51	1.03	1.86	16.74	11.91	50	17.47
5.	Flag leaf length (cm)	30.79	21.80	39.93	16.24	14.72	82	27.47
6.	Flag leaf width (cm)	1.40	1.08	1.81	16.57	14.68	78	26.80
7.	Peduncle length (cm)	23.22	18.50	28.26	13.00	9.76	56	15.10
8.	Ear length (cm)	8.74	6.73	10.26	12.05	10.81	80	19.97
9.	1000 grain weight (g)	2.35	1.70	3.00	14.65	12.07	67	20.48
10.	Biological yield plant^{-1} (g)	28.08	22.00	38.00	14.22	12.78	80	23.66
11.	Harvest index	25.31	19.89	30.80	13.19	10.98	69	18.85
12.	Grain yield plant^{-1} (g)	7.04	5.66	9.06	13.58	12.19	80	22.57

VR-1125. Maximum days to 50% flowering and lowest peduncle length exhibited by GPU-67. Maximum days to maturity recorded by PR-202. Maximum plant height recorded by TNEc-1311. Highest ear length recorded by DHFM4-9. Hence, these genotypes had highest value of above-mentioned desirable characters. These genotypes may be used as donor parent for transferring these characters in recipient parent in combination breeding programme.

3.1.1. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

Moderate magnitude of PCV was recordedfornumber of tillers followed by flag leaf width, flag leaf length, 1000 grain weight, biological yield per plant, grain yield per plant, harvest index, peduncle length, ear length and days to 50% flowering. Similar results were also reported by Keerthana et al. (2019) for grain yield per plant and number of tillers per plant and Singh et al. (2023) for peduncle length and 1000 grain weight.The low estimate of PCV was recorded for plant height and days to maturity.Similar findings were reported by Ganapathy et al. (2011) and Jahnavi and Lal (2023) for low PCV of days to maturity and Opole et al. (2018) (Figure 1).

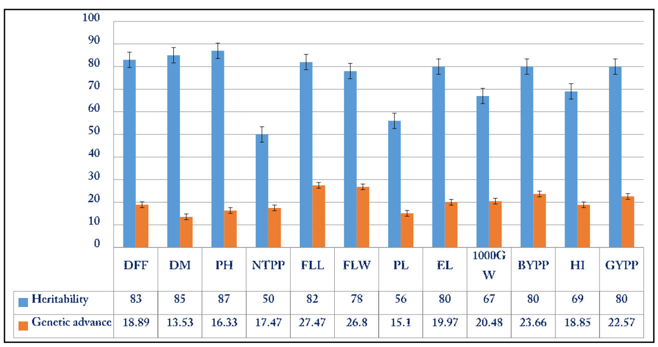

Figure 1: Phenotypic coefficient of variation, genotypic coefficient of variation

Similarly, moderate magnitudes of GCV were recorded for flag leaf length followed by flag leaf width, biological yield plant^{-1}, grain yield plant^{-1} and 1000 grain weight, tillers per plant, harvest index and days to 50% flowering. Similar findings were also reported by Singamsetti et al. (2018), Keerthana et al. (2019), while the low estimates of GCV were recorded by peduncle length, plant height, days to maturity. Similar results were also reported by Ganapathy et al. (2011) for days to maturity, Jahnavi and Lal (2023) for days to maturity and peduncle length, Karad and Patil (2013) and Opole et al. (2018).

The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all characters. This indicates the effect of environmental factors on these characters. This shows presence of large variation in the genotypes for these characters. Therefore, simple selection can be obtained for the improvement of these characters.

3.1.2. Heritability and genetic advance

The higher heritability estimates were recorded for plant height, days to maturity, days to 50% flowering, flag leaf length, ear length, biological yield per plant, grain yield per plant, flag leaf width, harvest index, 1000-grain weight. It indicated that these characters inherited from generation to generation without interference of environmental effects. High values indicate that heritability may be due to higher contribution of genotypic component. The similar results were also reported by Ganapathy et al. (2011), Priyadharshini et al. (2011) for plant height, harvest index and grain yield plant^{-1} and Jahnavi and Lal (2023) for plant height, days to maturity, days to 50% flowering, grain yield per plant, flag leaf width, harvest index, 1000-grain weight. While peduncle length and tillers plant^{-1} recorded moderate estimates of heritability (Figure 2).

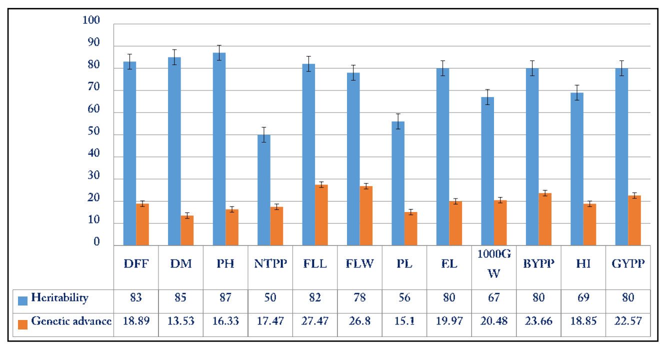

Figure 2: Heritability (broad sense) and genetic advance

The high heritability coupled with high genetic advance as percentage of mean was recorded for flag leaf length, biological yield plant^{-1}, grain yield plant^{-1}, flag leaf width and 1000-grain weight. It forces to conclude that these characters are governed by additive gene action. The similar results were also reported by Karad and Patil (2013) and Jahnavi and Lal (2023).

The characters plant height, days to maturity, days to 50% flowering, ear length, harvest index showed high heritability coupled with moderate genetic advance as percentage of mean. High heritability accompanied with moderate genetic advance % of mean indicated that the genotype, under study were diverse with innense genetic potential and further improvement in these traits are possible by practicing simple selection technique, similar result were also obtained by Priyadharshini et al. (2011), Karad and Patil (2013), Jahnavi and Lal (2023), while moderate heritability with moderate genetic advance recorded for peduncle length, tillers plant^{-1}.

4. CONCLUSION

The genotypes GPU-100, BR14-2 and TNEc-1311 showed better performance for yield components and can be used as parents in future improvement programme. The GCV and PCV were both observed to be good for biological yield plant^{-1}, grain yield plant^{-1}, tillers plant^{-1}. Thus, these characters provide a good source of variation and hence they are useful in improvement programme for finger millet. High heritability estimates were obtained for almost all the characters, indicating less influence from environmental effects.

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