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Characterization and evaluation of finger millet (*Eleusine coracana* L. Gaertn) genotypes for qualitative and quantitative traits

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Abstract

The research focused on studying the quantitative and qualitative traits of finger millet in order to characterise and evaluate the variability among 64 finger millet accessions. The research was carried out during the *Kharif* season of 2022 at the Instructional Cum Research Farm, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, IGKV, Raipur (Chhattisgarh), with an augmented complete block design as experimental framework. Observations were documented for 3 qualitative and 14 quantitative traits at different plant growth stages as per the guidelines for the test of conduct of DUS on Finger millet by PPV and FRA. For each trait, the analysis of variance revealed profoundly significant differences among the 64 genotypes. Among the accessions that were examined, traits like a semi-compact ear (30%), copper-coloured seeds (44%), and pigmentation at the leaf juncture (55%), were observed to be ubiquitous. Whereas, regarding quantitative traits, medium span for days to 50% flowering (72%), early maturation (92%), medium range of plant height (89%), flag leaf length (52%), finger length (46%), finger number (94%), and test weight (52%) were noticed to be more prevalent. A high range of biological and fodder yield was noticed to be prevalent. The highest GCV (19.29%) and PCV (22.10%) values were recorded for the trait grain yield. The quantitative traits that disclosed high heritability coupled with high genetic advance as percent of the mean were days to 50% flowering, finger length, grain yield, fodder yield, and biological yield. This indicated that the aforementioned characteristics were inherited through additive gene action, and direct selection may be advantageous for selection in upcoming breeding programmes. Overall, the research emphasizes the presence of variability in finger millet traits, showcasing the possibilities for selection and enhancement.

Keywords: Characterization, ANOVA, PCV, GCV and heritability

Introduction

Eleusine coracana (L.) Gaertn., sometimes referred to as African millet or Ragi, is a member of the Graminae or Poaceae family. Its common name, "Finger Millet," refers to the branching of the panicle that resembles fingers. It is a self-pollinating tetraploid ($2n = 36$) plant. There are eight diploid and tetraploid species of annual and perennial herbs in the genus *Eleusine* (Vidhate *et al.*, 2020) [16]. Finger millet is a sturdy, tufted, tillering annual grass that develops typically in 75–140 days and grows to a height of 30–150 cm. Among the world's millets, finger millet ranks fourth in significance, behind sorghum, pearl millet, and foxtail millet, and is nutritionally equivalent to rice and wheat (Mirza and Marla, 2019) [9]. It accounts for around 12% of the world's millet acreage and is grown in more than 25 nations across the African and Asian continents (Anjaneyulu *et al.*, 2014) [1]. 4.5 million tonnes of grain are produced annually from finger millet, which is grown on 5 million hectares of land worldwide. With a yield of 1238.7 thousand tonnes and a productivity of 1390 kg ha⁻¹, finger millet was grown on 890.9 thousand hectares of land in India (Anonymous, 2021). Finger millet is a resilient crop suitable for a wide range of environments, spanning from sea level to altitudes of approximately 2400m. It serves as a primary food source in regions prone to drought, making it a crucial element for ensuring food security. Notably, finger millet offers significant nutritional benefits, including a protein content ranging from 6% to 11%, calcium levels of 1.8g/kg to 4.8g/kg, iron concentrations of 21.7mg/kg to 65.23mg/kg, and zinc quantities of 16.5mg/kg to 25 mg/kg. Finger millet, also recognised as nutritious millet, is cultivated for various purposes such as food, fodder, and medicinal applications due to its remarkable nutritional value.

Characterization as well as evaluation are critical steps in maximising germplasm utilisation as well as recognising valuable genetic resources. Starting any systematic breeding effort requires a thorough understanding of the type and extent of genetic variety available in the gene pool, since the presence of significant genetic variability in the base material increases the likelihood that desirable plant types will evolve. (Bhavsar *et al.*, 2021)^[6].

2. Materials and Methods

The present investigation was carried out at the Instructional cum Research Farm of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar (C.G.). A specified portion of the field was selected, and good tilth was established by harrowing and ploughing. The experiment was carried out using a six-block augmented complete block design. Each block has 10 test accessions and 4 checks (IR 01, C.G. Ragi 02, GPU 28, and GPU 67), which together make up a total of 14 entries that are distributed at random within each block. Thus, the total entries were 64, including four checks. Two rows, each measuring three metres in length and spaced 22.5 cm apart with a 10 cm plant-to-plant gap, made up each accession. The crop was sown on August 27, 2022. The seeds were directly line-sown, and all suggested cultural procedures were used to raise a fruitful crop during the season.

During the experiment, data was collected by randomly selecting five plants from each plot at the ideal stage of growth for finger millet, based on specific DUS (Distinctness, Uniformity, and Stability) characteristics established by PPV&FRA (Plant Variety Protection and Farmer's Rights Authority). A total of 17 traits were selected for evaluation, including 14 quantitative traits and 3 qualitative traits. The average of all the plants for a particular trait was evaluated in each replication (Panse and Sukhathme, 1967)^[10]. The method proposed by Johnson *et al.* in 1955^[17] was employed to estimate the genotypic and phenotypic variance by utilising the mean square values obtained from the ANOVA table. By employing the Burton method, the phenotypic and genotypic coefficients of variance were determined. The heritability percentage (in the broad sense) was calculated using the method outlined by Allard in 1960, while the categorization of traits as having high, moderate, or low heritability was based on the approach described by Robinson *et al.* in 1949^[13]. The genetic advance was estimated using the methodology proposed by Johnson *et al.* in 1955^[17] and expressed as a percentage of the mean. The traits were classified as having high, moderate, or low genetic advance in accordance with the method proposed by Johnson *et al.*, (1955)^[17].

3. Results and Discussions

Qualitative traits

The qualitative traits that studied under this research were plant pigmentation at the junction of the leaves, ear shape, and seed colour. The presence or absence of pigmentation in the nodal region can serve as a characteristic for identifying different genotypes during the process of selection. Out of the 64 genotypes examined, 35 genotypes (55%) showed purple pigmentation at the leaf juncture, while the remaining 29 genotypes (45%) displayed green pigmentation, indicating the absence of pigmentation. The ear shape of finger millet was categorised into five types: compact, semi-compact, fist,

open, and droopy. Among the 64 finger millet genotypes studied, approximately 30% (19 genotypes) had a semi-compact shape, 25% (16 genotypes) displayed a compact shape, 23% (15 genotypes) showed an open shape, 19% (12 genotypes) exhibited a fist shape, and only 3% (2 genotypes) possessed a droopy shape. Seed colour was classified into four categories: white, light brown, copper brown, and dark brown. Among the genotypes studied, 22 genotypes (34%) had light brown seeds, 28 genotypes (44%) had copper brown seeds, 13 genotypes (20%) had dark brown seeds, and 1 genotype (2%) had black seeds, which was considered an exceptional case. None of the genotypes exhibited grains with a white colour. Similar results were documented by Basavaraj *et al.* (2021)^[4]; Patil *et al.* (2019)^[11].

Quantitative traits

Under this study, 14 quantitative characters were evaluated among the 64 genotypes of finger millet. The following discussion covers the findings for each character. For the trait days to 50% flowering, observed values existed in a range of 53 (ICO 477764, ICO 587981) to 103 (IR-01) DAS. Among 64 genotypes, 7 genotypes (11% of the total) showed early flowering, while 46 genotypes (72% of the total) required medium span for flowering. Furthermore, 11 genotypes (17% of the total) exhibited late flowering. Days to maturity spanned from 82 (ICO 587981) days to 131 (IR-01) days. Among the accessions assessed, 59 genotypes were classified as early (92%), 4 genotypes as medium (6%), and 1 genotype as late mature (2%). In this research most of the genotypes were early maturing which shows their ability to thrive in less rainfall conditions. A decrease in flowering and maturation intervals are manifestations of a crop's ability to thrive in conditions of low or erratic rainfall availability, and they can produce significant yields where other commonly grown cereal crops are unable to do so. The trait plant height at maturity ranged from 68.24 (ICO 477382) cm to 121.92 (GEC 238) cm. Of the 64 genotypes, six were short (9%), 57 were medium (89%), and one was tall (2%). The length of the flag leaf existed in a range of 21cm (GEC 251) to 37.58cm (GEC 370). Out of the evaluated accessions, 52% were classified as medium (33 genotypes), while the remaining 48% were classified as long (31 genotypes). Flag leaf width measurements ranged from 0.64 cm (observed in GEC 251 and GEC 46) to 1.58 cm (observed in GEC 170). Among the accessions investigated, 51 genotypes were with narrow flag leaf (80%), 13 genotypes were with medium flag leaf width (20%). The range of peduncle length measurements varied from 5.32 cm (observed in GEC 350) to 14.28 cm (observed in GEC 5). Out of 64 accessions studied, 21 genotypes (approximately 33%) had a peduncle length classified as very short, while 43 genotypes (about 67%) were classified as having a short peduncle length. Finger length and width determine ear size and are regarded as being particularly important because they harbour the grains above them and have an effect on a genotype's ability to act as a sink. The finger length spanned from 3.86 cm (GEC 350) to 12.12 cm (GEC 5). There were nine genotypes with short fingers (12% of the total), 34 genotypes with medium fingers (46% of the total), and 31 genotypes with long fingers (42%). The range of the number of fingers on the main ear varied from 4.8 (ICO 477831) to 8.6 (ICO 476959-X, ICO 476921). 1 genotype (1%) had a low number of fingers, 60 genotypes (94%) had a medium finger count, and 3 genotypes (5%) had a high

number of fingers. The number of grains per ear ranged from 895 (GEC 252) to 3239 (ICO 476959-X). Among 64 genotypes assessed, 28 genotypes (44%) had a high number of grains per ear and 36 genotypes (56%) had a low number of grains per ear. The fodder yield spanned the range of 27.51 q/ha (ICO 477312) to 69.41 q/ha (IR-01). Among all the genotypes analyzed, 33 genotypes (52%) demonstrated high fodder yield, whereas 31 genotypes (48%) showed low fodder yield. The test weight spanned the range of 1.83 g (ICO 477159) to 3.84 g (ICO 476877). Out of the accessions assessed, 2 genotypes (equivalent to 3%) displayed low test weight, while 33 genotypes (representing 52%) exhibited moderate test weight, and 29 genotypes (making up 45%) demonstrated high test weight. The harvest index ranged from 16.51% (GEC 370) to 38.78% (GEC 31). Among 64 genotypes examined, 28 genotypes (representing 44%) had a high harvest index, while 36 genotypes (representing 56%) had a low harvest index. The biological yield varied from 35.26 q/ha (ICO 477312) to 91.84 q/ha (IR-01). Low biological yield was observed in 34 genotypes, accounting for 53% of the total, while high biological yield was exhibited by 30 genotypes, representing 47% of the sample. The grain yield varied between 8.68 (ICO 477312) and 26.19 (GPU 28). Out of the genotypes analyzed, 27 (42%) exhibited high grain yield, while 37 genotypes (58%) displayed low grain yield. Similar findings were documented by Gopal *et al.* (2021) [8] and Patil *et al.* (2019) [11]. The adjusted mean of block differences and the mean of checks for all the studied traits in germplasm accessions are addressed in table 2.

All of the characters under study displayed significant mean sums of squares among block, check and test entries (Table 1). The diverse set of 64 finger millet genotypes displayed notable dissimilarities across various traits, indicating the presence of substantial genetic variation within the material. Conversely, comparable findings were made by Dhanalakshmi *et al.* (2013) [7], who discovered a significant difference in mean squares between treatments and checks, treatments per se, and check varieties.

Assessment of genetic variability parameters

The parameters for genetic variability were assessed and analyzed, as shown in Table 3. This analysis included the calculation of various parameters such as the mean, range, genotypic and phenotypic coefficients of variance (%), genetic advance as a percentage of the mean, and heritability in the broadest sense (%). The findings of the study showed that for all the traits analysed, PCV was higher than GCV. This indicates that the influence of the environment on the expression of genetic variability was significant and masked the genetic effects on the traits. The highest GCV (19.29%) and PCV (22.10%) values were recorded for the trait grain yield, whereas the lowest GCV (6.96%) and PCV (7.11%) values were found for the trait flag leaf length. The genetic parameters demonstrated moderate GCV coupled with moderate PCV for the characters: days to 50% flowering (12.39 and 12.42), flag leaf width (10.33 and 12.75), finger length (15.51 and 15.70), fodder yield (14.54 and 15.14), and biological yield (15.26 and 15.49), reflecting low genotype variability and the potential for future selection and improvement (Bezawele et al. 2007) [5]. Low GCV coupled with low PCV for the traits Days to maturity (8.16 and 8.27), Flag leaf length (7.45 and 7.59), and plant Height (6.96 and 7.11) indicate a narrow range of variability for these

traits and limit the scope for selection. Moderate GCV coupled with high PCV was noticed for the characters No. of grains per ear (15.87 and 21.64) and grain yield (19.29 and 22.10). Low GCV coupled with moderate PCV was noticed for peduncle length (9.24 and 10.34), number of fingers (9.23 and 11.17), and harvest index (8.68 and 11.40). In a similar way, low values of PCV and GCV for days to maturity were observed by Reddy *et al.*, 2013 [12] and Singamsetti *et al.*, 2018 [14]. Udamala *et al.*, 2020 [15], made comparable observations for GCV (days to 50% flowering, plant height, number of fingers, grain yield per plot, fodder yield per plant). Similar results for PCV (days to 50% flowering, finger length, number of fingers, fodder yield, harvest index, and test weight) were seen by Udamala *et al.*, 2020 [15].

The heritability of various quantitative traits was examined, revealing that days to flowering exhibited the highest heritability at 99.47%, while the number of grains per ear displayed the lowest heritability at 53.75%. Days to 50% flowering (99.47%), Days to maturity (97.22%), Flag leaf length (95.86%), Plant Height (96.36%), Flag leaf width (65.65%), Peduncle length (79.88%), Finger length (97.60%), Number of Fingers (68.23%), Test weight (61.93%), Fodder yield (92.27%), Biological yield (97.06%), and Grain yield (76.16%) were other characteristics that showed high heritability. These characters depicted their significance for selection. The traits of number of grains per ear (53.75%) and harvest index (57.98%) showed a medium range of heritability. Bhavsar *et al.*, (2020) [6] reported comparable outcomes in terms of various parameters such as days to 50% flowering, days to reach maturity, plant height, the number of fingers per ear head, and grain yield per plant. Similarly, Lad *et al.*, (2018) found similar results concerning days to 50% flowering, days to maturity, and finger length. Reddy *et al.*, (2013) [12] also observed similar trends in parameters such as traits days to 50% flowering, plant height, number of fingers per ear head, and days to maturity. The highest estimates for genetic advance as a percentage of mean observed in grain yield (34.67%), finger length (31.56%), biological yield (30.97%), fodder yield (28.77%), days to flowering (25.45%), and number of grains per ear (23.96%) whereas flag leaf length (14.04%), harvest index (13.61%), test weight (12.94%), flag leaf width (17.24%), peduncle length (17.01%), days to maturity (16.57%), plant height (15.07%), and number of fingers per ear (15.70%) were all observed to be moderate.

The combined assessment of heritability and genetic advance was deemed more valuable for evaluating traits compared to individual evaluation. The quantitative traits that exhibited high heritability and high genetic advance as percent of the mean were days to 50% flowering, finger length, grain yield, fodder yield, and biological yield. High heritability and high genetic advance as a percentage of the mean disclosed the presence of increased additive gene action in these traits, and selection would therefore be active in improving such traits. High heritability coupled with moderate genetic advance as percent of the mean was noticed in quantitative traits such as days to maturity, plant height, flag leaf length, flag leaf width, peduncle length, and number of fingers. Moderate heritability coupled with high genetic advance was observed in the trait of number of grains per ear. Moderate heritability coupled with moderate genetic advance was observed in the harvest index. None of the traits displayed low heritability or genetic advance. These findings concurred with studies by Udamala

et al. 2020 ^[15] (days to 50% flowering and grain yield), Bhavsar *et al.* (grain yield per plant), (days to 50% flowering, finger length, grain yield per plant), and Gopal *et al.* 2021 ^[8] (days to 50% flowering, finger length).

The analysis of variance revealed extremely significant differences among the 64 genotypes for each trait. The study demonstrated that all the traits displayed a substantial degree of variability, likely attributed to the diverse experimental

material used. The high heritability observed in the traits suggest that additive gene action plays a significant role. Additionally, the influence of the environment on character expression was evident, as indicated by slightly higher PCV values compared to GCV values. The safeguarding and further development of this germplasm is crucial, and a targeted improvement programme for finger millet may be implemented in the future.

Table 1: Mean squares for analysis of variance for check and test entries

Source of variation	Df	DF	DM	PH	FL L	FL W	PL	FL
Block	5	19.13**	16.42**	275.94**	8.68**	0.01**	2.51**	0.49**
Treat	63	189.05**	180.92**	157.08**	13.19**	0.03**	3.04**	3.05**
Checks	3	1500.33**	984.38**	654.20**	49.67**	0.03**	2.30**	7.05**
T. Entry	59	49.32**	46.95**	138.20**	10.70**	0.03**	3.31**	2.36**
Check vTest	1	4499.00**	5674.64**	-220.64**	50.86**	-0.01	-10.71**	31.58**
Error	15	0.33	1.71	1.95	0.19	0.002	0.24	0.02
Total	83	144.71	138.62	136.20	10.57	0.02	2.50	2.35
Source of variation	Df	No. F	G/E	TW	FY	BY	HI	GY
Block	5	1.15**	268777.4**	0.68**	97.22**	91.77**	40.39**	9.12**
Treat	63	1.11**	248366.5**	0.19**	137.60**	269.31**	19.87**	33.14**
Checks	3	9.84**	384994.7**	0.39**	222.02**	294.25**	21.06**	17.93**
T. Entry	59	0.62**	222305.2**	0.24**	75.00**	106.57**	21.19**	13.28**
Check vTest	1	3.88**	1376098.6**	-3.01**	3577.91**	9796.54**	-61.59**	1250.64**
Error	15	0.15	55363.6	0.03	3.74	2.69	3.87	3.13
Total	83	0.94	214716.0	0.19	110.98	210.43	18.21	26.27

*, ** significant at 5% and 1% level, respectively

Table 2: Comparison of mean, adjusted test mean, check mean and Standard error of 14 quantitative characters

Traits	Mean	Adjusted test mean	Check mean
DF	64.02	63.00	79.33
DM	94.76	93.62	111.88
PH	96.50	97.01	88.81
FL L	29.91	30.05	27.88
FL W	0.91	0.91	0.90
PL	10.47	10.46	10.59
FL	6.47	6.39	7.79
NoF	6.13	6.08	6.82
G/E	1598.58	1576.15	1935.09
TW	2.88	2.88	2.91
FY	45.94	44.91	61.48
BY	61.79	60.26	84.70
HI	26.61	26.45	28.97
GY	16.40	15.86	24.48

Table 3: Genetic variability parameters

Characters	Adj. Mean	Max	Min	Heritability (%)	Genetic advance at % mean	GCV %	PCV%
DF	64.02	53.00	103.00	99.47	25.45	12.39	12.42
DM	94.76	82.00	131.00	97.22	16.57	8.16	8.27
PH	96.50	68.24	121.92	96.36	15.07	7.45	7.59
FL L	29.91	21.00	37.58	95.86	14.04	6.96	7.11
FL W	0.91	0.64	1.58	65.65	17.24	10.33	12.75
PL	10.47	5.32	14.28	79.88	17.01	9.24	10.34
FL	6.47	3.86	12.12	97.60	31.56	15.51	15.70
NoF	6.13	4.80	8.60	68.23	15.70	9.23	11.17
G/E	1598.58	895.00	3239.00	53.75	23.96	15.87	21.64
TW	2.88	1.83	3.84	61.93	12.94	7.98	10.14
FY	45.94	27.51	69.41	92.27	28.77	14.54	15.14
BY	61.79	35.26	91.84	97.06	30.97	15.26	15.49
HI	26.61	16.51	38.78	57.98	13.61	8.68	11.40
GY	16.40	8.68	26.19	76.16	34.67	19.29	22.10

Key words: DF- Days to 50% flowering, DM- Days to maturity, PH- Plant height (cm), FLL-Flag leaf length (cm), FLW-Flag leaf width (cm), FL- Finger length (cm), NF-Number of fingers, G/E- Number of grains ear⁻¹, FY- Fodder yield (q ha⁻¹), GY- Grain yield (q ha⁻¹), HI- Harvest index(%), TW-Test weight (g), BY- Biological yield (q ha⁻¹); GCV-Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation

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