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Suryakant Sahu IGKV, Raipur, Chhattisgarh, India

Nomesh Kumar IGKV, Raipur, Chhattisgarh, India

Hemalata Rathiya IGKV, Raipur, Chhattisgarh, India

Bhagyasri Majhi IGKV, Raipur, Chhattisgarh, India

R. R. Kanwar IGKV, Raipur, Chhattisgarh, India

Prafull Kumar IGKV, Raipur, Chhattisgarh, India

Corresponding Author: Suryakant Sahu IGKV, Raipur, Chhattisgarh, India

Variability studies of little millet germplasm accessions under Bastar plateau for yield and adaptability

Suryakant Sahu, Nomesh Kumar, Hemalata Rathiya, Bhagyasri Majhi, R. R. Kanwar and Prafull Kumar

Abstract

The research was conducted on little millet (*Panicum sumatrense*) genotypes at New Upland Research Cum Instructional Farm, Lamker under the S.G. College of Agriculture and Research Station, Jagdalpur, Bastar (C.G.) during *Kharif* 2022. The research focused on studying the qualitative and quantitative traits of little millet in order to characterize and evaluate the variability among 28 little millet genotypes. The analysis of variance showed highly significant differences among the 28 genotypes for each trait. The variability analysis revealed that for the parameters flag leaf width, flag leaf length, fodder yield per plot, days to 50% flowering and number of productive tillers, high estimates of GCV and PCV were observed, showing the importance of selection for improving crop. The high heritability along with high genetic advance as percent of mean was recorded on the characters like days to 50% flowering, days to maturity, plant height, panicle length, fodder yield, number of productive tillers, flag leaf width, test weight, flag leaf length and grain yield per plot.

Keywords: Analysis of variance and Genetic Variability

Introduction

One of the underutilized small millets, little millet (Panicum sumatrense Roth. ex. Roem. and Schultz), is currently grown primarily in India and Nepal. It is thought to have originated in South East Asia. India is the world's largest producer, generating about 0.12 million tonnes annually. Karnataka, Andhra Pradesh, Tamil Nadu, Orissa, Bihar, Maharashtra, and Madhya Pradesh are among the states where it is grown extensively (Meena *et al.*, 2021)^[15]. Due to the presence of cleistogamous flowers, this crop is largely self-pollinated and is a member of the Poaceae family. With a chromosomal number of 2n = 4x = 36, little millet is an allotetraploid crop. It is the first food ingested by tribal people since it grows quickly, and it is a staple food for millions of people (Selvi et al., 2014)^[22]. The inflorescence of little millet is a panicle that is constricted or thyrsiform, 15–45 cm long, and 1–5 cm wide (Seetharam et al., 2003) ^[21]. The 2-3.5 mm long spikelet is persistent (Bor, 1960)^[4]. When panicle branches reach maturity, they appear scabrous and drooping. At the ends of the branches, spikelets develop on uneven pedicels, but they are solitary. A spikelet has two small blooms on it. The upper one, which lacks rachilla extension, is fertile or bisexual and the lower one is sterile. The fertile flower is enclosed by the lemma II and its Palea, while the staminate or sterile flower is enclosed by the lemma I and its palea. (Sundararaj and Thulasidas, 1976)^[23]. The spikelets are elliptical, dorsally compressed, and acut. It has three 1.5 mm long anthers. The glume that reaches the floret's apex is thinner than the fertile lemma; the lower glume is ovate, 0.7-1.2 mm long, membranous, without keels, 1-3 veined. In the lower glume, the lateral vein is missing, and its apex is acute. The upper glume is larger than the lower glume and also ovate and without keel, 11–15 veins are present (Nanda and Agrawal, 2008) ^[17]. In India, small millets are grown over an area of 6,19,000 ha, producing 4,41,000 tons (Gowari and Shivkumar, 2020)^[8]. In India's tribal regions of Madhya Pradesh, Chhattisgarh, Gujarat, Maharashtra, Odisha, and Andhra Pradesh, little millet is an important crop, 1.42 lakh tons of little millet was produced in India (Anonymous 2021)^[2]. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they are grown. Selection is also effective when there is presence of ample genetic variability among the individuals in a population. Hence, insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. Greater the variation in the material better is the chance for selecting promising and desired types.

The genetic variability is calculated from phenotypic observations, which are the results of interaction of genotypes and environment. (Patel *et al.* 2018) ^[18]. Any systematic breeding program should begin with a thorough understanding of the type and degree of genetic variability present in the gene pool. Therefore, an effort was made to determine the degree of diversity and character association for yield-contributing traits in 28 genotypes of little millet through the study of genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance that may help to formulate appropriate traits selection criteria and, consequently, genotypes for improvement in this crop.

Materials and Methods

The experiment was carried out at New Upland Research Cum Instructional Farm, Lamker under the S.G. College of Agriculture and Research Station, Jagdalpur, Bastar (C.G.) during Kharif 2022. There were 28 little millet genotypes including 1 check variety were studied under Randomized Block Design for 15 yield and morphological traits to find the elite genotypes that were producing high yields. Each genotype was planted with 22.5 cm×10 cm spacing between rows and plant. The standard agronomic practices were adopted for normal growth and development of crop. The observations were recorded as per the descriptor of IBPGR and PPV & FRA Rome. The average values were computed as treatment mean under each replication. Phenotypic and genotypic variability were calculated as per method proposed by Burton (1952)^[6]. Heritability estimates in cultivated plants were as suggested by Lush (1940) ^[13]. Genetic advance was worked out by using the formula suggested by Johnson et al. (1955) [11].

Results and Discussion Qualitative traits

All the genotypes were screened for various qualitative traits such as inflorescence shape, panicle compactness, seed shape and seed colour. With respect to inflorescence shape, genotypes were categorised as arched, diffused and globouselliptic. Out of 28 genotypes, 19 genotypes were arched (68%) whereas 9 genotypes showed diffused shape (32%). Character panicle compactness was easily distinguished in the field and was categorized into compact, intermediate and open. Out of 28 genotypes, 7 genotypes were compact (25%), 14 genotypes were intermediate (50%) and 7 were open (25%). With respect to seed colour, it was categorized as straw white/ cream (36%), golden yellow (14%), light brown (0%), brown (11%), grey (36%), and dark grey (3%). Seed shape was categorized in elliptical and oval shape. Out of 28 genotypes, in 20 genotypes seed shape was found to be elliptical (71%) and 8 genotypes showed oval shape (29%).

Quantitative traits

Under this study, 10 quantitative characters were evaluated among 28 genotypes of little millet. The analysis of variance revealed highly significant differences among the genotypes for all the characters under study. The following discussion covers the findings for each character. Days to 50% flowering varied from medium (40-50 days) to late (>50 days), Out of all 28 genotypes, 4 genotypes were medium and 25 genotypes were late. Maximum value for days to 50% flowering was recorded for IIMR LM- R21- 1001 (88 days) followed by WV

168(87 days) while, Minimum value was recorded for VS 33 (44 days). Days to maturity ranged from medium 72 to 119 days with a mean value of 100.85 Out of all 28 genotypes, earliest days to maturity was attained by VS 33 (72 days) followed by TNPSu 242 (75 days) while longest days to maturity was attained by WV 168 (119 days) followed by OLM 203 (118 days). Plant height varied from semi-dwarf (80.0-120.0 cm) to very tall (>160.0 cm). Among all, 7 genotypes were semi-dwarf (80.0-120 cm), 15 genotypes were tall (120.1-160.0 cm) and 6 genotypes were very tall (>160 cm). Minimum plant height was recorded for VS 33 (103.55 cm) followed by DLM 310 (104.89 cm) and maximum plant height was recorded for BL 2021-2 (173.26 cm) followed by IIMR LM-R21-1001 (172.07 cm). For No. of productive tillers, the 28 genotypes varied from DHLM 13-3 with a value of 1.07, while BULM-18-21 recorded with a value of 2.47. Maximum number of effective tillers were recorded for BULM-18-21 (2.47) followed by BL 6 (2.20) and VS 38 (2.13). Panicle length varied from short to medium (20.1-30 cm) to long (40.1-50 cm). Out of 28 genotypes, 6 genotypes were short to medium (20.1 - 30 cm), 18 genotypes were medium (30.1-40 cm)) and 4 genotypes were long (40.1-50 cm). Minimum panicle length was recorded for VS 33 (24.36 cm) followed by DLM 310 (25.33 cm) and maximum panicle length was recorded for BL 2021-2 (46.04 cm) followed by WV 146 (42.29 cm). For the character flag leaf length, the 28 genotypes varied from short (<20 cm) to medium (20.1-30 cm) and long (>30 cm). Out of 28 genotypes, 3 genotypes were having short flag leaf length, 15 genotypes were having medium flag leaf length and 10 genotypes were having long flag leaf length. Maximum flag leaf length was recorded in WV 146 (45.04 cm) and minimum flag leaf length was recorded in BULM-18-21 (17.67 cm). For flag leaf width, out of 28 genotypes, 17 genotypes were of narrow width (<1 cm) and 11 genotypes were of medium width (1-2 cm) whereas wide width genotypes were not found in current population. Maximum flag leaf width was recorded for BULM 18- 174 (1.62 cm) followed by BL 2021- 2 (1.60 cm) and minimum was recorded for VS 33 (0.71 cm) followed by TNPSu 242 (0.75) and DLM 310 (0.74 cm). Test weight varied from low (<2.0 g) to high (>3.0 g). Among all 28 genotypes, 3 genotypes were low (<2.0 g), 24 genotypes were medium (2.0-3.0 g) and 1 genotype was high (>3 g). Maximum test weight was recorded for IIMR LM- 8004 (3.06 g) and minimum test weight was observed in WV 168 and WV 146 (1.96 g). Among tested genotypes, the lowest fodder yield plot⁻¹ was recorded in VS 33 (1.43 kg) and highest in GPUL 13 (5.73 kg). The genotypes viz., BL 4 (local check), BULM- 18- 21, DPLN 1, WV 168, VS 38, IIMR LM- R21-1001 and IIMR LM- R21- 1158 recorded relatively higher fodder yield plot⁻¹. Seventeen genotypes recorded high fodder yield plot⁻¹ than the general mean of fodder yield (4.24 kg). Grain yield per plant ranged from 0.47 kg to 0.93 kg with a mean value of 0.73 kg. The highest yielding genotype was GPUL 13 (0.93 kg) whereas the genotype DHLM 13-3 (0.47 kg) manifested the lowest grain yield plot⁻¹. Fifteen genotypes recorded high grain yield plot⁻¹ than the general mean of grain yield.

For all the characters under study, phenotypic variances were higher than the corresponding genotypic variances showing the environmental factors influence the expression. The estimates of phenotypic coefficient of variation are higher than genotypic coefficient of variation for all the character. All the traits ranged from 14.04 to 29.99. High PCV was recorded for flag leaf width (29.99) followed by flag leaf length (29.66), fodder yield per plot (27.23), days to 50% flowering (21.38) and number of productive tillers (20.71). Similarly, the moderate estimates of PCV were recorded for grain yield per plot (18.35) followed by panicle length (16.17), test weight (15.86), plant height (15.18) and days to maturity (14.04). Genotypic coefficients of variation (GCV) were ranged from 12.56 to 27.93. High GCV was recorded for flag leaf width (27.93) followed by flag leaf length (27.92), fodder yield per plot (26.22) and days to 50% Flowering (21.24). Similarly, the moderate estimates of PCV were recorded for number of productive tillers (18.55) followed by grain yield per plot (17.28), plant height (14.23), panicle length (14.18), days to maturity (13.93) and test weight Similar results were reported earlier by (12.56). Nirmalakumari et al. (2010)^[25] Patil and Mane (2013)^[19], Brunda et al. (2014) [5] and Nandini et al. (2016) [26] respectively in little millet for panicle length; Selvi et al. (2010)^[22] and Venkataratnam (2019)^[24] in little millet for days to 50% flowering and number of productive tillers plant⁻¹

and panicle length.

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. High estimates of heritability in broad sense were recorded for days to 50% flowering (98.63%), days to maturity (98.40%), plant height (87.84%), panicle length (76.91%), fodder yield (92.71%), number of productive tillers (80.24%), flag leaf width (86.73%), test weight (62.69%), flag leaf length (88.65%) and grain yield per plot (88.68%). Similar findings were reported by Ganapathy et al. (2011) [7], Haradai et al. (2012) [10], Nagar (2017) ^[16] for all the above characters. A perusal of genetic advance (Table 1) revealed that it was high for days to 50% flowering (43.45%), days to maturity (28.47%), number of productive tillers (34.23%), plant height (27.47%), flag leaf width (53.58%), fodder vield (52.00%), panicle length (25.62), flag leaf length (54.16%), test weight (20.49%) and grain yield per plant (33.51%). It indicated that if selection is made based on above mentioned characters selection will be effective. High estimates of genetic advance as percent of mean were also reported by Dagnachew (2012)^[27] and Rawat $(2019)^{[20]}$.

Table 1:	Analysis	of variance	for yield and	d yield attributing	traits
	2		2	2	

Mean sum of square									
S. No.	Source of variation	Replication (df=2)	Treatment (df=31)	Error (df=62)					
1	Days to 50% flowering	1.87	694.03**	3.19					
2	Days to maturity	2.91	622.17**	3.35					
3	Plant height (cm)	350.76	1206.54**	53.21					
4	No. of productive tillers	0.112	0.362**	0.027					
5	Panicle length (cm)	9.58	75.76**	6.89					
6	Flag leaf length (cm)	2.13	212.90**	8.71					
7	Flag leaf width (cm)	0.015	0.265**	0.013					
8	Test weight (g)	0.427	0.321**	0.053					
9	Fodder yield (Kg/plot)	0.174	3.801**	0.097					
10	Grain yield (Kg/plot)	0.009	0.049**	0.002					

 Table 2: Descriptive analysis about various quantitative traits.

S.	Genotypes	Days to 50%	Days to	Plant height	No. of productive	Panicle length	Flag leaf length	Flag leaf width	Test weight	Fodder yield	Grain yield
110.		nowering	maturity	(cm)	tillers	(cm)	(cm)	(cm)	(g)	(kg/plot)	(kg/piot)
1	WV 168	87.00	119.00	151.59	1.47	40.71	37.46	1.56	1.96	5.13	0.86
2	VS 31	49.00	83.00	114.70	1.67	29.65	23.93	0.87	2.59	2.53	0.55
3	VS 33	44.00	75.00	103.55	1.27	24.36	20.25	0.71	2.21	1.43	0.54
4	IIMR LM- 8004	60.00	91.00	131.20	2.07	32.29	27.35	0.80	3.06	4.20	0.83
5	DHLM-11-3	70.00	100.00	137.59	1.87	32.83	22.82	0.79	2.87	4.43	0.87
6	RLM 204	59.00	89.00	110.95	1.73	33.97	26.68	0.99	2.15	2.70	0.63
7	DPLN 1	87.00	117.00	152.86	1.93	37.98	43.73	1.30	2.07	5.37	0.89
8	BULM- 18- 21	70.00	101.00	120.64	2.47	28.15	17.67	0.88	2.13	5.57	0.88
9	BULM- 18- 111	70.00	99.00	118.22	1.60	27.09	19.62	0.91	2.01	4.83	0.75
10	WV 146	87.00	117.00	162.77	1.40	42.29	45.04	1.40	1.96	4.07	0.70
11	BULM 18- 174	86.00	116.00	141.29	1.20	33.29	39.24	1.62	2.19	4.57	0.48
12	VS 38	87.00	116.00	160.99	2.13	38.71	34.25	1.27	2.25	5.47	0.81
13	DHLM 13-3	75.00	108.00	131.59	1.07	30.94	25.05	0.90	2.43	3.27	0.47
14	DHLM 14-5	74.00	102.00	140.23	1.93	33.32	22.97	0.83	2.81	4.53	0.70
15	BL 2021-2	86.00	115.00	173.26	1.40	46.04	43.12	1.60	2.18	4.37	0.55
16	TNPSu 242	46.00	73.00	117.76	2.13	30.62	24.36	0.75	2.36	2.20	0.86
17	TNPSu 244	45.00	75.00	126.33	1.87	31.77	25.20	0.90	2.45	2.67	0.67
18	IIMR LM- R21 1001	88.00	117.00	172.07	1.93	35.33	40.52	1.57	2.33	5.37	0.64
19	IIMR LM- R21 1002	86.00	117.00	164.49	1.63	40.35	37.89	1.37	2.26	4.37	0.66
20	IIMR LM- R21 1158	76.00	107.00	112.38	1.90	28.35	18.51	0.95	2.08	5.40	0.79
21	DLM 310	60.00	90.00	104.89	2.00	25.33	23.12	0.74	1.99	3.90	0.75
22	GPUL 13	67.00	98.00	138.03	2.20	34.19	36.84	0.83	2.96	5.73	0.93
23	GPUL 14	56.00	90.00	140.62	2.07	34.13	26.98	0.75	2.53	3.43	0.83
24	DHLM 36-3	71.00	102.00	145.74	2.07	35.79	25.50	0.82	2.64	4.53	0.76
25	OLM 203	87.00	118.00	161.00	1.43	36.25	40.56	1.21	2.15	4.47	0.70

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26	BL 6	60.00	89.00	137.43	2.20	33.16	26.04	0.89	2.90	4.47	0.74
27	CLMV 1	71.00	104.00	144.51	1.67	35.70	25.21	0.89	2.71	4.13	0.70
28	LOCAL CHECK	61.00	89.00	141.63	2.10	33.27	27.34	0.97	2.38	5.53	0.85
	Mean	70.25	100.85	137.80	1.80	33.78	29.54	1.04	2.38	4.24	0.73
	Min	45.00	77.67	103.55	1.07	24.36	17.67	0.71	1.96	1.43	0.47
	Max	94.33	125.67	173.26	2.47	46.04	45.04	1.62	3.06	5.73	0.93
	SE(d)	1.46	1.49	5.96	0.14	2.14	2.41	0.09	0.19	0.25	0.04
	C.D.	2.93	3.00	11.97	0.27	4.31	4.85	0.19	0.38	0.51	0.07
	C.V.	2.50	1.78	5.29	9.21	7.77	9.99	10.92	9.69	7.35	6.18

Table 3: Genetic variability parameters of various quantitative traits.

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	70.25	44.00	88.00	230.28	233.47	98.63	31.05	43.45	21.24	21.38
Days to maturity	100.85	73.00	119.00	206.27	209.62	98.40	29.35	28.47	13.93	14.04
Plant hight (cm)	137.80	103.55	173.26	384.45	437.65	87.84	37.86	27.47	14.23	15.18
No. of productive tillers	1.80	1.07	2.47	0.11	0.14	80.24	0.62	34.23	18.55	20.71
Panicle length (cm)	33.78	24.36	46.04	22.96	29.85	76.91	8.66	25.62	14.18	16.17
Flag leaf length (cm)	29.54	17.67	45.04	68.06	76.77	88.65	16.00	54.16	27.92	29.66
Flag leaf width (cm)	1.04	0.71	1.62	0.08	0.10	86.73	0.56	53.58	27.93	29.99
Test weight (g)	2.38	1.96	3.06	0.09	0.14	62.69	0.49	20.49	12.56	15.86
Fodder yield (kg/plot)	4.24	1.43	5.73	1.23	1.33	92.71	2.20	52.00	26.22	27.23
Grain yield (kg/plot)	0.73	0.47	0.93	0.02	0.02	88.68	0.24	33.51	17.28	18.35

Table 4: Number of genotypes and their frequency (%) in different categories for different characters

S. No.	Traits	Category	No of genotypes	Frequency %
1	Loof shooth pubeseenee	Present	7	25
1.	Lear sheath pubescence	Absent	21	75
		Arched	19	68
2.	Inflorescence shape	Globose-elliptic	0	0
		Diffused	9	32
		Compact	7	25
3.	Panicle compactness	Intermediate	14	50
	_	Open	7	25
4	Soud share	Elliptical	20	71
4.	Seed shape	Oval	8	29
5.		Straw white/cream	10	36
		Golden yellow	4	14
	Seed colour	Light Brown	0	0
	Seed colour	Brown	3	11
		Grey	10	36
		Dark Grey	1	3



Fig 1: Leaf sheath pubescence



Fig 2: Inflorescence Shape



Fig 3: Panicle compactness



Fig 4: Morphological description of seed colour.

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Conclusion

According to the findings of the experiment, it is indicated that future genetic improvements in little millet will benefit from the genetic variability documented for various features in relation to yield and the characters showing high heritability with high genetic advance *viz.*, plant height, days to maturity and days to 50% flowering should be utilized in direct selection.

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