J. Agric. Res. Technol., 47 (3) : 258-263 (2022) https://doi.org/10.56228/JART.2022.47303

Genetic Variability of Yield and its Components in Little Millet [*Panicum sumatrense* L.]. Local Germplasm

B. S. Matere[1], V. V. Bhavsar[2], P. A. Mate[3] and V. S. Girase[4]
Department of Botany , College of Agriculture, Dhule - 424 004 (India)
(Affiliated with Mahatma Phule Krishi Vidyapeeth, Rahuri - 413 712 (India)

Abstract

The fifty little millet genotypes were used to study Genetic variability, heritability and genetic advance. The highest estimates of GCV and PCV values were recorded seed yield plant^{-1} and iron content. Moderate estimates of GCV and PCV values were recorded panicle weight plant^{-1}, total number of tillers plant^{-1}, days to 50 per cent flowering and productive tillers plant^{-1}. Almost all the characters showed high percentage of heritability except productive tillers plant^{-1} and panicle length showed medium heritability, while number of branches panicle^{-1} showed low heritability. It indicates that charactersis least influenced by the environmental effect, suggesting scope for improvement of respective characters. The characters iron content, seed yield plant^{-1}, panicle weight plant^{-1}, total number of tillers plant^{-1} and productive tillers plant^{-1} showed high heritability accompanied with high genetic advance, it indicates that selection is effective for this characters.

Key words : Genetic variability,Heritability, Genetic advance, GCV and PCV, Little millet.

Millets are in the family of cereals grown in different parts of the world for human consumption and as feed and fodder for animal. Little millet (*Panicum sumatrense* L.) belongs to family *Poeceae* (*Graminae*), sub family *Panicoideae* and genus *Panicum*. It is considered as self-pollinated crop. Little millet is diploid (2n=36) in nature.It is known by different vernacular name in different states of India, is commonly called kutki and Shaban in Hindi. It is also known as sava,vari and halvi in Marathi, gajro and kuri in Gujrati, same and sama in Kannada, samai in Tamil, samalu in Telugu, sama in Bengali and swank in Panjabi.

Little millet is cultivated to a limited extent in India, Sri Lanka, Pakistan, Myanmar, and other South East Asian countries (Hiremath *et al*., 1990). In India it is important to tribes of the Eastern Ghat Mountains and grown in combination with other millets (Hiremath *et al*., 1990). The major little millet growing states are Orissa, Gujarat, Maharashtra, Karnataka, Andhra Pradesh and Madhya Pradesh. In India it is cultivated over an area of 2.34 lakh ha with total production of about 1.27 lakh tones and with productivity of 544 kg/ha during the year 2015-16. (Anonymous., 2018).

Little millet is a domesticated form of the weedy species *Panicum psilopodium* (De Wet *et al*., 1983). They are cultivated in diverse and adverse environments, mostly in the dry, semi-arid to sub-humid drought-prone agro ecosystems. It is a quick growing, short duration cereal which can withstand both drought and water logging. Its cultivation is restricted to hilly regions up to an altitude of 2000m. It cannot withstand colder temperatures below 10°C.

The little millet contains 8.7 gram protein, 75.7 gram carbohydrate, 5.3 gram fat and 1.7 gram mineral and 9.3 mg iron in per 100 gram grain. Its high fiber helps to reduce the fat depositions in the body. Little millet has a significant role in providing nutraceutical components such as phenols, tannins and phytates along with other nutrients.

Information on genetic variability, heritability and genetic advance is most essential for formulating effective selection schemes in any crop improvement programme. A very limited work of this kind has been previously done on little millet. Therefore, the present investigations were undertaken to determine genetic variability, heritability and genetic advance in moth bean.

Materials and methods

The experimental materials consisting fifty germplasm of little millet collected from NARP, research station Igatpuri, Nashik and remaining from Ahmednagar, Dhule and Nandurbar districts of Maharashtra (Table 2). Sowing of fifty genotypes of little millet on raised seed bed 2nd July, 2020 and transplanting was done on 31st July, 2020. The experiment was laid out in RBD with two replications at Department of Botany, College of Agriculture, Dhule (M.S.). By adopting a spacing of 30 cm between rows and 10 cm between plants respectively, at recommended package of practices were followed to raise good and healthy crop stand. Data were collected on twelve yield and yield contributing characters *viz*., days to 50% flowering, days to maturity, plant height (cm), total number of tillers plant^{-1}, productive tillers plant^{-1}, panicle length (cm), number of branches panicle^{-1}, panicle weight plant^{-1} (g), seed yield plant^{-1} (g), 100 ml volume weight, protein content (%) and iron content (mg).

The mean of five plants was subjected to statistical analysis. The data for different characters were statistically analyzed for significance by using analysis of variance technique described by Panse and Sukhatme (1985). The adapted design was Randomized Block Design (RBD) with two replications. The significance of mean sum of square for each character was tested against the corresponding error degrees of freedom using "F" Test (Fisher and Yates, 1967). The components of variances were used to estimate genetic parameters like phenotypic and genotypic coefficient of variation (PCV and GCV) as per the formula given by Burton and De Vane (1953). Heritability in broad sense was calculated according to the formula given by Allard (1960) and expressed in percentage. Genetic advance was estimated by using Burton (1955). Statistical analysis was done by using WINDOSTAT program.

Table 1. Analysis of variance for different characters in little millet

Characters	Mean sum of square		
	Replication	Genotype	Error
Days to 50 per cent flowering	1.0000	192.9722**	22.79592
Days to maturity	7.2900	226.3676**	32.18796
Plant height (cm)	80.4609	89.51078**	21.97355
Total number of tillers plant^{-1}	0.38440	0.751355**	0.11991
Productive tillers plant^{-1}	0.3249	0.645651**	0.165716
Panicle length (cm)	7.6176	7.214114**	2.112702
Number of branches panicle^{-1}	0.75516	2.575013**	1.365753
Panicle weight plant^{-1} (g)	12.9600	31.00144**	5.626939
Seed yield plant^{-1} (g)	1.3432	16.50176**	1.470063
100 ml volume weight (g)	9.4556	11.15253**	2.532317
Protein content (%)	0.000066	0.740318**	0.041422
Iron content mg 100^{-1} (g)	0.1844	4.919818**	0.046271

*, ** Indicates significance at 5% and 1% level, respectively.

Results and Discussion

Analysis of variance revealed significant differences among genotypes for all the characters. (Table 1). The characters seed yield plant^{-1} and iron content showed higher estimates of GCV and PCV, indicating presence of large variation among the genotypes for these characters (Table 3). Therefore, simple selection can be practiced for further improvement of these characters. These results were in conformity with the finding of Subramanian *et al*. (2010), Salini *et al*. (2010), Tyagi *et al*. (2011), Selvi *et al*. (2014), Nandini *et al*. (2016), Ashok *et al*. (2016 a), and Madhavilatha *et al*. (2020). The character panicle weight plant^{-1}, total number of tillers plant^{-1}, days to 50 per cent flowering and productive tillers plant^{-1}. Similar finding were also reported by Nirmalakumari *et al*. (2010) and Geetha *et al*. (2018) for days to 50 per cent flowering, Sasamala *et al*. (2015), Suryanarayana and Sekhar *et al*. (2018) for number of productive tillers plant^{-1}, days to 50 per cent flowering observed moderate GCV and PCV for these characters.

The charactersdays to maturity, panicle length, plant height, protein content, number of branches panicle^{-1} and 100 ml volume weightshowed low genotypic and phenotypic coefficient of variation. It indicates that low range of variation found in these characters thus offers little scope for further improvement of these characters. Similar results was recorded by Nirmalakumari *et al*. (2010) and Ashok *et al*. (2016 a) for plant height, Anuradha *et al*. (2017) for plant height, Brunda *et al*. (2014) for days to maturity andplant height, Savankumar *et al*. (2018) for days to maturity, number of branches panicle^{-1} and plant height and Selvi *et al*. (2014) and Madhavilatha *et al*. (2020) for panicle length.

High heritability coupled with high genetic

Table 2. List of little millet genotypes with origin

Genotype	Village	Tahsil	District
IGPLM-19-01	Khodala	Javhar	Thane
IGPLM-19-03	Dhondali	Igatpuri	Nashik
IGPLM-19-04	Vaitarana	Igatpuri	Nashik
IGPLM-19-05	Dhond-maryachi	Timbakeshwar	Nashik
IGPLM-19-08	Devgaon	Timbakeshwar	Nashik
IGPLM-19-10	Korapgaon	Igatpuri	Nashik
IGPLM-19-13	Devgaon	Timbakeshwar	Nashik
IGPLM-19-14	Dhargaon	Igatpuri	Nashik
IGPLM-19-16	Korapgaon	Igatpuri	Nashik
IGPLM-19-17	Bahuli kh	Igatpuri	Nashik
IGPLM-19-18	Ondasi	Igatpuri	Nashik
IGPLM-19-19	Devgaon	Timbakeshwar	Nashik
IGPLM-19-22	Dhondmar-yachiyate	Timbakeshwar	Nashik
IGPLM-19-24	Kalamwadi	Mokhada	Thane
IGPLM-19-26	Khodala	Javhar	Thane
IGPLM-19-27	Kalamwadi	Mokhada	Thane
IGPLM-19-28	Khodala	Javhar	Thane
IGPLM-19-29	Bahirwadi	Javhar	Thane
IGPLM-19-30	Dhargaon	Igatpuri	Nashik
IGPLM-19-31	Korapgaon	Igatpuri	Nashik
IGPLM-19-32	Bhavali	Igatpuri	Nashik
IGPLM-19-34	Devgaon	Timbakeshwar	Nashik
IGPLM-19-36	Khodala	Javhar	Thane
IGPLM-19-37	Dhargaon	Igatpuri	Nashik
IGPLM-19-38	Dhargaon	Igatpuri	Nashik
IGPLM-20-01	Manhere	Igatpuri	Nashik
IGPLM-20-02	Manhere	Igatpuri	Nashik
IGPLM-20-03	Gavande	Igatpuri	Nashik
IGPLM-20-04	Gavande	Igatpuri	Nashik
IGPLM-0-05	Bari	Igatpuri	Nashik
IGPLM-20-06	Bari	Igatpuri	Nashik
IGPLM-20-07	Gavande	Igatpuri	Nashik
IGPLM-20-08	Manhere	Igatpuri	Nashik
IGPLM-20-09	Manhere	Igatpuri	Nashik
IGPLM-20-10	Manhere	Igatpuri	Nashik
DHLM-1	Bhandardara-1	Akole	A'dnagar
DHLM-2	Bhandardara-2	Akole	A'dnagar
DHLM-3	Bhandardara-3	Akole	A'dnagar
DHLM-4	Khed	Akole	A'dnagar
DHLM-5	Rajur-1	Akole	A'dnagar
DHLM-6	Rajur-2	Akole	A'dnagar
DHLM-7	Charanmal	Sakri	Dhule
DHLM-8	Kudashi	Sakri	Dhule
DHLM-9	Nawapata	Sakri	Dhule
DHLM-10	Pimpalner	Sakri	Dhule
DHLM-11	Dhadgaon-1	Dhadgaon	Nandurbar
DHLM-12	Dhadgaon-2	Dhadgaon	Nandurbar
DHLM-13	Amli	Akkalkuwa	Nandurbar
DHLM-14	Amli Bari	Akkalkuwa	Nandurbar
Phule Ekadashi (check)	MPKV, Rahuri	Rahuri	A'dnagar

advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression (Panse, 1957). Lower values of genetic advance indicate the prevalence of narrow range of variability, high G X E interaction (non-additive gene action).

High heritability values recorded for most the characters. Iron content, protein content, seed yield plant^{-1}, days to 50 per cent flowering, days to maturity, total number of tillers per plant, panicle weight, 100 ml volume weight and plant height indicating least influence of environment on these characters. These results were conformity with Salini *et al*. (2010), Nirmalakumari *et al*. (2010 a), Ganapathy *et al*. (2011), Patil and Mane (2013), Sasamala *et al*. (2015), Jyothsna *et al*. (2016 a), Ashok *et al*. (2016, a) and Savankumar*et al*. (2018).

While medium heritability was observed for productive tillers plant^{-1}, panicle length. Similar finding were reported by Selvi *et al*. (2014) and low heritability was observed for number of branches panicle^{-1}.

In the present study, high heritability coupled with high genetic advance was observed for iron content followed by seed yield plant^{-1}, panicle weight plant^{-1}, total number of tillers plant^{-1} and productive tillers plant^{-1} suggesting that these characters are govern by additive genes and phenotypic selection for these characters may be effective. Previously similar results were reported by Subramaian *et al*. (2010), Selvi *et al*. (2014), Jyothsna *et al*. (2016, a), Ashok *et al*. (2016, a),Salini *et al*.(2010), Nirmalakumari *et al*. (2010, a), Ganapathy *et al*. (2011), Anuradha *et al*. (2017), Patel *et al*. (2018), Nirmalakumari *et al*. (2010, b), Patil and Mane (2013), Sasamala *et al*. (2015).

High heritability coupled with medium genetic advance was observed for protein content, days to 50 per cent flowering and days to maturity. This indicates the presence of both additive and non-additive gene action for these traits. Nirmalakumari *et al*. (2010 b) and Savankumar*et al*. (2018) for days to 50 per cent flowering are also reported similar result.

High heritability coupled with low genetic advance was observed for 100 ml volume weight and plant height suggesting preponderance of non-additive gene action and selection for these

Table 3. Parameters of genetic variability for different characters in Little millet

Characters	General mean	σ^2g	σ^2p	σ^2e	GCV (%)	PCV (%)	ECV (%)	h^2 (BS %)	GA	GA as per cent of mean
Days to 50% flowering	94.94	85.088	107.884	22.796	9.716	10.940	5.029	78.90	16.876	17.775
Days to maturity	129.43	97.090	129.278	32.188	7.613	8.785	4.383	75.10	17.591	13.591
Plant height (cm)	149.037	33.769	55.742	21.974	3.899	5.010	3.145	60.60	9.317	6.252
Total no. of tillers plant^{-1}	4.006	0.316	0.436	0.120	14.026	16.476	8.644	72.50	0.985	24.598
Productive tillers plant^{-1}	3.759	0.240	0.406	0.166	13.032	16.944	10.830	59.20	0.776	20.647
Panicle length (cm)	26.822	2.551	4.663	2.113	5.954	8.051	5.419	54.70	2.433	9.072
No. of branches panicle^{-1}	13.7451	0.605	1.970	1.366	5.657	10.212	8.502	30.70	0.887	6.456
Panicle weight plant^{-1} (g)	18.536	12.687	18.314	5.627	19.216	23.088	12.797	69.30	6.107	32.948
Seed yield plant^{-1} (g)	9.1081	75.16	8.986	1.470	30.100	32.912	13.312	83.60	5.156	56.707
100 ml volume weight (g)	73.8555	4.310	6.842	2.532	2.811	3.542	2.155	63.00	3.394	4.596
Protein content (%)	7.1064	0.349	0.391	0.041	8.318	8.798	2.864	89.40	1.151	16.203
Iron content mg 100^{-1} (g)	5.5762	2.437	2.483	0.046	27.995	28.259	3.858	98.10	3.186	57.129

traits may not be rewarding. Brunda *et al*. (2014) and Ashok *et al*. (2016, b) indicated same result for plant height.

Low heritability with low genetic advance was observed for character number of branches panicle^{-1} and panicle length suggesting that environment had a major role in their expression, indicating predominant role of non-additive gene action for this trait and selection would be ineffective. This was in conformity with the result of Selvi *et al*. (2014) for panicle length are also reported similar result.

In conclusion, the material chosen differed in their genotypic make up as evidenced by the significant differences among them in respect of all the quantitative characters studied. Phenotypic coefficients of variations estimate was slightly higher than the genotypic coefficients of variation for all the trait, indicating low environmental influence on the expression of all the traits.

References

Allard. R.W. 1960. Principles of plant breeding. John. Wiley and Sons.Inc. New York. pp. 20-24 and 88-89.

Anonymous. 2018. ICAR-AICRP on small millets, Bengalaru.

Anuradha, N., Patro, T. S. S. K., Divya, M., Rani, Y and Triveni, U. 2017. Genetic variability, heritability and correlation of quantitative traits in little millet genotypes. J. Pharmac.Phytochem., 6(6): 489-492.

Ashok, S., Patro, T. S. S. K., Divya, M., Sandhya Rani, Y., Triveni, U and Subba Rao, M. 2016a. Study of genetic parameters, character association and path analysis for grain yield and its components in little millet (Panicum sumatrense).Progressive.Res.Int.J., 11(4): 314-317.

Ashok, S., Patro, T. S. S. K., Jyothsna, S. and Divya, M. 2016b. Studies on genetic parameters, correlation and path analysis for grain yield and its components in foxtail millet (*Setaria italica*). Progressive. Res. Int. J.,11(3): 300-303.

Brunda, S. M., Kamatar, M. Y., Naveenkumar, K. L. and Hundekar, R. 2014. Study of genetic variability, heritability and genetic advance in foxtail millet in both rainy and post rainy season. J. Agric. Veter. Sci. 7(11): 34-37.

Burton, G. W. and Devene, H. E. 1953. Estimating heritability in tall fescue (*Festeca arundinaceae*) from replicated clonal material. Agron. J. 45: 478-481.

De Wet, J. M. J., Prasad, K. E. and Brink, D. E. 1983. Systematics and domestication of *Panicum sumatrense* (*Gramineae*). Journal d'agriculture traditionnelle et de botanique appliquée, 30: 159-168.

Fisher, R. A. and Yates. 1967. Statistical Tables for Biological Agricultural and Medical Research Oliver and Boyd, Edington.

Ganapathy, S., Nirmalakumari, A. and Muthiah, A. R. 2011. Genetic variability and inter relationship analysis for economic traits in finger millet germplasm. World J. Agric. Sci. 7(2): 185-188.

Geetha, N., Uma, M. S. and Ravishankar, P. 2018. Genetic variability for yield and yield attributing traits in elite germplasm lines of little millet. Int. J. Pure Appl. Bio-sci. 6(1): 1466-1471.

Hiremath, S. C., Patil, G. N. V and Salimath, S. S. 1990. Genome homology and origin of *Panicum sumatrense* (*Gramineae*). Cytologia, 55: 315-319.

Jyothsna, S., Patro, T. S. S. K., Rani, S. Y., Neeraja, B., Ashok, S. and Triveni, U. 2016a. Studies on genetic parameters, character association and path analysis of yield and components in little millet (*Panicum sumatrense*). Int. J. Agric. Sci. 8(6): 1018-1020.

Madhavlatha, L., Subbarao, M., ShanthiPriya, M and Hemanthkumar, M. 2020. Variability, character association and path analysis studies in little millet (*Panicum sumatrense*) Andra Pradesh Journal of Agriculture Science 6(1): 49-54, 2020.

Nandini, C., Sujata, B., Krishnappa, M. and Aruna, Y. R. 2016. Genetic variability, heritability, genetic advance and character association studies in F_3 generation of cross JK-8 x Peddasame (purple late) in little mille (*Panicum miliare* L.). Asian Journal of Bio Science. 11(2): 244-249.

Nirmalakumari, A. and Vetriventhan, M. 2010. Characterization of foxtail millet germplasm collection for yield contributing traits. Electronic J. Pl. Breed. 1(2).

Nirmalakumari, A., Salini, K. and Veerabadhiran, P. 2010, a. Morphological characterization and evaluation of little millet (*Panicum sumatrense* Roth. Ex-roem and schultz) germplasm. Elec. J. Plant Breeding. 1(2): 148-155.

Panse, V. G. and Sukhatme, V. P. 1985. Statistical methods for agricultural workers. ICAR, New Delhi. 4th Edition, pp. 97-156.

Patil, A. S and Mane, V. A. 2013. Studies on the genetic variation of yield and contributing traits in finger millet (*Eleusine coracana* L. Gaertn). Progressive Research. 8: 526-528.

Salini, K., Nirmalakumari, A., Muthiah, A. R. and Senthil, N. 2010. Evaluation of proso millet (*Panicum miliaceum* L.) germplasm collections. Elec. J. Pl. Breed. 1(4): 489-499.

Sasamala, A. C., Sahoo, L. P., Mohapatra, K. C. and Patra, C. 2015. Genetic variability and character association in little millet (*Panicum sumatrense*) germplasm collections of Odisha (India). Advances in Applied Agricultural Sciences. 3(1): 40-50.

Savankumar N. P., Patil, H. E., Harshalkumar M. Modi and Singh, J. T.2018. Genetic variability study in little millet (*Panicum miliare* L.) genotypes in relation to yield and quality traits. Int. J. Curr. Microbio. Appl. Sci. 7(6): 2712-2725.

Selvi, V. M., Nirmalakumari, A and Subramanian, A. 2014. Genetics and interrelationships of yield traits for enhancing productivity of little millet. Elec. J. Pl. Breed. 5(1): 82-86.

Subramanian, A., Nirmalakumari, A. and Veerabadhiran, P. 2010. Trait based selection of superior kodo millet (*Paspalum scrobiculatum* L.) genotypes. Elec. J. Pl. Breed. 1(4): 852-855.

Suryanarayana, L. and Sekhar, D. 2018. Studies on genetic variability, character association and path analysis in little millet (*Panicum sumatrense* L.) genotypes. The Pharma. J. 7(7): 908-910.

Tyagi, V., Ramesh, B., Kumar, D. and Pal, S. 2011.Genetic architecture of yield contributing traits in foxtail millet (*Setaria italica*). Curr. Advan. Agric. Sci. 3(1): 29-32.