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Extent of genetic variability for morpho-nutritional traits in foxtail millet [*Setaria italica* (L.) P. Beauv]

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Abstract

The present study was carried out to assess the nature and magnitude of genetic variability for yield and quality related traits in 52 genotypes of foxtail millet, carried at Agriculture Research Station Buldhana, during Akola *kharif*-2018-19 and *kharif*-2019-20. The analysis of variance revealed presence of significant differences for all the traits under study, indicating that the genotypes under study were genetically diverse for most of the traits. Coefficient of variation studies indicated that the estimates of GCV were lesser than the corresponding PCV values for all the traits indicating the influence of environment on expression of the characters under study. High variability existed for Fe content, number of productive tillers per plant, Zn content, fodder yield, and grain yield. High heritability with high Genetic Advance as percent Mean was recorded for panicle girth, Fe content, fodder yield, Zn content and grain yield per plant suggesting primarily additive nature of gene action which responds well to selection.

Keywords: foxtail millet, iron, zinc, genetic advance, heritability and variability

Introduction

Foxtail millet is well recognized as a short duration, rainy season crop. It belongs to genus *Setaria*, tribe *paniceae* and family *Poaceae* or *Graminae* in the grass family. There are about 125 species widely distributed in warm and temperate parts of the world. Foxtail millet (*Setaria italica* (L.) P. Beauv.) is an autogamous, diploid ($2n = 18$), C_4 panicoid crop species with a relatively small genome size of ~515 Mb (Li and Brutnell, 2011) [11] with haploid Chromosome number ($n = 9$). It is essentially grain crop of 90-100 days duration. Taxonomically, foxtail millet consists of two subspecies, *S. italica* subsp. *italica* and subsp. *viridis*. The geographical origin of foxtail millet based on cytological studies indicated that wild ancestor of foxtail millet is *S. viridis* (Kihara and Kishimoto, 1942; Li *et al.*, 1945) [9]. Based on the comparative morphology of the foxtail millet accessions, foxtail millet is classified into a European complex (Race *Moharia*) and a far Eastern complex (Race *maxima*) (Prasada Rao *et al.*, 1986) [16]. Race *Moharia* includes cultivars with relatively small inflorescences, while race *maxima* include pendulous inflorescences. Cultivars from India are morphologically different from those of Europe and the Far East and are recognized as race *indica* (Prasada Rao *et al.*, 1986) [16].

Genetic variability is the basis for any breeding programme as it is important for any population to adopt to the inevitable changes in the environment and helps to promote the survival of the species. As creation of variability being the essence of any plant breeding programme, any approach adopted strategically to create variation plays an important role in reaching the targets. For this, knowledge on the magnitude of variability present in a crop species for different traits is important, as it provides the basis for effective selection. It is also a pre requisite before initiating any breeding programme aimed at improving yield and quality characters under consideration.

Heritability measures the relative amount of the heritable portion of variability. But as heritability is also influenced by environment, the information on heritability alone fails to indicate response to selection and may not help in pin pointing characters enforcing selection. The heritability estimates along with genetic advance will be more reliable in formulating suitable and effective breeding methods. Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures (Johnson *et al.*, 1955) [6].

Materials and Methods

In the present investigation, 52 genotypes were evaluated at Agriculture Research Station, Buldhana, during Akola kharif-2018-19 and kharif-2019-20, which was collected from National Bureau of Plant Genetic Resources (NBPGR), Dr. PDKV, Akola. Genotypes were sown in a randomized block design (RBD) in three replications with a spacing of 30 × 10 cm per each entry.

The data was collected on five randomly selected plants per genotype for 12 metric traits *viz.*, days to 50% flowering, days to maturity, plant height, total number of tillers per plant, number of productive tillers per plant, panicle length, panicle girth, 1000 grain weight, fodder yield, iron content, zinc content, and grain yield per plant. However, days to 50 per cent flowering and days to maturity was recorded on plot basis. Analysis of variance and summary statistics were calculated as per Panse and Sukathme (1967) [15]. PCV, GCV values were classified as described by Sivasubramanian and Menon (1973) [21]. Heritability in the broad sense was categorised as per the classification given by Johnson *et al.*, (1955) [6].

Results and Discussion

The analysis of variance revealed presence of significant differences for all the traits under study, indicating that the genotypes under study were genetically diverse for most of the traits.

Possibility of achieving improvement in any crop plants depends largely on the magnitude of genetic variability. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and environmental components. The genotypic component being the heritable part of the total variability, its magnitude for yield and its component characters influence the selection strategies to be adopted by the breeders.

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters, indicating that the characters were less influenced by the environment. Therefore, selection for the improvement of these traits.

For the trait days to 50% flowering the PCV (6.78) and GCV (5.97) estimates were low indicating moderate variation among genotypes studied and such estimates of PCV and GCV were earlier reported by Nirmalakumari *et al.*, (2008) [14], Lakshmanan and Guggeri (2001) [10]. The estimates of PCV (4.55) and GCV (3.92) were low for days to maturity. These results are in agreement with Nirmalakumari *et al.*, (2008) [14], Nirmalakumari and Vetrivethan (2010) [13], Jyothsna *et al.*, (2016) [7] and Ashok *et al.*, (2016) [1]. The estimates of PCV (7.32) and GCV (5.66) were low for plant height indicating less variation among the genotypes studied. Similar results were reported by Brunda *et al.*, (2014) [2] and Jyothsna *et al.*, (2016) [7]. For the trait number of productive tillers per plant, the estimates of PCV (25.82) and GCV (18.82) were high and moderate. The difference between PCV and GCV value is more which indicates that there is high influence of environment in the observed variation. Similar results of high PCV and moderate GCV were reported by Nirmalakumari *et al.*, (2008) [14], Nirmalakumari and Vetrivethan (2010) [13], Prasanna *et al.*, (2013) [17], Yogeesh *et al.*, (2015) [23], Jyothsna *et al.*, (2016) [7], Ashok *et al.*, (2016) [1] and Kavya *et al.*, (2017) [8]. The estimates of PCV (12.83)

and GCV (8.70) were moderate and low for the character panicle length and the difference between PCV and GCV value is more indicating that there is high influence of environmental component in the observed variation. Similar results for moderate PCV and low GCV were earlier reported by Cill and Randhawa (1975) [3]. For the character test weight the estimate of PCV (8.78) and GCV (7.54) was low. Similar results for low PCV and GCV was reported by Cill and Randhawa (1975) [3]. The estimates of PCV (22.71) and GCV (18.18) were high and moderate for grain yield per plant. The difference between PCV and GCV value is more which indicates that there is high influence of environment in the observed variation. Similar results of high PCV and Moderate GCV were reported by Chidambaram and Palanisamy (1995) [4], Dasthagiraiah and Reddy (1995). The estimates of PCV (31.66) and GCV (30.51) were high for the character iron and these findings are in conformity with the results of Shingane *et al.*, (2016) [20] in foxtail millet. The GCV and PCV for trait fodder yield per plant was observed as moderate and high 19.75% and 24.32% respectively. Similar results were reported by Chidambaram and Palanisamy (1995) [4]. The estimates of PCV (22.92) and GCV (22.05) were high for zinc content.

Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to observed variation. The estimates of heritability revealed that all traits were found to have high magnitude of heritability. Heritability estimates alone cannot give a better idea in selecting suitable breeding method. So in order to fulfil the requirement we have also estimated genetic advance in addition to the heritability. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone and these will also give a better picture for having an idea of gene action involved. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance. Of the twelve characters concerned, high heritability coupled with high genetic advance was noted for panicle girth, fodder yield, Fe content, Zn content and grain yield per plant indicating the predominance of additive gene action, there by direct selection will be effective to obtain the desired results. The results were in accordance with Sirisha *et al.*, (2009) [19], Nirmalakumari and Vetrivethan (2010) [13], Tyagi *et al.*, (2011) [22], Govindaraj *et al.*, (2011) [5] in pearl millet, Brunda *et al.*, (2014) [2], Yogeesh *et al.*, (2015) [23], Ashok *et al.*, (2016) [1], Shingane *et al.*, (2016) [20] and Kavya *et al.*, (2017) [8]. High heritability coupled with moderate genetic advance were recorded for days to 50 % flowering and 1000 grain weight indicating the preponderance of both additive and non additive gene action indicating that simple selection will not be rewarding in improving this trait. Similar results were earlier reported by Nirmalakumari *et al.*, (2008) [14], Nirmalakumari and Vetrivethan (2010) [13] and Jyothsna *et al.*, (2016) [7]. Moderate heritability coupled with moderate genetic advance was recorded for the number of tillers per plant, number of productive tillers per plant and panicle length indicating that there is involvement of both additive and non-additive gene actions which may not be exploited through simple selection procedures. However different results of high heritability and moderate genetic advance as per mean were indicated by Prasad *et al.*, (1985) [16].

Table 1: Analysis of variance for 12 characters in foxtail millet (*Setaria italica* (L.) Beauv)

Sr. No.	Characters	Mean sum of square		
		Replication	Treatment	Error
1	Days to 50% flowering	3.61	74.22**	3.44
2	Days to maturity	0.009	77.02**	4.24
3	Plant height (cm)	0.01	3.68**	37.07
4	Total number of tillers per plant	0.13	3.33**	0.44
5	No. of productive tillers per plant	0.11	3.34**	0.42
6	Panicle length (cm)	2.99	16.67**	2.72
7	Panicle Girth (cm)	0.001	2.85**	0.24
8	Grain yield per plant (gm)	9.76	39.90**	3.4
9	Fodder yield per plant (gm)	25.44	145.68**	11.53
10	1000 grain weight (gm)	0.005	0.230**	0.012
11	Grain Fe content (mg/kg)	9.66	629.90**	7.95
12	Grain Zn content (mg/kg)	2.97	395.23**	5.25

*Significant at 5% level, ** Significant at 1% level

Table 2: Estimation of variability, heritability and genetic advance as percent of mean for 12 characters in 52 Foxtail millet germplasm accessions.

Sr. No.	Characters	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	h ² %	Genetic Advance	GA as% of mean (5 %)
1	Days to 50% flowering	11.88	15.32	5.97	6.78	77.5	6.25	10.83
2	Days to maturity	12.13	16.37	3.92	4.55	74.1	6.17	6.99
3	Plant height (cm)	55.21	92.29	5.66	7.32	59.8	11.84	9.03
4	Total number of tillers per plant	0.48	0.92	14.65	20.35	51.9	1.03	21.75
5	No. of productive tillers per plant	0.48	0.91	18.82	25.82	53.1	1.04	28.27
6	Panicle length (cm)	2.32	5.05	8.7	12.83	46.0	2.13	12.15
7	Panicle Girth (cm)	0.43	0.68	13.25	16.62	63.5	1.08	21.75
8	Grain yield per plant (gm)	6.08	9.48	18.18	22.71	64.1	4.06	31.01
9	Fodder yield per plant (gm)	22.35	33.89	19.75	24.32	66.0	7.91	33.05
10	1000 grain weight (gm)	0.03	0.04	7.54	8.78	73.9	0.33	13.33
11	Grain Fe content (mg/kg)	103.66	111.61	30.51	31.66	92.9	20.21	60.58
12	Grain Zn content (mg/kg)	64.99	70	22.05	22.92	92.5	15.97	43.69

GCV- Genotypic coefficient of variation ; PCV- Phenotypic coefficient of variation; h²- Heritability; GA- Genetic Advance

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

- Ashok S, Patro TSSK, Jyothsna S, Divya M. Studies on genetic parameters, correlation and path analysis for grain yield and its components in foxtail millet (*Setaria italica*). Progressive Research 2016;11(3):300-303.
- Brunda SM, Kamatkar MY, Hundekar R, Naveenkumar KL. Studies on genetic variability, heritability and genetic advance in foxtail millet in both rainy and post rainy season. IOSR-Journal of Agriculture and Veterinary Science 2014;7(2):34-37.
- Cill AS, Randhawa AS. Heritable variation and interrelationship in foxtail millet (*Setaria italica* (L.) P. Beauv.). Madras Agric. J 1975;62(5):253-258.
- Chidambaram S, Palnisamy S. Variability and correlation studies of dry matter with reference to selection criteria in foxtail millet (*Setaria italica*). Madras agric. J. 1995;82(1):1-3.
- Govindaraj M, Selvi B, Rajarathinam S, Sumathi P. Genetic variability and heritability of grain yield components and grain mineral concentration in India's pearl millet [*Pennisetum glaucum* (L) R. Br.] accessions. African Journal of Food, Agriculture, Nutrition and Development 2011;11(3):4758-4771.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soyabean. Agronomy Journal 1955;47:314-318.
- Jyothsna S, Patro TSSK, Rani YS, Ashok S, Neeraja B, Triveni U. Studies on genetic variability and inter-relationship between grain yield and its components in foxtail millet (*Setaria italica*). International Journal of Agriculture Sciences 2016;8(5):1015-1017.
- Kavya P, Sujatha M, Pandravada SR, Hymavathi TV. Variability Studies in foxtail millet [*Setaria italica* (L.) P. Beauv.]. International Journal of Current Microbiology and Applied Sciences 2017;6(9):955-960.
- Kihara H, Kishimoto E. Bastrade zwischen *Setaria italica* and *S. viridis*. (in Japanese with German summary). Bot. Mag. Tokyo 1942;56:62-67.
- Lakshmana D, Guggeri AK. Genetic variability studies in foxtail millet. Karnataka J Agril. Sci 2001;14(2):311-314.
- Li P, Brutnell TP. *Setaria viridis* and *Setaria italica* model genetic systems for the panicoid grasses. J Exp. Bot 2011;31:1-7.
- Marathe JP. Structure and characteristics of the world millet economy. Advances in small millets (Riley KW, Gupta SC, Seetharam A and Mushonga JN, eds.). New Delhi, India: Oxford & IBH. 1993, 159-178.
- Nirmalakumari A, Vetriventhan M. Characterization of foxtail millet germplasm collections for yield contributing traits. Electronic Journal of Plant Breeding. 2010;1(2):140-147.

14. Nirmalakumari A, Ganapathy S, Murugan R. Studies on variability and descriptive statistics in foxtail millet [*Setaria italica* (L.) Beauv.] germplasm. *Crop Research*. 2008;35(1-2):80-82.
15. Panse VG, Sukhatme PV. Statistically methods for agricultural workers. ICAR, New Delhi 1985, 359.
16. Prasada Rao KE, deWet JMJ, Brink DE, Mengesha MH. Intraspecific variation and systematic of cultivated *Setaria italica* (Graminae). *Econ. Bot* 1986;41:108-116.
17. Prasanna PL, Murthy JSVS, Kumar PVR, Rao SV. Nature of gene action for yield and yield components in exotic genotypes of Italian millet. [*Setaria italica* (L.) Beauv.]. *Journal of Plant Breeding and Crop Science*. 2013;5(5):80-84.
18. Selvarani M, Gomathinayagam SP. Genetic variability in foxtail millet [*Setaria italica* (L.) Beauv.]. *Crop Res* 2000b;20(3):553-554.
19. Sirisha ABM, Rao CP, Kumar PVR, Rao VS. Variability, character association and path coefficient analysis in italian millet [*Setaria italica* (L.) Beauv.]. *The Andhra Agricultural Journal* 2009;56(4):441-446.
20. Shingane S, Patil JV, Sunil G, Ganapathy KN. Genetic variability and association analysis for grain yield and nutritional quality in foxtail millet. *International Journal of Bio-Resource and Stress Management* 2016;7(6):1239-1243.
21. Sivasubramanian V, Madhavamenon P. Path analysis for yield and yield components of rice. *Madras Agric. J* 1973;60:1217-1227.
22. Tyagi V, Ramesh B, Kumar D, Sukrampal. Genetic architecture of yield contributing traits in foxtail millet (*Setaria italica*). *Current Advances in Agricultural Sciences* 2011;3(1):29-32.
23. Yogeesh LN, Shankar KA, Prashant SM, Lokesh GY. Genetic variation and morphological diversity in foxtail millet. *International Journal of Science, Environment and Technology* 2015;4(6):1496-1502.