



CHARACTERIZATION OF VARIABILITY AND DIVERSITY IN FOXTAIL MILLET (*SETARIA ITALICA*.BEAUV) GERMPLASM COLLECTION FOR YIELD AND ITS CONTRIBUTING TRAITS

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ABSTRACT

Foxtailmillet (*Setaria italica* L.Beauv) accessions were evaluated for extent of genetic variation and morphological diversity for seed yield and yield attributes.139 foxtailmillet accessions were collected from ICRISAT and NBPGR New Delhi. And were evaluated for variability and diversity in different characters at Department of Genetics and Plant Breeding, SamHigginbottom University of Agriculture, Technology and Sciences, Allahabad (U.P).The accessions were Experimented in Randomized Block Design Pradesh, 211007, India, with three replications observations were taken for quantitative traits Days to 50% flowering ,Days to 75% maturity Plant height, Leaf width, Leaf length, Peduncle length, Panicle length, Panicle weight, Biological yield, Grain yield.139 genotypes are grouped into 12 clusters. cluster V,XII is largest clusters having 23 genotypes followed by VII, IX(18), XI(15), VI(14), II (6), I, III, X(5),IV(4),VIII(3) the genotypes present in these clusters may be used as parents for Further hybridization programme to develop desirable types.

KEYWORDS: Genotypes, Variability, Diversity, Cluster, Foxtailmillet, hybridization.

INTRODUCTION

Foxtailmillet (*Setaria italica* L. Beauv), a self pollinating crop ($2n=18$) grouped under the family Graminae and Subfamily Ponicodeae (Fedoror,1974). It is cultivated in about 26 countries, and ranks second among the millets regarding world production. Around six million tons of foxtail millet is produced globally ; mostly in the southern part of Europe, in topical, sub-tropical and temperate Asia (Marathee,1993). Millets were domesticated same 8000 years ago in the highlands of central China (Amgai *et al.*, 2011). Foxtail millet is an Important cereal since old times and has critical role in advancement of human civilization in Asia and Europe (Li *et al.*, 1996; Lu *et al.*, 2009) foxtail millet is hardy and has the potential to develop well in draught stressed conditions (Singh *et al.*, 2015) foxtail millet generally grown in semi –arid regions has a low water requirement and can be considered as a second crop after wheat or barely, the major cereals. This is because of its short life cycle (Brink, 2006).

In India it is grown in semiarid regions of Andhra Pradesh, Karnataka, Maharashtra, Tamilnadu, Rajasthan, Madhya Pradesh, Uttar Pradesh and North Eastern states of our country. There are limited research and handful of Publication on this underutilized crop in this country Thus this research can act as a pivotal study as an initiation as well as a reference for further researches on foxtail millets the objective of this study was to evaluate the variability and a diversity among foxtail millet accession collected from ICRISAT and NBPGR New Delhi this research ultimately contribute exploitation of genetic makeup of available accessions and characteristics of plants for future breeding research.

MATERIALS & METHODS

Field Experiment was carried out at Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (U.P). About 139 accessions of foxtail millet collected from ICRISAT and NBPGR New Delhi. Accessions were sown in Randomized Block Design along with check and evaluated in field during *Kharif* 2017. The sowing was done on in July 15, 2017 and crop was raised with protective irrigation NPK Fertilizer dose was applied (40:20:0Kg/ha).The spacing between plant to plant 10cm and row to row 30cm was maintained. At the time of maturity 5plants are selected at random from each genotype were tagged in each replication and average of these five plants for each quantitative character was made to compute mean for further analysis the observations *viz.*, Days to 50% flowering, Days to 75% maturity, Plant height, Leaf width, Leaf length, Peduncle length, Panicle length, Panicle weight, Biological yield, Grain yield were recorded.

RESULTS AND DISCUSSION

Genetic Variability

Analysis of variance reveled all the genotypes exhibited significant difference in respect of Plant height, Leaf length, Days to 75% maturity, Days to 50% flowering indicating the presence of genetic variability and the choice of the material for the investigation is appropriate one of the ways to appreciate the extent of variability is examine the range which reflects the extent of phenotypic variability in respect of the trait under consideration, encompassing genotypic, environmental and interaction

components. In this present study foxtail millet genotypes exhibited considerable amount of variation for character Plant height, Days to 50% flowering, Days to 75% maturity, Leaf length, high range values indicate good scope for selection for any trait of interest for the breeder to exercise his selection.

Although range can provide a preliminary idea about the variability, it has to be confirmed by the magnitude of variance. Further for comparing the variability of one character with another coefficient of variation which is independent of unit of measurement is preferred. The phenotypic coefficient of variation and genotypic coefficient were low to high for characters. As expected the PCV values were greater than the GCV values for all the characters indicating considerable influence of environment on the expression of these characters under field conditions.

High estimates of genetic variability and phenotypic variability were recorded for Plant height, Leaf length, Days to 75% maturity, Days to 50% flowering there by indicating the presence of sufficient genetic variability over which selection can be more affective. In present investigation the estimates of heritability were found Plant height, Leaf width, Biological yield, Panicle weight, Grain yield, Days to 75% maturity, Days to 50% flowering, Peduncle length, Leaf length high value of heritability

indicates that the character is least influenced by environment. Genetic advance as percent of mean was high for Grain yield, Panicle weight, Biological yield, Panicle length, Leaf length, Leaf width, Days to 50% flowering. Genetic advance as percent of mean was moderate for Days to 75% maturity.

GENETIC DIVERSITY

139 accessions were grouped into 12 clusters. Cluster iv and xii had the maximum number of (23) genotypes, followed by cluster vii and ix (18), cluster xi (15), cluster vi (4), cluster ii (6), cluster I, iii, and v having (5) genotypes, cluster iv (4), cluster vii (3). As selected Murthy and Arunachalam (1966), this parallelism may be due to genetic drift and intense natural and human selection for diverse adaptive gene complexes under different environments causing greater diversity among genotypes rather than their geographic distance. Further genotypes present in the more distanced clusters will serve as good source of divergent genes which is very much required for breeding to exploit heterosis as reported by Gill *et al.* (1995) or end to get good transgressive segregants in the segregating population. Genotypes present in these clusters may be used as parents for hybridization programmes to develop desirable types.

TABLE1: Mean Sum of Squares different quantitative parameters in 139 Foxtail millet (*Setaria italica* L. Beauv) genotypes

S.No	Character	Mean Sum of Squares		
		Replications (d.f =2)	Treatments (d.f =138)	Error (d.f =276)
1.	Days to 50% flowering	2.91	162.17**	4.30
2.	Days to 75% maturity	11.94	174.06**	4.36
3.	Plant height	5.10	1013.43**	59.81
4.	Leaf width	0.006	0.24**	0.013
5.	Leaf length	1.76	182.80**	0.93
6.	Peduncle length	0.02	66.89**	0.92
7.	Biological yield	0.54	9.15**	0.31
8.	Panicle length	0.31	51.42**	1.032
9.	Panicle weight	0.098	1.84**	0.047
10.	Grain yield	0.04	1.40**	0.035

TABLE 2: GCV, PCV parameters for different quantitative characters in foxtail millet (*Setaria italica* L. Beauv)

S.No	Character	σ^2_g	σ^2_p	GCV	PCV	h^2 (B.S.)	GA	GA as % of mean
1	Days to 50% flowering	52.62	56.9	13.15	13.62	92.0	14.36	25.94
2	Days to 75% maturity	56.56	60.9	9.183	9.531	92.0	14.92	18.22
3	Plant height	317.8	377.6	21.98	23.96	84.0	33.69	41.55
4	Leaf width	0.078	0.09	18.88	20.43	85.0	0.53	35.97
5	Leaf length	60.62	61.50	23.35	23.53	98.0	15.91	47.75
6	Peduncle length	21.9	22.9	0.92	20.04	96.0	9.46	40.45
7	Biological yield	2.95	3.26	0.31	43.62	90.0	3.36	85.48
8	Panicle length	16.7	17.8	1.03	28.43	94.0	8.19	56.85
9	Panicle weight	0.59	0.64	0.04	49.22	92.0	1.53	97.62
10	Grain yield	0.45	0.49	0.03	55.25	92.0	1.33	109.61

TABLE 3: Clustering Pattern of Foxtail millet (*Setariaitalica*L.Beauv) accessions based on morphological traits

S.NO	Cluster number	Number of genotypes	Genotypes Included
1.	I	5	Ise2, Ise132, Ise375, Ise507, Ise710.
2.	II	6	ise1269,ise1299,ise1474,Gs86,ise1254,Ise1563.
3.	III	5	Ise1037, ise1161, ise719, ise1067, ise1187.
4.	IV	4	Ise1335, ise1209, ise1181,ise1335.
5.	V	23	Ise907,Gs490,Gs384,Gs309,Gs48,Gs45, Gs292,Gs354,Gs32,Gs63,Gs51,Gs586, Gs302,Gs314,Gs52,Gs50,Gs4,Gs330, GS3, GS300,Gs44,Gs1,Gs320
6.	VI	14	Ise1892,Gs306,ise963,Gs293,Gs6, GS313, GS349, ise745,Gs298,Gs299, GS18,Gs588,Gs291,Gs29.
7.	VII	18	GS19,Gs328,Gs60,Gs316,Gs62,Gs5, GS22,Gs85,Gs87,Gs326,Gs301,Gs350,Gs369,Gs294,Gs8,Gs35,Gs89, GS382.
8.	VIII	3	Ise1059, ise1685,ise1541.
9.	IX	18	Ise1305,ise1655,ise376,Gs337,Gs548, GS319,Gs303,ise375,ise1468,ise1820, GS11,Gs61,ise783,Gs9,Gs25,Gs584, GS297,Gs56.
10.	X	5	Ise1736,ise745 ,ise1704,Gs585,ise1302.
11.	XI	15	Ise1687,Gs37,Gs356,Gs295, GS385,Gs51,Gs2,Gs581,Gs30 GS38,Gs64,Gs304,Gs54,Gs36, GS54
12.	XII	23	GS386,Gs505,Gs296,Gs53, GS13,Gs329,ise1610,ise188, GGS305,Gs389,Gs368,Gs332, GS55,Gs23,Gs14,Gs307,Gs69 GS587,Gs380,Gs324,Gs47, GS222,Gs564

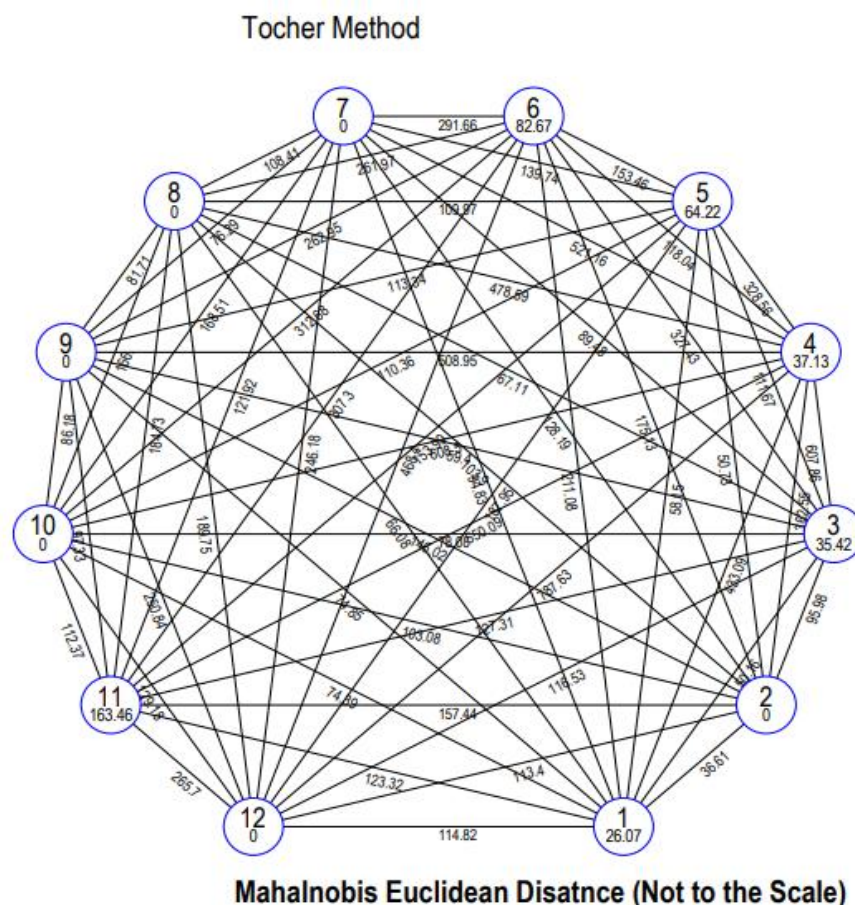


FIGURE 1: Intra and inter cluster distance diagram for different quantitative andphysiological characters in foxtail millet(*Setariaitalica*L.Beauv).

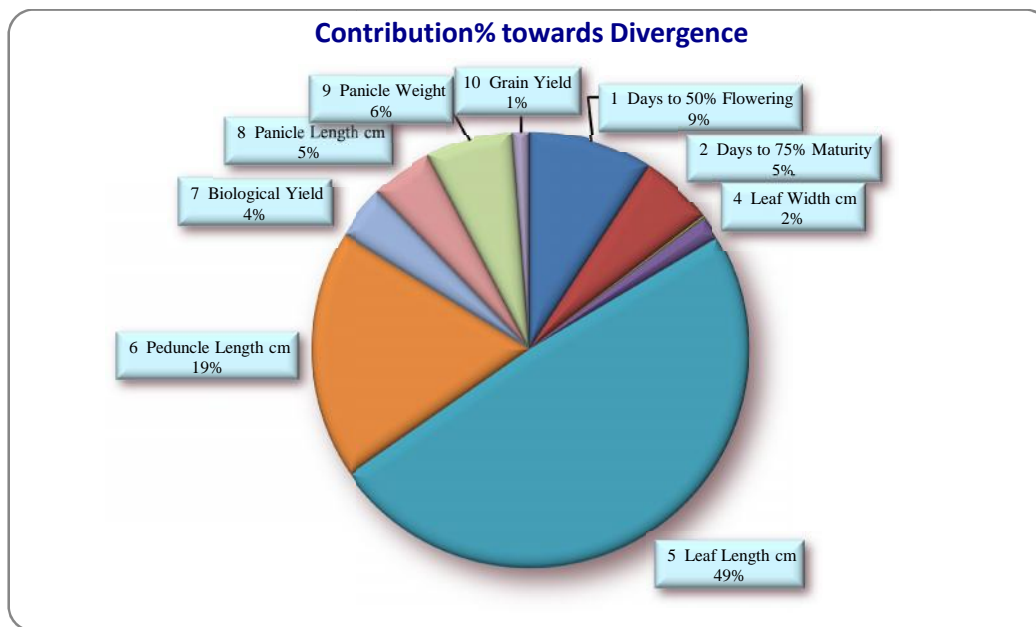


FIGURE 2: Contribution of % towards Divergence

CONCLUSION

On the basis of the results of the experiment it can be concluded that, considerable amount of genetic variability was observed in the studied genotypes for root and shoot traits. The values of PCV were higher in magnitude than GCV for all the characters, it means that little influence of environment on the expression of all traits and most of the characters exhibit high heritability with high genetic advance. 139 genotypes are grouped into 12 clusters. Cluster V, XII IS largest cluster having 23 genotypes followed by VII, IX(18), XI(15), VI(14), II(6), I, III, X(5), IV(4), VIII(3). This parallelism may be due to genetic drift and natural and human selection for diverse adaptive gene complexes under different environments causing greater diversity among genotypes rather than their geographical distances Breder have opportunity to select the divergent parents and he can go for further breeding work.

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