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Research Article

DIVERSITY STUDIES IN LITTLE MILLET THROUGH PCA ANALYSIS: MULTIVARIATE ANALYSIS

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Abstract- The present study was conducted to evaluate genetic diversity analysis for grain yield, its components as well as quality parameters along with 19 observations in 50 little millet genotypes under three environments *i.e.*, Waghai, Vanarasi and Navsari locations, Gujarat, India in year *Kharif*-2020. PCA analysis revealed that the first two components in the PCA analysis were with eigen values more than one and contributed to a maximum of 92.14 per cent of the variability among 50 genotypes evaluated for nineteen different traits. Based on scatter plot matrix, genotypes *viz*., WV 303, WV 275, WV 278, WV 281, WV 292, WV 299, WV 263, WV 296 and WV 259 were scattered across apart in the biplot indicated high genetic divergence across the genotypes. Genotypes viz., WV 287, WV 258, WV 260 and WV 272 were found to be closer to the origin and each other, indicated minimal genetic divergence. PCA analysis revealed that the first two PCs were more divergent along with different positive signifying genotypes for different characters would be utilized in hybridization programmes to produce superior recombinants in little millet breeding. These genotypes may be used in further breeding programme in little millet.

Keywords- *Little millet, Diversity, PCA analysis, Grain yield*

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Introduction

Little millet is one of the coarse cereals consumed in the form of rice. It is self-pollinated crop with a chromosome number of 2n=4x=36. Little millet belongs to the family Poaceae, sub-family Panicoideae and the tribe Paniceae [1]. Little millet's inflorescence is a panicle, contracted or thyrsiform and 15-45 cm long and 1-5 cm in wide [2]. The spikelet is persistent and 2-3.5 mm long. Panicle branches are scabrous and drooping at the time of maturity. Spikelets were produced on unequal pedicels but solitary at the end of the branches. Each spikelet consisted of two-minute flowers. The lower one is sterile; the upper one is fertile or bisexual without rachilla extension [3]. The lateral vein is absent in lower glume and its apex is acute. The upper glume is ovate and without keel but larger than lower glume [4]. The flowering progressed from the top to the bottom of the panicle. The anthesis occurred between 9.30 to 10.30 a.m. [5]. The glumes open for a short while and self-pollination is the rule. The whole process of the anthesis is very rapid and is completed within 2-5 min.

Little millet (*Panicum sumatrense* L.) is grown in India under various agro-ecological situations and commonly known as samai, samo, moraio, vari and kutki. Little millet is an important crop grown in the tribal belt of Madhya Pradesh, Chhattisgarh, Gujarat, Maharashtra, Odisha and Andhra Pradesh in India. In India, little millet having 1.42 lakh tones of production. In Gujarat, little millet is cultivated in an area of 10,634 hectares with 9,526 tonnes of production having the productivity of 896 kg/ha [6]. The area under this crop is mainly concentrated in the districts of Dangs, Valsad and Narmada of South Gujarat and Panchmahal of middle Gujarat.

Little millet is better as comparable to other cereals in terms of fiber, fat, carbohydrates, protein, calcium, iron and rich in phytochemicals included phenolic acids, flavonoids, tannins and phytate. Therefore, it could address nutritional sensitive agriculture, which aimed at nutritional enhancement to combat the present scenario of micronutrient malnutrition. Little millet is known for its drought tolerance and considered as one of the least waters demanding crop.

Crop improvement work carried out so far in this crop has thrown some success. In the recent past some improved cultivars were developed but have limited yield potential. The potentiality of little millet has not been exploited in India and the yield levels were very low there by indicated a greater scope for exploitation of little millet under Indian condition.

Principal component analysis (PCA) and cluster analysis had been very important for selecting genotypes for breeding program that could meet the objective of a plant breeder. The main advantage of using PCA over cluster analysis was that each genotype was assigned to one group only. Precise information on the nature and degree of genetic diversity could help the plant breeder in choosing the diverse parents for purposeful hybridization.

Materials and methods

The experiment was conducted during Kharif-2020 having 50 little millet genotypes, *viz*., WV 254, WV 255, WV 256, WV 257, WV 258, WV 259, WV 260, WV 261, WV 262, WV 263, WV 264, WV 265, WV 266, WV 267, WV 268, WV 269, WV 270, WV 271, WV 272, WV 273, WV 274, WV 275, WV 276, WV 277, WV 278, WV 279, WV 280, WV 281, WV 282, WV 283, WV 284, WV 285, WV 286, WV 287, WV 288, WV 289, WV 290, WV 291, WV 292, WV 293, WV 294, WV 295, WV 296, WV 297, WV 298, WV 299, WV 300, WV 301, WV 302 and WV 303 were evaluated in randomized block design at Hill Millet Research Station, Navsari Agricultural University, Waghai, Gujarat, India; Niger Research Station, Navsari Agricultural University, Vanarasi, Gujarat, India and College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India during Kharif-2020. The seedlings were planted at 22.5 x 10 cm^2 spacing. All recommended practices were followed and timely plant protection measures were taken to avoid damage through insect-pests and diseases.

The observations on five randomly selected plants were recorded for 19 characters *viz*., days to 50% flowering, days to maturity, plant height (cm),

productive tillers per plant, panicle length (cm), spikes per panicle, 1000 grain weight (g), grain yield per plant (g), fodder yield per plant (g), harvest index (%), hulling (%), chlorophyll content (mg/100g fresh weight), leaf area (cm^2), protein content (%), crude fiber (%), mineral matter (mg/100g), iron content (mg/100g), calcium content (mg/100g) and ash content (mg/100g). A method suggested by Karl Pearson (1901) [7] known as PCA is used as a powerful tool for quantifying the divergence in present studies.

Results and Discussions

Principal component analysis was applied as a reductionist approach of the multivariate data, to measure the importance and contribution of each component to total variance. PCA provided information on the independent impact of a particular trait to the total variance, wherein each coefficient of eigen vectors indicated the degree of contribution of every original variable, with which each principal component was associated.

PCA analysis revealed that the first two components in the PCA analysis were with eigen values more than one and contributed to a maximum of 92.14 per cent of the variability among 50 genotypes evaluated for nineteen different traits. These two principal components were retained based on the scree plot and threshold eigen value greater than 1 [Fig-1], [Table-1]. The principal component with eigen values less than one were considered as non-significant.

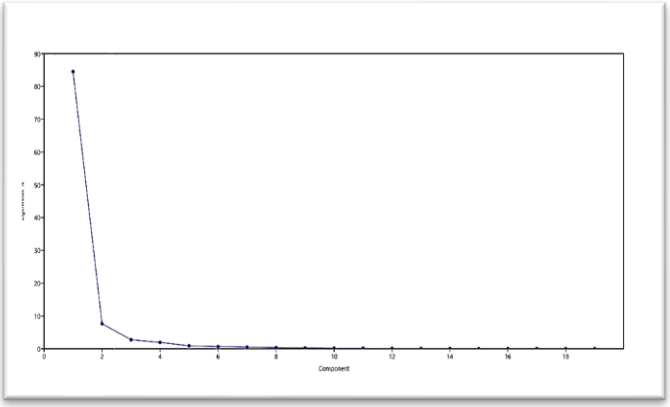

Fig-1 Scree plot formation on the basis of eigen values

Table-1 Principal components showing eigen values, proportion of variation and cumulative variance explained

Principal component	Eigen Value	Variation (%)	Cumulative variance (%)
PC-1	16.06	84.53	84.53
PC-2	1.45	7.61	92.14
PC-3	0.52	2.76	94.90
PC-4	0.37	1.94	96.84
PC-5	0.17	0.89	97.73
PC-6	0.13	0.68	98.41
PC-7	0.10	0.51	98.92
PC-8	0.07	0.35	99.27
PC-9	0.04	0.23	99.50
PC-10	0.03	0.15	99.65
PC-11	0.02	0.13	99.78
PC-12	0.02	0.09	99.87
PC-13	0.01	0.07	99.94
PC-14	0.01	0.04	99.97
PC-15	0.00	0.01	99.98
PC-16	0.00	0.01	99.99
PC-17	0.00	0.00	100.00
PC-18	0.00	0.00	100.00
PC-19	0.00	0.00	100.00

Ladumor *et al*. (2021) [8] assessed the important traits using principal component analysis which indicated that two principal components PC-1 and PC-2 contributed 74.89% and 24.26%, respectively of the maximum total variation.

Out of two principal components, only the first principal component showed 84.53 per cent of the entire variability. The first principal component revealed 84.53 per cent of total variability due to high and positive loading of days to 50% flowering, days to maturity, plant height (cm),productive tillers per plant, panicle length (cm), spikes per panicle, 1000 grain weight (g), hulling (%), chlorophyll content (mg/100g fresh weight), leaf area (cm^2), protein content (%), crude fiber (%), mineral matter (mg/100g), iron content (mg/100g), calcium content (mg/100g) and ash content (mg/100g) among two principal components.

Second principal component accounted for 7.61 per cent of total variability originated primarily due to high and positive loading of grain yield per plant (g), fodder yield per plant (g) and harvest index (%) among two principal components [Table-1 and 2].

Table-2 Principal component analysis for nineteen different traits in fifty little millet genotypes non-rotated loadings

Particulars	PC-1	PC-2
Days to 50% flowering	0.24	-0.21
Days to maturity	0.24	-0.21
Plant height (cm)	0.23	-0.22
Productive tillers per plant	0.24	-0.21
Panicle length (cm)	0.24	-0.22
Spikes per panicle	0.24	-0.22
1000 grain weight (g)	0.20	-0.12
Grain yield per plant (g)	0.20	0.46
Fodder yield per plant (g)	0.20	0.40
Harvest index (%)	0.18	0.47
Hulling (%)	0.23	0.13
Chlorophyll content (mg/100g fresh weight)	0.24	0.08
Leaf area (cm^2)	0.24	-0.03
Protein content (%)	0.23	-0.18
Crude fiber (%)	0.24	0.05
Mineral matter (mg/100g)	0.24	-0.07
Iron content (mg/100g)	0.23	0.15
Calcium content (mg/100g)	0.24	0.14
Ash content (mg/100g)	0.24	0.04

Dagnachew *et al*. (2012) [9] reported that first two principal components of grain yield per plant, 1000-seed weight and days to heading were the most important traits contributed more towards the total divergence. Jadhav *et al*. (2014) [10] reported that number of productive tillers per plant, ear weight per plant, days to maturity, days to 50% flowering, number of fingers per ear, plant height, 1000-seed weight, seed yield per plant and finger length contributed maximum towards divergence in PC-1. Ulaganathan and Nirmalakumari (2015) [11] reported that the characters *viz*., days to 50% flowering, days to maturity, finger numbers per panicle, productive tillers per plant, finger length, finger width, 1000-grain weight and grain yield per plant were the most important traits contributed for the overall variability to the first four principal components. Patil *et al*. (2017) [12] reported that first principal component had been positively accounted for all characters. PC-2 had been positively accounted for days to 50% flowering, days to maturity and plant height. Savankumar *et al*. (2017) [13] reported that first principal component had showed positive loading for all eight characters considered except for number of tillers per plant. The second principal component had positive loading for two characters *viz*., number of tillers per plant and grain yield. Patro *et al*. (2018) [14] reported that characters *viz*., days to 50% flowering, days to maturity, straw yield per plot and numbers of finger per ear found maximum lodging values toward total divergence in PC-1. Suman *et al*. (2019) [15] reported that characters included grain yield per plant, 1000-grain weight, productive tillers per plant, days to flowering, days to maturity, finger number per panicle, finger length and finger width were the most important traits contributing for the overall diversity. Ladumor *et al*. (2021) assessed PC1 axis which accounted for days to 50% flowering, days to maturity, plant height, main ear head length, finger length and harvest index contributed maximum towards divergence. On other axis, positive side of PC-2 which accounted for chlorophyll content was important traits contributed maximum towards divergence.

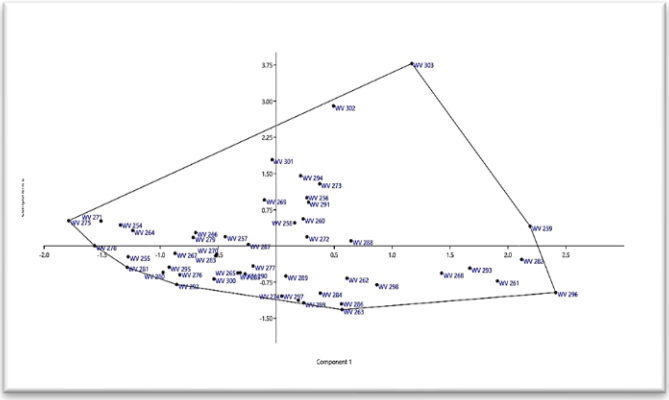

Fig-2 Bi-plot showing variation on basis of scores of fifty little millet genotypes in principal component analysis

The positive and negative loading showed the presence of positive and negative correlation trends between the components and the variables. Therefore, the characters which loaded positively contributed more to the diversity.

The first two PCs were used to create the biplot which showed the scattering pattern of 50 little millet genotypes. Bi-plot represented distribution of accessions based on PC-1 and PC-2 scores and relationship of different traits with PC-1 and PC-2 [Fig-2]. More similar genotypes were those that are dispersed closer to the origin and closer to one other, whereas genotypes that were scattered further apart were more divergent.

Genotypes *viz*., WV 303, WV 275, WV 278, WV 281, WV 292, WV 299, WV 263, WV 296 and WV 259 were scattered across apart in the biplot indicated high genetic divergence across the genotypes. Genotypes *viz*., WV 287, WV 258, WV 260 and WV 272 were found to be closer to the origin and each other, indicated minimal genetic divergence.

Genotypes selected based on PC score in PC 1 having high and positive values were WV 296, WV 259, WV 282, WV 261, WV 293, WV 268, WV 303, WV 298, WV 288, WV 262, WV 263, WV 286, WV 302, WV 284, WV 273, WV 291, WV 272, WV 256, WV 299, WV 260, WV 294, WV 297, WV 258, WV 289 and WV 274 [Table-3].

Table-3 Principal factor scores of fifty little millet genotypes in two major principal components

Genotypes	PC 1	PC 2	Genotypes	PC 1	PC 2
	X Vector	Y Vector		X Vector	Y Vector
WV 254	-1.34	0.43	WV 279	-0.72	0.18
WV 255	-1.28	-0.22	WV 280	-0.98	-0.55
WV 256	0.26	1.00	WV 281	-1.28	-0.44
WV 257	-0.44	0.19	WV 282	2.12	-0.28
WV 258	0.16	0.48	WV 283	-0.52	-0.20
WV 259	2.19	0.41	WV 284	0.38	-0.98
WV 260	0.23	0.56	WV 285	-0.31	-0.56
WV 261	1.91	-0.73	WV 286	0.56	-1.20
WV 262	0.61	-0.67	WV 287	-0.24	0.03
WV 263	0.57	-1.32	WV 288	0.64	0.11
WV 264	-1.24	0.32	WV 289	0.08	-0.62
WV 265	-0.33	-0.56	WV 290	-0.27	-0.58
WV 266	-0.69	0.28	WV 291	0.28	0.91
WV 267	-0.87	-0.15	WV 292	-0.86	-0.80
WV 268	1.43	-0.57	WV 293	1.67	-0.46
WV 269	-0.10	0.95	WV 294	0.21	1.45
WV 270	-0.51	-0.18	WV 295	-0.92	-0.44
WV 271	-1.51	0.52	WV 296	2.41	-0.97
WV 272	0.27	0.19	WV 297	0.19	-1.13
WV 273	0.37	1.29	WV 298	0.87	-0.80
WV 274	0.05	-1.04	WV 299	0.24	-1.18
WV 275	-1.79	0.52	WV 300	-0.54	-0.68
WV 276	-0.83	-0.60	WV 301	-0.03	1.79
WV 277	-0.20	-0.41	WV 302	0.49	2.90
WV 278	-1.57	0.01	WV 303	1.17	3.78

Genotypes selected on the basis of PC score in PC 2 having high and positive values were WV 303, WV 302, WV 301, WV 294, WV 273, WV 256, WV 269, WV 291, WV 260, WV 275, WV 271, WV 258, WV 254, WV 259, WV 264, WV 266, WV 257, WV 272, WV 279, WV 288, WV 287 and WV 278.

From the results it could be concluded that the genotypes *viz*., WV 296, WV 259, WV 282, WV 261, WV 293, WV 268, WV 303, WV 298, WV 288, WV 262, WV 263, WV 286, WV 302, WV 284, WV 273, WV 291, WV 272, WV 256, WV 299, WV 260, WV 294, WV 297, WV 258, WV 289 and WV 274 were accumulated positively on the side of PC1 axis which accounted for days to 50% flowering, days to maturity, plant height (cm),productive tillers per plant, panicle length (cm), spikes per panicle, 1000 grain weight (g), hulling (%), chlorophyll content (mg/100g fresh weight), leaf area (cm^2), protein content (%), crude fiber (%), mineral matter (mg/100g), iron content (mg/100g), calcium content (mg/100g) and ash content (mg/100g) that contributed maximum towards divergence.

On other axis PC-2, genotypes *viz*., WV 303, WV 302, WV 301, WV 294, WV 273, WV 256, WV 269, WV 291, WV 260, WV 275, WV 271, WV 258, WV 254, WV 259, WV 264, WV 266, WV 257, WV 272, WV 279, WV 288, WV 287 and WV 278 were accumulated positively on the side of PC-2 which accounted for grain yield per plant (g), fodder yield per plant (g) and harvest index (%) that contributed maximum towards divergence. PC-1 and PC-2 were providing maximum genetic variation. This type of results was reported by Dagnachew *et al*. (2012), Jadhav *et al*. (2014), Ulaganathan and Nirmalakumari (2015), Patil *et al*. (2017), Savankumar *et al*. (2017), Patro *et al*. (2018), Suman *et al*. (2019) and Ladumor *et al*. (2021).

Conclusion

The central idea of principal component analysis was to reduce the dimensionality of a data set in which there were many interrelated variables, while retaining as much as possible of the variation present in the data set. The positive signifying genotypes could be useful in little millet breeding.

Application of research: These genotypes could be utilized in hybridization programmes to produce superior recombinants.

Research Category: Millet Research

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Research project name or number: Research station study

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Study area / Sample Collection: Hill Millet Research Station, Waghai, 389151

Cultivar / Variety / Breed name: Little millet (*Panicum sumatrense* L.)

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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