Original Research Article

Multivariate ~~Analysis Through Principal Components~~analysis through principal components for ~~Yield Attributing Traits~~yield-attributing traits in Indigenous Moringa (*Moringa oleifera* L.) Germplasm Lines

Abstract:

The present investigation ~~entitled~~ was carried out ~~at~~at the Department of Vegetable Crops, Horticultural College and Research Institute (HC&RI), Tamil Nadu Agricultural University, Periyakulam during 2016 -2017. With twenty genotypes in order to study the genetic diversity for different yield attributing characters of Moringa by principal component analysis. In this study, out of twelve principal components, only five components exhibited eigenvalue and showed about 99.54% variability among the traits within the axes exhibited great influence on the phenotype of genotypes. The PC1 accounted for the highest variability (62.20%), followed by 28.86% (PC5), 6.25% (PC10), 1.01% (PC7) and 0.75% (PC4). ~~Thus~~Thus, the results of the principal component analysis ~~revealed,~~revealed that wide genetic variability exists in ~~this~~these Moringa genotype accessions.

Key words: Moringa (*Moringa oleifera* L.),Genotypes, PCA analysis, Eigen Values

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Introduction:

Moringa (*Moringa oleifera* L.), ~~belonging~~which belongs to the family Moringaceae, is a highly useful vegetable crop and native ~~of~~to India. In India it is grown all over the ~~subcontinent~~ region for its tender pods and also for its leaves and flowers. ~~The plants~~Plants have always been vital ~~for mankind~~to mankind, irrespective ~~of the~~of era and area, all over the ~~globe~~world since the beginning of life. Popularly known as ‘‘Drumstick’’ tree, horseradish tree, or Ben tree, *M. oleifera* is a deciduous-to-evergreen shrub or small tree with a height of 5 to 10 m (Morton, 1991).Unfortunately, limited work has been done on the understanding of its detailed germplasm characterization. Detailed studies of the distribution and genetic variability of moringa species are limited. However substantial variations in quantitatively inherited traits have been documented in natural population from India. In order to do breeding for increase the yield, information on genetic variability is the prerequisite since it is the source of variation and raw material for yield improvement work. Assessment of genetic variability is also needed for efficient parent selection in breeding program (Rahman *et al.*, 2011), ~~long term~~long-term selection gain and exploitation of heterosis(Rahman *et al.*, 2012).Moreover, the evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (N.Tomooka,1991).Principal component analysis (PCA) involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal component (C Chatfield and Collis, 1980).PCA is an important statistical method through which we can easily identify important polygenic characters which are of great importance in a plant breeding programme. PCA provides an idea for how to reduce a complex data set to a lower dimension to reveal the sometimes hidden, simplified structures that often underlie it. The eigenvalue of a particular principal component depicts the amount of variation present in traits ~~and~~and is explained by that principal ~~component~~component, which is very useful for the further breeding programme. Incomplete

Specific comment for your

The author should rewrite the research gab and a possible explanation of how these gab are addressed in the present study.

The author mentioned that the eigenvalue related to PCA is an important tool for elucidating the variability of the genotype, but the detail information from previous research on how to use the eigenvalue and its implication is poorly indicated. Furthermore, how the author

Comment [AT2]: Please rewrite it

Comment [AT3]: Is this vernacular name ?? verify

Comment [AT4]: I found that many research emphasis on genetic diversity of moringa oleifera were studied, as compared to the other species. However, environmental factor may be influencing this diversity and updating the recently diversity is important.
But please paraphrase your research gab accordingly and be sure that your research gab is not addressed elsewhere. Otherwise, your research report may be duplication effort with no scientific impact.

Comment [AT5]: Which yield leaf, seed or biomass production

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uses the eigenvalue to quantify the genetic variability could not be explained well. No clear objective.

Therefore, the author highly recommended revising the introduction part of the study.

Materials and Methods:

The present investigation was carried out to ~~know~~understand the variability through principal ~~component analysis~~components in Moringa (*Moringa oleifera* L.)germplasms cultivated in Telangana State at Department of Vegetable Crops, Horticultural College and Research Institute (HC&RI), Tamil Nadu Agricultural University, Periyakulam (PKM) during 2016 -2017.Twenty moringa accessions were collected from different regions of Telangana and the details of the plant materials used in the present study are listed in Table 1.

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Table .1. List of Moringa accessions ~~employed~~used in the study

S.No.	Name of the Accessions	Name of the Type	Place of collection & District	Latitude & Longitude
1.	MO 1	Long poded perennial type	Warangal, Warangal	18^0 0` 38.60N, 79^0 36'0 .10 E
2.	MO 2	Long poded perennial type	Malyal, Warangal	18^0 21' 48.80 N, 80^0 18' 23.66 E
3.	MO 3	Medium poded perennial type	Ghanpur, Warangal	17^0 49' 58.89 N, 78^0 59' 57.35 E
4.	MO 4	Short poded perennial type	Regonda, Warangal	18^0 23' 77.70 N, 79^0 77' 50.80 E
5.	MO 5	Long podedperennial type	Jagithyala, Karimnagar	18^0 46'0.66 N, 78^0 54'42 .83 E
6.	MO 6	Short poded perennial type	Peddapally, Karimnagar	18^0 37' 24.72 N, 79^0 22' 47.59 E
7.	MO 7	Short poded perennial type	Armor, Nizamabad	18^0 48' 37.14 N, 78^0 17' 7.00 E
8.	MO 8	Short poded perennial type	Nandipeta, Nizamabad	18^0 52' 34.06 N, 78^0 31' 14.68 E
9.	MO 9	MediumPoded perennial type	Rudrur, Nizamabad	18^0 34' 45.48 N, 77^0 52' 31.27 E
10.	MO 10	Short poded perennial type	Satyanarayanapuram,Nizamabad	18^0 32' 40.61 N, 77^0 53' 31.39 E
11.	MO 11	Medium poded perennial type	Basara, Nirmal	18^0 52' 40.63 N, 77^0 56' 57.01 E

12.	MO 12	Short poded perennial type	Mudhol, Nirmal	18^0 98' 26.81 N, 77^0 92' 05.10 E
13.	MO 13	Short poded perennial type	Ichoda, Adilabad	19^0 26' 1.02 N, 78^0 27' 14.82 E
14.	MO 14	Short poded perennial type	Adilabad, Adilabad	19^0 38' 53.14 N, 78^0 31' 14.68 E
15.	MO 15	Medium poded perennial type	Amaravathi,Manchiriyal	18^0 54' 15.05 N, 79^0 28' 58.30 E
16.	MO 16	Short poded perennial type	Doragaripalli, Manchiriyal	18^0 53' 59.5 N, 79^0 27' 41.2 E
17.	MO 17	Medium poded perennial type	Kyathanpalli, Manchiriyal	18^0 55'18.8 N, 79^0 28' 13.4 E
18.	MO 18	Short poded perennial type	Suryapeta, Nalgonda	17^0 14' 8.70 N, 79^0 36' 34.07 E
19.	MO 19	Medium poded perennial type	Gollapally, Nalgonda	17^0 31' 23.59 N, $80^0$52' 19.91 E
20.	MO 20	Short poded perennial type	Narayanapuram,Nalgonda	17^0 10' 36.74 N, 80^0 52' 19.91 E

Twenty moringa genotypes were evaluated by using IPGRI minimal descriptors. The recommended agronomic practices were followed.Observations were recorded for 12 morphological characters Principal component analysis (PCA) is an important multivariate method in modern data analysis because it is a simple, ~~non parametric~~nonparametric method for extracting relevant information from confusing data sets and it was applied for assessment of genetic diversity within moringa genotypes. Data were recorded on ten different ~~traits~~traits, *viz*. ~~plant~~Plant height stem girth (cm), leaf length (cm), number of leaves per rachis, length of leaf rachis, number of flowers per inflorescence, length of pod (cm), pod girth (cm), pod weight (g), number of pods per plant, number of seeds per pod, yield per plant (kg), The data on yield traits were statistically analyzed on the basis of a randomized complete block design. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an eigenvector for each axis and produces component scores for the characters (W. F. Massay, 1965), (I.T. Jolliffie, 1986).

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The authors presented poor methods that need major modification.

1. The author uses 20 genotypes and listed the collection site of each genotype but information on description of study area, agroecological description of the study area, inclusion criterion for genotype, planting and agronomic practice they applied during course of the trail, experimental layout and design were not included. The author advises to include this information and revise the methods section of the document.

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2. Among the listed 12 descriptors, some of them need explanation and it is recommended to add these explanations. When the authors recorded these descriptor? Please specify the exact time of data collection.
3. Which statistical software were used? Please specify the name and detail explanation for result interpretation

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Results and Discussion:

Twenty accessions of moringa collected from various parts of Telangana were evaluated for different morphological and biochemical traits. Observations on morphological, characters *viz.*, plant height (cm), stem girth(cm), leaf length (cm), number of leaves per rachis, length of leaf rachis, number of flowers per inflorescence, length of pod (cm), pod girth (cm), pod weight (g), number of pods per plant, number of seeds per pod, yield per plant(kg), Yield per plot.

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The accessions exhibited wide variability for morphological characters such as tree shape, tree nature, ~~colour of bark,~~bark colour, young shoot colour, foliage ~~density, nature of~~density, branch ~~lets,~~lets nature, leaflet shape, leaflet ~~apex, colour of~~apex, calyx and pod ~~maturity.~~maturity colour. Four morphological descriptors *viz*., duration of plant, type of planting material, shape of corolla and shape of calyx did not reveal any variation among the 20genotypes. The traits that ~~were showing~~showed variations revealed that most of the accessions possessed phenotypic variation among them.

PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set (W. F. Massay, 1965), (I.T. Jolliffie, 1986).The result of the PCA explained the genetic diversity of the moringagenotypes. There are no standard tests to prove the significance of proper values and coefficients. ~~Principal component~~The ~~analysis~~analysis of principal components has shown the genetic diversity ~~of the~~of germplasm lines. (Table 2) indicated that out of 12 principal components, only five components exhibited high eigenvalues and ~~showed~~showed a variability of about 99.54% variability among the traits studied. The PC1 had the highest variability (62.20%), followed by 28.86% (PC5), 6.25% (PC10), 1.01% ~~(PC7)~~(PC7), and 0.75% (PC4).

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Table 2 Eigen values, % variance and cumulative Eigenv alues of moriga germplasm

Traits	PC	Eigenvalue	Percentage of variation	Cumulative %
Plant height(cm)	PC1	2649.61	62.20	62.20
Stem girth(cm)	PC2	2.25	0.053	62.25

Leaf length(mm)	PC3	14.12	0.33	62.58
No.of leaves per rachis	PC4	32.08	0.75	63.34
Length of leaf rachis	PC5	1229.48	28.86	92.20
No of flower/infloresence	PC6	-2.08	-0.049	92.15
Length of pod(cm)	PC7	43.36	1.01	93.17
Pod girth(cm)	PC8	3.11	0.07	93.24
Pod weight(gr)	PC9	1.63	0.03	93.28
No of pods per plant	PC10	266.54	6.25	99.54
No of seeds per pod	PC11	15.42	0.36	99.90
Yield per plant(kg)	PC12	4.10	0.09	100.00

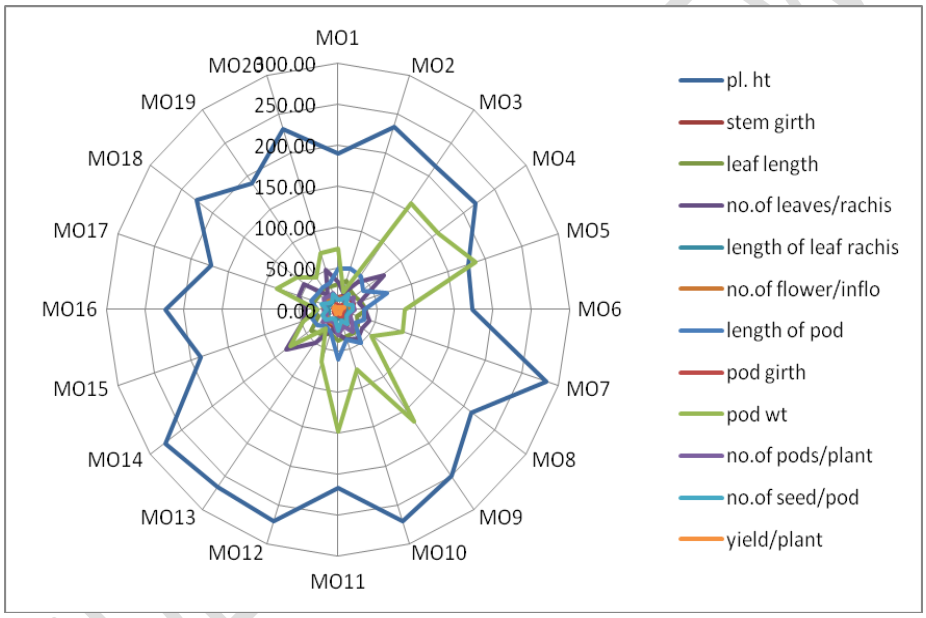

Figure 1: Radar diagram ~~showing~~showing the mean performance of 20 moringa germplasm lines for different yield traits

PC scores of genotypes

The PC scores of each component (PC1, PC2, PC3, PC4, PC5, PC6, PC7, PC8, PC9, PC 10, ~~PC11,~~PC11 and PC12) had positive and negative values (Table 3).In this pc score PC1, PC5, PC10, PC7 and PC4 or given high pc score ~~values These score~~values, these scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by

each principal component. A high PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype.

Table 3 PCA scores of moringa genotypes

Genotype	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
MO 1	5.926	20.841	11.157	16.129	10.557	61.487	14.830	200.187	18.472	6.201	3.466	41.701
MO 2	8.826	24.421	-4.302	17.494	12.464	70.445	15.679	231.834	20.405	5.828	4.10	-17.818
MO 3	9.801	22.129	19.591	17.334	11.383	52.714	13.755	243.949	27.398	14.740	3.50	119.532
MO 4	9.0280	19.058	51.668	14.773	10.750	52.310	14.964	249.686	28.665	-0.255	7.066	116.888
MO 5	9.438	24.090	2.652	16.157	11.771	56.790	14.522	211.174	29.096	8.777	8.866	155.363
MO 6	6.659	30.529	18.274	15.736	11.862	45.098	12.324	187.533	29.975	6.144	3.20	54.240
MO 7	8.143	18.603	19.994	17.591	13.014	52.620	14.964	295.488	22.169	6.807	4.133	33.407
MO 8	10.77	25.938	21.089	16.651	10.852	45.965	13.885	220.035	26.577	2.626	3.766	13.585
MO 9	9.632	27.914	18.995	18.321	12.683	53.608	15.095	279.457	39.805	3.322	6.50	119.361
MO 10	8.672	25.480	15.366	18.440	16.001	55.598	15.494	279.878	26.749	3.207	4.70	25.655
MO 11	10.231	28.840	3.475	15.021	13.360	60.951	13.869	242.304	40.651	6.729	4.00	108.928
MO 12	11.179	25.470	6.403	16.205	13.250	45.772	13.110	277.670	22.096	4.220	5.10	14.253
MO 13	10.644	27.503	30.404	18.695	13.424	55.442	14.855	265.256	21.835	5.374	4.20	-22.496
MO 14	6.480	31.126	59.697	20.097	9.358	67.293	15.221	287.228	32.739	5.766	4.30	23.743
MO 15	11.851	18.335	27.406	15.339	11.940	54.348	16.691	192.465	25.169	12.323	2.20	14.728
MO 16	7.074	23.847	22.790	16.196	14.461	51.379	11.644	223.917	24.986	4.091	4.466	-15.621
MO 17	8.910	24.832	34.332	17.474	14.919	52.565	14.570	187.257	28.143	12.501	4.966	51.645
MO 18	12.008	21.309	34.444	17.440	14.400	54.497	15.835	235.756	28.390	2.742	5.233	23.593
MO 19	10.281	23.868	5.321	14.849	11.004	46.524	13.201	195.610	24.460	2.084	6.066	13.202
MO 20	7.809	20.815	31.522	16.653	13.863	54.345	15.510	240.507	30.160	8.476	4.10	29.349

Where is the dendrogram tree?

Contribution of each variable/ descriptor for each PC is not included

Detail explanation about mean genotype contribution is expected

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Authors requested to revise the result and provide detail and sufficient discussion for each result

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Conclusion:

The phenotypic value of each trait measures the importance and contribution of each component to the total variance. The component contributed the maximum for phenological traits, plant height, number of pods per ~~plant,~~plant, and yield per plant are the chief contributors towards genetic divergence in moringa genotypes. Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability and ~~have~~having the tendency to remain ~~together this~~together may be kept into consideration during the utilization of these characters in the breeding program.

Comment [AT13]: needs modification

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Plate.1. Morphological variation in leaves of moringa genotypes

Plate.2. Morphological variation in leaves of moringa genotypes

Plate.3. Morphological variation in pods of moringa genotypes

Plate.4. Morphological variation in pods of moringa genotypes