Electronic Journal of Plant Breeding, 7(3): 767-770 (September 2016)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2016.00101.0

Research Note

Morphological diversity study in horsegram (*Macrotyloma uniflorum* (Lam.) Verdc) based on Principal Component Analysis (PCA)

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(Received:12 Aug 2015; Accepted:15 Jul 2016)

Abstract
Horsegram is an important arid legume known to grow in the tropical countries of Asia and Africa. A total of 500 accessions from NBPGR regional center, Thrissur and landraces maintained in AICRP on arid legumes UAS, Bangalore were evaluated for seven different quantitative traits and screened for Yellow Mosaic Virus disease resistance. The data collected on seven quantitative parameters and YMV reactions were subjected for Principle Component Analysis (PCA) and eight Principal Components (PC) explained the total (100%) variation in the entire collection. Based on PCA the accessions were grouped into seven clusters. Among them, cluster II had maximum number of accessions followed by cluster V. An over view of the seven clusters indicated that genotypes coming under cluster I had better performance for days to 50% flowering, pods per plant, seeds per pod. Cultivars PHG 9, BGM 1 and DPI 2278 categorized under cluster II had better performance for plant height, branches per plant, seeds per pod, and 100 seed weight.

Keywords
Horsegram, *Macrotyloma*, genetic Diversity, PCA (Principal Component Analysis)

Horsegram (*Macrotyloma uniflorum* (Lam.) Verdc) belongs to the genus *Macrotyloma* in the fabaceae family, mostly grown in the tropical countries of Asia and Africa under dry-land agriculture in marginal and sub marginal soils, well known for its hardiness and adaptability to poor soil, adverse climatic conditions that are unsuitable for most other crops. It is cultivated most extensively in southern India (Smartt, 1990). It has multipurpose uses, as food for human beings. The chemical composition of grain is comparable with commonly cultivated legumes and it is an excellent source of iron and molybdenum. But this crop has been neglected in research and development and consequently our understanding of its genetic diversity is limited. There are few studies limited to some agro ecological regions are reported (Dasgupta *et al., 2*005, Gupta *et al.,* 2010, Sunil *et al.,* 2008, Geetha *et al.,* 2011, Prakash *et al.,* 2010, Chahota *et al*.,2005). The necessity for finding out genetic divergence among the genotypes is more pronounced because genetically diverse parents if included in the hybridization programme are likely to produce high heterotic effect and a wide spectrum of variability could be expected in the segregating generation of crosses involving distantly related parents. Characterization can be done using morphological traits, molecular markers or both. In this experiment, focus was given on morphological characterization where scoring is easily detected and characteristics are highly heritable.

In the present study five hundred horsegram genotypes collected from NBPGR, regional center Thrissur and local landraces maintained in AICRP on arid legumes, GKVK were characterized and evaluated for seven different quantitative traits *viz.*, days to 50 per cent flowering, plant height, branches per plant, pods per plant, seeds per pod, 100 seed weight, and seed yield per plant. The experiment was laid out in augmented design along with checks (PHG 9, BGM 1). Each accession was planted in 3m rows, with an inter row spacing of 60cm and an inter plant spacing of 10cm.were. The data collected on seven quantitative parameters and for YMV reaction under field condition. The per cent transmission of disease in each genotype was recorded at weekly interval and they were grouped based on disease scoring scale into different categories. (Vishwanatha *et al.,* 2009) All eight variables were subjected to Principal Component Analysis as per (Anderson ,1963) and analysis was done using MINITAB software. By considering PC I in X-axis and PC II in Y-axis graph was plotted. Based on the result of PCA accessions were grouped into different clusters.

The eight principal components (PC) obtained from the present study explained total (100%) of variation in the collection of the horsegram germplasm. The first principal component accounted for 18.3 per cent of the total variation in eight characters (Table 1). Plant height, branches per plant, pods per plant and seeds per pod were most important traits contributing to

variation. The Eigen value of PC I was 1.46. Whereas second principal component which described about 13.8 per cent of the total variance originated mainly from days to 50 per cent flowering, 100 seed weight, YMV reaction and seed yield per plant. Eigen value of PC II was 1.10. First two principal components accounted for 32.1 per cent of the total variation. In a similar study it was found that days to flowering, days to physiological maturity, plant height and grain yield per plant had the highest contributions to the genetic variability in Horsegram (Gupta *et al.*, 2010). Similarly sufficient genetic diversity was reported in days to maturity, plant height and number of pods per plant by Chahota *et al*. 2005 in Horsegram. In the present investigation, important traits contributing towards the genetic diversity were Plant height, branches per plant, pods per plant and seeds per pod. The study indicated that Plant height contributed maximum to the total variation followed by pods per plant. There is always a difference of opinion in specifying the trait that is contributing high or low towards the genetic diversity. The contribution mainly depends upon the genotypes included in the study and the environmental influence over the character. 100 seed weight contributed least to the total variation. The minimum contribution by this trait reveals that this trait was least affected in course of evolution.

The first principal component had maximum vector loading for plant height and PC II for seed yield per plant by considering these two characters graph was plotted by calculating graph value for both PC I in X-axis and PC II in Y-axis. Details of the graph are shown in Figure 1. Based on the distribution of different genotypes with respect to PC I and PC II, we have grouped seven clusters, which include extreme genotypes for all the seven characters studied. The characters, plant height, branches per plant, pods per plant and seeds per pod showed maximum vector loadings in cluster I and days to 50 per cent flowering, 100 seed weight and seed yield per plant had maximum vector loading in cluster II. The clusters I, II, III, IV, V, VI and VII had 27, 466, 3,1,3,1 and 1 genotypes each, respectively.

The clustering of the entries suggested that the exchange of genetic stocks, genetic drift, spontaneous variation and natural and artificial selections applied for developing varieties suited to local needs may all have played an important role in generating genetic diversity (Arunachalam and Ram, 1967). Genotypes belonging to different eco-geographical areas were included in the same cluster. This indicated that there was no association between clustering pattern and eco-geographical distribution of genotypes. Hence, selection of varieties for hybridization should be based on genetic diversity rather than geographic diversity. The similar observation is also made earlier [Dasgupta *et al.*, 2005, Prakash *et al.*, 2010] in Horsegram.

An over view of the seven clusters indicated that genotypes coming under cluster I had better performance for days to 50% flowering, pods per plant, and seeds per pod 100 seed weight. Five YMV resistant genotypes were included in cluster I (AK21, AK26, AK34, AK36 and AK38). Genotypes (466) in cluster II performed better for plant height, Branches per plant, Seeds per pod, 100 seed weight and included PHG-9, DPI 2278 and BGM1. Cluster III included the genotypes TCR 208, TCR 244 and TCR 256 which performed better for pods per plant and seeds per pod. Seven genotypes grouped under Cluster IV had high *per se* performance for branches per plant and pods per plant. The genotypes TCR 116, TCR 152 and TCR 360 which performed better for plant height, seeds per pod and 100 seed weight with susceptible reaction to YMV were categorized under cluster V. The genotype TCR 133 which performed better for plant height was categorized under cluster V. The genotype TCR 293 showed better performance for plant height and seed yield per plant and was categorized under cluster VII.

Selected diverse genotypes from different clusters with extreme characters will be used as parents for hybridization and development of mapping population for linkage mapping and identification and validation of YMV resistance linked markers.

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Table 1. Vector loadings and percentage of variation explained by the eight principal components

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to 50% flowering	-0.142	**0.624**	0.07	0.448	-0.402	0.069	-0.465	-0.056
Plant Height	**-0.516**	-0.182	-0.257	-0.326	-0.127	0.024	-0.247	-0.672
Branches per plant	**-0.454**	0.097	-0.305	-0.048	-0.192	-0.673	0.193	0.403
Pods per plant	**-0.498**	-0.288	0.168	-0.072	0.079	0.438	-0.35	0.561
Seeds per pod	**-0.43**	0.189	0.404	0.101	-0.118	0.272	0.703	-0.151
100 seed weight	-0.086	**0.393**	0.541	-0.447	0.443	-0.315	-0.219	-0.045
YMV reaction	0.208	**0.349**	-0.2	-0.683	-0.417	0.32	0.098	0.207
Seed yield per plant	-0.152	**0.416**	-0.558	0.096	0.629	0.273	0.107	0.022
Eigen values	1.4637	1.1033	1.052	1.0095	0.9121	0.8919	0.8325	0.7349
Per cent of total variance explained	18.3	13.8	13.1	12.6	11.4	11.1	10.4	9.2
Cumulative *per cent* of total variance explained	18.3	32.1	45.2	57.9	69.3	80.4	90.8	100

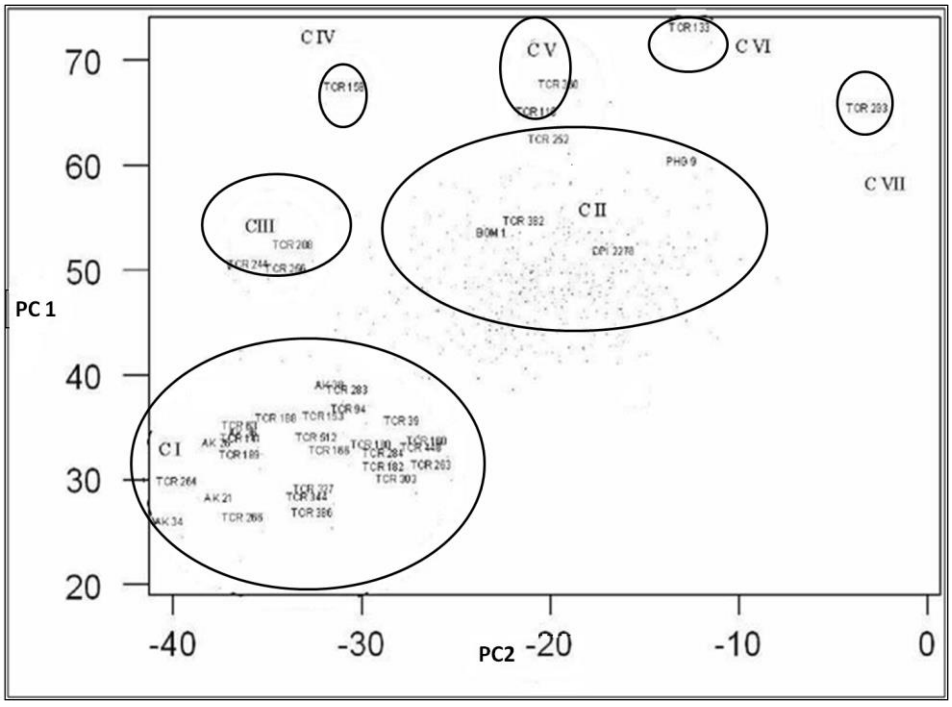

Fig.1 Clustering of Horsegram genotypes