



Principal component analysis and genetic diversity for seed and fodder yields in cowpea

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Abstract

The present investigation consisted of forty three diverse germplasm lines of cowpea (*Vigna unguiculata* (L.) Walp.) in which PCA analysis and divergence were studied. The analysis of variance for phenotypic traits revealed that differences among genotypes were highly significant for all traits. High GCV, PCV, heritability and genetic advance was observed for grain yield, number of branches per plant, number of seeds per pod and 100-seed weight. The first four principal components showed 65.17% of total variability among the genotypes. The first principal component explained 23.21% of total variation. The second, third and fourth principal components explained 15.83%, 14.62% and 11.50% of total variance, respectively. Grain yield, fodder yield, plant height, seeds per pod, 100-seed weight, pod length and number of primary branches per plant contributed mainly to PC1. Fodder yield, days to 50% flowering, pod length and days to maturity contributed mainly to PC2. On the basis of cluster distances, all the 43 genotypes of cowpea were grouped into five clusters. Cluster pattern revealed that cluster I was the largest group consisting of 15 genotypes followed by cluster II (11 genotypes), cluster III (8 genotypes), Cluster V (7 genotypes) and IV (2 genotypes). For improving the seed yield, fodder yield, number of branches, pod length and number of seeds per pod the genotypes like CPD-290, CPD-317, CPD-261, CPD-320, CPD-330, CPD-269, CPD-119 and RC 101 in cluster III would be crossed with genotypes with other clusters having low yielding genotypes. Cluster analysis provided an opportunity to yielding desirable segregants from crossing between the selected desirable diverse lines and brings together different gene combinations.

Keywords: Cowpea, Diversity, Principal component, Variability parameters