

## GENETIC DIVERGENCE IN FODDER LABLAB

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### ABSTRACT

D<sup>2</sup> analysis of divergence in thirty genotypes of lablab for seventeen fodder characters revealed that the genotypes are genetically divergent for all the characters studied. Number of leaves contributed maximum towards genetic diversity, followed by dry matter production and plant height. It was suggested that the genotypes DL 3196, FD 1067, FD 1364 and MS 9478 can be utilized as parents in the hybridization programme to develop a high yielding fodder lablab with high qualitative characters.

**Key words:** Genetic divergence, fodder lablab.

To estimate the nature and magnitude of genetic diversity and to identify promising types to initiate crossing programme for fodder characters in lablab (*Lablab purpureus* (L.) Sweet), Mahalanobis' D<sup>2</sup> statistic described by Rao [1] was used. As many as seventeen characters of developmental, economical traits and chemical parameters, viz., germination, primary leaf area, plant height, No. of primary and secondary branches, No. of leaves, total leaf area, green fodder yield, dry weight/plant, dry weight of leaf and stem, leaf/stem (L/S) ratio, dry matter production, crude protein, phosphorus, potassium, and calcium contents, were studied in thirty genotypes of lablab collected from India, Australia and Thailand. The genotypes were sown in randomised block design with three replications during rabi 1984-85 at Tamil Nadu Agricultural University, Coimbatore, in a plot size of 300 m<sup>2</sup>. Observations were recorded on five randomly selected plants in each replication at 50% flowering stage.

### RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters except for potassium content. All the 30 genotypes were grouped into 10 clusters on the basis of D<sup>2</sup> values. Among these, cluster I was the largest having twelve

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genotypes, whereas clusters II, III, IV and VI had three genotypes each. Cluster V consisted two genotypes and the remaining clusters had one genotype each.

The intracluster  $D^2$  values ranged from 14.1 to 15.6. Maximum intracluster distance was recorded by cluster II, which included three genotypes, and minimum by cluster V with only two genotypes. The highest intercluster distance was found between clusters V and X (41.5), and minimum between clusters VI and X (11.5).

The clustering pattern indicated that genotypes MS 9478, FD 1364, FD 1067, and DL 3196 were genetically distant among themselves as well as from the other genotypes which formed most divergent single-genotype clusters, viz., VII, VIII, IX and X. The highest mean green fodder yield (736.3 g) was recorded in cluster X. This cluster also had the highest dry weight/plant (246.8 g), dry weight of stem (183.4 g), and dry matter production (229.8 g). Cluster VII with one genotype (MS 9478) recorded the highest crude protein content (17.08%), cluster VIII, L/S ratio, and cluster IX total leaf area. Intercrossing among these clusters may result in a wide spectrum of variability and selection for these characters would result in increased green and dry matter production with high protein content.

The results of the present investigation indicate that the genotypes are genetically divergent for all the characters studied. Similar results were reported in fodder cowpea [2] and soybean [3]. Number of leaves contributed maximum towards genetic diversity, followed by dry matter production and plant height. Manoharan [2] reported that green fodder yield contributed maximum towards genetic diversity, followed by dry matter production in fodder cowpea. It was suggested that the genotypes DL 3196, FD 1067, FD 1364, MS 9478 can be utilized as parents in hybridization based on their cluster means and genetic divergence to develop a high yielding fodder lablab with high quality characters.

#### REFERENCES

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