

“Biochemical characterization of taro (*Colocasia esculenta* (L.) Schott)”

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By

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Summary

Thirty taro accessions were collected from the hot spot areas of Western Ghats viz., Peringammala and Kulathupuzha grama panchayaths under Thiruvananthapuram and Kollam districts respectively, raised in experimental field and harvested after 120 days. The cormels collected were subjected to biochemical analysis in triplicate for nine biochemical characters (dry matter, starch, sugar, protein, and fat percentages of cormels, mineral levels of cormels viz; calcium, iron and phosphorus (mg/100g), and leaf protein percentage). Detailed accession-wise characterization with respect to these biochemical characters has been attempted.

Statistical analysis in respect of various parameters like variability, heritability, genetic advance, coefficient of variation and correlation coefficient of 9 biochemical characters has been made. Values of GCV and PCV were suggestive of high degree of variability among the accessions with regard to the characters studied. The difference between GCV and PCV was meagre suggesting that variability is primarily due to genotypic difference for these characters. All the characters studied showed high heritability and got values above 90%. GCV coupled with high heritability and genetic advance were observed for characters like cormel weight, number of cormels, corm weight and sheathed petiole length. Significant positive correlation was observed between majority of characters at both 5% and 1% levels.

Divergence analysis based on the data from nine biochemical characters grouped the 60 accessions into 11 clusters of which Cluster I was the largest with 8 accessions followed by cluster II with 6 accessions. There were five solitary clusters (VII – XI) comprising single entries. The intra-cluster D^2 values ranged from 111.07 (within V) to 734.66 (within VI). The intercluster distance was high between cluster IX and cluster XI (2768.9) followed by cluster V and cluster XI (2561.9). The intercluster

distances were greater than intracluster distances, revealing considerable amount of genetic diversity among the genotypes studied. The cluster means for cormel starch content showed maximum variation, and the values were high in majority of the clusters, and was highest in cluster XI (22.63), followed by cluster III (21.75).

Cormel weight and number of cormels are considered as the main yield attributing traits. The cultivar Co-20 belonging to cluster IX is identified as the highest yielder followed by Co-17 belonging to cluster XI. Highest mineral content (Ca, Fe and P) is also observed in cluster XI. Similarly highest leaf protein content is observed in Cluster VII (4.95), followed by cluster VIII (4.58). Highest cormel protein content is observed in cluster IX (3.23) followed by cluster III (3.00). Crosses between accessions under the clusters, viz; III, VII, VIII, IX and XI may yield good cultivars with highest starch, cormel protein, mineral contents and with highest leaf protein content. The clustering pattern of accessions suggest that geographic diversity is not always related to genetic diversity, and therefore it is not adequate as an index of genetic diversity.

The intraspecific biochemical characterization and analytical studies on the accessions at the lower taxonomic level has been attempted for the first time.