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EVALUATION OF GENETIC DIVERSITY IN ESTATE SELECTIONS OF TEA (*Camellia sinensis* L.) USING FLORAL CHARACTERISTICS AND SSR MARKERS

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Evaluation of genetic diversity of the tea germplasm is a vital requirement for its conservation and utilization in a tea yield improvement programme. The objectives of this study were to evaluate the genetic diversity of estate selections while investigating ancestral relationships among them and to compare the genetic relatedness with geographical locations using SSR markers. Fifty estate selections were selected to represent all the tea growing Agro Ecological Regions (AER) in Sri Lanka.

The floral characterization was done using five standard morphological descriptors that revealed considerable variation among the estate selections. Correlation analysis among the floral traits illustrated a significant negative correlation between split pattern of style and style length/column length ratio. Floral data were subjected to Principle Component Analysis and 74% of the total variability was explained by the first two Principle Components. The resultant biplot clearly categorized estate selections into four groups *viz* Assam, China, Cambod and Assam – Cambod hybrids. A majority of the estate selections were grouped into Assam and Cambod types while China types were poorly represented in the germplasm studied.

Highly informative eight SSR primers specially developed for the genus *Camellia* were used for the molecular assay which generated 33 polymorphic bands. The average polymorphism was 93.75% where the Polymorphism Information Content value for primers ranged from 0.5 to 0.91. Data obtained by the SSR primers were subjected to genetic variation analysis, according to which the diversity among the estate selections originating from different AERs ranged from 0.02 to 0.63. The population derived from the WM2a region clustered with the highest distance in the dendrogram indicating that this population is genetically diverse from the others. The dissimilarity matrix generated from the genetic variation analysis showed that genetic distance among estate selections ranged from 0.03 to 0.82 indicating wide genetic variation. Ten clusters were obtained for the cluster analysis and six estate cultivars (TC 10, CV 4B1, CH 13, QT 4/4, CV 5B1 and MO 241) were identified as diverse phenotypes in the neighbour joining tree and could be used as diverse parents in tea breeding programs after they have been evaluated for traits such as the quality of made tea, resistance to drought, pests and diseases. Molecular characterization of the evaluated estate cultivars showed a different clustering pattern as compared to the grouping pattern resulting from floral characterization. This indicated that molecular characterization does not reflect the sub-species level variation of the tea germplasm.