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Molecular characterization of Sri Lankan tea [*Camellia sinensis* (L.) O. Kuntze] genotypes with diverse origins using SSR markers for future breeding programmes

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The tea plant [*Camellia sinensis* (L.) O. Kuntze] is one of the most popular non-alcoholic beverage crops worldwide. Tea germplasm is the most valuable and fundamental resource for breeding high yielding, climate resilient, and quality tea cultivars. Therefore, efforts were made to characterize the existing genetic diversity of Sri Lankan tea using simple sequence repeat (SSR) markers. A total of 91 tea accessions including exotic, estate selections, improved quality and diverse cultivars were selected for the diversity estimations. Eleven informative highly polymorphic SSR markers selected based on inferences of previous studies (EST, miRNA and traits associated SSR markers) were used in this study. Genetic relationships were analyzed by a neighbor-joining (NJ) tree constructed using DARwin software. Genetic structure analysis was performed by the Bayesian clustering model using STRUCTURE analysis and the optimum delta K was generated. Genetic diversity analysis grouped all the accessions into three major clusters. Further, structure analysis complemented the cluster analysis and revealed three genetic populations (China types with Korean origins, Assam types with ASM4/10 ancestral relationship and mixture of different origins) in the Sri Lankan tea germplasm. Newly recommended TRI5001, TRI5002, TRI5003 and TRI5004 cultivars have shown affinities with five Assam introductions and grouped together in the same cluster. Interestingly, five high yielding TRI developed cultivars (TRI2023, TRI2025, TRI3013, TRI3055 and TRI3073) having an ancestral relationship with the parent ASM4/10 were also grouped together. Likewise, seven accessions of Azerbaijan origin were remained together. The estate selections were scattered in the three clusters. The inferences of the current study provide molecular evidence for the genetic diversity and population structuring of the tea germpalsm and will help the selection of the potential parental group for the future cultivar development programme of Sri Lanka.

Keywords: *Camellia sinensis*, Genetic diversity, Simple sequence repeats, Tea breeding