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MICROSATELLITE BASED ESTIMATION OF GENOMIC SIMILARITIES OF CULTIVATED TEA (*Camellia sinensis* L.) AND NON-TEA (*Camellia spp.*) TYPES IN THE GENUS *Camellia*

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The genetic base of cultivated tea (*Camellia sinensis* L.) is narrow due to recurrent use of a limited number of accessions as parents in the tea breeding programmes. Exploitation and conservation of genetic resources is of paramount importance for sustainability of any crop species. Non-tea species which belong to the genus *Camellia* is a source which can be used to enrich the poor gene pool of tea. However their genetic diversity and genetic relationships are not well documented. In the present study, genomic similarities of cultivated tea and non-tea were assessed by the microsatellite (Simple Sequence Repeat - SSR) marker technique.

Fifteen tea accessions representing six 'TRISL developed improved cultivars', two 'Estate cultivars', 3 old seedling teas (OSD), 2 distinct tea types ('China' and 'Yabukita') and two ornamental tea accessions (*Camellia japonica* and *Camellia rosaeflora*) were used. Isolation of DNA was carried out using five methods including three commercial kits, one mini-prep method and STE/CTAB method. A total of seven SSR primer pairs, including genomic (2) and EST (Expressed Sequence Tag) derived SSR (5) primers were used for PCR amplification. Amplification products were separated and detected by 6% denaturing polyacrylamide gels stained with silver nitrate. Only intensely stained, unambiguous bands were visually scored for their presence (1) or absence (0). Data were entered in a data matrix and were analyzed using 'RAPDistance' and 'Phylip' softwares. Nei and Li's similarity coefficient was employed to generate the genetic distance matrix. Dendrograms were constructed to find genetic relationships using the above software.

A total of 78 alleles were amplified and out of that 58 were generated by 5 EST-SSR primers and the remaining 20 were generated by two genomic SSR primers. The highest genetic distance (0.80) was between accessions TRI 62/1 and *Camellia japonica* and the lowest (0.20) was between two TRI developed accessions (TRI 777 and TRI 4085). The dendrogram generated using 78 SSR loci, separated 15 tea accessions into two main groups. The first group comprised two non-tea species and three OSD accessions. The second group of the dendrogram comprised all the cultivated tea accessions and two distinct types.

A considerable degree of genetic diversity was observed between cultivated tea and non-tea species used in this study, reflecting their potential for widening the tea genetic pool. This study also revealed that SSR primers generated for the cultivated tea could be used for cross amplification of SSRs in non-tea types, which would facilitate further studies on non-teas.