

Characterization of a new tea (*Camellia sinensis*) hybrid progeny based on SSR markers and morphological traits

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Hybridization is the main method for creating genetic variation and breeding new cultivars in tea (*Camellia sinensis*) which is vegetatively propagated. To add variations to existing tea germ plasm, 118 putative hybrids of tea were generated from crossing two diverse parents, TRI2043 which is characterized with high pubescence density, pigmented leaves, resistance to blister blight disease, production of silvertips and higher yield, and TRI3055 a non-pigmented stem, canker resistant cultivar with less leaf hairs. A reciprocal cross also was made. The total progeny was characterized for five morphological traits; anthocyanin pigmentation in petiole, leaf vestiture, average number of pubescence of leaf, immature leaf colour, and petiole colour following IPGRI and UPOV guidelines for tea. Using these data, a dendrogram was constructed based on Nei's genetic distance analysis by using the software "Tree view" version 1.0.

Average number of pubescence in lower surface of the second leaf varied from 5 to 149 per 7.0174 mm² with a mean of 62. Parental cultivar TRI2043 recorded the highest average number of pubescence and TRI3055 had the lowest. Among the progenies, 93 individuals contained anthocyanin pigmentation in petiole which is the characteristic feature of silvertip producer TRI2043. The degree of pigmentation and the intensity of the leaf colour varied among hybrid progenies. In the morphological dendrogram, progenies were grouped into four different clusters. Forty individuals showed close resemblance with the parent TRI2043 and 21 individuals were grouped with cultivar TRI3055. Rest of the individuals shared both parental morphological characteristics which show economically important qualities.

Based on the morphological diversity 42 individuals were selected and subjected to molecular genotyping using four tea specific SSR primers. A total of 24 alleles were generated ranging from 120 to 400 bp. In the molecular clustergram, eighteen progenies were grouped with the parent TRI 3055 and the rest of 24 with TRI2043. The hybrid progeny 100 strongly resembled the parent TRI 3055 while the hybrid progeny 57 strongly resembled the parent TRI 2043.

There were discrepancies between morphological and molecular clustering. Tea progenies in matching clusters between the two schemes can be reliably deployed in future breeding programmes.