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Pedigree-based genetic diversity estimates of parental lines and recommended tea (*Camellia sinensis* L.) cultivars in Sri Lanka

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Crop genetic uniformity is today a main concern of plant breeders. Although detail pedigree information is available for recommended cultivars of tea in Sri Lanka, that information was not utilised for analysing genetic diversity in tea. Coefficient of parentage (COP) is a realistic estimate of diversity based on pedigree information. The objectives of this study were to quantify the level of genetic diversity/similarity among the tea cultivars recommended by the Tea Research Institute of Sri Lanka, with the aim of identifying material that contributed most to the present cultivated gene pool as well as to assign genotypes into groups of genetic similarity. In the present study, fifty-seven cultivars, including their parental lines were analysed based on pedigree information and COP.

COP values estimated for pair-wise combinations of the 57 cultivars ranged from 0.00 to 0.75 with a group mean COP of 0.097 (COD, Coefficient of diversity: 0.903). Yet parental lines ASM 4/10 and CY 9 contributed most to the present gene pool, while the contribution by the other six parental lines (N2, DT 95, TRI 777, DN, DT1 and NAY 3) were marginal, suggesting that the present recommended cultivars is constituted by a restricted and mainly the adapted germplasm as ancestral genotypes.

Among the pair wise relationships computed, 31.09% had 0.00 COP suggesting that there is more potential to be tapped in future breeding programmes. Group mean COP of the different TRI cultivar series (TRI 2000 series: 0.18; TRI 3000 series: 0.08; TRI 4000 series: 0.11) further indicate restricted utilisation of the genetic resources in tea breeding programmes conducted in the past.

Identifying genealogically similar groups and estimations of genetic diversity within and among the groups as revealed in this study are of immense value in developing effective breeding strategies in future programmes.

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