

Abstract

Tea is the most popular non-alcoholic beverage worldwide and is one of the most important tree cash crops in East Africa. However, no comprehensive study has been carried out on the genetic structure and diversity of tea germplasm for this region to date. In the present study, 193 tea accessions held at the ex situ Germplasm Bank of the Tea Research Institute (TRI), Kenya, were analysed using genetic data from 23 polymorphic simple sequence repeat (SSR) loci. A total of 266 alleles were detected with the number of alleles per locus ranging from 4 to 19 with an average of 7.88. Genetic clustering by STRUCTURE was used to correct misidentified accessions based on morphological characters. After reassignment of the tea accessions, *Camellia assamica* exhibited the lowest genetic diversity ($H_s = 0.648$) despite being the most widely cultivated tea type in the East African region. *C. assamica* subsp. *lasiocalyx* showed the highest genetic diversity ($H_s = 0.76$), which supported its origin by hybridization among tea types. Tea cultivars cultivated across the region exhibited lower genetic diversity ($H_s = 0.661$) compared to material held at the ex situ Germplasm Bank of TRI. Tea accessions clustered in the neighbour-joining tree on the basis of geographical origin, pedigree and leaf pigmentation, indicating their common origin. Our results indicated further that East African tea germplasm has a complex breeding history with a majority of the hybrids being F2 generation and backcross plants. *C. assamica* contributed significantly more genetic materials in the tea breeding programmes in East Africa. This study highlights the importance of ex situ germplasm banks to conserve the highest genetic diversity, which is an important resource for future tea crop improvements in East Africa.