

## Abstract

The mating system parameters of tea (*Camellia sinensis*) were determined in four isolated biclonal seed orchards using two PCR-based marker technologies, Randomly Amplified Polymorphic DNA (RAPD) and Inter-Simple Sequence Repeats (ISSR), in an open-pollinated array of 180 progeny from six genotypes. The genotypes consisted of the three cultivated varieties of tea, namely China, Assam and Cambod, with 60 progeny of each. High-value multi-locus ( $t_m = 0.995 \pm 0.094$ ) and single-locus ( $t_s = 0.971 \pm 0.011$ ) estimates of out-crossing rates indicated predominant out-crossing and suggested maintenance of adequate genetic variability within families. The  $t_m$  estimated from RAPD markers ( $0.988 \pm 0.051$ ) was higher than that estimated based on ISSR markers ( $0.936 \pm 0.022$ ). The difference between  $t_m - t_s$  ( $0.024 \pm 0.094$ ) was low, indicating negligible biparental in-breeding. Likewise, the estimated correlation of paternity ( $r_p = 0.070$ ) was low, indicating that many of the offspring did not share the same paternal genitor, despite the isolation of the two putative parents, which is an indication of high pollen contamination rate and long-distance mating. These results suggest that a review of the current isolation distances between orchards is necessary, to increase the pollination efficiency between two isolated breeding cultivars.