

Abstract

Camellia sinensis is a beverage tree crop native to Southeast Asia and introductions have been made into several nonindigenous countries. No systematic assessment of genetic variability in tea has been done anywhere. In this study, random amplified polymorphic DNA (RAPD) analysis was used to estimate genetic diversity and taxonomic relationships in 38 clones belonging to the three tea varieties, *assamica*, *sinensis*, and *assamica* ssp. *lasiocalyx*. Extensive genetic variability was detected between species, which was partitioned into between and within population components. Seventy percent of the variation was detected within populations. Analyses based on band sharing separated the three populations in a manner consistent with both the present taxonomy of tea and with the known pedigrees of some clones. RAPD analysis also discriminated all of the 38 commercial clones, even those which cannot be distinguished on the basis of morphological and phenotypic traits. *Key words*: genetic diversity, RAPDs, *Camellia sinensis*.