

## Abstract

Genetic variation and resulting variable groupings in tea (*Camellia sinensis*) and its wild *Camelia* relatives were assessed using Random Amplified Polymorphic DNA (RAPD) and Amplified Fragment Length Polymorphic (AFLP) markers. Numerous polymorphic bands were generated, of which 266 unambiguous ones were scored. The highest level of polymorphism as determined by the expected heterozygosity ( $H_{av}$ ) was detected with AFLPs. Three major groups were recognized in the germplasm based on the parsimony method of cluster analysis. Two of the groups corresponded to varieties *assamica* and *sinensis* while the third group consisted of a heterogeneous mix of tea cultivars and related wild species. The Taiwan *yamacha*, unique tea cultivars grown predominantly in the highlands of Taiwan for the production of pan-fired semi-fermented (Oolong and Pouchong) tea clustered in this group. Analysis of phenotypic diversity based on the generated RAPD and AFLP profiles revealed that population diversity ( $H$ ), decreased in the order; Wild *Camellia* . >. India . >. China . >. Kenya . > . Sri-lanka . >. Vietnam . >. Japan . >. Taiwan. Analysis of molecular variance (AMOVA) revealed that most variation resided among individuals within populations (72%). Calculation of genetic distances and nested AMOVA further revealed a significant degree of structuring among the populations based on the country of origin.