

## Abstract

The variation in three NADP-linked dehydrogenase enzymes; glucose-6-phosphate dehydrogenase, 6-phosphogluconate dehydrogenase and shikimate dehydrogenase as well as alpha and beta esterases was determined in 24 cultivars of *Camellia sinensis* and 2 other species of *Camellia*; *C. japonica* and *C. irrawadiensis*, using specific activity staining. The isozyme profiles partitioned the cultivars according to their phylogenetic origins; (China, Assam, Cambodia and Japan). At all the loci studied, tea cultivars from China expressed the highest number of alleles followed by the Assam/Cambodia cultivars while the Japanese cultivars expressed the least. *Camellia irrawadiensis* and *C. japonica* showed unique isozyme profiles. The F<sub>1</sub> progeny from an interspecific cross between *C. sinensis* and *C. japonica* displayed the normal Mendelian allelic segregation, while progeny from a *C. sinensis* and *C. irrawadiensis* cross displayed 'distorted' segregation for some alleles. Analysis of the catechin expression patterns using HPLC, also showed that Chinese teas expressed the highest number of prominent catechins while Japanese tea expressed the least. These results show that the catechin biosynthetic pathway is most diverse in China and least in Japan tea. Since the quality and pharmacological importance of tea is mainly derived from catechins and catechin precursors like the aromatic amino acids, these results have important implications in breeding strategies especially in connection with tea germplasm enrichment and quality.