Abstract

Chinese Assam tea (Camellia sinensis var. assamica) is an important tea crop with a long history of cultivation in Yunnan, China. Despite its potential value as a genetic resource, its genetic diversity and domestication/breeding history remain unclear. To address this issue, we genotyped 469 ancient tea plant trees representing 26 C. sinensis var. assamica populations, plus two of its wild relatives (six and three populations of C. taliensis and C. crassicolumna, respectively) using 16 nuclear microsatellite loci. Results showed that Chinese Assam tea has a relatively high, but comparatively lower gene diversity (HS ¼ 0.638) than the wild relative C. crassicolumna (HS ¼ 0.658). Clustering in STRUCTURE indicated that Chinese Assam tea and its two wild relatives formed distinct genetic groups, with considerable interspecific introgression. The Chinese Assam tea accessions clustered into three gene pools, corresponding well with their geographic distribution. However, NewHybrids analysis indicated that 68.48% of ancient Chinese Assam tea plants from Xishuangbanna were genetic intermediates between the Puer and Lincang gene pools. In addition, 10% of the ancient Chinese Assam tea individuals were found to be hybrids between Chinese Assam tea and C. taliensis. Our results suggest that Chinese Assam tea was domesticated separately in three gene pools (Puer, Lincang and Xishuangbanna) in the Mekong River valley and that the hybrids were subsequently selected during the domestication process. Although the domestication history of Chinese Assam tea in southwestern Yunnan remains complex, our results will help to identify valuable genetic resources that may be useful in future tea breeding programs.