Studies of genetic diversity and the establish of the molecular data base of Taiwan tea cultivars

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ABSTRACT

In this study, different tea varieties preserved in Taitung Tea Research and Extension Station (TTES) were used as materials. Tea leaves were manufactured to green tea and 10 kinds of tea catechins were determined by HPLC, and to study the genes Diversity based on these chemical markers. Principal component analysis and UPGMA clustering analysis based on the contents of tea catechins have been used in the study of correlations between manufacturing suitabilities and agronomic traits. Molecular markers, including the nucleotide sequences of pITS2, trnL intron, trnL-trnF IGS were also used in determining the genetic diversity of teas preserved in Tea Research and Extension Station of tea in Taiwan. Our results have shown that the breed tea varieties are generally have higher total catechin content. TTES No.4 has the highest methylation catechins of 3.3 tea (g/100g d.w.), with the greatest potential used in anti-allergy products, for all the tea species tested. Catechins contents in wild Camellia speciesis generally low. Even though these indigenous tea species are much more resist to the environment stress. Unfortunately, more or less negative agronomic traits will be carriered. Total catechins (TC) content is correlated to the contents of caffeine, EC, ECG, EGC, EGCG and four methylated catechin content. Caffeine ’s content is correlated to the content of EGCG, ECG. Principal component analysis (PCA) results have shown that Taiwan wild camellia Tea fell the third and fourth quadrant. Taiwan wild camellia Tea is best for making black tea, and most of the tea cultivars located in third and fourth quadrant are suitable for manufacturing black tea too. For those tea cultivars suitable for manufacturing green tea are scattering in all four quadrantswith overlapping some cultivars suitable for manufacturing Fermented tea. PCA results also indicated that the content and distribution of catechins are correlated with the tea varieties and the manufacturing suitablility and are valuable data for future tea breeding reference. The higher content of caffeine and EGCG are related to the capacities ofinsect resistance of tea, such as anti-mite, anti-leaf beetle, anti-thrips and leaf beetle resistance. Cluster analysis for tea varieties based on UPGMA method using MVSP software has separated two wild Camellia Tea (TD85 and TD100) can be species with other into an independent cluster, showing their genetic pecificity. Single nucleotide polymorphisms were observed based on three multiple sequence alignments of pITS2 sequence of 112 tea varieties, 104 trnL intron sequences, and 98 trnL-trnF IGS sequencespITS2 has the highest nucleotide sequence polymorphism with sequence similarity between 0.379 ~ 0.994, and up to 149 variable sites. Two cpDNA sequences are relatively conserved in these two area, with sequence similarity of 0.948~1.000 for trnL intron and sequence similarity of 0.979 to 1.000 for trnL-trnF IGS. The sequence variation of pITS2 can be used in establishing the molecular fingerprinting database for Taiwan tea plants. Phylogenetic trees constructed based on nucleotide sequence of pITS2 using Neighbor Joining Method, Minimum Evolution methods and Mmaximum parsimony methods can clustered wild teas in Taiwan into two independent clustersalong with other five groups. Our results in genetic diversity is important in future tea breeding selection program.

Keywords : tea、catechins、molecular markers、germplasm resource、genetic diversity

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