Phylogenetic and Taxonomic Study of Native *Eriobotrya* in Taiwan

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**Abstract**


The native *Eriobotrya* plants in Taiwan are the wild relative of loquat crop, and they distribute across the entire island of Taiwan. The taxon of native *Eriobotrya* in Taiwan was treated inconsistently in past decades, either as species, variety, or forma. This study was conducted to reassess the systematic status of native *Eriobotrya* plants in Taiwan by investigations of the internal transcribed spacers (ITS) region sequences of nuclear ribosomal DNA (nDNA), partly *matK* gene sequences of chloroplast DNA (cpDNA), and morphological features of leaves, inflorescences, and pollens. Results of ITS sequences analysis showed that only 7 variation sites were detected in 593 base pairs (bp) of ITS sequences obtained from the 14 samples of *Eriobotrya* plants collected in Taiwan. In addition, no variation sites were detected in 658 bp of partial *matK* gene sequences. Phylogenetic analysis showed that the native *Eriobotrya* in Taiwan belonged to one monophyletic group which was well separated from other referenced taxa from National Center for Biotechnology Information (NCBI). However, the distinction among three taxa of the native *Eriobotrya* in Taiwan was still unclear. If affirmed by more other nucleotide sequences would support to clarify the taxon under *Eriobotrya deflexa*.

**Key words:** *Eriobotrya deflexa*, Rosaceae, ITS sequences, *matK* sequences, Phylogeny.