Molecular phylogenetic relationship of the family Colchicaceae (Liliales)

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The Colchicaceae comprising 250 species and 15-19 genera of rhizomatous or cormous perennials, the moderate sized family in Liliales, distributes widely through the temperate and tropical areas of Africa, Asia and North America. The division of two subfamilies in Colchicaceae is still unclear because of different results in previous studies. Moreover, sister taxa of this family has not been determined. In genus level, it was uncertain that whether expand circumscription of three genera of Colchicum, Gloriosa, and Wurmbea which are include Androcymbium, Littonia and Onixotis, respectively, is reasonable or not. In this study, three coding genes of atpB, matK and *rbcL* were analyzed to reconstruct phylogenetic relationship of Colchicaceae and both of maximum parsimony (MP) and Bayesian analysis were conducted. Among three genes, matK region was most variable and provided more parsimony-informative sites, whereas the *atpB* and *rbcL* regions were similar in the variation and number of informative characters. Monophyly of Colchicaceae was strongly supported and it was divided into two subfamilies (Wurmbeoideae and Uvulariodeae). Uvularia-Disporum clade, comprises the subfamily Uvularioideae, is a sister of the rest Colchicaceae and subsequently differentiated Burchardia was a sister within subfamily Wurmbeoideae. Burchadia was used to be supposed to be a sister of the family in the previous studies. It was clear the monophyly and phylogenetic relationship among six tribes *sensu* Vinnersten and Manning (2007) within the family. In addition, the expanded circumscription of three genera was also strongly supported; Colchicum-Androcymbium (BP99), Wurmbea-Onixotis (BP100), and Littonia-Gloriosa (BP100). Here, we propose a re-circumscription among taxa of Colchicaceae.

Key words : Colchicaceae, Molecular phylogeny, subfamilial circumscription, coding genes