

전사체 데이터에 의한 산형아과 (Apioideae)의 계통과 적응진화

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Phylotranscriptomics of the Subfamily Apioideae (Apiaceae)

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Due to the abundance of information in Nuclear DNA, it has a magnificent phylogenetic resolution. Moreover, because they show biparental inheritance, it has proven to be superior to organelle DNA, which has a limited number of genes and only shows maternal lineage. In particular, the transcriptome, which includes much nuclear DNA but is relatively inexpensive to analyze, can provide valuable insights into evolution through selection analysis and enable gene function research. This study's dataset includes 45 transcriptomes (16 generated for this study). It aims to explore the evolutionary history of Apioideae by comparing the results of the phylogenetic analysis with gene tree discordance and chloroplast phylogeny. The results confirmed the taxonomic positions of *Peucedanum terebinthaceum*, *Ligusticum tachiroei*, and *Cymopterus melanotilingia* and proposed a genus change for *Glehnia littoralis*. High gene tree discordances were identified in recently diverged clades, suggesting frequent hybridization and introgression. In the most recently diverged tribe of Selineae, the highest number of PSGs (positively selected genes) has been confirmed, which is inferred to be due to the geological and climatic diversity of their originated habitat, Central Asia. These genes include those related to responses to growth and drought, oxidative, and salt stress. In particular, the CYP97A gene confirmed as PSGs in *Bupleurum latissimum* is inferred to be a result of adaptation to the light-limited environment of Ulleungdo Island, as it is associated with the efficiency of photosynthesis.

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