

Morphological and molecular systematic for selected *Blechnum* from Peninsular Malaysia

ABSTRACT

Systematic of *Blechnum* spp. using both morphological and molecular studies were resolved in a monophyletic tree. The use of coding *rbcL* and non-coding *trnH-psbA* genes amplified from chloroplast were used to support the morphological differences. From the study, five species of *Blechnum*, *Blechnum fraseri*, *Blechnum vestitum*, *Blechnum indicum*, *Blechnum orientale* and *Blechnum finlaysonianum* were clustered independently according to morphological characters of scales, rhizome, stipe, rachis, laminae and their fertile and sterile pinnae. On the basis of morphological similarity, both *B. fraseri* and *B. vestitum* were lomarioid species; their fertile pinnae much reduced in size compared to their sterile pinnae. This result was supported by molecular analyses by having 0.034 genetic distances and the phylogenetic tree represented here shown both of them more related. However, some of the relationships have been previously suspected on the basis of morphological similarity and supported as well by the DNA analyses were shown in this study for *B. orientale* and *B. finlaysonianum*. They were similar in rhizome, scales and laminae characters. Most importantly, both of them are eublechnoid species; the fertile and sterile pinnae are similar in size and the genetic distance for *B. orientale* and *B. finlaysonianum* is 0.017. However, *B. indicum* was independently because of morphological distinct and no obvious relatives to other species. Morphological and molecular variations were consistently complemented to each other, and may be useful for further phylogenetic and taxonomical studies.

Keyword: *Blechnum*; Peninsular Malaysia; Phylogeny; Taxonomy; Chloroplast *rbcL*; *trnH-psbA* DNA sequences