

# **Preliminary molecular phylogeny of Bornean *Plagiostachys* (Zingiberaceae) based on DNA sequence data of internal transcribed spacer (ITS)**

## **Abstrak**

A molecular phylogenetic analysis based on DNA sequence data of internal transcribed spacer region (ITS 1, ITS 2) and 5.8S gene and re-evaluation of morphological characters were performed in order to examine the relationships of *Plagiostachys* and related genera, and to elucidate the previous informal grouping of Bornean *Plagiostachys*. A total of 111 taxa, including 25 taxa of *Plagiostachys* were included in the analysis. The strict consensus tree (length = 1094; CI = 0.482; HI = 0.518) showed that *Plagiostachys* consisted a strong supported (BS = 96%) clade with some *Alpinia* species that belong to section *Alpinia*. However, species of *Plagiostachys* comprised three subclades (A, B and C) and each subclade was moderately to strongly supported with relatively high bootstrap values. The three subclades of *Plagiostachys* were also recognized morphologically by the combination of inflorescence and capsule characters. Poor resolved tree prevent us to conclude phylogenetic status of the genus *Plagiostachys*, but at the moment we propose this genus remain an independent genus and wait for further analysis. Previous informal grouping of Bornean *Plagiostachys* was not supported from both molecular and morphological analyses.