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.