CHAPTER I

GENERAL INTRODUCTION

The Annonaceae is a pantropical family, with approximately 200 genera and 2500 species. There are two related North America genera, but the remaining taxa are all tropical, displaying high continental generic endemism (Keßler, 1993; Doyle and Le Thomas, 1996). Annonaceae have been included in the order Magnoliales by various taxonomists (APG II, 2003). Morphological and more recent molecular cladistic analyses have continued to place Annonacece in the Magnoliales along with Magnoliaceae, Degeneriaceae, Himantandraceae, Eupomatiaceae and Myristicaceae (Donoghue and Doyle, 1989; Chase et al., 1993; Doyle and Endress, 2000; Soltis et al., 2000). Eupomatiaceae which were previously included as a subfamily within Annonaceae and have always been considered closely related based on morphological characters (Morawetz, 1988) was proposed by Qiu et al. (2000) as the sister to Annonaceae. From the analysis using *rbcL* and *trnL-F* DNA sequence data, Richardson et al. (2004) separated Annonaceae into 3 groups, namely the basal grade, the long branch clade and the short branch clade.

The genus *Goniothalamus* Hook. f. & Thomson, belonging to the long branch clade is one of the largest and most important genera of Annonaceae, with over 150 species distributed throughout tropical south-east Asia; the center of diversity lies in Indochina and western Malesia (Sumatra, Peninsular Maleysia and Borneo) (Saunders, 2003). Based on molecular clade, the estimated age of *Goniothalamus* is in the range of 3.6-4.8 ± 1.5 Myr ago (Richardson et al., 2004). Little is known of the evolution and biogeographical history of this genus. Many morphological characters are ambiguous and reveal little phylogenetically useful information. Thus molecular systematics has become an alternative approach for determining evolutionary relationships because morphological and other phenotypic characters are either absent or change too rapid to be useful for phylogenetic inference. So far, many studies in the genus *Goniothalamus* are based on morphological characters, thus it is impossible to conduct any tests on morphological homology and/or evolutionary changes in this genus. The objectives of

this dissertation were (1) to investigate the delimitations and phylogenetic relationships of the genus *Goniothalamus*, (2) to test the monophyly of *Goniothalamus*, (3) to infer the phylogenetic relationships within and among the genus *Goniothalamus* and related genera using nuclear and chloroplast genes, and (4) to use the phylogenetic reconstruction as a framework to infer character evolution in this group. These regions have been widely used to infer phylogenetic relationships within the Annonaceae (Doyle, Bygrave and Le Thomas, 2000; Meade, 2000; Erken, 2002; Mols, Keßler and Gravendeel, 2002; Chatrou et al., 2002; Richardson et al., 2004; Scharaschkin and Doyle, 2005)

The results from this study enable a clarification of the relationships and phylogeny within the genus *Goniothalamus* and related genera and understanding the evolutionary history and biogeography of this genus. Moreover, this study was to realize which morphological characters are phylogenetically informative in *Goniothalamus*.