

CHAPTER I

INTRODUCTION

The genus *Aeschynanthus* Jack (Gesneriaceae, subfamily Cyrtandroideae, tribe Trichosporeae) contains about 160 species widely distributed in subtropical and tropical forests in the Indo-Malayan region. *Aeschynanthus* (Lipstick vine) are evergreen subshrubs, climbers, or trailing perennials. Most species are epiphytes in the wild, growing on trunks and branches of forest trees, and a few species are semi-terrestrial. They are attractive plants with twiggy, arching or flexuous pendulous stems and numerous pairs of leaves. The flower colour is commonly brilliant red, more rarely orange, yellow or greenish-brownish while the calyx varies from green to red or purple. *Aeschynanthus* is therefore an attractive ornamental plant having high commercial value, both in Thailand and abroad. Several common species have been cultivated for their exotic flowers whereas some rare plants are usually collected from the wild. The later case has raised recent concerns about potential biodiversity threats to the genus.

In taxonomic point of view, species identification and sectional classification of this genus rely mostly on their flower and seed morphology. *Aeschynanthus* capsule-like fruits contain many anatropous ovules, with one or more appendages (hair) at the hilar end and another one at the apical end. The number of hilar appendage has been use to subdivide

the genus in to five section (Bentham, 1876; Clark, 1883; Burt and Woods, 1975). Later work by Wong (1984) added the sixth Chinese-endemic section based on corolla colour. Recent seed Scanning Electron Microscope (SEM) studies and molecular analyses proposed a sectional revision leading to a new unnamed section and sub generic classification (Dendaungboripant *et al.*, 2001; Mendum *et al.*, 2001; Christie and Mendum, 2002). Previous works on molecular genetic relationship of *Aeschynanthus* come from those of Dendaungboripant and Cronk (2000 and 2001) and Dendaungboripant *et al.* (2001). They used internal transcribed spacer (ITS) regions of nuclear ribosomal DNA (nrDNA) amplified from 50 species of *Aeschynanthus* grown in Royal Botanic Garden of Edinburgh, United Kingdom, to study their evolutionary genetic relationships. The results of these phylogenetic analyses combined with other previous morphological studies (for example, Mendum, 1999) revealed a natural history and evolutionary pattern of the genus.

Although those previously studied 50 *Aeschynanthus* came mostly from many places in Asia, covering almost all distribution areas of the genus, only some species were from Thailand. Several foreign researchers have surveyed and collected specimen *Aeschynanthus* in Thailand for decades. So far, they have reported about 20 species of *Aeschynanthus* found distributing in many areas across the country. Although *Aeschynanthus* is one important plant for ornamental business in Thailand, there is no researcher working specially on the Thai species. This thesis therefore was initiated to study

a genetic relationship of some *Aeschynanthus* species found in Thailand compared with those of countries. This research had mainly used molecular phylogenetic techniques, particularly on DNA sequences of ITS regions of nuclear ribosomal DNA following an approach in Denduangboripant *et al.* (2001). An advantage of ITS regions as phylogenetic tool is that they are fast evolving areas being useful for accessing relationship at species level. Leaf materials were sampled from the living collection of the Royal Botanic Garden Edinburgh, and wild-collected in Chiangmai. Combining with cytogenetic investigation on chromosome numbers of some *Aeschynanthus* species, this molecular systematic study could help solving long-time taxonomic problems of some *Aeschynanthus* in Thailand.

Because the reproduction parts of *Aeschynanthus* in the wild are usually unavailable, causing a great identification problem to most taxonomists, molecular identification technique based on ITS sequences of several different morphotypes of *Aeschynanthus* cultivars and those of some wild samples was performed with a previously reported data of 73 *Aeschynanthus* species. This molecular identification was successfully performed. Knowledge gained from all of these studies are an important background for the future research in taxonomy biodiversity and conservation biology of the genus *Aeschynanthus* and the family Gesneriaceae in Thailand and other countries.

Research objective

This thesis aims to investigate an importance of molecular phylogenetics as a useful mean to study genetic relationship of some *Aeschynanthus* in Thailand based on *Aeschynanthus* molecular phylogeny reconstructed from ITS sequences and cytogenetic investigation on chromosome numbers of some *Aeschynanthus* species.



ศูนย์วิทยทรัพยากร
จุฬาลงกรณ์มหาวิทยาลัย