

CHAPTER 8

RESULTS – MOLECULAR PHYLOGENETIC ANALYSIS

The ITS and 5.8S sequences of six species of *Curcuma* were obtained in this study and sequences of nine species of *Curcuma* and seven species each from different genera were taken from Genbank. In total, sequences of 22 taxa were used in cladistic analysis.

The total lengths of ITS genome in this analysis vary from 578 to 604 bp (table 32). The length of each region was determined by comparison with sequences from Genbank. The lengths of ITS-1 vary from 185-199 bp, while lengths of 5.8S sequences vary from 152-157 bp and the lengths of ITS-2 sequence vary from 235 to 247 bp. Alignment of ITS sequences of 22 taxa resulted in 648 bp. Among them, 463 characters are constant, 93 characters are autapomorphic and 92 characters are parsimony-informative.

Table 9 Sequence characteristics of ITS and 5.8S nuclear ribosomal DNA.

Taxon	Length (base pair)			
	Total	ITS-1	5.8S	ITS-2
<i>Curcuma caesia</i>	602	200	157	245
<i>Curcuma cochinchinensis</i>	582	190	152	235
<i>Curcuma flaviflora</i>	578	186	152	235
<i>Curcuma longa</i>	604	200	157	247
<i>Curcuma parviflora</i>	578	192	157	238
<i>Curcuma</i> sp. (Pitsanulok)	578	192	157	238

The three most parsimonious cladograms resulted from branch and bound method has 306 steps with CI = 0.696, RI = 0.731, RC = 0.509 (appendix A). The strict consensus tree of the three most parsimonious trees is given in Figure 45.

The *Curcuma* species appear in four major groups. *C. cochinchinensis* is separated first, combine with *Smithatris* with 100% bootstrap support and form a basal clade of the remaining species of *Curcuma*. The second group is *C. ecomata*, comprising *C. bicolor*, *C. ecomata* and *C. flaviflora*. This group has moderate support.

The third group comprises *C. alismatifolia*, *C. harmandii*, *C. parviflora* and *C. sp.* (Pitsanulok) which is sister group of the genus *Stahlianthus*. The last group is composed of *C. aeruginosa*, *C. amada*, *C. comosa*, *C. longa*, *C. petiolata*, *C. roscoeana* and *C. rubescens* which includes genus *Hitchenia* and *Paracautleya*.

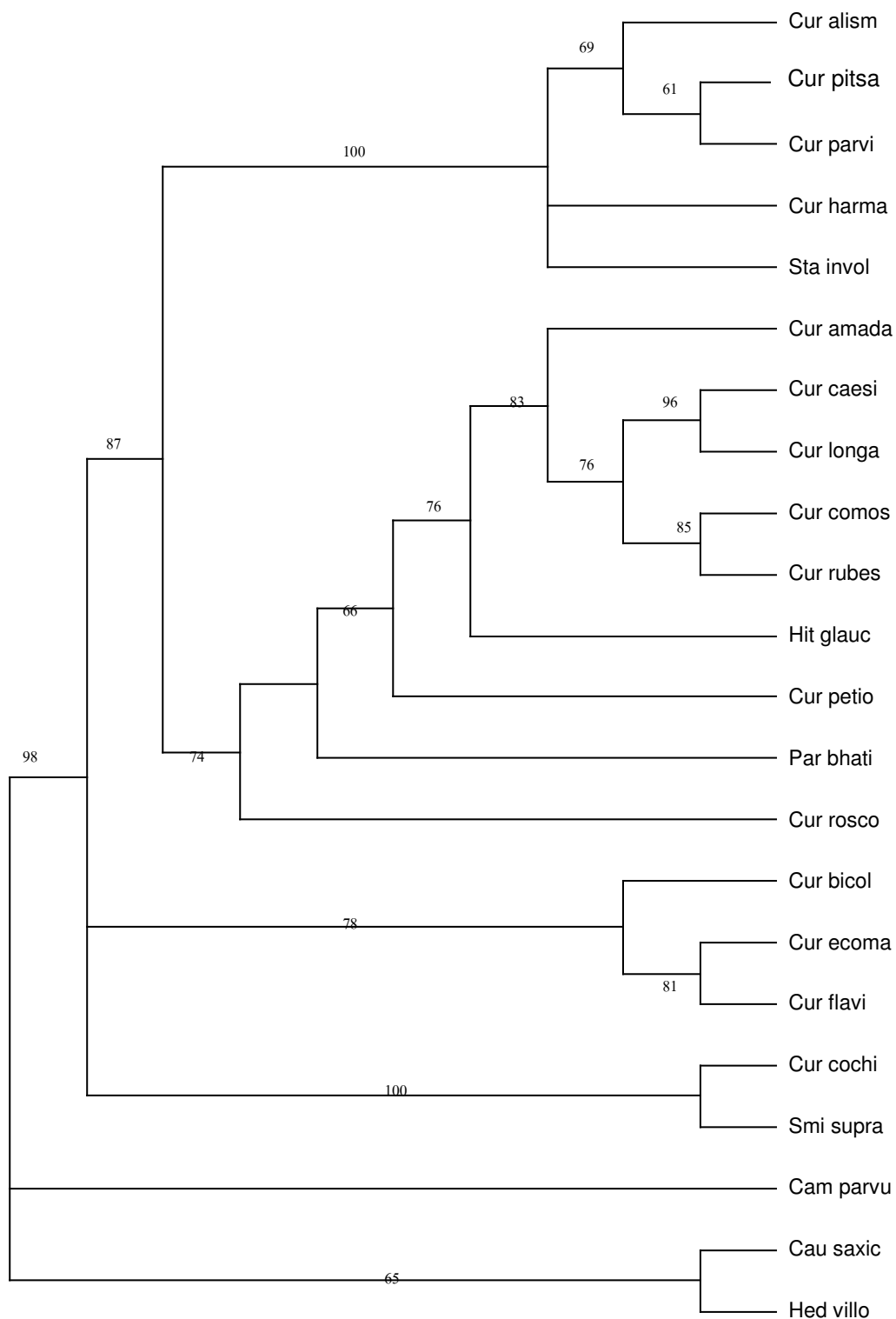


Figure 45. Strict consensus tree of 3 most parsimonious trees resulted from cladistic analysis of ITS and 5.8S nuclear ribosomal DNA with 308 steps (CI = 0.698, RI = 0.731, RC = 0.510). Bootstrap values shown above branches. The values lower than 50% are not shown.