

## CHAPTER 1

### INTRODUCTION

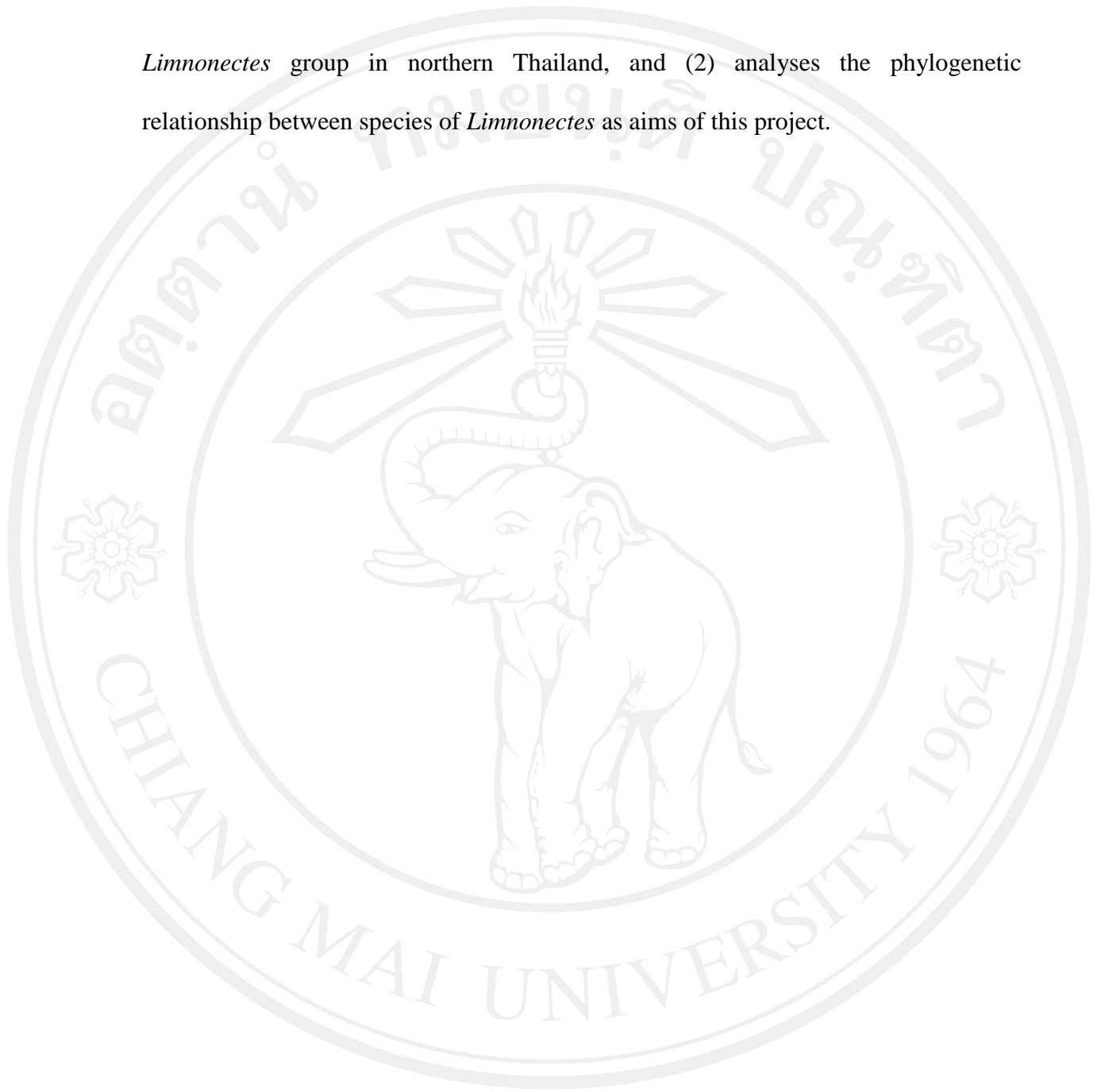
Genus *Limnonectes* (Fanged frog) has distributions throughout Southeast Asia and could be found in every parts of Thailand. *Limnonectes* being classified in the IUCN categories of Near Threatened (NT) or Least Concern (LC) in which it seems to be a serious underestimate. This can be illustrated briefly by a case study of *L. kuhlii*. McLeod (2010) stated that the data need to be continually updated and revised, particular, newly described species have been added as 16 more new species discovered still waiting to be classified. *Limnonectes* tends to exhibit morphologically cryptic species within taxa that were previously considered to be a single species which have been hindered progression in taxonomic study as well as conservative plan. These findings imply that species diversity of Southeast Asian frogs remains significantly underestimated.

Since the early 1990s, the development of suitable tools has resulted in a leading role for DNA markers, mostly mitochondrial DNA and nuclear DNA, in characterisation of population genetics for the reconstruction of phylogenetic relationships of closely related species, for the estimation of divergence times in the context of historical biogeography, and for simple taxonomic purposes, e.g., to detect and differentiate species that are morphologically indistinguishable. The application of molecular phylogenetic techniques has permitted fine-scale examination of species-level differences. In the last decade, numerous studies have uncovered cryptic diversity in nominal species of amphibians, reptiles, fishes, and other organisms with

the use of molecular data (Matsui *et al.*, 2011; Oliver *et al.*, 2012; Pierce and Stepien, 2012). Genetic diversity is one of the key factors in evolution because it provides the genetic foundation for selection to act upon. The variation in genetic diversity among species or populations arises from a combination of genetic processes, such as mutations, genetic drift, gene flow, and ecological selection resulting from spatial and temporal differences in the environment (Arioli *et al.*, 2010). High genetic variation can have a crucial role for the viability of a species or population because it offers the potential to persist and to adjust to changing or new environments. Conversely, the loss of genetic diversity may have a direct negative impact on the viability of the species or population. As mentioned above fanged frog (*Limnonectes* spp.) populations from Thailand are considered to be Near Threatened (NT) in IUCN, 2012 since they are a vulnerable animal and poorly protected. Populations of this frog are rapidly decreasing because of habitat destruction and human disturbance. Basic information regarding patterns of genetic diversity of these populations is unknown, making it difficult to adopt scientifically guided management measures to ensure their conservation. Advances in genetics, especially the introduction of polymerase chain reaction (PCR) and the analyses of differences in nuclear DNA and mitochondrial DNA, have benefited conservation genetics by enhancing knowledge of the population structure and phylogeography of a growing number of species (Avisé, 1998; Sweijd *et al.*, 2000) and could be useful to reveal an unprecedented genetic pattern of the *Limnonectes* populations.

The classification of *Limnonectes* spp. in this study was based on morphological and genetic characteristics. Both mitochondrial DNA and nuclear DNA data were used to (1) study the systematic relationships among members of the

*Limnonectes* group in northern Thailand, and (2) analyses the phylogenetic relationship between species of *Limnonectes* as aims of this project.



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