

TABLE OF CONTENTS

	Page
ACKNOWLEDGEMENT	iii
ABSTRACT (ENGLISH)	vi
ABSTRACT (THAI)	viii
LIST OF TABLES	xi
LIST OF FIGURES	xiii
CHAPTER 1 INTRODUCTION	1
CHAPTER 2 REVIEW OF THE LITERATURE	4
CHAPTER 3 MATERIALS AND METHODS	23
CHAPTER 4 RESULTS AND DISCUSSION	42
CHAPTER 5 CONCLUSION	76
REFERENCES	78
APPENDIX	95
CURRICULUM VITAE	105

LIST OF TABLES

Table		Page
1	Samples of <i>Limnonectes</i> spp. collected in the present study	25
2	Morphological parameters used in this study	29
3	Morphometric measurements for <i>L. blythii</i>	45
4	Morphometric measurements for <i>L. gyldenstolpei</i>	46
5	Morphometric measurements for <i>L. taylori</i>	47
6	Morphometric measurements for <i>L. magastomias</i>	48
7	Morphometric measurements for <i>L. jarujini</i>	49
8	Factor loading on the four principal components extracted from a correlation matrix of seven morphological parameters for five species male and female individuals of fanged frogs from Thailand	50
9	Summary of identification based on each species consensus barcodes sequence using BOLD Identification System (BOLD-IDS) and BLASTN search from GenBank	53
10	Molecular diversity of fanged frog species (Haplotype (h) and nucleotide (π) diversity estimates \pm standard deviations) for all compared foraging aggregations	56
11	Mean pairwise genetic distances between fanged frog species of mtDNA in this study under Kimura 2-Parameter Model (K2P)	59

LIST OF TABLES (CONTINUED)

Table		Page
12	Mean pairwise genetic distances between fanged frog Species of nuDNA in this study under Kimura 2-Parameter Model (K2P)	60
13	Mean genetic distances between species of 16s rRNA gene in this study by the Kimura 2-parameter model (K2P)	62

LIST OF FIGURES

Figure		Page
1	Map showing distribution of <i>L. blythii</i> (Boulenger, 1920) in northern Thailand	7
2	Map showing distribution of <i>L. gyldenstolpei</i> (Andersson, 1916) in northern Thailand	9
3	Map showing distribution of <i>L. taylori</i> (Matsui, Panha, Khonsue, and Kuraishi, 2010) in northern Thailand	10
4	Map showing distribution of <i>L. limborgi</i> (Sclater, 1892) in northern Thailand	12
5	Variously characterised of family Dicroglossidae (out-growths of the lower jaw bone)	14
6	Gene organisations of the <i>L. bannaensis</i> the mitochondrial genome	19
7	Map showing the collecting stations for frogs used in the present study	24
8	Morphological characters measured in this study	30
9	Scatterplot of principal component scores (PC1 and PC2) for female which are five <i>Limnonectes</i> from Thailand	51
10	Scatterplot of principal component scores (PC1 and PC2) for female which are five <i>Limnonectes</i> from Thailand	51

LIST OF FIGURES (CONTINUED)

Figure		Page
11	Phylogenetic consensus tree of eight fanged frog species constructed using Maximum Parsimony (MP) Method.	63
12	The maximum likelihood (ML) phylogenetic tree analysis of mitochondrial genes (mtDNA). Numbers indicates clades supported by bootstrap (2000 replicates)	65
13	The maximum likelihood (ML) tree for mitochondrial genes (mtDNA) sequences of <i>L. taylori</i> clade. The ML tree was constructed under the K2P model. Bootstrap support values of > 80% from 2000 replicates are shown	66
14	The maximum likelihood (ML) tree for mitochondrial genes (mtDNA) sequences of <i>L. taylori</i> in northern Thailand. Bootstrap support values of > 80% from 2000 replicates are shown	67
15	Map of northern Thailand showing the known distributions of the <i>L. taylori</i> complex	68
16	Phylogenetic consensus tree of eight fanged frog species constructed using Maximum Parsimony (MP) Method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (2000 replicates) is shown next to the branches. <i>Amolops spinapectoralis</i> and <i>Huia melasma</i> used as an outgroup	69

LIST OF FIGURES (CONTINUED)

Figure		Page
17	The maximum likelihood (ML) phylogenetic tree analysis of nuclear genes (nuDNA). Numbers indicates clades supported by bootstrap (2000 replicates)	71