

CHAPTER IV

Results

Morphological Description

Chirodropid medusa belonging to the genus *Chironex* (Table 3). Live specimen cube shape with transparent bell (Figure 6.1A). Maximum bell height (BH) about 150 mm. and maximum bell width (BW) about 185 mm, mouth length about 2/3 of BH. Pedalia claw-like with up to twelve tentacles (Figure 6.1B). Pedalial canal bend bulbous shaped (Figure 6.1C). Tentacles flat in life as in *C. fleckeri* and *C. yamaguchii*, rounded in preserved specimens (Figure 6.1D). Gastric phacellae V-shaped; numerous and unbranched gastric cirri (Figure 6.2A). Blooming white champaca shaped manubrium hanging from the ceiling connecting to gastric saccule at the base (Figure 6.2B). Gastric saccule cock's comb shape (Figure 6.2C). Perradial lappets smooth and triangular shaped with a single frenulum on each side of the bell (Figure 6.2D). Velarial canals numerous and highly branched (Figure 6.3A), as in *C. fleckeri* and *C. yamaguchii*. Rhopalial niche ostia dome shaped. Four sets of eyes, containing six eyes in each set (Figure 6.3B), located in each of four rhopalia.

Remarks

All 4 *Chironex* sp. A specimens share the same morphological characters, especially the bulbous shaped pedalial canal which is a distinguishing character, except in *Chironex* sp. A3 which has a cinder cone volcano shaped pedalial canal on one side of pedalia (Figure 6.4).

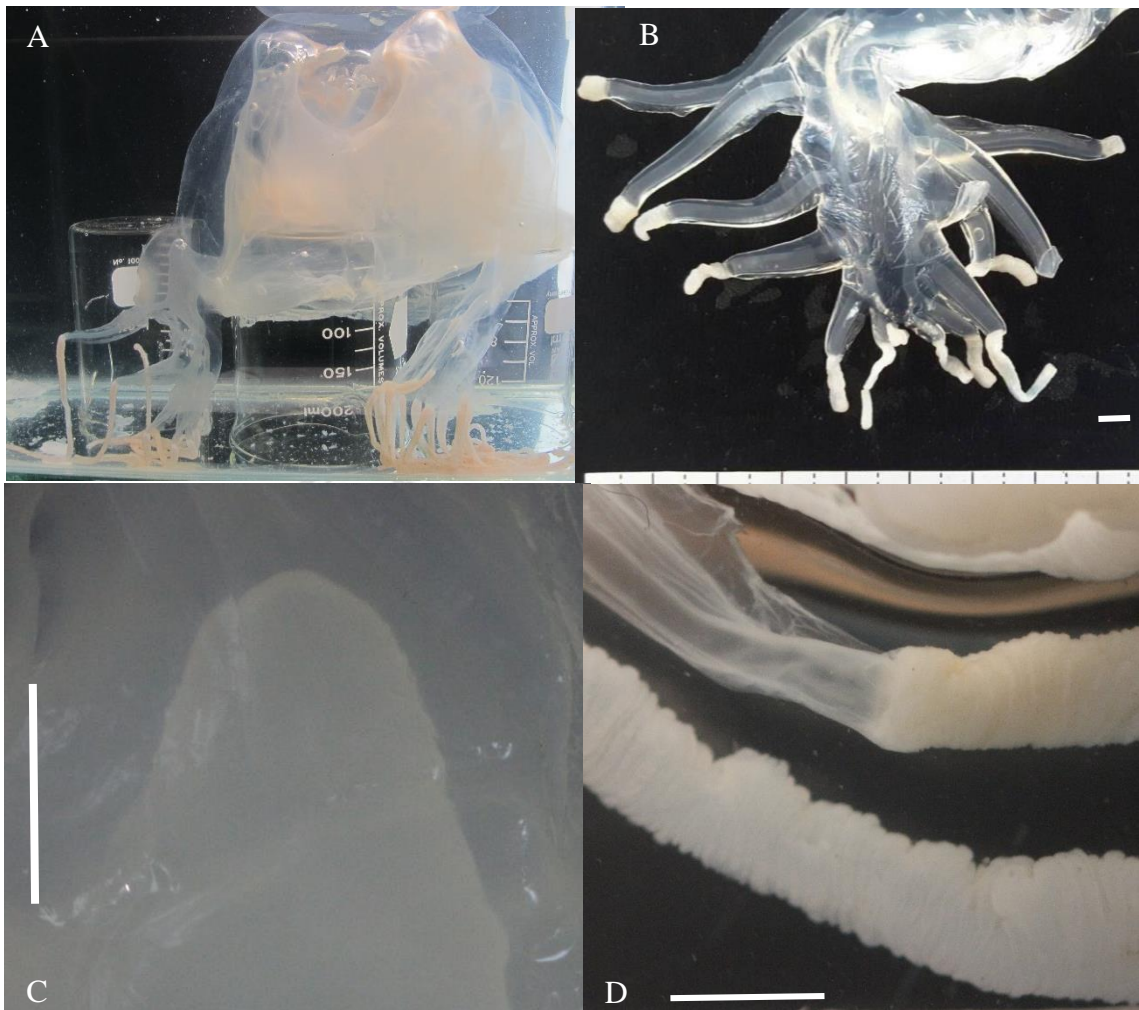


Figure 6.1 A: Transparent bell of *Chironex* sp. A; B: Claw-like pedalia; C: Bulbous shape pedalia canal; D: Rounded tentacles in preserved specimen.

Scale bar represented 0.5 cm.

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Figure 6.2 A: Numerous gastric cirri; B: Blooming white champaca shaped manubrium connecting to gastric saccule at the base (red arrow); C: Cock's comb shaped gastric saccule; D: A single frenulum on each side of the bell

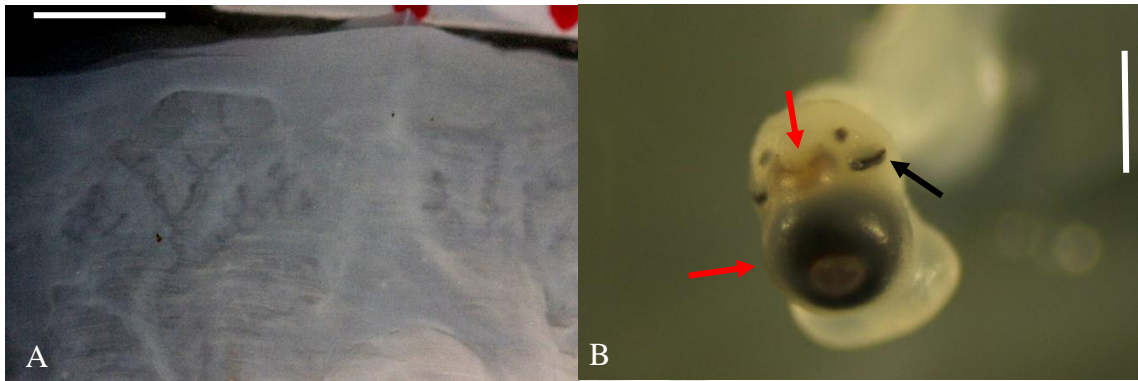


Figure 6.3 A: branched velarial canal, scale bar represented 0.5 cm.; B: Rhopalia comprises of 2 median lensed eyes (red arrows) and 4 slit eyes (black arrow), scale bar represented 0.3cm

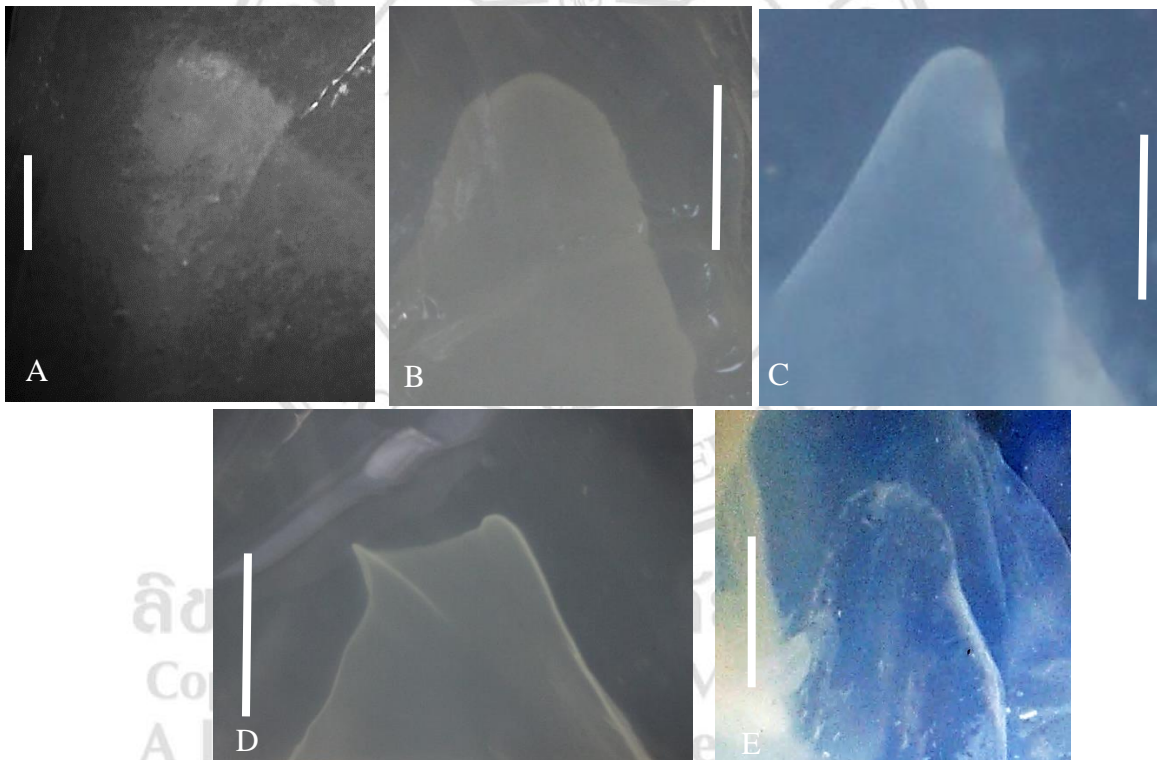


Figure 6.4 A-C: Bulbous shaped pedalia canal in *Chironex* sp. A1, A2 and A4 respectively. D and E: Bulbous shaped and cinder cone volcano shaped on each side of pedalia canal in *Chironex* sp. A3. Scale bars represented 0.5 cm.

Table 3 Comparison of genera within the Chirodropidae adapted from Gershwin (2006)

	Saccule shape	Tentacles	Pedialial canal bend
<i>Chirodectes</i>	Absent	9-11	Spike
<i>Chirodropus</i>	Elongate, tapered, with numerous axial processes, or absent	9-21	Spike
<i>Chironex</i>	Cock's comb	5-15	Spike, volcano and bulbous

Table 4 Comparison of species within the *Chironex*

	Tentacles	Pedialial canal bend
<i>Chironex fleckeri</i>	12-15	Spike
<i>Chironex yamaguchii</i>	5-9	Volcano
<i>Chironex</i> sp. A	12	Bulbous

Systematic results

Phylum Cnidaria Verrill, 1865 (Hatschek, 1888)

Subphylum Medusozoa Petersen, 1979

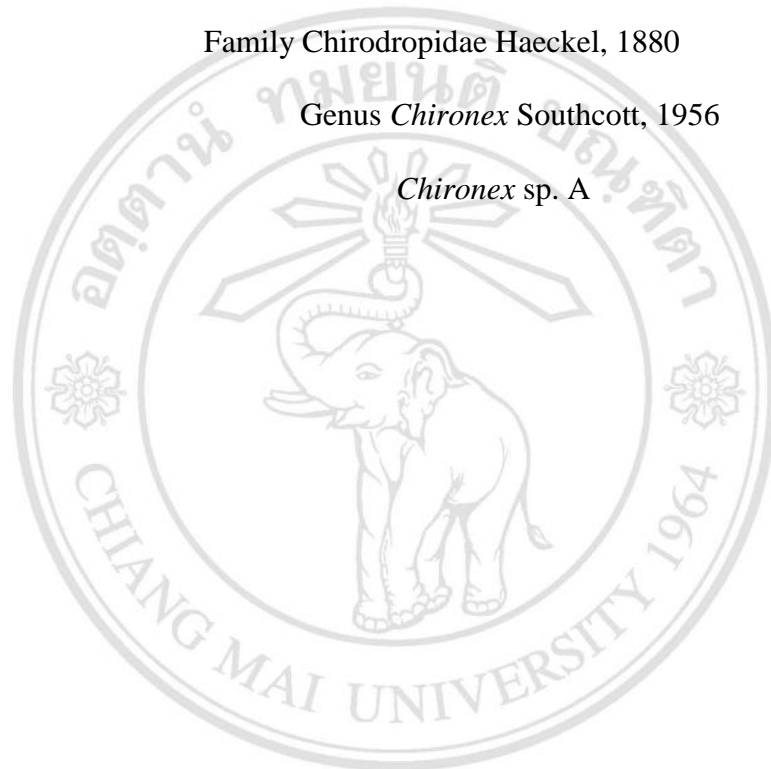
Class Cubozoa Werner, 1973

Order Chiropoda Haeckel, 1880

Family Chiropidae Haeckel, 1880

Genus *Chironex* Southcott, 1956

Chironex sp. A



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Molecular identification

Mt-COI and 18S rRNA were amplified. The former generated about 680 bp products (Figure 7.1) and the latter generated approximately 600 bp products (Figure 7.2) by primers from Geller *et al.* (2013) and Gershwin (2005) respectively.

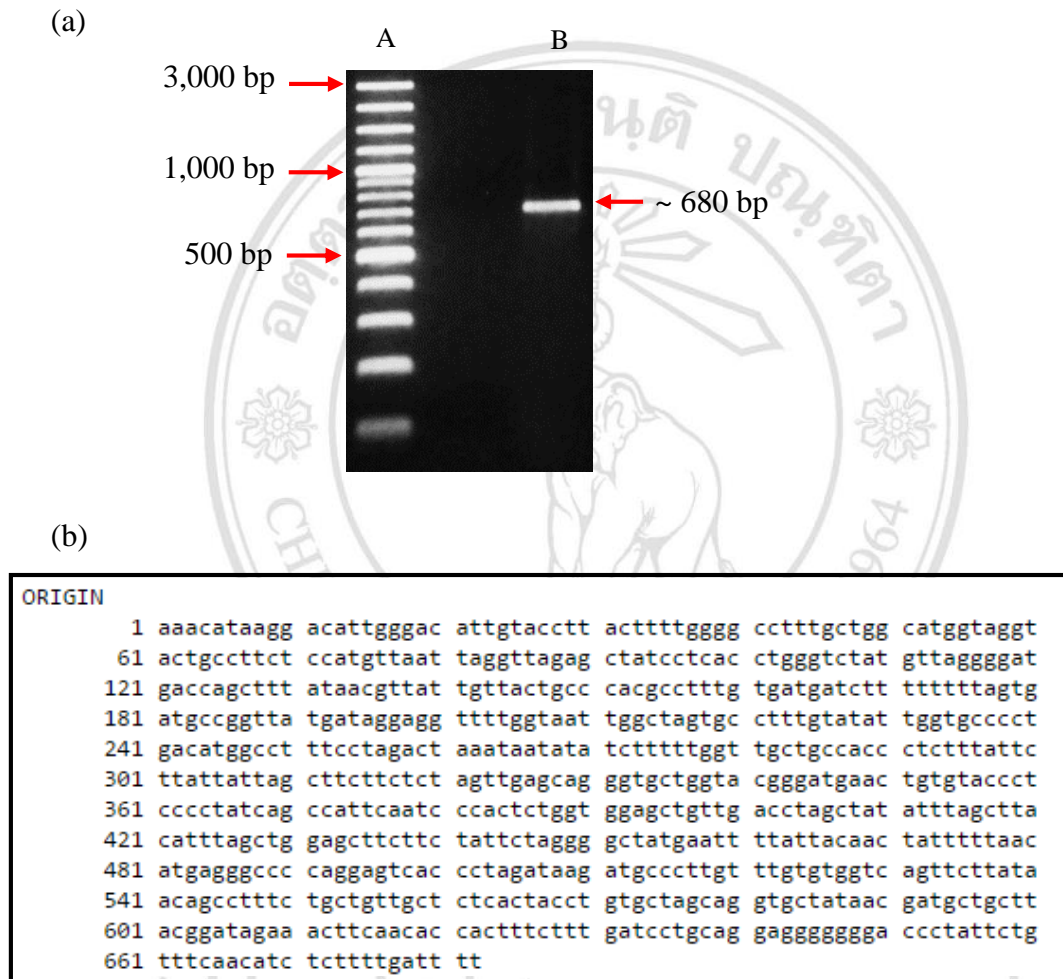
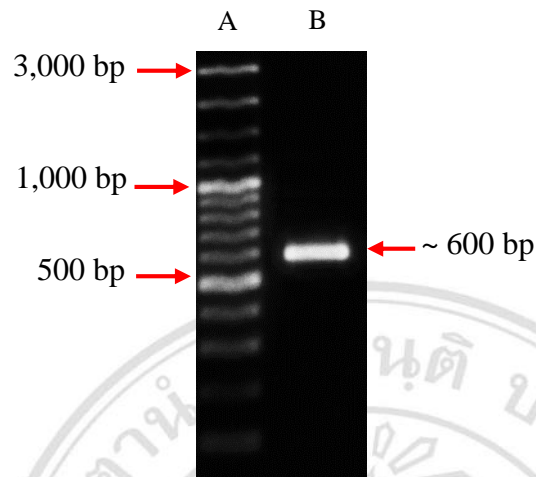


Figure 7.1 (a) PCR product was visualized by 1.5% agarose gel electrophoresis, A: GeneRuler 100 bp DNA ladder, B: *Chironex* sp. A1 (b) Approximately 680 bp of COI gene sequence from *Chironex* sp. A1

(a)

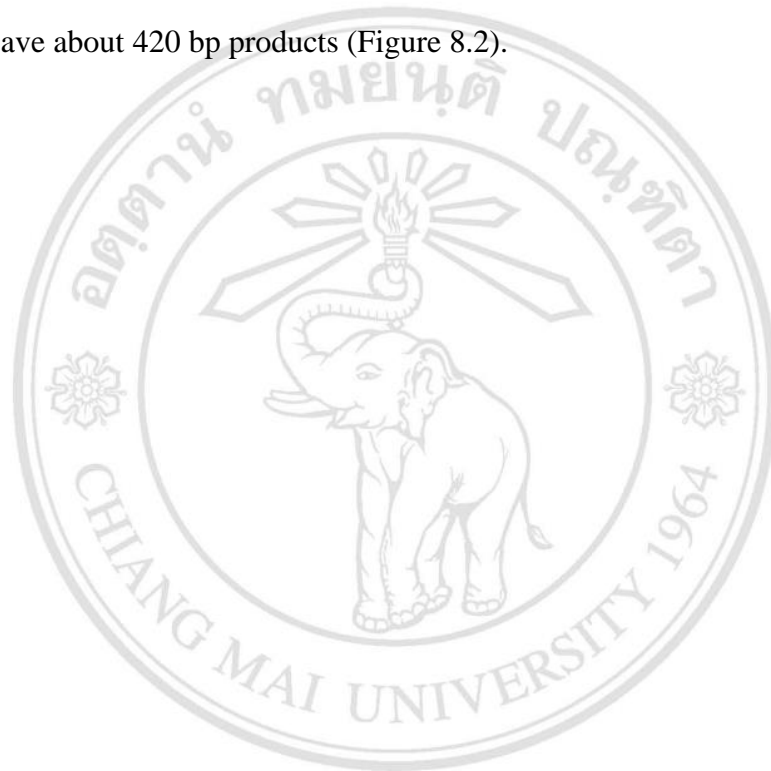


(b)

```
ORIGIN
  1 tccgaattcg tcgacaacct ggttgatcct gccagtagtc atatgcttgt ctcaaagatt
 61 aagccatgca tgtccaagta taagcatttg tactgtgaaa ctgcgaatgg ctcattaaat
121 cagttatcgt ttacttgatc gtatccatta catggataac cgtggtaatt ctagagctaa
181 tacatgcgac aagtcccagc ctctggaagg gatgtattha ttagactaaa aaccaatact
241 ggtttcacga ccagttcaat tggtgattca tgataacttc tcgaatcgca cgggcttagt
301 accggcgatg ttccattcaa atatctgccc tatcaactgt cgatggtaag gtagtggcct
361 accatggttg taacgggtga cggagaatta gggttcgatt ccggagaggg agcctgagaa
421 atggctgcca catccaagga aggagcagg cgcgcaaatt acccaatcct caaagagggg
481 ggtagtgaca agaaataaca atacggggcc atcttggctc cgtaattgga atgagtacaa
541 tttaaatcct ttaacgagga tctattggag ggcaagtctg gtgccagcag ccgcgggtaa
601 ttcaaaa
```

Figure 7.2 (a) PCR product was visualized by 1.5% agarose gel electrophoresis, A: GeneRuler 100 bp DNA ladder, B: *Chironex* sp. A1 (b) Approximately 600 bp of 18S gene sequence from *Chironex* sp. A1

Primers for 16S rRNA were designed from chironomidae members. All sequence from NCBI were aligned to search for conserved region within these group. After that, forward primer (P16sf: 5' AAG GGC CGC GGT AAC TCT G 3') and reverse primer (S16sr: 5' ACC CTG TTA TCC CCG TGG T 3') were designed by Primer-BLAST (Figure 8.1). The designed primers were successfully amplified *chironex* sp. A1-A4 samples and gave about 420 bp products (Figure 8.2).

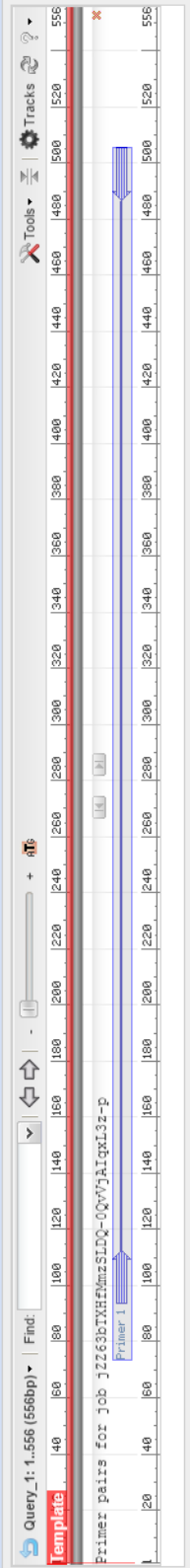


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NCBI/Primer-BLAST : results: Job id=JZ63bTXHfMmzSLDQ-0QvYjIqxL3z-p [more...](#)

Input PCR template
 Range 1 - 556
 Primer pairs are specific to input template as no other targets were found in selected database: Refseq mRNA (Organism limited to Homo sapiens)
[Other reports](#) [Search Summary](#)

Graphical view of primer pairs

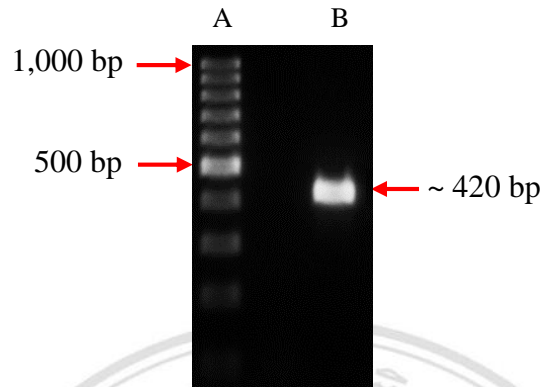


Detailed primer reports

Primer pair 1	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AAGGGCGCGGTAACCTCG	Plus	19	94	112	62.31	63.16	6.00	2.00
Reverse primer	ACCCTGTTATCCCCGTTGGT	Minus	19	505	487	60.23	57.89	4.00	2.00
Product length	412								

Figure 8.1 Forward primer and reverse primer were designed by Primer-BLAST

(a)



(b)

```
ORIGIN
  1 tagggccgcg gtaactctga cctgctaa gtagcataat caatogccat gtaatttatg
 61 gctagaatga atggctttac aagtoctoct ctgtotcaac tttaccccta ctgaaattaa
121 atatgttgtg aagatgcaac ttactcttgg aaggacgaga agaccocgtt gagcttaact
181 cctgttcccc cacctttaa cttaaactct agggaacagt aggtacttgg aggaaaagga
241 gtttggttgg ggcgaccacc taaatagaag caacttaggt aaaccaaggt taacaatcaa
301 tatagtaagc ctaactaata gactgataag ttagttagat agtagtcata gctaagttat
361 agtgaccctc catcataagg agaaattaga taaaagttac cacggggata acagggta
```

Figure 8.2 (a) PCR product was visualized by 1.5% agarose gel electrophoresis, A: GeneRuler 100 bp DNA ladder, B: *Chironex* sp. A1 (b) Approximately 420 bp of 16S gene sequence from *Chironex* sp. A1

Mitochondrial COI gene sequences from *Chironex* sp. A1 and A3 were added to NCBI database, accession numbers are KT223648.1 and KU646841.1 respectively. All sequenced were compared with NCBI database using BLAST (Basic Local Alignment Search Tool). The result showed 85% identical to *Chironex yamaguchii*, accession number: FJ665180.1 (Figure 9.1). The variation among *C. yamaguchii*, *C. fleckeri* and *Chironex. sp A* were computed by MEGA 6 (Figure 9.2). The result showed a distinctive genetic variation among the species. The genetic difference between *C. yamaguchii* (Accession number FJ665180.1) and *Chironex. sp A1* (Accession number KT223648.1) was 14.0% with genetic distance of 0.18. Also, the genetic variation and genetic distance between *C. fleckeri* (Accession number FJ665181.1) and *Chironex. sp A1* (Accession number KT223648.1) was 15.3% and 0.21 respectively. Likewise, the genetic variation between *C. yamaguchii* (Accession number FJ665180.1) and *C. fleckeri* (Accession number FJ665181.1) was 15.3% and genetic distance was 0.19. Variation among 4 *Chironex. sp A* samples were less than 1 percent (Table 5).

Phylogenetic trees were constructed by Maximum likelihood and Kimura 2-parameter model in order to observe relationship among species. The result demonstrated that all *Chironex* sp. A samples were the monophyletic clade with the root of other chirodropids (Figure 9.3).

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chironex yamaouchii voucher USNM1121555 cytochrome c oxidase subunit I (COI) gene, partial cds: mitochondrial	621	621	87%	6e-174	85%	FJ665180.1
Palvthoa aff. mutuki ANK-2014 voucher HeSu13 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	348	348	88%	1e-91	77%	KJ776762.1
Palvthoa aff. mutuki ANK-2014 voucher LaSu7 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	348	348	88%	1e-91	77%	KJ776760.1
Palvthoa aff. mutuki ANK-2014 voucher HeWi2 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	342	342	85%	5e-90	77%	KJ776765.1
Palvthoa aff. mutuki ANK-2014 voucher HeSu19 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	342	342	85%	5e-90	77%	KJ776764.1
Palvthoa aff. mutuki ANK-2014 voucher HeSu18 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	342	342	85%	5e-90	77%	KJ776763.1
Palvthoa aff. mutuki ANK-2014 voucher LaSu14 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	342	342	85%	5e-90	77%	KJ776761.1
Palvthoa aff. mutuki ANK-2014 voucher LaSu1 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	342	342	85%	5e-90	77%	KJ776759.1
Parazoanthid sp. yellow polyp' mitochondrial CO1 gene for cytochrome oxidase subunit 1, partial cds	339	339	88%	7e-89	76%	AB247358.1
Palvthoa tuberculosa voucher HeWi3 cytochrome oxidase subunit I (COI) gene, partial cds: mitochondrial	337	337	88%	2e-88	76%	KJ776768.1

Figure 9.1 Sequences from *Chironex* sp. A1-A4 were compared with NCBI database using BLAST (Basic Local Alignment Search Tool)

Table 5 Localities and genetic variation among *Chironex* sp. A1-A4 of COI gene (671 bp)

Localities	Specimens	Identity (%)	Nucleotide differences at position					
			5	167	473	663	666	667
Chao Lao beach, Chanthaburi	<i>Chironex</i> sp. A1	100	G	C	A	A	G	C
Suan Son beach, Rayong	<i>Chironex</i> sp. A2	99.25	A	T	•	T	C	T
Suan Son beach, Rayong	<i>Chironex</i> sp. A3	99.55	A	T	G	•	•	•
Pha Ngan island, Surat Thani	<i>Chironex</i> sp. A4	99.85	•	T	•	•	•	•

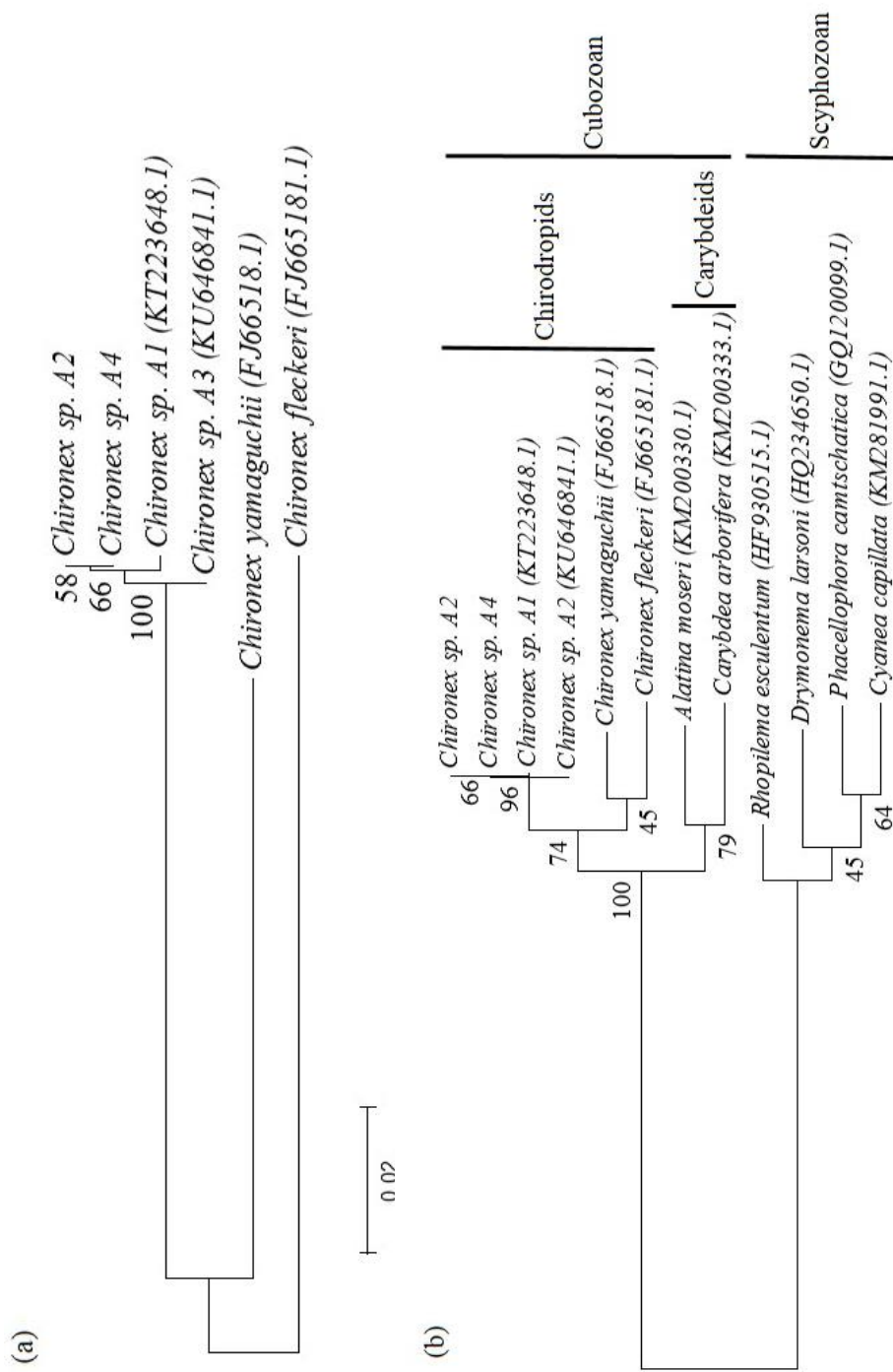
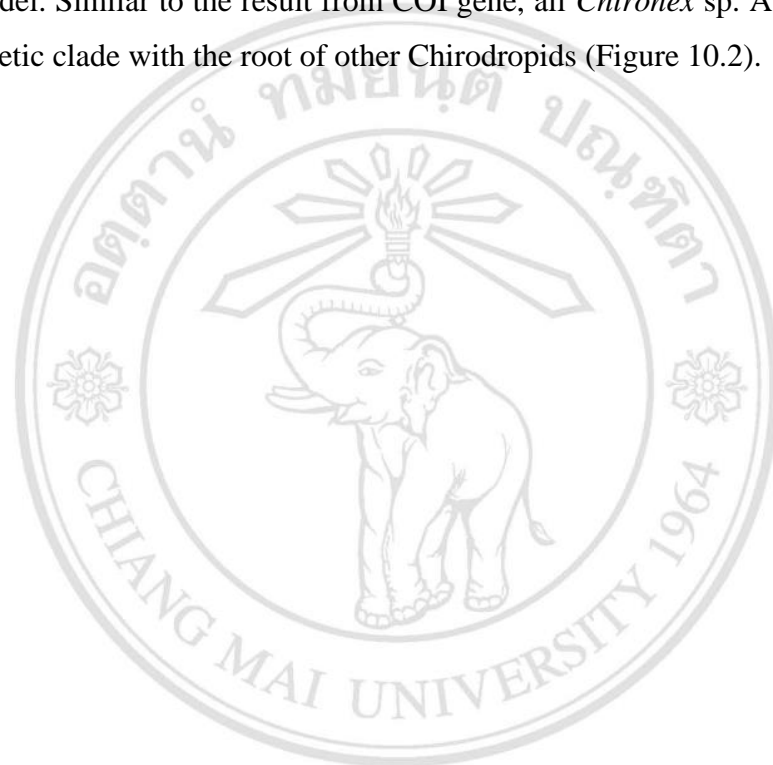


Figure 9.3 (a): Phylogenetic tree of genus *Chironex* based on mt-COI gene; (b): Phylogeny of members from scyphozoa and cubozoa based on mt-COI gene.

For the sequence from 18S rRNA, a sequence from *Chironex* sp. A1 was added into NCBI database, the accession number is KU097000.1. Sequences data from *Chironex yamaguchii* (GQ849076.1), *Chironex fleckeri* (GQ849074.1) and *Chironex* sp. A1-A4 were calculated. The variation among congener calculated by MEGA 6 was less than 1% (Figure 10.1).

Evolutionary trees were constructed by Maximum likelihood and Kimura 2-parameter model. Similar to the result from COI gene, all *Chironex* sp. A samples were the monophyletic clade with the root of other Chirodropids (Figure 10.2).



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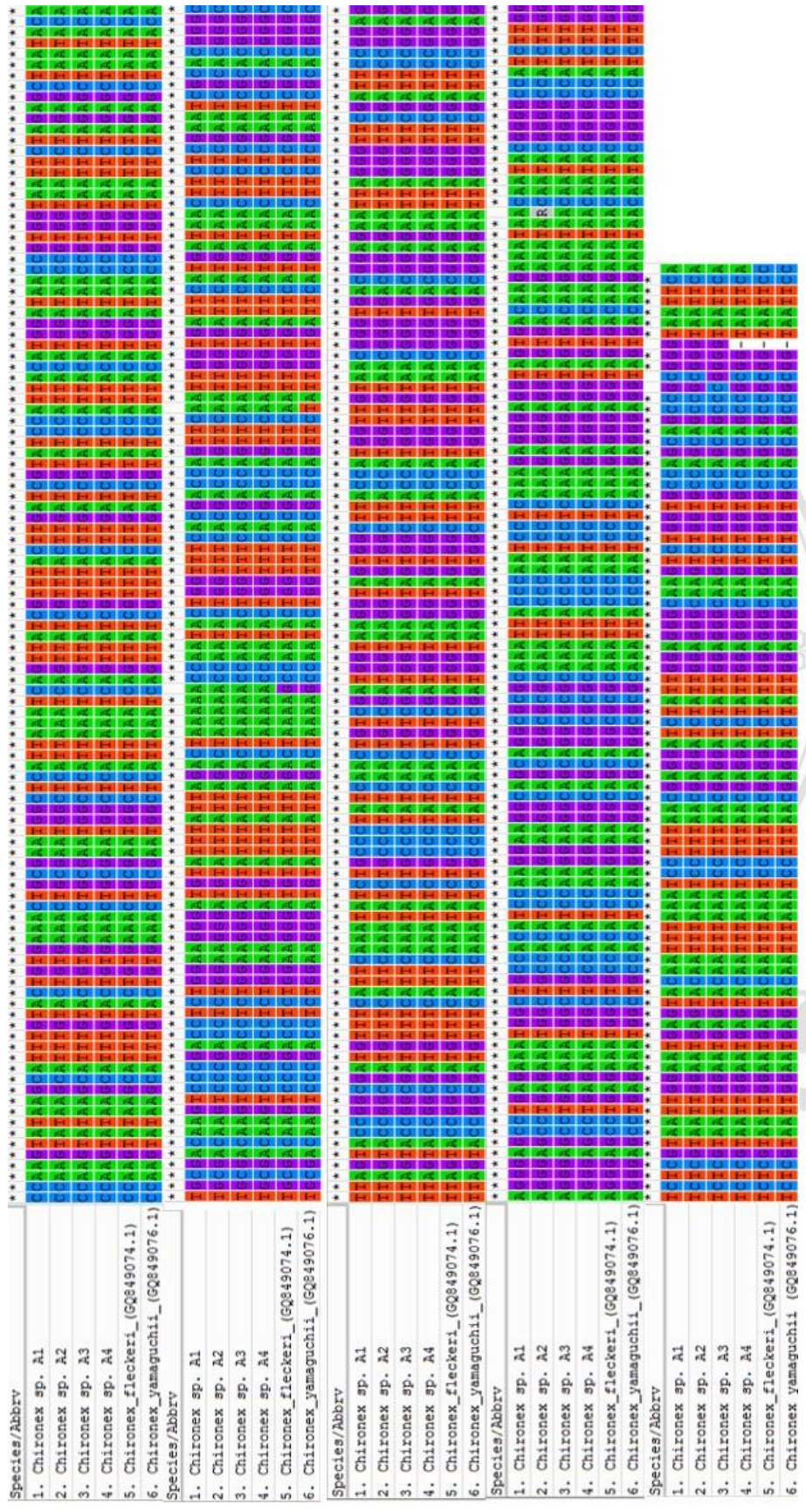


Figure 10.1 18S gene alignment of *Chironex* spp. by MEGA 6

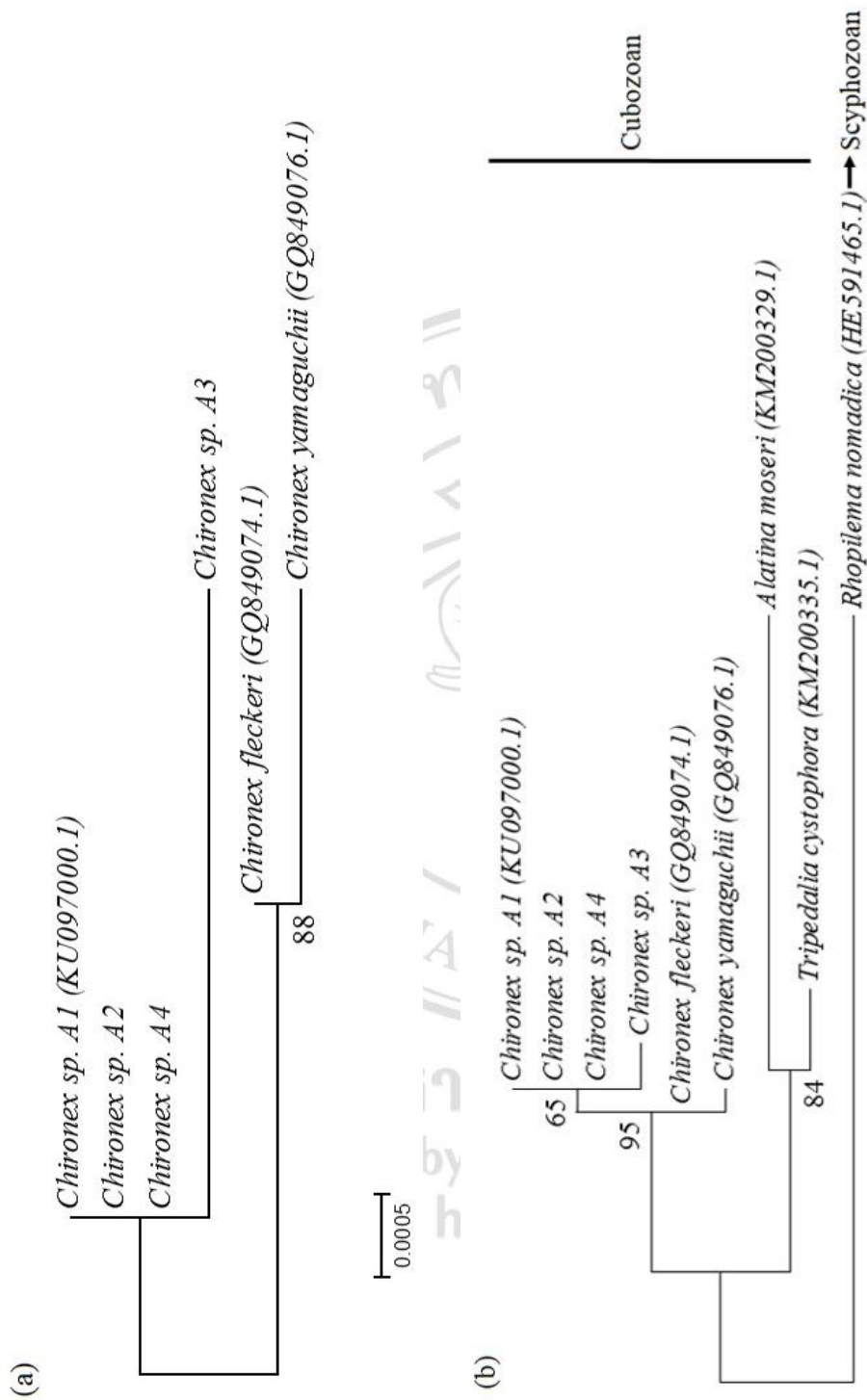


Figure 10.2 (a): Phylogenetic tree of genus *Chironex* based on 18S rRNA; (b): Phylogeny of members from scyphozoa and cubozoa based on 18S rRNA

For 16S sequences, sequences from *Chironex yamaguchii* (from Dr. Allen Collins by personal contact), *Chironex fleckeri* (GQ849103.1) and *Chironex* sp. A1 (KX065499) *Chironex* sp. A4 were computed by MEGA 6. Genetic difference between *Chironex fleckeri* and *Chironex* sp. A1 was 17% while the variation within *Chironex* sp. A1-A4 was relatively low (0.0%) (Figure 11.1).

Phylogeny based on 16S gene were constructed using Maximum likelihood and Kimura 2-parameter model. According to the trees, *Chironex* sp. A1-A4 were separated from *Chironex fleckeri*. Furthermore, the result revealed that *Chironex* sp. A1- A4 samples, were the monophyletic clade with the root of other chirodropids and separated from other scyphozoan (Figure 11.2).

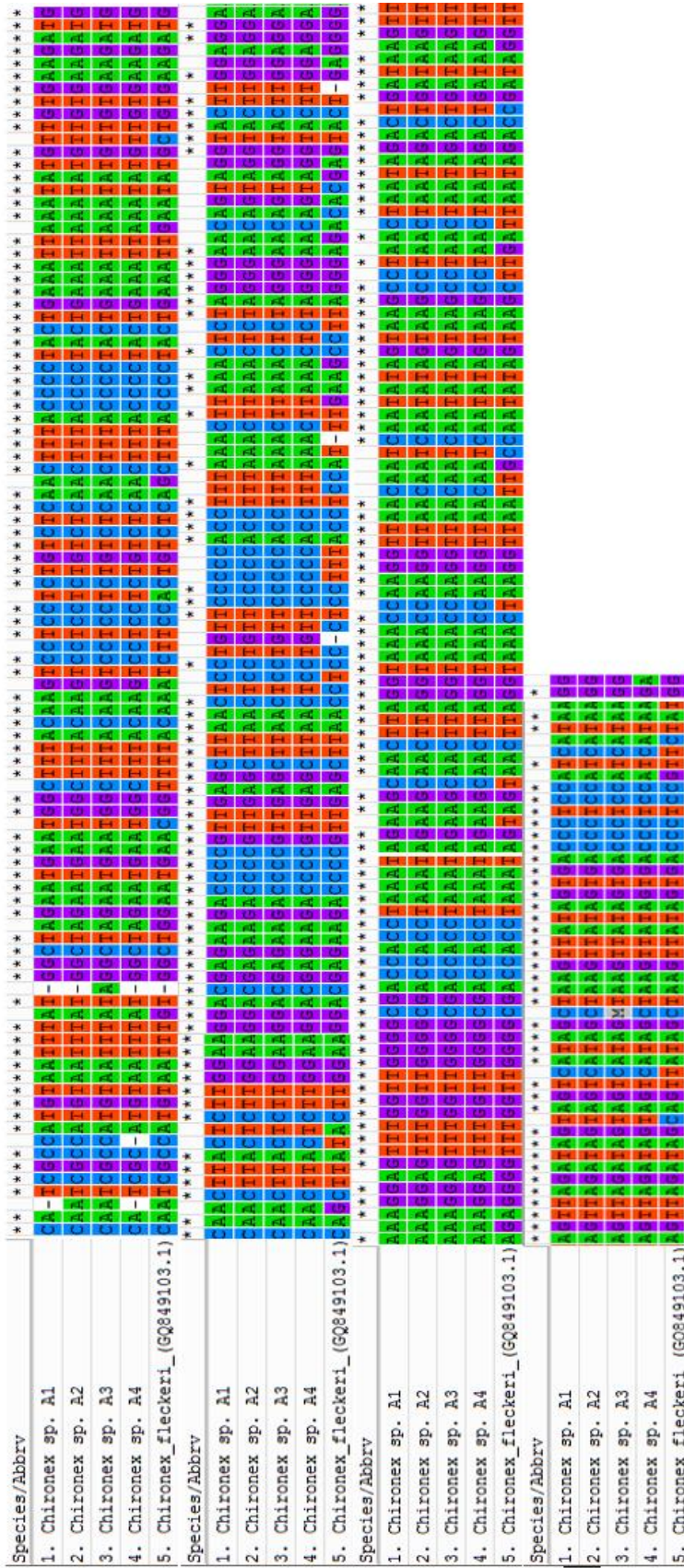


Figure 11.1 Alignment of *Chironex* members based on 16S gene



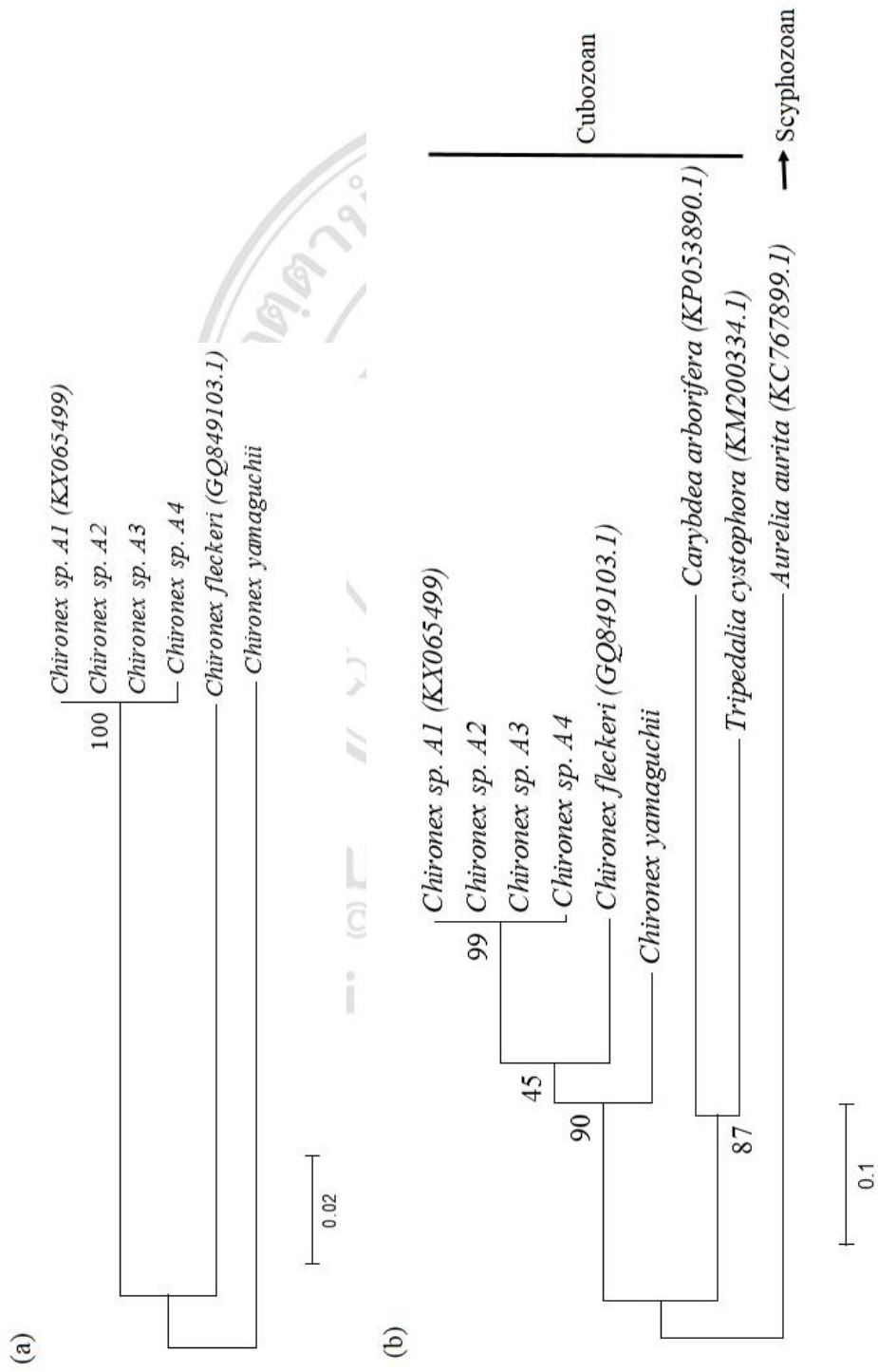


Figure 11.2 (a): Phylogeny of genus *Chironex* based on 16S rRNA; (b): Phylogeny of members from scyphozoa and cubozoa based on 16S rRNA

DICHOTOMOUS KEY TO THAI CUBOZOA

- 1A. Cubomedusae with more than one tentacle arise from each corner of the bell4
- 1B. Cubomedusae with only one tentacle arise from each corner of the bell.....2
- 2A. Frown-shaped rhopalial niche ostium, prominent thorn pedalial canal bend,
exumbrella nematocyst warts present.....3
- 2B. Orange and brown tentacles, bright orange gonads, exumbrella nematocyst warts
absent, phacellae present.....*Carybdea sivickisi*
- 3A. Phacellae absent, 2 eyes per rhopalium, pedalial lappets present.....*Morbakka fenneri*
- 3B. Phacellae present, 6 eyes per rhopalium, pedalial lappets absent...*Tamoya haplonema*
- 4A. Each corner bearing 3 tentacles, frown shaped rhopalial niche ostium, gastric saccule
absent, perradial lappet absent, exumbrella nematocyst present
.....*Tripedalia cystophora*
- 4B. Each corner bearing more than 3 tentacles, gastric saccule present, perradial lappets
present, exumbrella nematocyst absent.....5
- 5A. Finger-shaped gastric saccule, unilaterally branched pedalia, Thorn shaped pedalial
canal, each side of the corner bearing 5-6 tentacles.....*Chiropsoides buitendijki*
- 5B. Cock's comb shaped gastric saccule, claw-like pedalia, doubly uniserial branched
pedalia.....6
- 6A. Volcano shaped pedalial canal bend, 5-9 tentacles arise from the rim
.....*Chironex yamaguchii*
- 6B. More than 11 tentacles arise from each corner of the bell.....7
- 7A. Upward-pointing thorn pedalial canal bend, up to 15 tentacles arise from each corner
of the bell.....*Chironex fleckeri*
- 7B. Dome shaped pedalial canal, 11-12 tentacle arise from each corner of the bell.....
.....*Chironex* sp. A1-A4