ADDITIONAL RECORDS AND PHYLOGENETIC RELATIONSHIPS OF *Fejervarya moodiei* (Taylor, 1920) (ANURA: DICROGLOSSIDAE) FROM VIETNAM

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SUMMARY
Kurniwan et al. (2010) specified the distribution of *F. cancrivora* to the south of the Isthmus of Kra and a large area in the North of the Isthmus of Kra, including Vietnam, is the distribution range of *F. moodiei,* but the samples analyzed in that study did not include samples collected from Vietnam. Based on the results of morphological and genetic analyses on two mitochondrial gene fragments (16S and Cytb) of populations of *Fejervarya moodiei* and *F. cacrivora*, this study confirmed that the Northern Crab-eating Frog *F. moodiei* distributed in Vietnam. In addition, we recorded the distribution of this species in the mangrove areas of the Thai Binh and Thua Thien Hue provinces as well as Hai Phong city. Although the *Fejervarya moodiei* populations are widely distributed from the Philippines to Bangladesh, the genetic differences in the 16S and Cytb genes are insignificant (from 0.2 to 1.5% on 16S gene). Morphological data of specimens of *F. moodiei* from Vietnam and China are also provided.
Keywords: Distribution, *Fejervarya*, new record, taxonomy.

1. INTRODUCTION

The genus *Fejervarya* currently comprises 14 species, distributed in Eastern India, Eastwards to Southern China and Japan, throughout the Indochina region and Southwards to Papua New Guinea (Frost, 2022). In Vietnam, two species are currently known, viz. *F. limnocharis* and *F. moodiei* (Frost, 2022).

The Crab-eating Frog, *Fejervarya cancrivora*, was previously considered a widespread species in the Asian region, from the Andaman and Nicobar Islands of India, Guangxi and Hainan Island of China, Vietnam, Peninsular Thailand, Malaysia, Singapore, the Greater Sundas, the Philippines, and the Lesser Sundas as far as Flores (Frost, 2007; Kurniwan et al., 2010). Kurniwan et al. (2010) specified the distribution of *F. cancrivora* to the South of the Isthmus of Kra and a large area in the North of the Isthmus of Kra, including Vietnam, is the distribution range of *F. moodiei*.

In Vietnam, Nguyen et al. (2009) and Nguyen et al. (2016) recorded *F. moodiei* in Ho Chi Minh City, Kien Giang, Ca Mau and Ba Ria – Vung Tau provinces under the name *F. cancrivora*. Zheng et al. (2021) reported the species from Xuan Thuy National Park, Nam Dinh province, Northern Vietnam but still used the name *F. cancrivora.*

During our fieldwork in Thua Thien Hue province in 2016, in Hai Phong city in 2016 and in Thai Binh province in 2018, a frog collection was sampled and it was assigned to *Fejervarya moodiei* based on morphological and molecular data. We herein provide additional records of this species from Northern and Central localities of Vietnam.

2. RESEARCH METHODOLOGY

Sampling: Field surveys were conducted in 2016 and 2018. Specimens were collected from 19:00 to 24:00. After being taken photographs specimens were anaesthetized in a closed vessel with a piece of cotton wool containing ethyl acetate, fixed in 85% ethanol for 5 hours and subsequently stored in 70% ethanol. For molecular analysis, tissue samples were taken and preserved in 90% ethanol. A total of 17 preserved specimens were collected from Hai Phong, Nam Dinh, Thai Binh, and Thua Thien Hue provinces. Specimens were deposited in the Institute of Ecology and

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Biological Resources (IEBR), Hanoi, Vietnam and the Chengdu Institute of Biology (CIB), Sichuan province, China.

Molecular analyses: DNA extraction and sequencing. Extraction of genomic DNA from 22 tissue samples (Table 1) was carried out using the TIANamp Genomic DNA kit (Tiangen Biotech, Beijing, China), following the manufacturers' instructions. We amplified a 1979 base pair (bp) fragment that encodes part of the 12S rRNA gene, the complete tRNA Val gene, and part of the 16S rRNA gene (Hoang et al., 2021). The polymerase chain reaction (PCR) was performed using an Eppendorf PCR machine in 25 µl reactions containing 12 µl of Mastermix, 6 µl of water, 1 µl of each primer at a concentration of 10 pmol/µl, and 5 µl of DNA. We have amplified in multiple fragments: the first fragment with primers 12SAL (5'-AAACTGGGATTAGATACCCCACTAT-3'; forward), 16S2000H (5'-GTGATTAYGCTACCTTTGCACGGT-3'; reverse) (Zhang et al., 2008); and the second fragment with primers LR-N-13398 (5'-CGCCTGTTTACCAAAAACAT -3'; forward), LR-J 12887 (5'-CCGGTCTGAACTCAGATCACGT -3'; reverse) (see Simon 1994). PCR conditions were at 94°C for 5 minutes of initial denaturation; with 35 cycles of denaturation at 94°C for 30s, annealing at 56°C for 30s, and extension at 72°C for 45s; and the final extension at 72°C for 7 minutes. In addition, we amplified a 654 base pair (bp) fragment that encodes part of the Cytb rRNA gene. The polymerase chain reaction (PCR) was performed using an Eppendorf PCR machine in 25 µl reactions containing 12 µl of Mastermix, 6 µl of water, 1 µl of each primer at a concentration of 10 pmol/µl, and 5 µl of DNA. We have amplified in multiple fragments: Fragmet fisrt, primers: Cytb69R (5'-TCTGCTTAATTGCYCAAATYGC-3'; forward), Cytb780F (5'-AARAGGAARTATCAYTCWGGTTTAAT-3'; reverse) (Liu et al., 2018) used in the PCR and sequencing. PCR conditions: an initial denaturing step at 95°C for 5 min; 35 cycles of denaturing at 94°C for 1 min, annealing at 55°C for 1 min, and extension at 72°C for 1 min; and a final extension step of 72°C for 10 min. PCR products were sent to Tsingke Biological Technology company for sequencing (http://www.tsingke.net). The obtained sequences were deposited in GenBank under the accession numbers ON870696–ON870717 and ON936022-ON936033 (Table 1).

Table 1. Samples of *Fejervarya moodiei* and *F. cancrivora* representatives used in molecular analyses

No	Species	Voucher No	Genbank No		Locality	Reference
			16S	Cytb		
1	*Fejervarya moodiei*	IEBR A.5085	ON870696	ON936022	Vietnam: Nam Dinh	This study
2	*Fejervarya moodiei*	IEBR A.5086	ON870697		Vietnam: Nam Dinh	This study
3	*Fejervarya moodiei*	IEBR A.5087	ON870698		Vietnam: Nam Dinh	This study
4	*Fejervarya moodiei*	IEBR A.5088	ON870699		Vietnam: Nam Dinh	This study
5	*Fejervarya moodiei*	IEBR A.5089	ON870700	ON936023	Vietnam: Nam Dinh	This study
6	*Fejervarya moodiei*	IEBR A.5090	ON870701		Vietnam: Nam Dinh	This study
7	*Fejervarya moodiei*	IEBR A.5091	ON870702	ON936024	Vietnam: Nam Dinh	This study
8	*Fejervarya moodiei*	IEBR A.5092	ON870703		Vietnam: Nam Dinh	This study

No	Species	Voucher No	Genbank No		Locality	Reference
			16S	Cytb		
9	*Fejervarya moodiei*	IEBR A.5093	ON870704	ON936025	Vietnam: Nam Dinh	This study
10	*Fejervarya moodiei*	IEBR A.5094	ON870705	ON936027	Vietnam: Nam Dinh	This study
11	*Fejervarya moodiei*	IEBR A.5096	ON870706	ON936026	Vietnam: Thua Thien Hue	This study
12	*Fejervarya moodiei*	IEBR A.5097	ON870707	ON936028	Vietnam: Thua Thien Hue	This study
13	*Fejervarya moodiei*	IEBR A.5098	ON870708	ON936031	Vietnam: Hai Phong	This study
14	*Fejervarya moodiei*	IEBR A.5099	ON870709	ON936032	Vietnam: Hai Phong	This study
15	*Fejervarya moodiei*	IEBR A.5100	ON870710		Vietnam: Ca Mau	This study
16	*Fejervarya moodiei*	IEBR A.5101	ON870711	ON936029	Vietnam: Ca Mau	This study
17	*Fejervarya moodiei*	IEBR A.5102	ON870712		Vietnam: Ca Mau	This study
18	*Fejervarya moodiei*	IEBR A.5103	ON870713	ON936033	Vietnam: Ca Mau	This study
19	*Fejervarya moodiei*	IEBR A.5104	ON870714		Vietnam: Ca Mau	This study
20	*Fejervarya moodiei*	IEBR A.5105	ON870715	ON936030	Vietnam: Ca Mau	This study
21	*Fejervarya moodiei*	IEBR A.5106	ON870716		Vietnam: Ca Mau	This study
22	*Fejervarya moodiei*	IEBR A.5107	ON870717		Vietnam: Ca Mau	This study
23	*Fejervarya moodiei*		AB070738	AB444706	Philippines: Manila	Kurniawan et al., 2010
24	*Fejervarya moodiei*	ROM 1059	AF206473		Philippines: Negros Island	Chen et al., 2005
25	*Fejervarya moodiei*		AB444691		Thailand: Bangkok	Kurniawan et al., 2010
26	*Fejervarya moodiei*		AB444692	AB444708	Thailand: Trat	Kurniawan et al., 2010
27	*Fejervarya moodiei*		AB372018	AB372070	Bangladesh: Khulna	Islam et al., 2008
28	*Fejervarya moodiei*		EU652694	EU652694	China: Hainan	Ren et al., 2009
29	*Fejervarya cancrivora*		AB444690	AB444703	Indonesia: Bany	Kurniawan et al., 2010

Phylogenetic analyses: In addition to the 22 sequences of 16S rRNA in this work, we used eight available sequences from GenBank for phylogenetic analyses. The sequences of *Fejervarya limnocharis* and *Hoplobachachus rugolosus* were included in the analyses as the outgroups (Fig. 1A). In addition to the 11 sequences of Cytb rRNA in this work, we used six available sequences from GenBank for phylogenetic analyses. A sequence of *Quasipaa shini* was included in the analyses as the outgroup (Fig. 1B). For locality and accession numbers for all sequences used in the analysis see Table 1. Phylogenetic trees were constructed by using maximum likelihood (ML) and Bayesian inference (BI)

analyses. Chromas Pro software (Technelysium Pty Ltd., Tewantin, Australia) was used to edit the sequences, and then aligned using the ClustalW (Thompson et al., 1997) option in MEGA 11 (Tamura et al., 2021) with default parameters and subsequently optimized manually in BioEdit 7.0.5.2 (Hall, 1999). We then checked the initial alignments by eye and adjusted slightly. Evolutionary and genetic distance analyses were conducted in MEGA11. The number of base substitutions per site from between sequences are shown. Analyses were conducted using the Maximum Composite Likelihood model (Tamura et al., 2004). The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The differences in the composition bias among sequences were considered in evolutionary comparisons (Tamura and Kumar, 2002). This analysis involved 30 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). Prior to Bayesian tests, phylogenetic analyses were performed in MrBayes 3.2 (Ronquist et al., 2012). We chose the optimum substitution models for entire sequences using Kakusan 4 (Tanabe, 2011) based on the Akaike information criterion (AIC). The BI summarized two independent runs of four Markov Chains for 10^7 generations. A tree was sampled every 100 generations and a consensus topology was calculated for 70,000 trees after discarding the first 30,001 trees (burnin = 3,000,000). We checked parameter estimations and convergence using Tracer version 1.7 (Rambaut et al., 2018). The strength of nodal support in the ML tree was analyzed using non-parametric bootstrapping with 1,000 replicates. We regarded tree nodes in the ML tree with bootstrap values of 75% or greater as sufficiently resolved (Hillis and Bull, 1993; Huelsenbeck and Hillis, 1993), and nodes with a BPP of 95% or greater as significant in the BI analysis (Leaché and Reeder, 2002).

Morphological analysis: Measurements were taken with digital callipers to the nearest 0.1 mm. Morphological measurements were conducted using characters previously described by Djong et al. (2007), Islam et al. (2008) and Kurniwan et al. (2011), following 31 characters: Snout-vent length (SVL), head length (HL), head width (HW), snout tympanum length (STL), mouth angle-snout length (MSL), distance from nostril to tip of snout (NS), distance from front of eye to tip of snout (SL), nostril tympanum length (NTL), distance from front of eye to nostril (EN), tympanum-eye distance (TEL), tympanum diameter (TD), distance from back of mandible to nostril (MN), distance from back of mandible to front of eye (MFE), distance from back of mandible to back of eye (MBE), inter-narial space (IN), eye length (EL), inter-orbital distance (IOD), maximum width of upper eyelids (UEW), hand length (HAL), forelimb length (FAL), lower arm length (LAL), hindlimb length (HLL), thigh length (THIGHL), tibia length (TL), foot length (FOL), length of tarsus and foot (TFOL), third finger length (3FL), first finger length (1FL), fourth toe length (4TL), length of inner metatarsal tubercle (IMTL), and inner toe length 1 (ITL). Taxonomic identification was based on descriptions of Taylor (1962) and Kurniawan et al. (2011).

3. RESULTS AND DISCUSSION

3.1. Sequence variation

The final alignment of 16S rRNA gene contained 487 characters. Of these, 434 sites were conserved and 48 sites exhibited variation, with 41 characters being parsimony-informative. The estimated Transition/Transversion bias (R) is 2.77. Substitution pattern and rates were estimated under the Tamura (1992) model. The nucleotide frequencies are A = 26.39%, T/U = 26.39%, C = 23.61%, and G = 23.61% (data for ingroup only). The final alignment of Cytb rRNA gene contained 487 number of

characters. Of these, 434 sites were conserved and 48 sites exhibited variation, with 41 characters being parsimony-informative. The estimated Transition/Transversion bias (R) is 2.77. Substitution pattern and rates were estimated under the Tamura (1992) model. The nucleotide frequencies are A = 26.39%, T/U = 26.39%, C = 23.61%, and G = 23.61% (data for ingroup only).

3.2. Interspecific uncorrected p-distance on 16S rRNA gene

In Vietnam, there are no genetic differences between populations from Nam Dinh and Thua Thien Hue provinces and Hai Phong city. The genetic divergence of the population from Ca Mau province and the above three populations (Nam Dinh, Hai Phong and Thua Thien Hue) is approximately of 0.2–0.4%. The genetic divergence ranged from 0.2 to 0.4% between the populations from Vietnam and the populations from the Philippines (the type locality of *Fejervarya moodiei*). These values were insignificant compared to the genetic distances between the populations from the Philippines (of *F. moodiei*) and the populations from Indonesia (of *F. cancrivora*) (14.3–15.5%) or the populations from Malaysia (of *F. cancrivora*) (14.3–15.5%) (Table 2).

Table 2. Uncorrected ("p") distance (%, 16S rRNA) between populations of *Fejervarya moodiei* and *F. cacrivora*

	Populations	1	2	3	4	5	6	7	8	9	10
1	*Fejervarya moodiei* Vietnam: Nam Dinh	**0**									
2	*Fejervarya moodiei* Vietnam: Thua Thien Hue	0	**0**								
3	*Fejervarya moodiei* Vietnam: Hai Phong	0	0	**0**							
4	*Fejervarya moodiei* Vietnam: Ca Mau	0.2–0.4	0.2–0.4	0.2–0.4	**0–0.2**						
5	*Fejervarya moodiei* the Philippines	0–0.4	0–0.4	0–0.4	0.2–0.9	**0–0.4**					
6	*Fejervarya moodiei* Thailand	0	0	0	0–0.4	0–0.4	**0**				
7	*Fejervarya moodiei* Bangladesh	1.5	1.5	1.5	1.1–1.3	1.5–2	1.3	**0**			
8	*Fejervarya moodiei* China: Hainan	0	0	0	0.2–0.4	0–0.4	0	1.5	**0**		
9	*Fejervarya cancrivora* Indonesia	14.3	14.3	14.3	14.3–14.8	14.3–15.5	13.6	14.6	14.3	**0**	
10	*Fejervarya cancrivora* Malaysia	14.8	14.8	14.8	14.8–15.3	14.8–16.1	14.1	15.1	14.8	0.2	**0**

3.3. Phylogenetic relationships on 16S rRNA and Cytb rRNA genes

BI and ML analyses of obtained similar topologies (Fig. 2) that differed only at several poorly supported basal nodes. Our matrilineal genealogy showed that there is no separation between populations from Vietnam and other populations from the Philippines (the type locality of *Fejervarya moodiei*) as well as from the countries of the north of the Isthmus of Kra (China, Thailand, Bangladesh). Our results also supported those of Kurniawan et al. (2010) that populations distributed north of the Isthmus of Kra (including Vietnam) should be assigned to *F. moodiei* (Fig. 1).

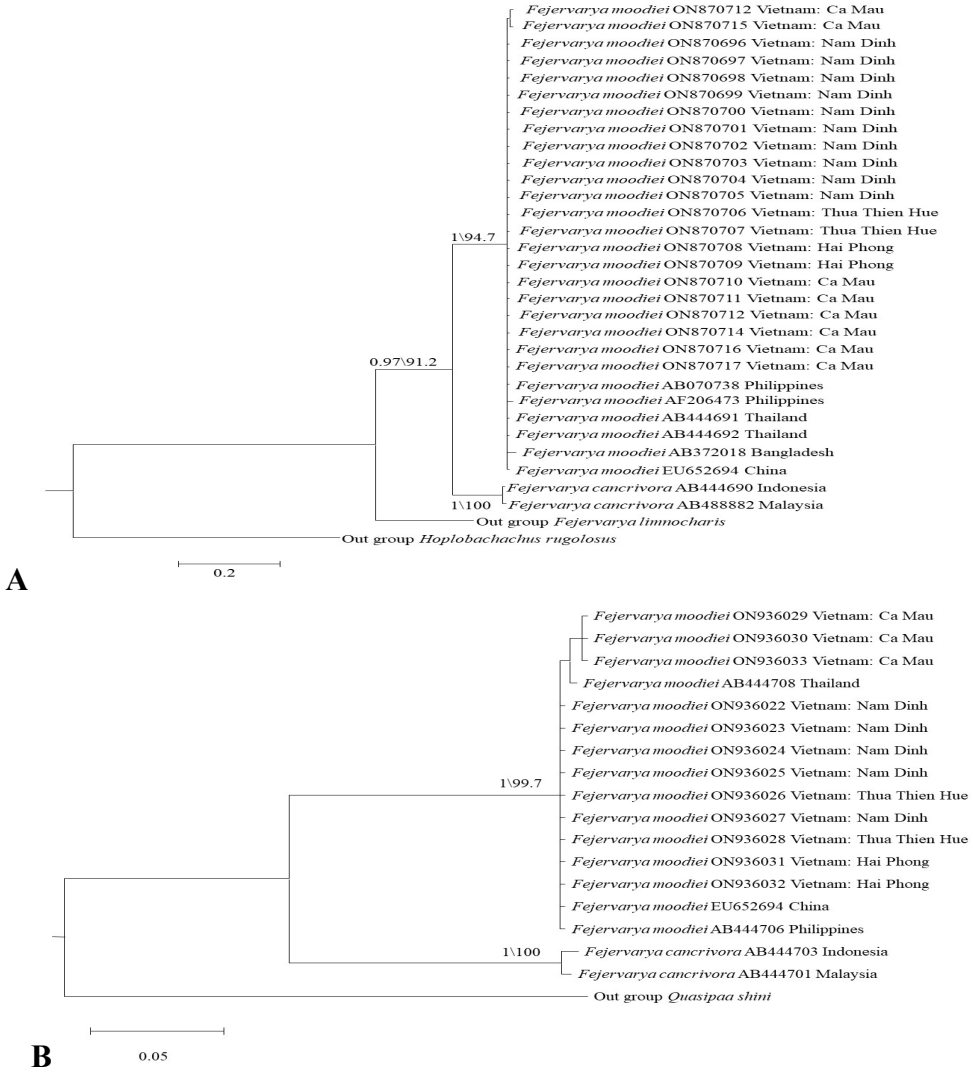

Figure 1. BI tree based on the mitochondrial 16S gene (A), Cytb gene (B) of *Fejervarya moodiei* and *F. cancrivora*. Bootstrap support values are listed in order for the BI/ML analyses. The scale bar represents 0.2(A) and 0.05(B) nucleotide substitutions per site

3.4. Description of *Fejervarya moodiei* (Taylor, 1920) from Vietnam/Northern Crab-eating Frog/Ếch cua (Fig. 2)

A **B**

Figure 2. Dorsolateral view (A) and ventral view (B) of *Fejervarya moodiei* (IEBR A.5096) in life

Specimens examined: IEBR A.5085–5090 (Field no. NĐ2013.6–11), IEBR A.5091, A.5093, A.5094–5095 (Field no. NĐ 2014.1, 2014.3, 2014.5–6), ten adult females, IEBR A.5092 (Field no. NĐ 2014.2), one adult male, collected on 13 December 2013 by C.T. Pham and T.T. Nguyen from Xuan Thuy National Park (20°14'46.2"N 106°34'46.9"E, at an elevation of ~0 m), Giao Thuy district, Nam Dinh province, Vietnam; IEBR A.5096–5097

(Field no. HVC 2016.15, 2016.24), two adult females, collected on 25 December 2016 by C.V. Hoang from Tam Giang - Cau Hai Lagoon, (16°33'27.6"N 107°36'42.4"E, at an elevation of ~0 m), Phong Dien district, Thua Thien Hue province, Vietnam; IEBR A.5098–5099 (Field no. VNMN 06910, 06911) two adult females, collected in December 2016 by T.V. Nguyen from Dinh Vu Seaport (20°51'06.0"N 106°46'20.7"E, at an elevation of 0 m), Hai Phong city, Vietnam; IEBR A.5108, 5109 (Field no. TB 2018.1, 2018.2), two adult females, collected on 13 December 2018 by T.V. Nguyen from Thai Thuy district (20°30'34.1"N 106°34'57.2"E, at an elevation of ~0 m), Thai Binh province, Vietnam; IEBR A.5100, A.5107 (Field no. CM 2018.1, 2018.8), two adult females, IEBR A.5101–5106 (Field no. CM 2018.2–2018.7), five adult males, collected in 2018 by K.V. Nguyen from Dat Mui National Park, Ca Mau province, Vietnam.

Referred specimens: CIB 58046, 58048, two adult females, CIB 5807, one adult male, collected from Hai Nam province, China.

Description: Morphological characters of the specimens from Vietnam (Table 3) agreed well with the description of Taylor (1920) and Fei et al. (1999). Size medium (SVL 51.0–91.3 mm, n = 6 adult females; 55.4–59.3 mm, n = 5 adult males). Head large, triangular, longer than wide (HL/HW 1.01–1.07, adult females; 1.01–1.06, adult males); snout nearly round in dorsal view (SL/HL 0.37–0.43 in females; 0.37–0.43 in males); canthus rostralis distinct, loreal region concave; nostrils round, much closer to snout tip than to eye (NS/EN 0.61–0.89 in females; 0.68–0.80in males. Eye large (EL/HL 0.24–0.30, EL/SVL 0.09–0.11 in females; EL/HL 0.26–0.30, EL/SVL 0.10–0.12 in males); maximum width of upper eyelid greater than interorbital distance (IOD/UEW 0.60–0.75, UEW/EL 0.72–0.85, UEW/SVL 0.07–0.09 in females; IOD/UEW 0.57–0.65, UEW/EL 0.70–0.8, UEW/SVL 0.07–0.09 in males); interorbital space convex, greater than interorbital distance (IOD/IN 0.86–0.97 in females; IOD/IN 0.80–0.97 in males). Tympanum round, smaller than eye length (TD/EL 0.6–0.84, TEL/TD 0.59–0.74 in females; TD/EL 0.64–0.75, TEL/TD 0.47–0.69 in males); vomerine teeth present; tongue cordiform, notched posteriorly; external vocal sac present on either side of the throat. Arm moderately long, robust (FAL/HAL 0.78–0.96, FAL/SVL 0.18–0.25, HAL/SVL 0.19–0.28 in females; FAL/HAL 0.9–0.98, FAL/SVL 0.21–0.22, HAL/SVL 0.22–0.24 in males). Fingers small, free of webbing, tips round. The relative length of fingers II<IV<I<III; tips of fingers bluntly round; fingers dermal ridge weakly developed. Subarticular tubercles prominent, round, single tubercle per digit; supernumerary tubercles absent; two capsule-shaped, distinct palmar tubercles; finger I of males with nuptial pad. Hind limbs are relatively long, longer than tibia length (TL/SVL 0.43–0.56, THIGHL/TL 0.91–1.00, FOL/SVL 0.44–0.57 in females; TL/SVL 0.48–0.49, THIGHL/TL 0.90–1.00, FOL/SVL 0.50–0.54 in males); foot length longer than half of length of tarsus and foot (FOL/TFOL 0.64–0.72 in females; FOL/TFOL 0.68–0.70 in males). Toes long, thin, tips round; webbing between toes weakly developed, webbing formula I1–1II1–1III1–2IV2–1V. Relative lengths of toes I<II<V<III<IV; distinct fringe of skin the on outer side of toe V. Inner metatarsal tubercle elongated, present at base of first toe; outer metatarsal tubercle oval, distinct; subarticular tubercles well developed, nearly oval. Skin dorsal surface smooth, tubercles present, arranged in row; tiny granules on upper eyelids and cloacal region. Dorsal surface of forelimb, thigh and tarsus glandular. Throat, chest, abdomen and ventral part of the thigh and tibia smooth. Colour in life: Dorsal and lateral surface of head, body, forelimbs and hindlimbs brown with a few dark irregular spots; slightly darker brown streak marking between two eyeballs; eyes brown; irises oblique, black; gular region, chest and anterior part of abdomen white cream with dark brown spot; belly, thing and shanks white cream; pectoral glands white. Coloration in preservative: Ground color and pattern are faded. Eyes color turns white.

Ecological notes: Specimens were found at night, between 19:00 and 23:00 on the alluvial ground or grass land. Surrounding habitat was mangrove forest.

Table 3. Morphological characteristics of *Fejervarya moodiei* from Vietnam and China

Voucher No	CIB58047	IEBR A.5100	IEBR A.5107	IEBR A.5096	IEBR A.5097	IEBR A.5089			CIB58048	CIB58046	IEBR A.5104	IEBR A.5101	IEBR A.5105		
Local	**Hainan**	**Ca Mau**	**Ca Mau**	**Thua Thien Hue**	**Thua Thien Hue**	**Nam Dinh**			**Hainan**	**Hainan**	**Ca Mau**	**Ca Mau**	**Ca Mau**		
Sex	F	F	F	F	F	F	Min	Max	M	M	M	M	M	Min	Max
SVL	68.4	66.6	66.7	57.4	51.0	91.3	51.0	91.3	59.3	57.4	58.4	55.4	59.0	55.4	59.3
HL	29.5	27.6	27.0	21.6	19.6	32.6	19.6	32.6	22.6	21.1	22.8	22.3	23.8	21.1	23.8
HW	28.6	26.3	25.7	21.4	18.5	30.5	18.5	30.5	21.6	20.8	21.5	21.2	23.1	20.8	23.1
STL	23.5	20.2	20.6	16.8	15.4	29.4	15.4	29.4	17.7	15.9	17.3	15.7	17.9	15.7	17.9
MSL	27.4	21.1	22.7	18.5	16.1	27.2	16.1	27.4	14.9	22.1	18.6	17.4	19.4	14.9	22.1
NS	4.9	5.4	5.1	3.5	3.3	5.6	3.3	5.6	3.9	3.5	4.3	3.4	4.3	3.4	4.3
SL	12.7	11.1	11.1	8.8	7.9	12.2	7.9	12.7	9.7	8.1	8.8	8.3	9.0	8.1	9.7
NTL	19.0	15.9	16.3	13.6	13.0	19.3	13.0	19.3	14.0	12.3	18.9	13.1	14.3	12.3	18.9
EN	7.3	6.1	6.1	5.8	4.5	6.4	4.5	7.3	5.5	4.5	5.3	5.0	5.9	4.5	5.9
TEL	3.9	3.4	4.0	2.9	2.3	3.8	2.3	4.0	2.9	2.1	2.6	2.7	3.0	2.1	3.0
TD	6.0	5.4	5.4	4.1	4.0	5.2	4.0	6.0	4.3	4.4	4.6	4.3	4.4	4.3	4.6
MN	27.3	24.1	24.2	20.5	17.5	28.4	17.5	28.4	20.3	19.7	20.2	19.2	21.4	19.2	21.4
MFE	20.6	18.1	18.3	14.8	12.9	21.3	12.9	21.3	15.2	14.3	19.7	14.2	15.5	14.2	19.7
MBE	14.4	12.6	12.8	10.0	7.8	12.9	7.8	14.4	9.4	8.6	9.2	8.9	9.5	8.6	9.5
IN	4.4	4.2	3.9	3.4	3.2	5.1	3.2	5.1	3.6	3.4	3.8	3.2	3.8	3.2	3.8
EL	7.1	6.8	6.8	5.9	5.8	8.6	5.8	8.6	6.6	5.9	6.9	5.7	6.8	5.7	6.9
IOD	3.9	3.6	3.8	3.2	2.9	4.4	2.9	4.4	3.5	3.3	3.0	3.1	3.6	3.0	3.6
UEW	5.9	4.9	5.1	5.0	4.7	6.8	4.7	6.8	5.3	4.1	5.3	4.3	4.8	4.1	5.3
HAL	18.9	14.9	15.9	13.4	13.5	17.6	13.4	18.9	14.2	13.2	14.1	12.2	13.8	12.2	14.2
FAL	17.4	13.7	13.0	12.1	10.5	16.8	10.5	17.4	13.1	11.9	13.0	12.0	12.8	11.9	13.1
LAL	11.8	13.1	13.1	10.0	10.1	13.2	10.0	13.2	9.2	10.3	13.2	10.1	10.4	9.2	13.2
HLL	117.7	104.7	105.2	88.5	87.2	120.0	87.2	120.0	90.2	85.7	93.3	86.3	92.7	85.7	93.3
THIG HL	36.6	29.9	30.8	27.5	27.4	37.2	27.4	37.2	25.9	26.0	27.6	25.8	28.8	25.8	28.8
TL	38.6	32.9	31.6	28.0	27.5	39.3	27.5	39.3	28.8	27.4	27.9	26.3	28.7	26.3	28.8
FOL	38.6	32.4	34.4	28.2	29.3	40.2	28.2	40.2	30.3	28.8	30.8	28.7	31.8	28.7	31.8
TFOL	57.7	50.4	49.9	41.8	42.0	56.1	41.8	57.7	44.1	41.6	44.4	42.2	45.2	41.6	45.2
3FL	10.1	9.5	10.8	7.7	7.8	10.5	7.7	10.8	7.8	6.5	9.2	7.7	8.5	6.5	9.2
1FL	14.8	12.1	12.7	1.4	10.6	13.7	1.4	14.8	9.7	10.1	12.0	9.7	11.0	9.7	12.0
4TL	21.1	29.0	29.3	21.1	20.6	31.3	20.6	31.3	16.9	17.4	23.9	21.9	23.1	16.9	23.9
IMTL	4.7	3.4	2.8	3.3	2.5	4.7	2.5	4.7	3.5	3.5	3.4	2.6	2.7	2.6	3.5
ITL	7.1	7.4	7.6	4.9	5.5	8.1	4.9	8.1	4.3	4.4	6.6	5.6	5.9	4.3	6.6

3.5. Distribution

In Vietnam, *Fejervarya moodiei* was recorded in Nam Dinh, Ho Chi Minh City, Kien Giang and Ca Mau provinces (Nguyen et al., 2009; Zheng et al., 2021; as *F. cancrivora*). This is the first record of *F. moodiei* from Hai Phong City, Thai Binh and Thua Thien Hue provinces. Elsewhere, this species has been reported from India, the Andaman Islands, Bangladesh, Cambodia, Thailand, Myanmar, China, and the Philippines (Frost, 2022).

Remark: Although the *Fejervarya moodiei* populations are widely distributed from the Philippines to Bangladesh, the genetic differences in the 16S and Cytb genes are insignificant.

4. CONCLUSION

The crab frog species distributed in Vietnam is *Fejervarya moodiei.* In Vietnam, *F. moodiei* was recorded in Nam Dinh, Ho Chi Minh City, Kien Giang and Ca Mau provinces (Nguyen et al., 2009; Zheng et al., 2021; as *F. cancrivora*). This study is the first record of *F. moodiei* from Hai Phong City, Thai Binh and Thua Thien Hue. Although the *F moodiei* populations are widely distributed from the Philippines to Bangladesh, the genetic differences in the 16S and Cytb genes are insignificant.

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GHI NHẬN BỔ SUNG PHÂN BỐ VÀ QUAN HỆ DI TRUYỀN CÁC QUẦN THỂ CỦA LOÀI *Fejervarya moodiei* (Taylor, 1920) (ANURA: MEGOPHRYIDAE) Ở VIỆT NAM

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TÓM TẮT

Loài Ếch cua *Fejervarya moodiei* đã được Kurniawan và cộng sự (2010) ghi nhận phân bố ở phía Bắc eo Kra (bao gồm Việt Nam), nhưng các mẫu vật sử dụng trong nghiên cứu đó không bao gồm các mẫu vật thu từ Việt Nam. Dựa trên kết quả phân tích đặc điểm hình thái và di truyền trên hai đoạn gen ty thể (16S và Cytb) của các quần thể của hai loài Ếch cua *F. moodiei* và *F. cacrivora,* nghiên cứu này xác nhận loài Ếch cua phân bố ở Việt Nam là *F. moodiei*. Đồng thời, chúng tôi ghi nhận bổ sung phân bố của loài này tại các vùng rừng ngập mặn của thành phố Hải Phòng và các tỉnh Thái Bình và Thừa Thiên Huế. Mặc dù các quần thể của loài *F. moodiei* có phân bố rộng từ Bangladesh về phía Nam đến Philippines nhưng sự khác biệt về mặt di truyền giữa các quần thể địa lý là không đáng kể (chỉ từ 0,2 đến 1,5% trên đoạn gen 16S). Dữ liệu mô tả hình thái của các mẫu vật loài *F. moodiei* ở Việt Nam và Trung Quốc cũng được cung cấp.

Từ khóa: Ghi nhận mới, *Fejervarya*, phân bố, phân loại.

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