Phylogenetic relationship and morphological characters of common house gecko *Hemidactylus frenatus* (Squamata: Gekkonidae) in Nghe An province

Ma Seo Seng[1#], Bui Thuy Linh[1#], Dam Thanh Nga[2], Bui Van Thang[1], Ha Bich Hong[1], Luu Quang Vinh[1*]

[1]*Vietnam National University of Forestry*

[2]*Vinschool the Harmony Highschool – Hanoi, Vietnam*

Quan hệ di truyền và đặc điểm hình thái của loài Thạch sùng đuôi sần *Hemidactylus frenatus* (Squamata: Gekkonidae) tại tỉnh Nghệ An

Ma Seo Sèng[1#], Bùi Thùy Linh[1#], Đàm Thanh Nga[2], Bùi Văn Thắng[1], Hà Bích Hồng[1], Lưu Quang Vinh[1*]

[1]*Trường Đại học Lâm nghiệp*

[2]*Trường THPT Vinschool the Harmony*

[#]*Both authors have contributed equally as the first author*

**Corresponding author: vinhlq@vnuf.edu.vn*

https://doi.org/10.55250/jo.vnuf.10.1.2025.071-080

Article info:
Received: 21/02/2025
Revised: 24/03/2025
Accepted: 22/04/2025

Keywords:
Cytb gene, Gekkota, Genetics, ND2 gene, Taxonomy.

ABSTRACT

Hemidactylus frenatus Duméril & Bibron (Gekkonidae) is a fairly common species and has a wide distribution from Asia, Americas, Africa, Australia, and a number of tropical islands worldwide. Although this species is distributed from the North to the South in Vietnam, studies on morphological characters and genetic diversity are limited. In this study, we used two mtDNA sequences, Cytb (Cytochrome b) and ND2 (NADH dehydrogenase subunit 2), to evaluate the genetic relationships of five H. frenatus specimens in Nghe An province. The genetic distances between the studied samples were relatively low, 0.3% and 0.1% for Cytb and ND2 sequences, respectively. Phylogenetic analyses based on Cytb and ND2 sequences showed that all five samples were grouped together with H. frenatus on GenBank with significant support (100%). The genetic divergence between the H. frenatus specimens in Nghe An and the H. frenatus specimens on GenBank were also small, ranging from 0.0% to 0.6%, while high genetic distance between the five H. frenatus specimens and othe species in the genus Hemidactylus was observed, ranging from 29% to 46%. In addition, the morphological characters of H. frenatus species in Nghe An are also described to provide additional biological data for studies on genetic relationships and the invasion process of the species.

Từ khóa:
Cytb gene, Gekkota, Genetics, ND2 gene, Taxonomy.

TÓM TẮT

Thạch sùng đuôi sần (Hemidactylus frenatus) là một loài phổ biến với phạm vị phân bố rộng, xuất hiện ở nhiều khu vực thuộc châu Á, châu Mỹ, châu Phi, Úc và một số đảo nhiệt đới. Tại Việt Nam, loài này phân bố từ Bắc tới Nam, tuy nhiên các nghiên cứu liên quan đến đa dạng di truyền và đặc điểm hình thái của loài vẫn còn hạn chế. Trong nghiên cứu này, nhóm tác giả sử dụng hai trình tự DNA ty thể gồm Cytochrome b (Cytb) và NADH dehydrogenase subunit 2 (NADH) để phân tích quan hệ di truyền năm mẫu Thạch sùng đuôi sần thu thập tại tỉnh Nghệ An. Kết quả phân tích cho thấy mức độ sai khác di truyền giữa các mẫu là thấp, với khoảng cách di truyền 0,3% đối với trình tự Cytb và 0,1% đối với trình tự ND2. Cây phát sinh chủng loại được xây dựng dựa trên trình tự Cytb và ND2

cho thấy cả năm mẫu nghiên cứu được nhóm cùng với nhau và với loài H. frenatus trên GenBank với giá trị bootstrap ủng hộ rất cao (100%). Mức độ phân hóa di truyền giữa các mẫu tại Nghệ An và các mẫu H. frenatus trên GenBank dao động từ 0,0% đến 0,6%, trong khi khoảng cách di truyền giữa các mẫu này với các loài khác trong giống Hemidactylus dao động từ 29% đến 46%, cho thấy sự khác biệt rõ rệt về mặt di truyền. Ngoài ra, các đặc điểm hình thái của loài Thạch sùng đuôi sần tại Nghệ An cũng được mô tả chi tiết, nhằm bổ sung thông tin sinh học cho các nghiên cứu về quan hệ tiến hóa, cấu trúc quần thể và tiềm năng xâm lấn của loài này.

1. INTRODUCTION

The speciose gekkonid genus *Hemidactylus* Goldfuss, 1820, is one of the most diverse genera within the Gekkonidae family, comprising 195 species, seven of which are known from Vietnam [1]. The Common House Gecko, *Hemidactylus frenatus*, is native to South east Asia but has been introduced to the Americas, Africa, Australia, and several tropical islands worldwide [1, 2]. In Vietnam, this species has a wide distribution range, from the North to the South [3] .

Preliminary analyses of genetic diversity based on mtDNA of this species have been performed in many different regions of the world such as the Western Pacific islands [4]; Moorea, French Polynesia [5]; South America [6]; Indian Ocean [7]. However, there is limited information regarding the genetic data and morphological characteristics of this species in Vietnam. During a field survey in Con Cuong district, Nghe An province, we collected five specimens of the *Hemidactylus* genus. Based on the analysis of morphological traits and genetic relationships, we provide, for the first time, information on the genetic relationships and morphological features of *Hemidactylus frenatus* from Nghe An province.

2. RESEARCH METHODS

2.1. Sampling

Field surveys occured during the evening hours in October 2023 Con Cuong district, Nghe An province, Vietnam. After photographing the newly collected specimens, they were euthanized in a sealed container with a cotton wool pad soaked in ethyl acetate [8], fixed in 85% ethanol, and then transferred to 70% ethanol for long-term storage. Tissue samples were preserved separately in 70% ethanol. The specimens were later deposited in the collection of the Vietnam National University of Forestry (VNUF) in Hanoi, Vietnam.

2.2. Genetic data

A total of 05 collected samples of *Hemidactylus* species from Nghe An province along with 34 species from GenBank were included in the analyses (Table 1).

Table 1. List of samples used for the phylogenetic analyses.

Species	DNA sequence	Catalog no.	Location	GenBank accession no.
	Cytb, ND2	**LD 13**	**Nghe An, Vietnam**	-
		LD 14	**Nghe An, Vietnam**	-
		LD 15	**Nghe An, Vietnam**	-
		YK 06	**Nghe An, Vietnam**	-
		YK 07	**Nghe An, Vietnam**	-
	Cytb	LELU-UR05	Curacao, Dutch Antilles	MH541093.1
		HEMA-UR69		MH541094.1
		HEMA-GU57		MH541095.1
		HEMA-GU58		MH541096.1
		HEMA-GU59		MH541097.1
	Cytb	-	China	EU549816.1

Species	DNA sequence	Catalog no.	Location	GenBank accession no.
Hemidactylus frenatus	Cytb	MTCP	China	FJ971015.1
	Cytb	HEFR-AW-18-02-cytBS1L/cytbH15	Aruba	MT666059.1
	Cytb	HEMA-UR29 HEMA-UR68	Curacao	MG049673.1 MG049674.1
H. shihraensis	Cytb	JS57	-	KC818865.1
H. gubanensis	Cytb	NMP-P6V 76683	Northern Somaliland	PP756140.1
H. adensis	Cytb	NHM-BS N41904	Yemen and Ethiopia	KP238268.1
H. dawudazraqi	Cytb	COMU-ZM-B5	Jordan: Azraq	HQ833753.1
H. turcicus	Cytb	Hdeg01	Egypt	OR133206.1
H. lavadeserticus	Cytb	JOR22_51	Jordan	OR133199.1
H. granosus	Cytb	JIR549	Jordan	OR133191.1
H. isolepis	Cytb	NMP-P6V 74446/3	Ethiopia	MN538002.1
H. awashensis	Cytb	NMP6V 74978/2	Yemen and Ethiopia	KP238259.1
H. haitianus	Cytb	NMP6V 73365/3	Cameroon	HQ833764.1
H. mindiae	Cytb	NMP6V 72739/1	Jordan	HQ833748.1
H. frenatus	ND2	DJ1259	Maldives	MK559042.1
	ND2	RMB 3534; TNHC 62814	Philippines	HM559630.1
	ND2	DJ640	Maldives	MK559055.1
H. parvimaculatus	ND2	DJ3431	Maldives	MK559035.1
H.brookii parvimaculatus	ND2	ADS36	USA	GQ458053.1
H. sankariensis	ND2	NCBS-BH682	India	MK569844.1
H. aaronbaueri	ND2	CES14023	India	MN482222.1
H. benguellensis	ND2	CAS 263324	Angola	MN843782.1
H. paivae	ND2	FKH-0455	Angola	MZ616987.1
H. sushilduttai	ND2	CES11079/NCBS-AU157	India	MK569852.1
H. scabriceps	ND2	CES12008	India	MH454769.1
Lepidodactylus lugubris	Cytb	HEMA-CU18	Curacao	MG049682.1
	ND2	SYNU210417	China	ON416995.1

2.3. Morphological data and analyses

Measurements and meristic characters followed by Narayanan et al. (2023) [9]. Measurements and meristic data from the collected specimens for this study were taken under an Olympus SZ61 stereo microscope and using a Mitutoyo digital vernier caliper (accuracy 0.1 mm). Selective abbreviations were as follows: snout vent length (SVL, from tip of snout to the cloacal opening; axilla to groin length (AGL, from posterior mar-gin of forelimb insertion to anterior margin of hind–limb insertion); tail length (TL, from the cloacal opening to tip of tail); tail width (TW, taken at the base of the tail immediately posterior to the postcloacal swelling); head length (HL, distance from the posterior margin of the retroarticular process to the tip of the snout); head width (HW, maximum width of head); head depth (HD, maximum head depth at occiput); eye to snout distance (SE, distance between anterior margin of eye and tip of ; orbital diameter (OD, greatest diameter or bony orbit); maximum width of body (BW); LD4A: length of finger IV; LD4P: length of toe IV; forearm length (FL, from posterior margin of elbow while flexed 90º to distal end of wrist); crus length (CL, from the posterior surface of the knee while flexed 90º to the base of the heel); femur L: femur length, from limb

insertion to knee. Additional meristic characters include: the number of paravertebral tubercles between limb insertions (PVT); the number of ventral scale rows at midbody between the lowest rows of dorsal scales (MVSR); femoral pores (FP) in the femoral region in males; the number of pore-less scales between the series of femoral pores and the number of undivided lamellae on all the digits in manus and pes.

2.4. Molecular data and phylogenetic analyses

Total genomic DNA was extracted from liver samples using the animal DNA isolation Kit (AnalytikJena, Germany). A fragment of ND2 (NADH dehydrogenase subunit 2) and Cytb (cytochrome b) gene in the mitochondrial genome were amplified using the primer pairs ND2f101A (5'-CAACAGAAGCCACAACAAAAT-3')/ HemiR (5'-GAAGAAGAGGCTTGGKAGGCT-3') [10] and L1419 (5'-AACCACCGTTGTTATTCAACT-3')/H16064 (5'-CTTTGGTTTACAAGA ACAATGCTTTA-3') [11], respectively.

The PCR volume consisted of 15 µL of Taq PCR master mix 2X (AnalytikJena, Đức), 12 µL of water, 1 µL of each primer at 10 pmol/µL and 1 µL of DNA or higher depending on the quantity of DNA in the final extraction solution). The following temperature profile for PCR was used: 95°C for 5 min; 40 cycles at 95°C for 30 s, 50°C for 45 s (for ND2f101A/ HemiR primer), and 46°C for 30 s (for L1419/ H16064 primer), 72°C for 60 s, and the final extension at 72 °C for 6 min. PCR products were visualized using electrophoresis through a 1.0% agarose gel, DNA ladder 100 bp, 1X TAE and stained with RedSafe Nucleic Acid Staining Solution and photographed under UV light of Geldoc system (Quantum CX5, Villber, France).

Successful amplifications were purified to remove PCR components and unspecific amplifications using an innuPREP gel extraction Kit (Analytikjena – Germany) for ND2 gene and innuPREP PCR pure Kit (Analytik Jena, Germany) for Cytb gene. Purified PCR products were sent to FirstBase (Malaysia) for sequencing in both directions.

Sequence data were aligned in BioEdit v.7.2.5 [12]. Phylogenetic trees were performed using maximum likelihood (ML) on MEGA ver. 7.0 [13] software with 1000 bootstrap replicates. Genetic distances among species were calculated using MEGA ver. 7.0 [13].

3. RESULTS AND DISCUSSION

3.1. Molecular analyses

Cytb and ND2 fragments were amplified successfully with 1200 bp and 700 bp in length, respectively (Figure 1). Alignment of sequences shows five different positions in Cytb sequences, in which LD13 and LD15 are 100% similar 100%, LD14 and YK6 differ at two nucleotide positions, and YK7 differs at only one nucleotide position (Figure 2A). The genetic distance between five *Hemidactylus* sp. samples is 0.3%. Between these five samples and *Hemidactylus frenatus* species on GenBank vary from 0.00 to 0.6%. However, genetic divergence is 33% - 45% between the five studied samples and other species of *Hemidactylus* genus (Table 2).

The phylogenetic results constructed based on Cytb sequences indicated that five *Hemidactylus* sp. samples were placed in the same clade as *Hemidactylus frenatus* with a strong bootstrap value (100%) (Figure 3).

For the ND2 sequences, four samples, including LD14, LD15, YK6 and YK7, is 100% identity. LD13 sample had a different at one nucleotide position (Figure 2B). Genetic distance among five samples is 0.1% while this value between the five studied samples with *Hemidactylus frenatus* and other species in *Hemidactylus* genus on GenBank ranges from 0.0% to 0.5% and 29% to 46%, respectively (Table 3). In phylogenetic tree, all five samples were clustered in the same clade with three *Hemidatylus frenatus* species from GenBank (100% bootstrap value).

In the field, the five samples were identified

as an unknown species and Cytb as well as ND2 sequence analyses confirmed they were *Hemidactylus frenatus* (Table 1). Both phylogenetic analyses based on Cytb and ND2 sequences showed the same result, that is, all five samples were grouped with *H. frenatus* on GenBank with significant support. However, other species of the genus *Hemidatylus* showed significant genetic divergence with *H. frenatus* group, this is probably due to the limited data available on GenBank.

Rocha et al. (2022) supposed *H. frenatus* appears to be a species complex, with variation between the samples from mainland India and Sri Lanka and the island populations ranging up to 14 and 11%, respectively, using Cytb sequences [7].

Smid et al. (2019) analyzed the sequences of two mitochondrial genes (12S and Cytb) and four nuclear genes (cmos, mc1r, rag1, rag2) of the genus *Hemidactylus* in Africa and confirmed that the *Hemidactylus* species in Africa are separated into a separate clade compared to the Arabian clade [14].

Torres - Carvajal (2015) also used Cytb sequences and found no variation across Ecuador, Colombia, Hawaii, and Papua New Guinea while intraspecific genetic distances between individuals of *H. frenatus* from Papua New Guinea/Hawaii/South America and individuals from India and Myanmar included in the analysis varied between 6.9%–13.2%. Besides, four samples come from geographically close localities (India and Myanmar), their genetic distances vary between 7.6% – 13.5% [6].

In this study, genetic diversity among *H. frenatus* from Nghe An province is relatively low, with only 0.3% for Cytb sequences and 0.1% for ND2 sequences. This contrasts with the high genetic diversity of invasive *H. frenatus* recently reported from the remote Pacific island of Moorea, French Polynesia [5].

Toniene et al. (2011) supposed that invasive species often have reduced genetic diversity, but the opposite can be true if there have been multiple introductions and genetic admixture. Reduced diversity is most likely soon after establishment, in remote locations, when there is lower propagule pressure and with stepping-stone colonization [5]. The low genetic diversity of *H. frenatus* in Nghe An may require further analysis of more samples to examine the possibility of species invasion.

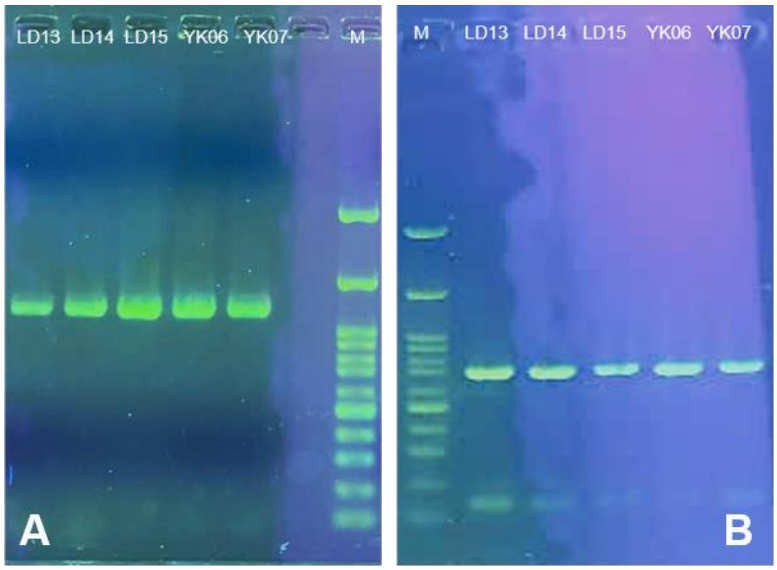

Figure 1. Agarose gel electrophoresis of PCR products of Cytb (A) and ND2 (B) gene. Annotated ladder (M) size is 100 bp

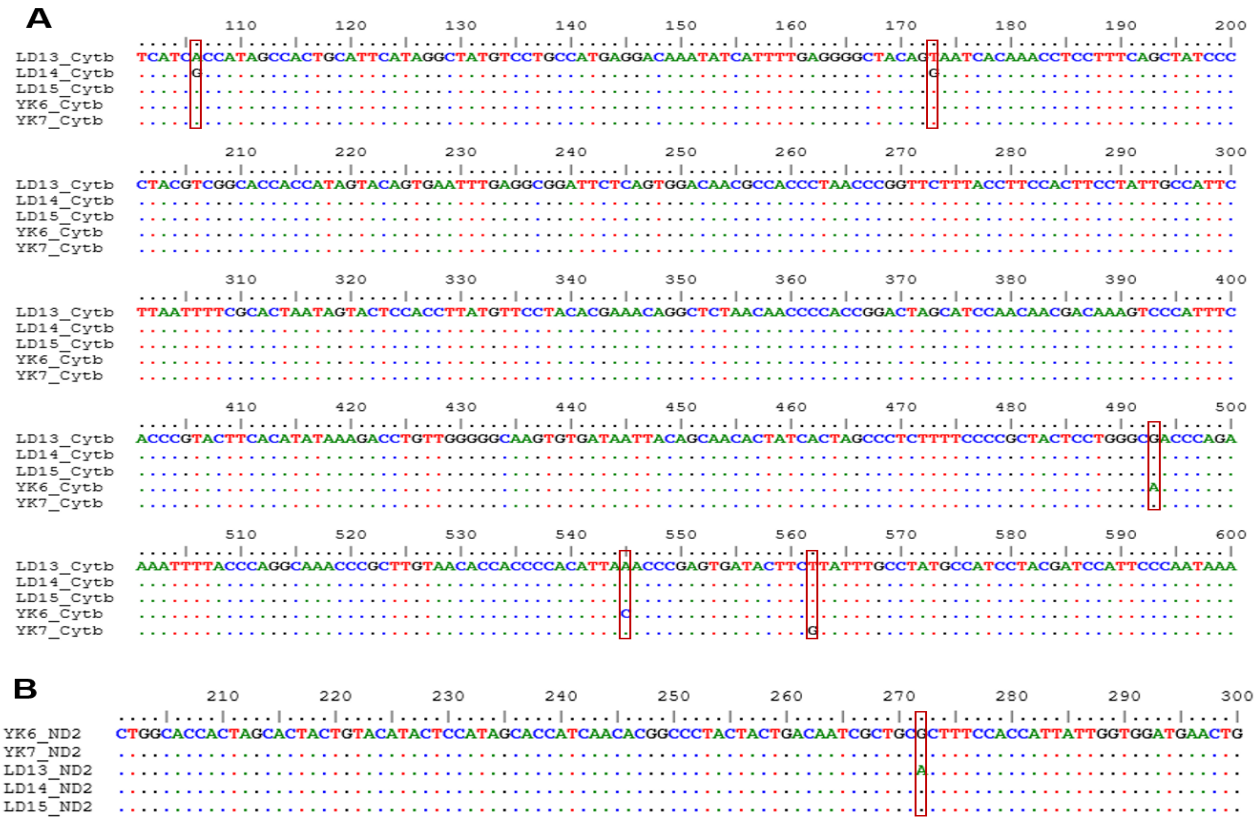

Figure 2. Multiple sequence alignment of nucleotide sequences of Cytb gene (A) and ND2 gene (B). Color dots show similar nucleotides and color letters (A, G, C, T) present different nucleotides

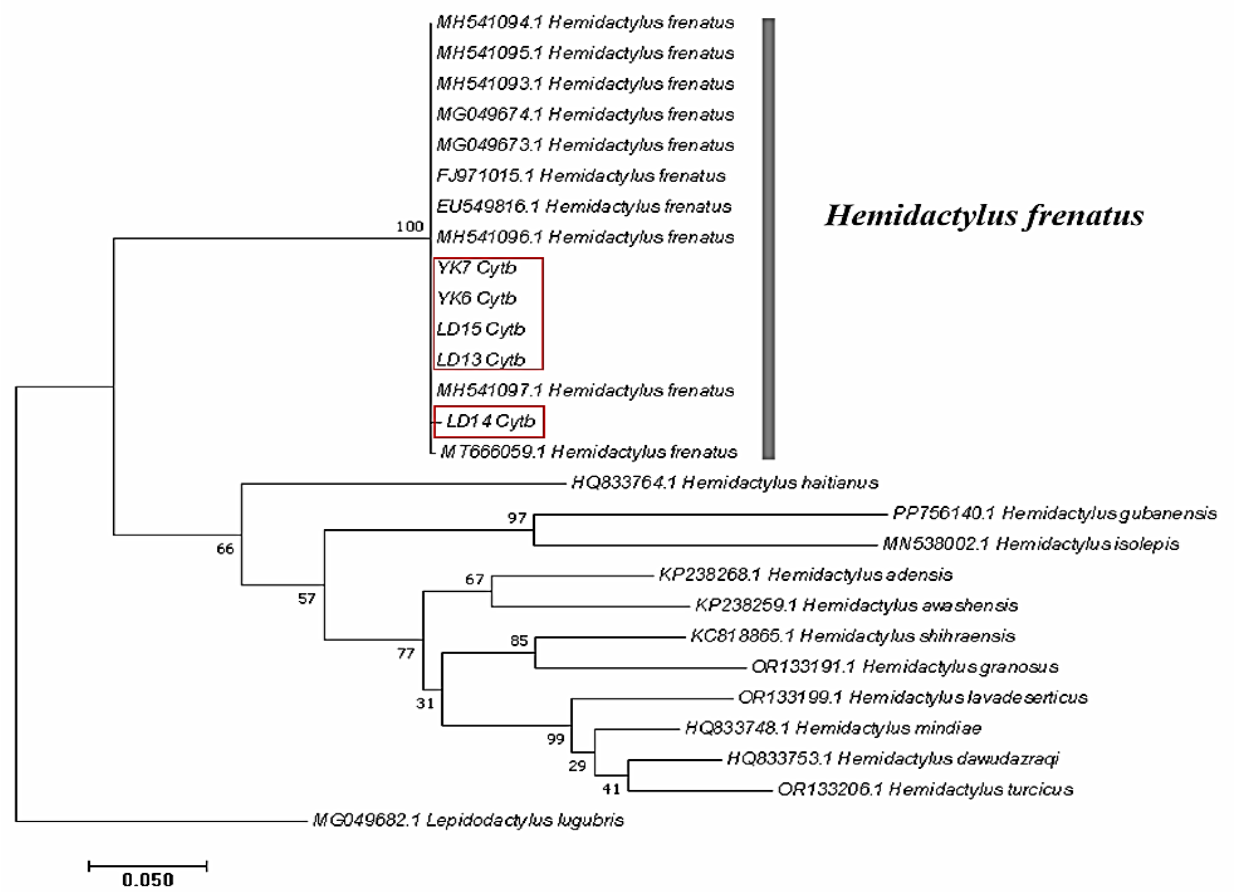

Figure 3. Phylogenetic analysis using Maximum Likelihood method of Cytb nucleotide sequences. The numbers above branches are ML ultrafast bootstrap values

Table 2. Matrix showing percentage pairwise genetic distance between different species using Cytb sequences

Voucher/ species name	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1. LD 13																	
2. LD14	0.003																
3. LD15	0.00	0.003															
4. YK 6	0.003	0.007	0.003														
5. YK 7	0.002	0.005	0.002	0.005													
6. *H. frenatus*	0.00 – 0.002	0.004– 0.006	0.00 – 0.002	0.00 – 0.002	0.00 – 0.002	0.00 – 0.002											
7. *H. shihraensis*	0.33	0.34	0.33	0.33	0.33	0.33											
8. *H. gubanensis*	0.45	0.45	0.45	0.45	0.45	0.45	0,37										
9. *H. adensis*	0.34	0.34	0.34	0.34	0.34	0.34	0,19	0.39									
10. *H. dawudazraqi*	0.36	0.37	0.36	0.36	0.36	0.36	0,21	0.36	0.18								
11. *H. turcicus*	0.34	0.35	0.34	0.34	0.34	0.34	0,19	0.39	0.19	0.10							
12. *H. lavadeserticus*	0.36	0.37	0.36	0.35	0.36	0.36	0,21	0.40	0.22	0.13	0.14						
13. *H. granosus*	0.34	0.35	0.34	0.34	0.34	0.34	0,16	0.41	0.21	0.22	0.22	0.24					
14. *H. isolepis*	0.45	0.45	0.45	0.45	0.45	0.45	0,37	0.35	0.33	0.37	0.33	0.37	0.38				
15. *H. awashensis*	0.39	0.41	0.39	0.39	0.39	0.39	0,19	0.38	0.16	0.19	0.20	0.23	0.20	0.35			
16. *H. haitianus*	0.34	0.35	0.34	0.34	0.34	0.34	0,31	0.44	0.28	0.31	0.29	0.34	0.32	0.47	0.31		
17. *H. mindiae*	0.35	0.37	0.36	0.35	0.35	0.35	0,20	0.39	0.19	0.09	0.11	0.11	0.22	0.36	0.21	0.28	

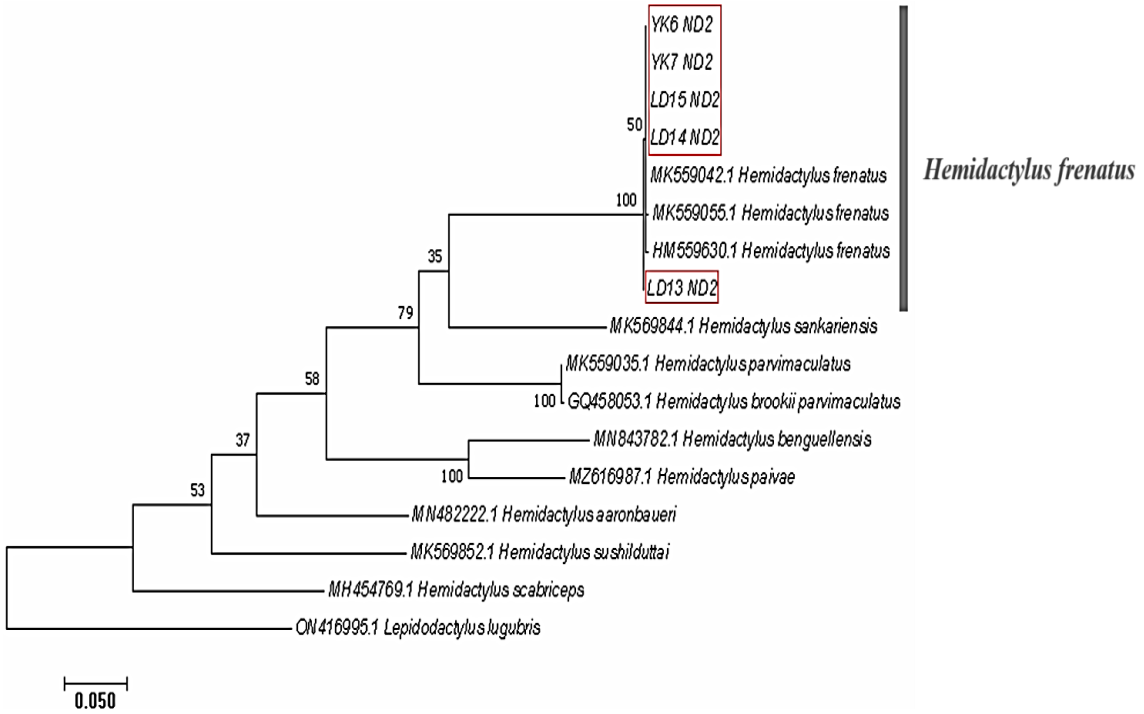

Figure 4. Phylogenetic analysis using Maximum Likelihood method of ND2 nucleotide sequences. The numbers above branches are ML ultrafast bootstrap values

3.2. Taxonomic treatment

Table 3. Matrix showing percentage pairwise genetic distance between different species using ND2 sequences

	Voucher/ species name	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1.	LD 13														
2.	LD14	0.002													
3.	LD15	0.002	0.00												
4.	YK 6	0.002	0.00	0.00											
5.	YK 7	0.002	000	0.00	0.00										
6.	*H. frenatus*	0.002 – 0.005	0.00 – 0.002	0.00 – 0.002	0.00 – 0.002	0.00 – 0.002									
7.	*H. parvimaculatus*	0.29	0.29	0.29	0.29	0.29	0.29								
8.	*H. brookii parvimaculatus*	0.29	0.29	0.29	0.29	0.29	0.29	0.00							
9.	*H. sankariensis*	0.27	0.27	0.27	0.27	0.27	0.27	0.28	0.28						
10.	*H. aaronbaueri*	0.37	0.37	0.37	0.37	0.37	0.37	0.32	0.32	0.35					
11.	*H. benguellensis*	0.36	0.37	0.37	0.37	0.37	0.37	0.33	0.33	0.38	0.41				
12.	*H. paivae*	0.38	0.39	0.39	0.39	0.39	0.39	0.37	0.37	0.33	0.40	0.16			
13.	*H. sushilduttai*	0.36	0.37	0.37	0.37	0.37	0.37	0.44	0.44	0.45	0.34	0.34	0.41		
14.	*H. scabriceps*	0,45	0.46	0.46	0.46	0.46	0.46	0.52	0.52	0.39	0.41	0.44	0.50	0.33	

Specimens examined (n=5): Three adult males (LD 13, LD 14, LD 15) and two adult females (YK6, YK7) were collected between 05 and 08 October 2023 by Luu Quang Vinh, Vilay Phimpasone, Dinh Thi Quynh, Lung Long Thanh in the karst forest of Con Cuong district, Nghe An province.

A large gecko of the genus *Hemidactylus*, medium–size (SVL) 47.3-56.3 mm (mean ± SD: 51.05 ± 3.58 mm); tail length (TL) 38.2-54.3 (mean ± SD: 45.73 ± 5.85 mm), the tail base has 3–4 rows of spines in straight lines, varying by individual; tail width (TW) 5.4-6.3 mm (mean ± SD: 5.75 ± 0.35 mm); head elongated, depressed (mean HW/mean HL 0.67 mm), distinct from neck; loreal region concave; snout long (mean SE/mean HL 0.38 mm), longer than the diameter of the orbit (mean OD/mean SE

0.53 mm); snout scales small, granular; eye large (mean OD/mean HL 0.20 mm), pupils vertical; ear oval shaped, small; rostral wider than high, rostral bordered by a nostril, and first supranasal on each side; nares round, surrounded by supranasal, rostral, first supralabial, and three postnasals; mental triangular; two postmentals, enlarged, in broad contact posteriorly, bordered by mental anteriorly, first infralabial laterally, and an enlarged chin scale posteriorly; 11 supralabials on each side; 9–10 infralabials. Dorsal scales granular; dorsal tubercles round, subconical, small, gradually increasing in size and becoming conical towards the flanks, each surrounded by 9-11 granular scales; 7–13 the paravertebral tubercles between limb insertions; 34-39 ventral scales across midbody scales, smooth, medial scales 2 or 3 times larger than dorsal scales, round; enlarged femoral scales present on both male and female, 25-39 in male and 0-12 in female; femoral pores are elongated, forming a straight line along the crus from left to right in males, 0–12 pitted precloacal pores in females; 2 or 3 postcloacal tubercles, but one individual (LD14) lacking them on one side; subcaudals enlarged; no tubercles on the dorsal surface of fore and hind limbs; fingers and toes with indistinct webbing; 15 or 16 lamellae under fourth fingers, 17 or 18 under fourth toes; 7 or 8 lamellae under first fingers and 9 beneath first toes.

Male: Stocky body (SVL: 53.15 ± 1.55 mm); Tail length (TL: 50.65 ± 3.65 mm) slightly shorter than the body; trunk relatively longer (AGL: 23.70 mm) and head longer than wide (HL: 16.20 ± 0.10 mm, HW: 10.95 ± 0.15 mm); big eyes (OD: 3.25 ± 0.05 mm); long snouts (SE: 6.15 ± 0.25 mm); narrow cross-section (BW: 11.45 ± 0.25 mm); robust forearms (FL: 6.95 ± 0.35 mm), thin limbs with femur length (FemurL: 8.05 ± 0.05 mm) and crus length (CrusL: 7.50 ± 0.20 mm); robust fourth toe (LD4A: 3.95 ± 0.25 mm) and broad toe pad (LD4P: 6.10 ± 0.00 mm).

Female: Proportionate body (SVL: 50.45 ± 4.45 mm) with a shorter tail (TL: 40.80 ± 3.68 mm); elongated body (AGL: 21.35 ± 3.18 mm); Shorter and narrower head than the males (HL: 14.80 ± 1.41 mm, HW: 9.85 ± 0.21 mm); moderately sized eyes (OD: 2.95 ± 0.21 mm); relatively long snout (SE: 5.60 ± 0.28 mm); lean cross-section body (BW: 10.05 ± 0.35 mm); average forearm length (FL: 6.25 ± 0.49 mm), thin limbs with femur length (FemurL: 7.00 ± 0.78 mm), and crus length (CrusL: 3.80 ± 3.68 mm); average length of the fourth toe (LD4A: 4.15 ± 0.07 mm) and average width of the toe pads (LD4P: 5.35 ± 0.35 mm).

Figure 6. *Hemidactylus frenatus* samples LD 13 (A, E), LD 15 (B), YK 6 (C, F) and YK 7 (D) from Nghe An province

Coloration: The dorsal coloration is dull brown, with a series of four or five pale transverse saddles running from the occiput to the sacrum, and the tail displays distinct alternating light and dark bands. The limbs blend into the body color. The head is identical in color to the dorsum, and the eyes are large with dark pupils surrounded by lighter irises.

4. CONCLUSION

The phylogenetic analyses of five *Hemidactylus frenatus* samples from Nghe An province indicate that the genetic distance within the population is relatively low, only 0.3% and 0.1% for Cytb and ND2 sequences, respectively. The genetic divergence between the *H. frenatus* specimens in Nghe An and the *H. frenatus* specimens on GenBank were also small, ranging from 0.0% to 0.6%. Besides, morphological characteristics of this species in Nghe An are also described to provide additional data on the biodiversity of the widely distributed but little-studied species.

Acknowledgements

We are grateful to Vilay Phimpasone, Dinh Thi Quynh, Lung Long Thanh for their assistance in the field. This research is funded by the Vietnam National Foundation of Science and Technology Development (NAFOSTED, grant No. 106.06-2021.28).

REFERENCES

[1]. Peter Uetz, Sami Cherikh, Glenn Shea, Ivan Ineich, Patrick D Campbell, Igor V Doronin, Jose Rosado, Addison Wynn, Kenneth A Tighe & Roy McDiarmid (2019). A global catalog of primary reptile type specimens. Zootaxa. 4695(5): 438–450.

[2]. J Lindley McKay & Olga Milenkaya (2020). The Asian House Gecko (Hemidactylus frenatus) established in natural vegetation of Oaxaca, Mexico. Reptiles & Amphibians. 27(3): 479-484.

[3]. Nguyen Van Sang, Ho Thu Cuc & Nguyen Quang Truong (2009). Herpetofauna of Vietnam. Edition Chimaira.

[4]. C Moritz, TJ Case, DT Bolger & S Donnellan (1993). Genetic diversity and the history of Pacific island house geckos (*Hemidactylus* and *Lepidodactylus*). Biological Journal of the Linnean Society. 48(2): 113-133.

[5]. Maria A Tonione, Natalie Reeder & Craig C Moritz (2011). High genetic diversity despite the potential for stepping-stone colonizations in an invasive species of gecko on Moorea, French Polynesia. PLoS One. 6(11): e26874.

[6]. O Torres-Carvajal (2015). On the origin of South American populations of the common house gecko (Gekkonidae: *Hemidactylus frenatus*). NeoBiota. 27: 69-79.

[7]. Sara Rocha, Alexandra Trinks, D James Harris, Greger Larson & Anthony S Cheke (2022). The global and Western Indian Ocean dispersal of house geckos from Asia using historical and mitochondrial DNA perspectives. Frontiers in Ecology & Evolution. 10: 791762.

[8]. Dwayne D Simmons (2002). Development of the inner ear efferent system across vertebrate species. Journal of neurobiology. 53(2): 228-250.

[9]. Surya Narayanan, Peter Christopher, Kothandapani Raman, Nilanjan Mukherjee, Ponmudi Prabhu, Maniezhilan Lenin, Sivangnanaboopathidoss Vimalraj & V Deepak (2023). A new species of rock-dwelling *Hemidactylus* Goldfuss, 1820 (Squamata: Gekkonidae) from the South ern Eastern Ghats, India. Vertebrate Zoology. 73: 499-512.

[10]. Truong Quang Nguyen, Tanja Lehmann, Minh Duc Le, Ha Thuy Duong, Michael Bonkowski & Thomas Ziegler (2013). A new species of *Hemiphyllodactylus* (Reptilia: Gekkonidae) from Northern Vietnam. Zootaxa. 3736(1): 89-98.

[11]. Peng Guo, Qin Liu, Yan Xu, Ke Jiang, Mian Hou, Li Ding, R Alexander Pyron, Frank T Burbrink (2012). Out of Asia: natricine snakes support the Cenozoic Beringian dispersal hypothesis. Molecular phylogenetics & evolution. 63(3): 825-833.

[12]. Tom A Hall (1999). BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic acids symposium series. Oxford. 95-98.

[13]. Sudhir Kumar, Glen Stecher, Koichiro Tamura (2016). MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Molecular biology & evolution. 33(7): 1870-1874.

[14]. Jiří Šmíd, Tomáš Mazuch, Lucie Nováková, David Modrý, Patrick K Malonza, Hassan Sh Abdirahman Elmi, Salvador Carranza & Jiří Moravec (2019). Phylogeny and systematic revision of the gecko genus *Hemidactylus* from the Horn of Africa (Squamata: Gekkonidae). Herpetological Monographs. 33(1): 26-47.