



Genetic Diversity of Vietnamese Native Ducks Based on Sequences of the Mitochondrial Dna D-Loop Region

NGUYEN THI VINH¹, PHAM KIM DANG², TRAN BICH PHUONG¹, NGUYEN THI PHUONG GIANG¹, DO DUC LUC¹, HA XUAN BO¹, BUI HUY DOANH¹, NGUYEN VAN DUY³, NGUYEN VAN THONG¹, BUI BINH AN⁴, NGUYEN QUOC TRUNG⁴, NGUYEN HOANG THINH^{1*}

¹Faculty of Animal Science, Vietnam National University of Agriculture; ²Department of Livestock Production, Ministry of Agriculture and Rural Development; ³Daixuyen Duck Breed and Research Center; ⁴Faculty of Biotechnology, Vietnam National University of Agriculture

Abstract | Indigenous ducks contribute significantly to communities in Vietnam as cheap and highly nutritional protein sources. At present, most native ducks are often raised on a small scale in household using traditional farming methods. This study analyzed the polymorphisms of five Vietnamese duck breeds, namely Na Tau (VNT), Dom (VD), Co (VC), Co Lung (VCL), and Troi (VT) by the mtDNA D-loop region to have more genetic information to aid in the conservation and maintenance of these breeds. Fifteen mutation sites were detected in the sequence analyses and formed 17 haplotypes. A low genetic diversity of Vietnamese indigenous ducks was found with an average haplotype and nucleotide variants of 0.051 (Hd) and 0.099% (Pi), respectively. Tajima's D index was significantly negative in the VNT population ($P < 0.10$). The genetic distances among breeds ranged from 0.189–0.347. The neighbor-joining phylogenetic tree indicated that the Vietnamese indigenous ducks have close relationships with both *Anas platyrhynchos* and *Anas zonorhyncha*.

Keywords | Conservation, Genetic diversity, Mitochondrial D-loop, Vietnamese duck.

Received | May 17, 2024; **Accepted** | June 15, 2024; **Published** | December 18, 2024

***Correspondence** | Nguyen Hoang Thinh, Faculty of Animal Science, Vietnam National University of Agriculture, Trau Quy, Gia Lam, Ha noi, Viet Nam; Email: nhthinh@vnua.edu.vn

Citation | Vinh NT, Dang PK, Phuong TB, Giang NTP, Luc D, Bo HX, Doanh BH, Duy NV, Thong NV, An BB, Trung NQ, Thinh NH (2025). Genetic diversity of Vietnamese native ducks based on sequences of the mitochondrial DNA d-loop region. Adv. Anim. Vet. Sci. 13(1): 73–80.

DOI | <https://dx.doi.org/10.17582/journal.aavs/2025/13.1.73.80>

ISSN (Online) | 2307-8316; **ISSN (Print)** | 2309-3331



Copyright: 2025 by the authors. Licensee ResearchersLinks Ltd, England, UK.

This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

INTRODUCTION

Vietnam is one of the countries with the potential for biodiversity and serves as the cradle of domestication of many livestock. Vietnamese indigenous duck breeds are an important part of livestock genetic diversity and their

distribution throughout the country has been has been raised by farmers using different traditional husbandry methods. Indigenous duck breeds have the common advantage of adaptation to local environmental conditions, including climate, feed, technology of rearing and use of animals, diseases and parasites, and other specifics, and they

are adapted to the ever-changing socio-economic demands and environmental conditions (FAO, 2007). The meat and eggs of ducks are widely used by Vietnamese people due to their unique taste and high nutritional value. However, most native ducks are not very efficient in terms of productivity and have a longer rearing period (Hong *et al.*, 2012).

In the context of population explosion and unfavorable environmental changes, food and feed safety are a top concern of countries around the world as well as in Vietnam. In addition, due to the rapidly increasing demand for food as population and incomes have increased, high-yielding exotic breeds have been massively imported. This has led to a decrease in the number of local breeds, declines in population sizes, and the extinction of a few breeds with a resultant decline in genetic diversity (Seo *et al.*, 2016). Indigenous livestock breeds are valuable and have diverse genetic resources for exploitation, development, and hybridization to create commercial varieties, creating sustainable agricultural systems (Blott *et al.*, 2003). Therefore, it is very important to retain these genetic resources for the future. In recent years, in countries around the world, more and more attention has been paid to the protection and management of indigenous breeds (Susanti *et al.*, 2017). The government of Vietnam has recently approved the Program with the aim of preserving, using and developing and sustainable use genetic resources, which emphasizes the promotion of the application of biotechnology (Hoat *et al.*, 2022).

Mitochondrial DNA (mtDNA) is commonly used to evaluate phylogenetic relationships or population genetics because of its lack of recombination and the rate of nucleotide substitution is 5 to 10 times higher than that of nuclear DNA markers (Brown *et al.*, 1979; Mannen *et al.*, 2004). Mitochondrial DNA has two major functional regions, of which the coding region makes up 93% of the mitochondrial genome and the remaining region, called the D-loop (displacement loop), is a noncoding region with high variation, and therefore, the mtDNA D-loop sequencing could be an effective tool for determining phylogenetic relationships, including genetic distances and genetic variability among breeds (Pfeiffer *et al.*, 2005). This study explored the sequences of mtDNA D-loop of Vietnamese native ducks for genetic diversity and their relationships with other reference sequences found in NCBI GenBank. Our findings could provide evidence to better understand duck domestication in Vietnam and a genetically based tool for effective conservation programs.

MATERIALS AND METHODS

The animals for this study were VNT, VD, VC, VCL, and VT ducks. VNT is mainly distributed in Na Tau Commune, Dien Bien District, Dien Bien Province in Northwestern Vietnam (21o23' N 103o1' E). It has a chubby body and

short neck. The male has a blue head and neck feathers with a pearlescent sheen, a flaming stork chest, blue secondary wing feathers, stone-gray body feathers, a yellow-green beak, and yellow feet. The female has split-winged feathers, yellow feet, and black webbed feet. VD originated in Lang Son Province (21o45' N 106o30' E), where the ethnic people usually call it "Pat Lai". They have light sparrow-colored feathers and are a medium sized duck. VC has its root in Van Dinh Commune, Ung Hoa District, Ha Noi City (20°43' N 105°46'17"E). They have a small body size with mainly sparrow-colored feathers. The males have a light green beak and blue neck feathers. VCL, also known as a Quoc Thanh or Muong Khuong duck, is an indigenous breed originating in Co Lung commune, Ba Thuoc district, Thanh Hoa Province (19o48' N 105o46' E). Co Lung duck has its own signature characteristics that are considered to be peculiar to this breed: a short neck, small and short legs, the neck and head are covered with smooth feathers, and the male duck has curly tail feathers and blue neck feathers with a pearlescent sheen. VT is a quite familiar wild bird in Vietnam with settled populations in the North and South, and migratory populations wintering in the North and Central regions. In this study, VT were raised in Thuan Thanh District, Bac Ninh Province (21o2' N 106o4' E). In general, adult VT ducks have gray-black body feathers with many stripes like sparrows. The fur on the underside of the neck is light and smooth (no stripes), while the fur on the belly is lighter. They are small in size and have a long neck, gray beak, and orange-red duck feet.

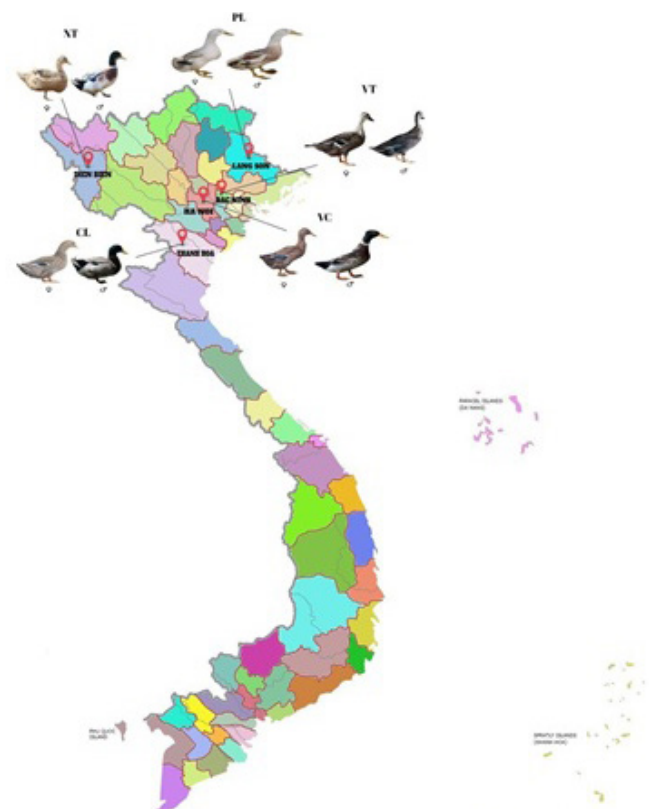


Figure 1: Geographic distribution of the studied duck breed.

Blood samples were collected from the wing vein of the ducks in the province where they live (Figure 1). The blood sampling process followed the standards of animal welfare in Vietnam. Currently in Vietnam there is no law on animal welfare, however all blood sampling processes completely followed the Law of Livestock (2018) and Veterinary (2015). A total of 84 blood samples of the five duck breeds, namely 13 VNT, 16 VD, 25 VC, 18 VCL, and 13 VT, were collected. For each animal, a 1.0 ml blood sample was collected and placed in a 3-ml tube containing ethylenediaminetetraacetic acid (EDTA). After collection, the samples were transported in a thermo box with ice. Analyses were immediately carried out when the samples is delivered to the laboratory.

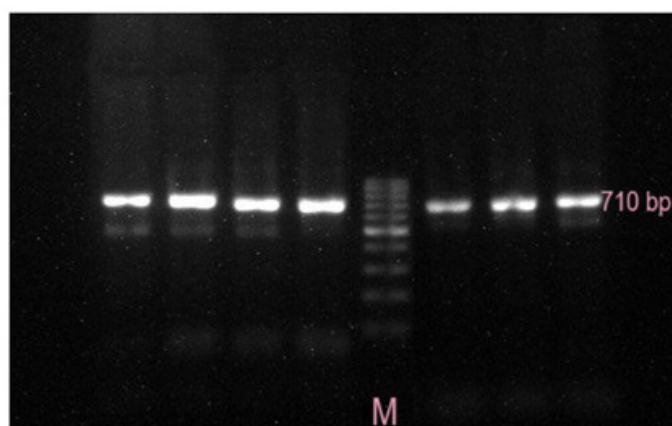


Figure 2: PCR amplicon of D-loop gene of Vietnamese duck used agarose gel.

The DNA extractions were performed according to the procedure of (Albariño and Romanowski, 1994) with slight modifications. The purity and concentration of the DNA were determined by electrophoresis on 1% agarose and measured by a spectrophotometer (Nanodrop™2000 spectrophotometer, Thermo Fisher). The sequence region of mtDNA D-loop was amplified using specific primers according to (Sorenson et al., 1999) (Forward was 5'- GTT ATT TGG TTA TGC ATA TCG TG - 3'; and reverse was 5'- CCA TAT ACG CCA ACC GTC TC - 3'). The 50 µL reaction consisted of 50 ng of genomic DNA, 1.5 mM MgCl₂, 0.2 mM dNTPs, 0.5 µM primers and 2U of Taq DNA polymerase. The PCR amplifications were performed in a Astec Thermal Cyclers Gene Atlas (Japan) with the following amplification conditions: 5 min at 95°C for pre-denaturation, 45 sec at 95°C for 35 cycles of denaturation, 45 sec at 60°C for annealing, and 1 min at 72°C for extension. The ended cycle was 5 min at 72°C for extension. Then, the purified PCR products were sequenced at 1st BASE Pte Ltd company, Singapore.

All duck mtDNA sequences were examined using Chromas 2.6.4 software, and edited using BioEdit Sequence Alignment Editor version 5.0.9. The sequenced products

also were compared and aligned using ClustalX 2.1 software (Thompson et al., 1994). Similarities in the mtDNA sequences of the samples identified in the same haplotype group were analyzed using DnaSP 6.10. In addition, the number of haplotype, nucleotide variable sites, haplotype diversity (Hd), nucleotide diversity (Pi), Tajima's D (P values) were calculated. Analysis of pairwise genetic distances (Ds) were computed by using GenAlEx version 6.51b2. A phylogenetic tree was built based on MEGA-X software with Bootstrap analysis at 1000 repetitions and with Maximum Composite Likelihood analysis. Reference D-loop sequences were obtained from GenBank data (NCBI) with the accession codes of *Anas platyrhynchos* (FJ213596.1) and *Anas zonorhyncha* (Mz593724.1)

RESULTS AND DISCUSSION

PCR AMPLIFICATION AND SEQUENCING mtDNA D-LOOP REGION

The PCR product visualization showed a uniform band size of 710 bp for all the samples (Figure 2). These products indicated that the D-loop gene of Vietnamese ducks could be amplified by the primers developed by (Sorenson et al., 1999). The brightness and thickness of the bands were specific and well amplified DNA fragments of the D-loop sequence region in the five populations of Vietnamese indigenous ducks. The PCR products were sequenced and then the mt DNA- D-loop sequences from nucleotide 15 to 685 were later analyzed

GENETIC VARIATION

In the five duck populations, the average nucleotide composition was 22.8% A, 24.3% G, 26.6% C, and 26.3% T, equivalent to 49.1% A + T and 50.9% G + C (Table 1). The sequences obtained were analyzed using BioEdit software and then uploaded to NCBI's BLAST program. The results indicated that all the samples were homogeneous with wild mallard ducks (*Anas platyrhynchos*) and with spot-billed ducks (*Anas zonorhyncha*) at 98-100% (Genbank Acc Number FJ213596.1) and at 97-98% (Genbank Acc Number MZ593724.1), respectively.

Table 1: Percentage of nucleotide compositions.

Population	A	T	G	C
VC	23.4	26.9	25.4	24.3
VNT	22.8	26.8	24.7	25.6
VD	23.4	25.9	27.8	22.8
VCL	21.8	26.4	22.5	29.3
VT	22.6	25.5	21.1	30.7
Mean	22.8	26.3	24.3	26.6

Fifteen polymorphic sites were found and these mutation types were transversions and transitions. Nucleotide deletions

Table 2: The identified haplotype with the mitochondrial D-loop sequence polymorphism in Vietnamese duck.

Haplotype	Position of nucleotide substitution															
	124	146	157	195	208	217	232	263	279	286	306	349	352	375	405	
Reference sequence FJ213596.1	T	C	A	A	A	A	T	A	C	T	T	A	T	C	G	
Hap 1	A	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
Hap 2	*	*	*	*	*	*	*	T	*	*	*	*	G	*	T	
Hap 3	*	A	*	*	T	*	*	*	A	G	*	*	*	*	*	
Hap 4	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
Hap 5	*	*	G	*	*	*	*	*	*	*	*	*	*	*	*	
Hap 6	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
Hap 7	*	*	*	T	*	T	*	*	A	*	G	*	*	*	*	
Hap 8	*	*	*	*	T	T	*	*	A	G	*	*	*	*	*	
Hap 9	A	*	*	*	*	*	*	*	*	*	*	*	G	*	*	
Hap 10	*	*	*	*	*	*	*	*	*	*	*	*	*	T	*	
Hap 11	*	A	*	*	*	*	*	*	*	*	*	C	*	T	*	
Hap 12	*	*	*	*	*	*	*	*	*	*	*	*	*	T	T	
Hap 13	*	*	*	*	C	T	*	*	*	*	*	*	*	*	T	
Hap 14	*	*	T	T	*	*	*	*	A	G	G	*	*	T	*	
Hap 15	*	*	G	*	*	*	A	*	*	*	G	*	*	T	*	
Hap 16	*	A	*	*	*	*	*	*	A	*	*	*	*	*	*	
Hap 17	A	*	*	*	C	*	*	*	A	G	*	*	*	*	*	

Table 3: Haplotype distribution in 5 Vietnamese duck breeds.

No.	Haplotype	Position of nucleotide substitution	Population
1	Hap 1	T124A	VC, VCL, VT
2	Hap 2	A263T T352G G405T	VC, VNT, VD
3	Hap 3	C146A A208T C279A T286G	VC, VD
4	Hap 4	-	VC
5	Hap 5	A157G	VC
6	Hap 6	-	VC
7	Hap 7	A195T A217T C279A T306G	VC
8	Hap 8	A208T A217T C279A T286G	VCL
9	Hap 9	T124A T352G	VCL
10	Hap 10	C375T	VCL, VNT
11	Hap 11	C146A A349C C375T	VNT
12	Hap 12	C375T G405T	VT, VNT
13	Hap 13	A208C A217T G405T	VT
14	Hap 14	A157T A195T C279A T286G T306G C375T	VCL, VT, VNT, VD
15	Hap 15	A157G T232A T306G C375T	VT, VNT, VD
16	Hap 16	C146A C279A	VD
17	Hap 17	T124A A208A C279A T286G	VD

and insertions were not obtained. The distribution of polymorphic sites are presented in Figure 3. The sequence between base pairs 124–200 contained four polymorphic sites (26.67%), between base pairs 201–300 contained six polymorphic sites (40%), between base pairs 301–400 contained four polymorphic sites (26.67%), and between base pairs 401–500 contained one polymorphic site (6.66%)(Table 2).

From all polymorphic sites, 17 haplotypes were formed(Table 3). Among the 17 haplotypes, haplotype 14 presented in all the duck breeds except in the VC ducks (Table 3), followed by haplotypes 1, 2, and 15, which each appeared in three breeds. There were several haplotypes that appeared in only a single breed, namely haplotypes 4–7 (VC), 8–9 (VCL), 11 (VNT), 13 (VT), and 16–17 (VD).

GENETIC DIVERSITY

The number of haplotypes, haplotype diversity (Hd), nucleotide diversity (Pi), and Tajima's D were calculated for each duck population and are presented in Table 4. Most notably, the native duck populations in this study had a high number of haplotypes. In the VC population, the number of haplotypes obtained was the largest with 7 haplotypes, followed by VD and VNT (6), and lower numbers were found in VT (5) and VCL (4). The average Hd, Pi, and Tajima's D values in the five duck populations were 0.515, 0.099, and 0.357, respectively. The highest genetic diversity (Hd = 0.838, Pi = 0.166) was observed in VNT. A non-significant positive Tajima's D index ($P > 0.10$) was observed in four breeds (VC, VT, VCL, and VD) while a significant negative value of -0.00276 ($P < 0.10$) was observed for VNT.

PHYLOGENETIC RELATIONSHIPS

The genetic divergence between studied populations ranged from 0.189 to 0.347 (Table 5). Among the five indigenous duck breeds, the lowest Ds value was found between VCL and VT (0.189), followed by VNT and VD (0.196). The highest Ds value was presented between VC and VCL (0.347).

Table 4: Haplotype diversity in Vietnamese duck breeds.

Breed	Number of sequences	Number of Haplotypes	Hd	Pi (%)	Tajima's D
VC	24	7	0.216	0.106	0.504
VT	11	5	0.348	0.038	0.212
VD	17	6	0.647	0.085	0.589
VNT	12	6	0.838	0.166	-0.00276
VCL	20	5	0.525	0.099	0.483

The results of the neighbor-joining analysis (Figure 3) indicated that Vietnamese ducks and another *Anas* breed formed two distinct clusters. The first cluster consisted of the entire population of VT, six individuals of VNT, the wild mallard ducks (*Anas platyrhynchos*), and the spot-billed ducks (*Anas zonorhynchos*). The second one consisted of the other Vietnamese duck breeds with sub clusters of VCL, VC, and VD, in which VNT had genetic shares in the three branches of the other three duck breeds.

Table 5: Pairwise of Nei's genetic distance calculation.

Breeds	VC	CL	NT	VT
CL	0.347			
NT	0.338	0.306		
VT	0.380	0.189	0.208	
VD	0.222	0.282	0.196	0.304

Among the five studied duck populations, the most common type of mutation was transversion, and then transition. No insertions or deletions were found, which was similar to

the finding of (Li *et al.*, 2010) and (Gaur *et al.*, 2017), however, this result was different from those of (Kulikova *et al.*, 2004; 2005).

The G + C content in ducks was higher than that of A + T, and the C content was highest, which was almost identical to the values indicated by (Gaur *et al.*, 2017). The content of G + C in our study was higher than that finding of (Kulikova *et al.*, 2004; 2005) who studied the mtDNA sequence region of *Anas platyrhynchos* and reported the A + T and G + C contents as 51.2% and 48.8%, respectively. The proportion of polymorphic nucleotide sequences were highest between base pairs 201-300, which had six polymorphic sites (40%). This result is inconsistent with the report of (Susanti *et al.*, 2017) in that the highest proportion was in the 56-100 region (18 polymorphic sites). Many previous studies have shown that the D-loop of mitochondria has two regions with high mutation rates, which are hypervariable region 1 (HV1) and hypervariable region 2 (HV2). (Susanti *et al.*, 2017) stated that these variations could be the result of mutation, natural selection, or mating. Genetic variations in Vietnamese duck populations may be the result of random selection within the population and/or interbreeding. Genetic diversity will increase if there is high inbreeding in a population.

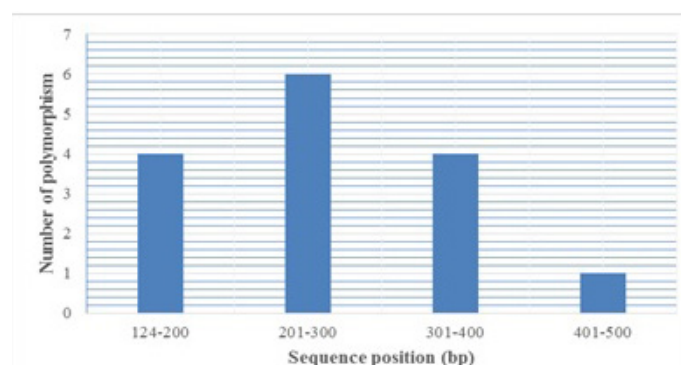


Figure 3: Distribution of polymorphic site of mtDNA D-loop in Vietnamese duck.

The largest number of haplotypes was found in the VC ducks, which indicated that this breed had a high number of polymorphisms in the D-loop mtDNA region. Haplotype and nucleotide diversity indices are often used to evaluate the mtDNA variation and genetic diversity of populations or breeds. Larger Hd and Pi values indicate greater genetic diversity (Li *et al.*, 2010). The Hd in the present study was higher than in Nigerian duck breeds (0.381), but lower than in four Fujian duck breeds (0.645) (Li *et al.*, 2010), and *Anas platyrhynchos* (0.987) (Kulikova *et al.*, 2005). The average nucleotide diversity observed in this study was 0.099%, which is higher than reported in previous studies. When study on seven duck breeds in Korea, (Jin *et al.*, 2014) found that Pi values ranged from 0.004 to 0.019. (Qu *et al.*, 2009) reported the highest (0.01100) and the

lowest (0.00087) Pi were found in seven duck breeds of China. However, (Li *et al.*, 2010) found a high Pi (0.115%) in 26 indigenous duck breeds of China, and a very high Pi (0.83%) was found in *Anas platyrhynchos* in the study of (Kulikova *et al.*, 2005). In the present study, genetic diversity (haplotype and nucleotide diversity) was highest in VNT and lowest in VT and VC ducks. The results reported here suggest that special attention or conservation strategies are needed for VC and VT breeds because they have low genetic diversity.

is more clearly shown when looking at the phylogenetic tree (Figure 4) as some VNT individuals are in the branch with *Anas platyrhynchos* and *Anas zonorhyncha*.

Our findings about the genetic distances among Vietnamese duck populations agreed with the report of (Pham *et al.*, 2021) who observed genetic distances among four Vietnamese duck breeds (Singcheng, Bauben, Minhhuong, and Muongkhieng) from 0.16 to 0.40, with the lowest Ds found in Minhhuong and Muongkhieng (0.16). These results led to a phylogenetic tree showing Sincheng and Bauben representing independent branches while the Muongkhieng and Minhhuong are in the same branch. The phylogenetic trees of the five Vietnamese ducks with *Anas platyrhynchos* and *Anas zonorhyncha* formed two clusters in which all the individual VT ducks and six of the VNT ducks joined in the first cluster with *Anas platyrhynchos* and *Anas zonorhyncha*. As mentioned above, in the VNT population, several animals had rare alleles, and these alleles helped determine the origin of VNT ducks. Regarding the evolutionary origin of domestic duck breeds around the world, there are two hypotheses. One hypothesis is that ducks originated from the wild mallard ducks (*Anas platyrhynchos*) (Sultana *et al.*, 2016). The other is that the domestic ducks were domesticated from a cross between wild mallard and spot-billed ducks (Johnson and Sorenson, 1999). Our phylogenetic tree indicated that Vietnamese native duck populations could have originated from more than two maternal lineages, indicating that the indigenous duck breeds of Vietnam were probably domesticated from the mixture of mallard and spot-billed ducks.

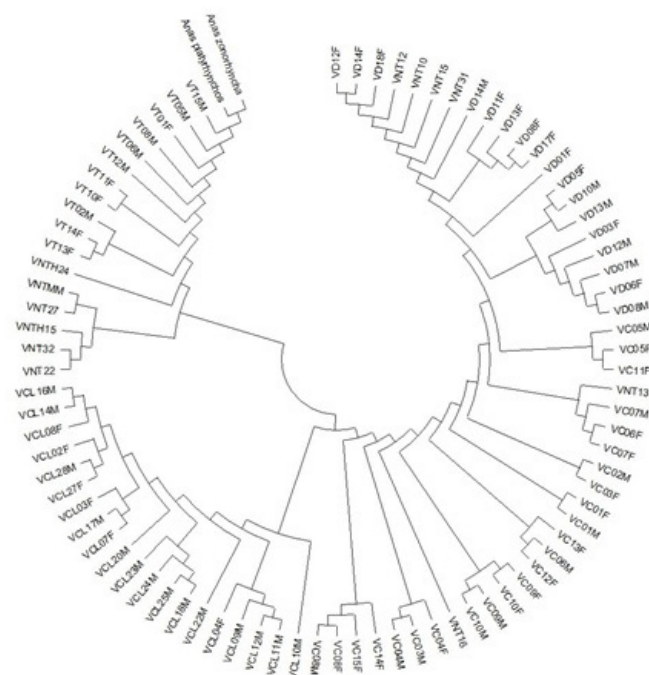


Figure 4: The unrooted neighbour-joining phylogenetic tree of D-loop sequence for Vietnamese duck and other anas breed from GenBank.

Among the five Vietnamese native duck breeds, a non-significant positive of Tajima's D test index was found in four breeds (VC, VT, VCL, and VD) while a significant negative was observed for VNT. According to (Tajima, 1996), a positive Tajima's D indicates low levels of both low and high-frequency polymorphism. This suggests population size reduction and/or balancing selection is occurring in the population. If Tajima's D value is negative, it shows an excess of low-frequency polymorphism compared to expectations, indicating an expansion of population size. Therefore, with the significant negative Tajima's D value, the VNT population in Dien Bien province is evolving by random selection, and the population expansion might be due to separation and rare alleles appearing in the population at high frequencies. The VNT duck population has departed from equilibrium, which may be the result of a past/recent population expansion or bottleneck effect (Tajima, 1996). (Pang *et al.*, 2009) suggested that based on rare haplotypes or rare alleles, the evolutionary origin of breeds could be determined. This result of the VNT breed

CONCLUSIONS AND RECOMMENDATIONS

Based on the analysis of polymorphism on D-loop mtDNA, a total of 15 mutation sites and 17 haplotypes were found in five indigenous Vietnamese duck breeds. VC and VT both showed low genetic diversity and conservation practices should be adopted to protect these indigenous duck resources. Phylogenetic analysis indicated that Vietnamese ducks are closely related to both *Anas platyrhynchos* and *Anas zonorhyncha*.

ACKNOWLEDGMENTS

This project (T2021-0204-TĐ) was supported by Vietnam National University of Agriculture in the framework of Research Fund 2021.

NOVELTY STATEMENT

This study aimed to determine the genetic diversity of Vietnamese native ducks through exploring the sequences of

mtDNA D-loop, thereby providing evidence of the genetic relationship between duck breeds and information for the conservation and development of native duck breeds in Vietnam.

AUTHOR'S CONTRIBUTIONS

Nguyen Thi Vinh: Conceptualization, methodology, investigation, data analysis, and writing original draft preparation, editing.

Nguyen Hoang Thinh: Supervision, conceptualization, review and editing.

Pham Kim Dang: Review and editing.

Tran Bich Phuong: Writing, validation, review and editing.

Nguyen Thi Phuong Giang: review and editing.

Do Duc Luc: Writing- Review and editing.

Ha Xuan Bo: Review and editing.

Bui Huy Doanh: Review and editing.

Nguyen Van Duy: Data analysis, Review and editing.

Nguyen Van Thong: Review and editing.

Bui Binh An: Review and editing.

Nguyen Quoc Trung: Review and editing.

CONFLICT OF INTEREST

We certify that there is no conflict of interest in the finances or data used in this manuscript.

REFERENCES

- Albariño CG, Romanowski V (1994). Phenol extraction revisited: a rapid method for the isolation and preservation of human genomic DNA from whole blood. *Mol Cell Probes.*, 8(5): 423-7. doi: 10.1006/mcpr.1994.1060.
- Blott S, Kim JJ, Moisisio S, Schmidt-Küntzel A, Cornet A, Berzi P, Cambisano N, Ford C, Grisart B, Johnson D, Karim L, Simon P, Snell R, Spelman R, Wong J, Vilkkilä J, Georges M, Frédéric F, Coppieters W (2003). Molecular dissection of a quantitative trait locus: a phenylalanine-to-tyrosine substitution in the transmembrane domain of the bovine growth hormone receptor is associated with a major effect on milk yield and composition. *Genetics*, 163:253-266. <https://doi.org/10.1093/genetics/163.1.253>
- Brown WM, George JM, Wilson AC (1997). Rapid evolution of animal mitochondrial DNA. *Proc. National Acad. Sci. U. S. A.*; 76:1967-1971. <https://doi.org/10.1073/pnas.76.4.1967>
- FAO (2007). The State of the World's Animal Genetic Resources for Food and Agriculture Food and Agriculture Organization of the United Nations, Rome, Italy.
- Gaur U, Tantiya MS, Mishra B, Settypalli TBK, Ramesh KV, Ashok C (2017). Mitochondrial D-loop analysis for uncovering the population structure and genetic diversity among the indigenous duck (*Anas platyrhynchos*) populations of India. *Mitochondrial DNA Part A*, 1-8. <https://doi.org/10.1080/24701394.2016.1267158>
- Hoat PC, Dung TH, Tiem PV (2022). Conservation of pet general resources in Vietnam in the context of the fourth industrial revolution. *Vietnam J. Sci., technol. Eng.*, 10: 36-38.
- Hong EC, Choo HJ, Kang BS, Kim CD, Heo KN, Lee MJ, Hwangbo J, Suh OS, Choi HC, Kim HK (2012). Performance of growing period of large-type Korean native ducks. *Korean J. Poult. Sci.*, 39: 143-149. <https://doi.org/10.5536/KJPS.2012.39.2.143>
- Jin SD, Hoque MR, Seo DW, Paek WK, Kang TH, Kim HK, Lee JH (2014). Phylogenetic analysis between domestic and wild duck species in Korea using mtDNA D-loop sequences. *Mol. Biol. Rep.*, 41: 1645-52. <https://doi.org/10.1007/s11033-013-3012-6>
- Johnson KP, Sorenson MD (1999). Phylogeny and biogeography of dabbling ducks (Genus: *Anas*): A comparison of molecular and morphological evidence. *Auk.*, 116:792-805. <https://doi.org/10.2307/4089339>
- Kulikova IV, Zhuravlev YN, McCracken KG (2004). Asymmetric hybridization and sex-biased gene flow between eastern spot-billed ducks (*Anas zonorhynchos*) and mallards (*Anas platyrhynchos*) in the Russian Far East. *The Auk.*, 121: 930-949. <https://doi.org/10.1093/auk/121.3.930>
- Kulikova IV, Drovetski SV, Gibson DD, Harrigan RJ, Rohwer S, Sorenson MD, Winker K, Zhuravlev YN, Cracken KGM (2005). Phylogeography of the mallard (*Anas platyrhynchos*): Hybridization, dispersal, and lineage sorting contribute to complex geographic structure. *Auk.*, 122, 949-965. <https://doi.org/10.1093/auk/122.3.949>
- Mannen H, Kohno M, Nagata Y, Tsuji S, Bradley DG, Yeo JS, Nyamsamba D, Zagdsuren Y, Yokohama M, Nomura K, Amano T (2004). Independent mitochondrial origin and historical genetic differentiation in north eastern Asian cattle. *Mol. Phylogenet. Evol.*, 32: 539-544. doi: 10.1016/j.ympev.2004.01.010.
- Pfeiffer I, Voelkel I, Brenig B (2005). Phylogenetics of the European Dahomey miniature cattle based on mitochondrial D-loop region DNA sequence. *Anim. Genet.*, 36(2): 160-190. <https://doi.org/10.1111/j.1365-2052.2005.01245.x>
- Pang JF, Kluetsch C, Zou XJ, Zhang AB, Luo LY, Angleby H, Ardalan A, Ekström C, Sköllerö M, Lundeberg J, Matsumura S, Leitner T, Zhang YP, Savolainen P (2009). mtDNA data indicate a single origin for dogs south of Yangtze River, less than 16,300 years ago, from numerous wolves. *Mol. Biol. Evol.*, 26(12): 2849-2864. <https://doi.org/10.1093/molbev/msp195>
- Pham LD, Do DN, Le QN, Nguyen BV, Pham NH, Doan TP, Pham SV, Pham TC (2021). Evaluation of genetic diversity and population structure in four indigenous duck breeds in Vietnam. *Anim. Biotechnol.*, 33(6): 1065-1072. <https://doi.org/10.1080/10495398.2020.1868485>
- Qu LJ, Lui W, Yang FX, Hou ZC, Zheng JX, Xu GY, Yang N (2009). Origin and domestication history of Peking ducks determined through microsatellite and mitochondrial marker analysis. *Science of China Series C: Life Sci.*, 52: 1030-1035. <https://doi.org/10.1007/s11427-009-0145-x>
- Seo D, Bhuiyan MSH, Sultana H, Heo JM, Lee JH (2016). Genetic diversity analysis of South and East Asian duck populations using highly polymorphic microsatellite markers. *Asian-Australas J. Anim. Sci.*, 29(4): 471-478. <https://doi.org/10.5713/ajas.15.0915>

- Sorenson MD, Ast CJ, Dimcheff DE, Yuri T, Mindell DP (1999). Primers for a PCR-Based Approach to Mitochondrial Genome Sequencing in Birds and Other Vertebrates. *Mol. Phylogenet. Evol.*, 12: 105-114. doi: 10.1006/mpev.1998.0602.
- Sultana H, Seo D, Bhuiyan M, Choi NR, Lee JH (2016). Genetic Diversity and Phylogenetic Analysis of South-East Asian Duck Populations Based on the mtDNA D-loop Sequences. *Asian Australas. J. Anim. Sci.*, 29(12): 1688–1695. doi: 10.5713/ajas.15.1017.
- Susanti R, Iswari RS, Fibriana F, Sari RI (2017). Mitochondrial D-loop sequence variation among Central Javanese Duck in Indonesia. *Acta Sci. Anim. Sci.*, 449-456. <https://doi.org/10.4025/actascianimsci.v39i4.34352>
- Tajima F (1996). The amount of DNA polymorphism maintained in a finite population when the neutral mutation rate varies among sites. *Genetics*, 143: 1457–1465. <https://doi.org/10.1093/genetics/143.3.1457>
- Thompson JD, Higgins DG, Gibson TJ (1994). CLUSTAL W: improving the sensitivity of progressive multiple alignment through sequence weighing, position specific gap penalties and weight matrix choice. *Nucleic Acids Res.*, 22: 4673–4680. <https://doi.org/10.1093/nar/22.22.4673>