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BRIEF REPORT

COMPLETE MITOCHONDRIAL GENOME OF DONG TAO CHICKEN BREED (*GALLUS GALLUS DOMESTICUS*) OF VIETNAM

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SUMMARY

The complete mitochondrial genome of Dong Tao chicken breed (*Gallus gallus domesticus*, Dong Tao) was obtained by PCR and sequencing. The complete mitogenome was 16,783 bp in length, with the nucleotide composition for A, T, C, G was 30.29%, 23.75%, 32.48%, and 13.48%, respectively. The mitogenome of Dong Tao chicken contained a non-coding control region (D-loop), 2 rRNA genes, 13 protein-coding genes, and 22 tRNA genes. Phylogenetic analysis revealed that breed Dong Tao chicken breed was sister-close to *G. gallus* breed Guangxi, and paraphyletic to *G. spadiceus*, *S. jabouillei*, and a range of Chinese indigenous, ie. breeds Rugao and Taoyuan.

Keywords: *mitogenome, D-loop, rRNA gene, Dong Tao breed chicken, Gallus gallus domesticus*

Dong Tao chicken is an indigenous and rare breed of the Vietnamese chicken, mainly rearing in Khoai Chau district, Hung Yen province of Vietnam. The Dong Tao chicken breed has the imposing figure, healthy body and stout legs covered with reddish scales. The chicken is far more expensive than other Vietnamese native chicken because of high demand for its meat, which is considered as delicious and nutritious traditional food.

The blood sample of Dong Tao chicken breed (DT347) was collected from Khoai-Chau District, Hung-Yen Province, Vietnam and stored in the Biobank of National Institute of Animal Husbandry, Vietnam. The genomic DNA was extracted from blood tissue using method as described (Sambrook, Russell, 2001). A set of primers was designed according to the report (Nishibori *et al.*, 2001) to amplify and sequence complete mitochondrial genome. SeqScape 3.0 software (Thermo Fisher Scientific Inc.) was used to analyze mitochondrial DNA sequence. The distribution of all genes in the genome was analyzed by using transfer RNA (tRNA) Scan-SE 1.21 (Lowe, Eddy 1997) and MITOS tool (Bernt *et al.*, 2013). The complete mitochondrial sequence of Dong Tao chicken has

been deposited in GenBank with accession number KY094500.

The entire mitogenome of Dong Tao chicken breed of 16,783 bp in length was obtained, with the nucleotide composition of A (30.29%), T (23.75%), C (32.48%), and G (13.48%). The mitogenome contained a non-coding control region (D-loop), 2 rRNA genes, 13 protein-coding genes, and 22 tRNA genes, which are similar to those of other reported fowls (Snyder *et al.*, 2015, Xie *et al.*, 2016, Yan *et al.*, 2016, Zhang *et al.*, 2016).

Most of mitochondrial genes were located on the H-strand, except 8 tRNA genes (tRNA-Gln, tRNA-Ala, tRNA-Asn, tRNA-Cys, tRNA-Tyr, tRNA-Ser, tRNA-Pro and tRNA-Glu) and ND6 gene, which are similar to the typical mitogenome of vertebrates (Boore, 1999, Snyder *et al.*, 2015). The initiation codon for 12 of 13 mitochondrial genome proteins was ATG except the initiation codon of *COX1* was GTG. The stop codon for *ND1*, *COX2*, *ATPase8*, *ATPase6*, *ND3*, *ND4L*, *ND5*, *CytB* and *ND6* was TAA, while the stop codons for *ND2* and *COX1* were TAG and AGG, respectively. An incomplete stop codon “T--” was found for *COX3* and *ND4*. These features are common among

vertebrate mitochondrial genomes (Anderson *et al.*, 1981). We found one base insertion at position 10,956, but reading frame was presumably maintained by translational frameshift of RNA. The 12S and 16S ribosomal RNA genes were separated

by tRNA-Val and located between the tRNA-Leu and tRNA-Phe. The deduced 22 tRNA genes were distributed in rRNA and protein-coding genes, ranging from 65 to 76 bp in size. D-loop region was 1231 bp in length.

Table 1. Location of genes and elements on the mitochondrial genome of Dong Tao chicken breed.

Genes and elements	Position		Length	Strand	Codon	
	From	To			Start	Stop
tRNA-Phe	1233	1302	70	H		
12S rRNA	1302	2277	976	H		
tRNA-Val	2277	2349	73	H		
16S rRNA	2353	3971	1619	H		
tRNA-Leu	3973	4046	74	H		
NADH-dehydrogenase subunit 1 (ND1)	4056	5024	969	H	ATG	TAA
tRNA-Ile	5031	5102	72	H		
tRNA-Gln	5108	5177	70	L		
tRNA-Met	5177	5245	69	H		
NADH-dehydrogenase subunit 2 (ND2)	5246	6280	1035	H	ATG	TAA
tRNA-Trp	6285	6360	76	H		
tRNA-Ala	6367	6435	69	L		
tRNA-Asn	6439	6511	73	L		
tRNA-Cys	6513	6578	66	L		
tRNA-Tyr	6579	6648	70	L		
Cytochrome oxidase subunit 1 (COX1)	6659	8191	1533	H	TGT	AGG
tRNA-Ser	8192	8266	75	L		
tRNA-Asp	8269	8337	69	H		
Cytochrome oxidase subunit 2 (COX2)	8339	8962	624	H	ATG	TAA
tRNA-Lys	9023	9090	68	H		
ATPase subunit 8 (ATP8)	9092	9250	159	H	ATG	TAA
ATPase subunit 6 (ATP6)	9247	9927	681	H	ATG	TAA
Cytochrome oxidase subunit 3 (COX3)	9930	10713	784	H	ATG	T--
tRNA-Gly	10714	10782	69	H		
NADH-dehydrogenase subunit 3 (ND3)	10783	11131	348	H	ATG	TAA
tRNA-Arg	11136	11203	68	H		
NADH-dehydrogenase subunit 4 light chain (ND4L)	11204	11497	294	H	ATG	TAA
NADH-dehydrogenase subunit 4 (ND4)	11494	12871	1378	H	ATG	T--
tRNA-His	12872	12940	69	H		
tRNA-Ser	12941	13007	67	H		
tRNA-Leu	13008	13078	71	H		
NADH-dehydrogenase subunit 5 (ND5)	13079	14884	1806	H		
Cytochrome B (CytB)	14913	16037	1125	H	ATG	TAA
tRNA-Thr	16047	16115	69	H		
tRNA-Pro	16116	16185	70	L		
NADH-dehydrogenase subunit 6 (ND6)	16195	16713	519	L	ATG	CAT

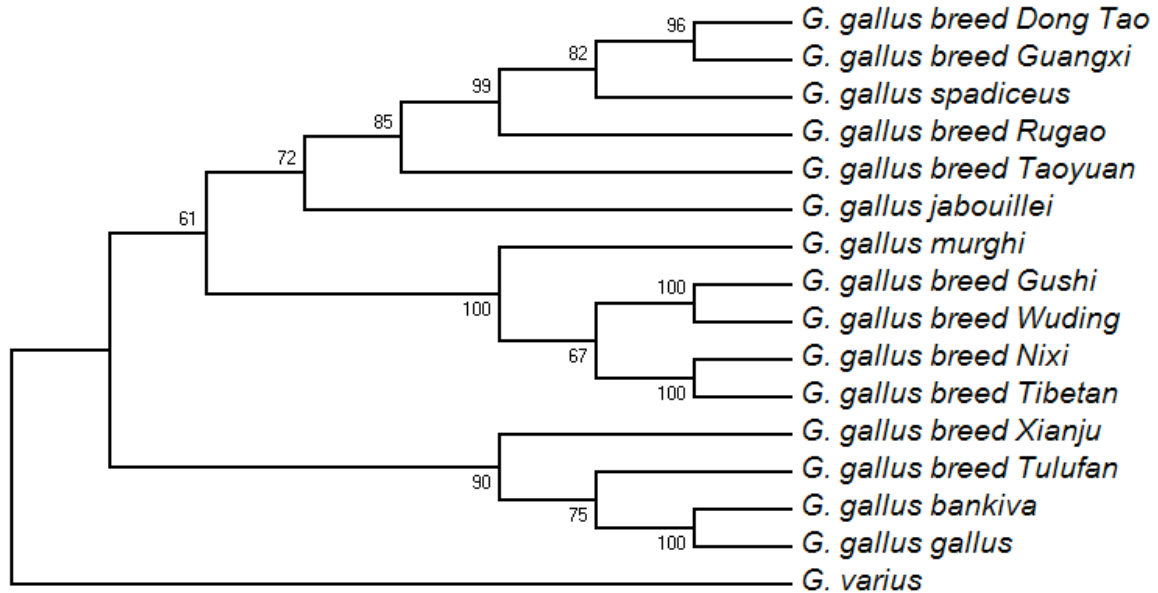


Figure 1. Molecular phylogenetic analysis of the complete mitogenome of Dong Tao chicken breed and 15 other mitogenomes of *Gallus* genus by Maximum Likelihood method. Complete mitogenomes were downloaded from GenBank with accession number as follows: AP003323 (*G. gallus bankiva*), KP681581 (*G. gallus* breed Guangxi), GU261678 (*G. gallus* breed Gushi), GU261711 (*G. gallus* breed Nixi), KP742951 (*G. gallus* breed Rugao), KF981434 (*G. gallus* breed Taoyuan), DQ648776 (*G. gallus* breed Tibetan), GU261683 (*G. gallus* breed Tulufan), GU261676 (*G. gallus* breed Wuding), GU261677 (*G. gallus* breed Xianju), AP003322 (*G. gallus gallus*), GU261696 (*G. gallus jabouillei*), GU261709 (*G. gallus murghi*), AP003321 (*G. gallus spadiceus*), AP003324 (*G. varius*)

The complete mitogenome sequence of *Gallus gallus* breed Dong Tao together with other 15 mitogenomes of *G. gallus* species and *G. varius* were used for phylogenetic analysis. The phylogenetic tree was conducted in MEGA7 (Kumar *et al.*, 2016) by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura, Nei 1993), with mitogenome of *G. varius* as an outgroup. Phylogenetic analysis revealed that Dong Tao chicken breed was sister-close to *G. gallus* breed Guangxi, and paraphyletic to *G. spadiceus*, *S. jabouillei*, and a range of Chinese indigenous, ie. breeds Rugao and Taoyuan. The result showed that Dong Tao chicken breed close related to the other *G. gallus* species, with the sister position of *G. gallus* breed Guangxi (Figure 1).

Complete mitogenome was used to reconstruct the history of animal domestication, such as in cattle (Achilli *et al.*, 2009, Achilli *et al.*, 2008, Bonfiglio *et al.*, 2010), pigs (Wu *et al.*, 2007), chicken (Miao *et al.*, 2013) and sheep (Lancioni *et al.*, 2013). This is the first mitochondrial genome of the Dong Tao chicken, which is the native chicken of Vietnam, has

been sequenced. The complete mtDNA data initially contributes to the study of the conservation of indigenous chicken breeds in Vietnam.

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TRÌNH TỰ HOÀN CHỈNH HỆ GEN TY THỂ GIỐNG GÀ ĐÔNG TẢO (*GALLUS GALLUS DOMESTICUS*) CỦA VIỆT NAM

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TÓM TẮT

Sử dụng phương pháp PCR và giải trình tự Sanger, chúng tôi đã xác định trình tự hoàn chỉnh của DNA ty thể giống gà Đông Tảo (*Gallus gallus domesticus*). Trình tự hoàn chỉnh của genome ty thể của giống gà Đông

Tảo có chiều dài là 16.783 bp, với tỷ lệ các base nito A, T, C, G tương ứng là 30,29%, 23,75%, 32,48% và 13,48%. Genome ty thể của gà Đông Tảo gồm vùng điều khiển (D-loop), 2 gen mã hóa rRNA, 13 gen mã hóa cho các protein và 22 gen mã hóa cho các tRNA. Phân tích cây phát sinh chủng loại đã chỉ ra rằng giống gà Đông Tảo có quan hệ rất gần gũi với giống gà *G. gallus* Guangxi và có quan hệ họ hàng xa với các loài *G. spadiceus*, *S. jabouillei* và một số giống gà bản địa của Trung Quốc như giống Rugao và Taoyuan.

Từ khóa: *mitogenome, D-loop, rRNA gene, gà Đông Tảo, Gallus gallus domesticus*