



Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome sequence of the Canada goose
(*Branta canadensis*)

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Abstract

The Canada goose (*Branta canadensis*) entire mitochondrial genome of a bird from Western Pennsylvania has 16,760 bp (GenBank accession number NC 007011) and has been analyzed for gene locations, length, start codon and stop codons. This genome from a bird harvested during the non-migratory season is the REFSEQ and the haplotype is designated GCC-A. There are two rRNAs, 22 tRNAs, 13 protein-coding regions, and 1 displacement loop region. The base composition of mtDNA was A (30.2%), G (15.1%), C (32.1%), and T (22.6%), so the percentage of A and T (52.8%) was slightly higher than G and C. All genes except ND6 and eight tRNA genes (Gln, Ala, Asn, Cys, Tyr, Ser, Pro and Glu) are encoded on the heavy strand. The gene arrangement is the same as most birds and differs from mammals by an inversion of the mtDNA at the connection between the D-loop and the ND5 junctions.

Keywords

Branta canadensis, mitochondrial DNA, start codons, stop codons

History

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The Canada goose (*Branta canadensis*) is ubiquitous across the US and is often a nuisance species. Its mtDNA sequence will help characterize the migratory and non-migratory populations and define genetic relationships among various species and subspecies of Canada and other geese. The 16,760 bp mtDNA genome of a Canada goose harvested in Mercer County, Pennsylvania, USA during the non-migratory season is reported (NCBI NC_007011.1, REFSEQ, haplotype GCC-A).

Liver mtDNA was separated from nuclear DNA using Perfectprep Plasmid Mini spin kits (Eppendorf, Westbury, NY) (Ray et al., 2005). Mitochondrial DNA is purified with the same chemistry as plasmid isolation from *E. coli* DNA (Ray et al., 2005). Primer design procedures (Lowe et al., 1990; Ray et al., 2005) using the *Anser albifrons* (white-fronted goose) (GenBank accession number NC 004539) sequences were successful. Polymerase Chain Reaction (PCR) and PCR-based di-deoxy

sequencing was performed (Ray et al., 2005) in Grove City College's Applied Biosystems Model 310 sequencer. Combinations of 38 primer sets were used to circumnavigate the entire genome. Substantial non-homology between Canada goose and white-fronted goose mtDNA in the D-loop control region required authentic Canada goose sequences for primer design to complete the Canada goose genome. The genome was compiled from 220 contig sequences using Seqman II software (DNASTAR, Inc., Madison, WI).

The 16,760 bp mtDNA genome contains 2 rRNAs, 22 tRNAs, 13 protein-coding regions, and 1 displacement loop region (control region, Table 1). The genes are all encoded on the heavy stand (H-strand) except for ND6 and eight tRNA genes (Gln, Ala, Asn, Cys, Tyr, Ser, Pro and Glu). The gene arrangement in the mtDNA of the Canada goose was identical to other *Anatidae* family birds, including the white fronted goose, thus unlike the novel gene order located in most sub-oscine species (Mindell et al., 1998). The non-novel goose gene arrangement differs from mammalian mtDNA since the bird mtDNA segment coding for CytB-Thr-tRNA-Pro-tRNA-ND6-Glu-tRNA-Glu-tRNA is inverted 180 degrees in the mammalian mtDNA (Anderson et al., 1981). ATG is the start codon for most proteins, but GTG is the start codon for COXI, COXII, and ND5. AGG is the stop codon for ND1 and COXI, TAG is the stop codon for ND2 and ND6, AGA is the stop for ND5. TAA is the stop codon for six proteins (COXII, ATPase 8, ATPase 6, ND3, ND4L and Cyt b). The incomplete stop codon T is located

Table 1. The mitochondrial DNA genome of *Branta canadensis* (REFSEQ Gene Bank Accession Number NC_007011).

	Amino acid	Position	bp length	Space (+) or Overlap (–)	Strand	Number of amino acids	Start codon	Stop codon
F	tRNA-Phe	1–69	69	0	H			
	12S rRNA	70–1054	985	0	H			
V	tRNA-Val	1055–1125	71	0	H			
	16S rRNA	1126–2731	1606	0	H			
L	tRNA-Leu	2732–2805	74	(+6)	H			
	ND1	2812–3789	978	(+10)	H	325	ATG (Met)	AGG
I	tRNA-Ile	3799–3869	71	(+7)	H			
Q	(tRNA-Gln)	3877–3947	71	(–1)	L			
M	tRNA-Met	3947–4014	68	0	H			
	ND2	4015–5055	1041	(+2)	H	346	ATG (Met)	TAG
W	tRNA-Trp	5055–5128	74	(+5)	H			
A	(tRNA-Ala)	5134–5202	69	(+1)	L			
N	(tRNA-Asn)	5204–5276	73	(+3)	L			
C	(tRNA-Cys)	5280–5345	66	(–1)	L			
Y	(tRNA-Tyr)	5345–5415	71	(–1)	L			
	COXI	5417–6967	1551	(+2)	H	516	GTG (Val)	AGG
S	(tRNA-Ser)	6959–7031	73	(–6)	L			
D	tRNA-Asp	7034–7102	69	(+1)	H			
	COXII	7104–7790	687	(+4)	H	228	GTG (Val)	TAA
K	tRNA-Lys	7792–7860	69	(–1)	H			
	ATPase 8	7862–8029	168	(–7)	H	55	ATG (Met)	TAA
	ATPase 6	8020–8703	684	(+2)	H	227	ATG (Met)	TAA
	COXIII	8703–9486	784	(+1)	H	261	ATG (Met)	T–
G	tRNA-Gly	9487–9555	69	0	H			
	ND3	9556–9907	352	(+4)	H	116	ATG (Met)	TAA
R	tRNA-Arg	9909–9979	71	0	H			
	ND4L	9980–10,276	297	(–4)	H	98	ATG (Met)	TAA
	ND4	10,270–11,647	1378	(+1)	H	459	ATG (Met)	T–
H	tRNA-His	11,648–11,716	69	0	H			
S	tRNA-Ser	11,717–11,783	67	(–1)	H			
L	tRNA-Leu 2	11,783–11,853	71	0	H			
	ND5	11,854–13,677	1824	(+2)	H	607	GTG (Val)	AGA
	Cyt b	13,677–14,819	1143	(+5)	H	380	ATG (Met)	TAA
T	tRNA-Thr	14,822–14,889	68	(+8)	H			
P	(tRNA-Pro)	14,898–14,966	69	(+13)	L			
	(ND6)	14,977–15,498	522	0	L	173	ATG (Met)	TAG
E	(tRNA-Glu)	15,499–15,566	68	0	L			
	Control Region	15,567–16,760	1192	0	H			
	Total genome		16,760					

in the stop position of COXIII and ND4 and is thought to be completed by polyadenylation of the mRNAs after cleavage of their primary transcripts (Anderson et al., 1981.) There are 18 areas of intergenic spaces ranging from one to 13 bp and 8 places that genes overlap ranging from 1 to 7 bp. For the Canada goose, the ND5 protein is 1 amino acid longer and TAA instead of TAG stop codon for ND3 is located in the Canada goose as compared to the white fronted goose. This mtDNA genome will help further the future knowledge of species variants and evolutionary relationships.

Declaration of interest

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the article. This work was solely funded by Grove City College and the Janicki Research Fund.

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