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FEATURES OF MITOCHONDRIAL DNA FOR THE ARABIAN CAMEL (*Camelus dromedarius*)

Sayed A.M. Amer
Department of Biology, Faculty of Science, Taif University, Taif, 888, Saudi Arabia

ABSTRACT

The complete mitochondrial genome of the Arabian camel (*Camelus dromedarius*) has been previously sequenced and deposited in the Genbank database by some researchers. Three mitogenomes were found in the Genbank, two for Arabian camel from United Arab Emirates with total length of 16643 bp and one was from Morocco with a total length of 16665 bp. The only published was the mitogenome of the Moroccan sample, while the two Arabian mitogenomes were cited in the NCBI as unpublished data. The present study used these data to compare the mitogenomes of the Arabian and the Moroccan camel samples. The features of these genomes were described and compared in details. The base differences were also presented. The present study is one of the bioinformatics clues for investigating the molecular biodiversity of the domesticated camel in a trial for managing their conservation.

Key words: Arabian camel, biodiversity, breeds, mitochondrial DNA, mitogenome

The Old World Camelina and the New World Lamini are the only two tribes of the family Camelidae. The first contains two species, bactrian camel (*Camelus bactrianus*) and dromedary (*C. dromedarius*) and the second contains four species, guanaco (*Lama guanicoe*), Lama (*L. glama*), alpaca (*L. pacos*) and vicuna (*L. vicugna* or *Vicugna vicugna*) (Novoa, 1989; Stanley *et al,* 1994). Approximately 12 camel complete mitochondrial genomes were found in GenBank database, three of which are belonging to *Camelus dromedarius*.

The genome organisation and features were described for the wild *Camelus bactrianus* (Cui *et al*, 2007), while that of the Arabian camel have not been described yet. The present study therefore, was conducted to describe the already sequenced Arabian camel mitogenome. The genome data were taken from the Genbank, have been manipulated by bioinformatics and described in a comparison to that of the wild camel.

Materials and Methods

The complete mitochondrial genome of the wild *C. bactrianus* (GenBank: NC_009629) and the Arabian *C. dromedarius* (GenBank: NC_009849 and JN632608) were obtained from the NCBI database. Multiple alignments were performed with the CLUSTAL W (Thompson *et al,* 1994). Gene identification was conducted using DNASIS and MacClade programs.

Results and Discussion

Genome organisation

The mitochondrial genome of *Camelus dromedarius* is 16,643 bp for Arabian breed and 16,665 bp for Moroccan breed (GenBank: NC_009849 and JN632608, respectively). The latter is 22 bp longer than the first. This length variation occurred in the tandem repeat (ACGTAC)n of the control region where this repeat was typically found in the Arabian breed with some deletions (Fig 1) inducing the sequence length difference. The gene arrangement and content were identical to those of other mammals having nearly similar gene lengths of that of the wild Bactrian camel. It consisted of 13 protein-coding genes as subunits of three cytochrome c oxidase, seven NADH ubiquinone oxidoreductase complex, one ubiquinol cytochrome b oxidoreductase complex and two ATP synthases. It also contained the small and large ribosomal RNA genes and 22 tRNA genes (Table 1). The replication origin of the light strand within a WANCY tRNA gene cluster was identified in the Arabian breed while its counterpart in the Moroccan breed did not acquire stem-and-loop structure of this replication origin (Fig 2).

Protein-coding genes

Thirteen protein-coding genes (Table 1) were annotated in the genome of both breeds, including start and stop codons (nine ATGs, three ATAs, one GTG, seven TAAs, one TAG, one GTA and one

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Fig 1. The alignment control region nucleotides for the Moroccan (M) and Arabian (A) camel breeds. Dotes denote similarity while dashes refer to gaps.

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M      GCTTGGTAAGAAGAGGGCTCTCACCTCTGTCTTTAGATTTACAG-TCCAATGCCTACT
A      TCT----------ACTTCTCCCGCCGCGAGAAAAAAAAAAGGCGGGAGAAGCCCCGGCA
       **                    *      ***  *.**  *  .  .:::*.*::  .*.*  :  .*.    **  .*:
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Fig 2. The alignment of the origin of light strand replication (OL) for both Moroccan (M) and Arabian (A) camel breeds. * refers to identity, - refers to gaps, dots denote transitions and : refers to transversions.

AGA). The genes nd2, cox3 and nd4 have stopped with "T" which was provided later with "A" via post-transcriptional polyadenylation in the cellular translation process (Ojala *et al,* 1981). Acquiring such nontypical start and stop codons was shared by most of the vertebrate mitochondrial genomes and it was similar herein to that found in the Bactrian camel. ATP6 and ATP8 genes showed an overlap of a 32-bp sequence which was 42-bp sequence in the Bactrian camel.

Transfer RNA genes

Twenty two tRNA genes have been identified in mtDNA of the Arabian camel and as has been found in the Bactrian camel, 21 of them were capable of folding into the cloverleaf structure of the vertebrate mitochondrial genome. Only tRNAser consisted of 29 nucleotides and did not acquire the typical cloverleaf structure of the vertebrate mitochondrial genome. It lacked both dihydrouridine loop and the anticodon and thus, it could be a pseudogene or may be inactive (Wolstenholme, 1992).

Non-coding region

The control region of *Camelus dromedarius* was 1222-bp in the Arabian breed and 1236 bp in the Moroccan one. All the characteristic domains of the control region that found in the genome of the wild camel were also found in that of the Arabian ones. These domains were the termination-associated sequence (TAS) motifs and eight putative conserved sequence blocks (CSB1-3 and B-F) that were important to the regulation of mtDNA replication (Clayton, 1991). Among these domains, CSBC-B differed by one base from that of the wild camel but it resembled that of alpaca.

Conclusions

There are some base differences, mainly a length variation, between the mitochondrial genomes of *Camelus dromedarius* from Morocco and from Arabia. This length variation occurred in the tandem repeat $(ACGTAC)_n$ of the control region. Moreover, the replication origin of the light strand within a WANCY tRNA gene cluster was found in the Arabian breed and was not found in the Moroccan

Table 1. Gene organisation for the complete mitochondrial genome of Arabian (Moroccan) camel breeds.

Gene/element	Position	Start	Stop
tRNA-Phe (H)	1–67	-	-
12S rRNA(H)	68–1033	-	-
tRNA-Val(H)	1034–1099	-	-
16S rRNA(H)	1105–2663	-	-
tRNA-Leu(H)	2664–2741	-	-
nd1(H)	2742–3697	ATG	TAA
tRNA-Ile(H)	3698–3766	-	-
tRNA-Gln(L)	3764–3836	-	-
tRNA-Met(H)	3838–3906	-	-
nd2(H)	3907–4948	ATA	T.. (TAG)
tRNA-Trp(H)	4949–5016	-	-
tRNA-Ala(L)	5022–5090	-	-
tRNA-Asn(L)	5092–5164	-	-
O_L	5161–5208	-	-
tRNA-Cys(L)	5197–5264	-	-
tRNA-Tyr(L)	5265–5331	-	-
cox1(H)	5333–6877	ATG	TAG
tRNA-Ser(L)	6879–6947	-	-
tRNA-Asp(H)	6954–7020	-	-
cox2(H)	7021–7704	ATG	TAA
tRNA-Lys(H)	7708–7774	-	-
atp8(H)	7776–7979	ATG	TAA
atp6(H)	7937–8617	GTG(ATG)	TAA
cox3(H)	8617–9400	ATG	T . .
tRNA-Gly(H)	9401–9470	-	-
nd3(H)	9468–9817	ATA(ATG)	GTA(TA.)
tRNA-Arg(H)	9818–9885	-	-
ND4L(H)	9886–10182	ATG	TAA
nd4(H)	10176–11553	ATG	T . .
tRNA-His(H)	11554–11622	-	-
tRNA-Ser(H)	11623–11681	-	-
tRNA-Leu(H)	11683–11752	-	-
nd5(H)	11753–13570	ATA	TAA
nd6(L)	13554–14081	ATG	TAA
tRNA-Glu(L)	14083–14151	-	-
cytb(H)	14156–15295	ATG	AGA
tRNA-Thr(H)	15296–15364	-	-
tRNA-Pro(H)	15364–15429	-	-
d-loop(H)	15430–16643	-	-

breed. Otherwise both genomes were identical. This difference could refer, most probably, to a breed variation.

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