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## MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of domestic sheep, *Ovis aries*Xiao-di Hu<sup>1</sup> and Li-zhi Gao<sup>1,2</sup><sup>1</sup>Faculty of Life Science and Technology, Kunming University of Science and Technology, Kunming, China and <sup>2</sup>Plant Germplasm and Genomics Center, Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, the Chinese Academy of Sciences, Kunming, China

## Abstract

In this study, we report a complete mitochondrial (mt) genome sequence of the Texel ewe, *Ovis aries*. The total genome is 16,615 bp in length and its overall base composition was estimated to be 33.68% for A, 27.36% for T, 25.86% for C, and 13.10% for G indicating an AT-rich (61.04%) feature in the *O. aries* mtgenome. It contains a total of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and a control region (D-loop region). Comparisons with other publicly available sheep mitogenomes revealed a bunch of nucleotide diversity. This complete mitgenome sequence would enlarge useful genomic information for further studies on sheep evolution and domestication that will enhance germplasm conservation and breeding programs of *O. aries*.

## Keywords

Comparative mitochondrial genomics, *Ovis aries*, Texel ewe

## History

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Domesticated sheep, *Ovis aries*, have had an important part in human settlement, providing a farmed source of food, wool and hide since the Neolithic Agricultural revolution approximately 8000–9000 years ago (Ryder, 1984). Mitochondrial genome has long been recognized as an important organelle related to disease, apoptosis, aging and metabolism (Boore, 1999). The complete mitochondrial (mt) genome sequencing and analyses of a number of haplotype groups identified in domestic sheep and its wild relatives have given in-depth insights into the sheep mtgenome-wide variation and their evolutionary relationships (Hiendleder et al., 1998; Hiendleder, 1998; Lancioni et al., 2013; Meadows et al., 2011; Miller et al., 2012). These obtained findings indicate that more representatives of sheep reference mtgenomes would better provide evidence of its origins and domestication and further enhance the germplasm conservation and breeding programs. Here, using the Velvet package (Zerbino & Birney, 2008), we assembled and characterized the complete mitochondrial genome of the Texel ewe, *O. aries*, with the Illumina sequencing dataset released by Jiang et al. (2014). This mitochondrial sequence will enlarge genomic resources of a global sheep reference mtgenome panel that would greatly help germplasm conservation and utilization of *O. aries*.

The complete mitochondrial genome (GenBank Accession Number: KJ954145) of *O. aries* (16,615 bp in length) harbored a

total 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and two non-coding regions: the origin of light-strand replication (*OL*) and control region (*D-loop*) (Table 1). The total base compositions are 33.68% A, 27.36% T, 25.86% C, and 13.10% G; the percentage of A + T (61.04%) was found to be higher than G + C (38.96%). Most of these genes are encoded on the H-strand, except for the *ND6* gene and 8 tRNA genes that are encoded on the L-strand. All protein-coding genes are 11,373 bp in length, which together encode 3805 amino acids. A total of 13 open reading frames of protein-coding sequences have the typical ATN initiation codon. Seven genes used TAA as their termination codon, whereas *ND2* and *Cyt b* use with TAG and AGA, respectively. In addition, there are four genes (*COX3*, *ND3*, *ND4* and *ND6*) that were found with an incomplete stop codon.

The mitgenome of *O. aries* contains a small subunit of 12S rRNA (958 bp), a large subunit of 16S rRNA (1574 bp) and a typical set of 22 tRNA genes. These ribosomal subunit genes are located between the *tRNA-Phe* and *tRNA-Leu* genes and further separated by the *tRNA-Val* gene. The total length of all tRNAs is 1510 bp, varying from 64 bp (*tRNA-phe*) to 75 bp (*tRNA-Leu*). The *OL* is 32 bp in length, which is located between *tRNA-Asn* and *tRNA-Cys* genes within the WANCY cluster (*tRNA-Asn*, *tRNA-Cys*, *tRNA-Trp*, *tRNA-Ala* and *tRNA-Tyr*). The control region (CR) or *D-loop* is 1180 bp in length and is positioned between *tRNA-Pro* and *tRNA-Phe*.

We next compared the complete Texel ewe mitochondrial genome with seven *O. aries* breeds and three *Ovis* species (*O. vignei*, *O. ammon* and *O. canadensis*) (Hiendleder et al., 1998; Hiendleder, 1998; Lancioni et al., 2013; Meadows et al., 2011; Miller et al., 2012) (Table 1). Our results show that the gene order and base composition were expectedly conserved one another; however, SNPs and genome sizes varied slightly within *O. aries* but higher levels of variation were detected among different *Ovis* species.

Table 1. Features of the *Ovis aries* mitochondrial genome of Texel breed and comparisons with other *Ovis aries* mitochondrial genomes.

Genes	Position		Length (bp)	Codons		Strand
	Start	End		Start	Stop	
<i>tRNA-Phe</i>	1	66	66			+
<i>12S rRNA</i>	67	1024	958			+
<i>tRNA-Val</i>	1026	1092	67			+
<i>16S rRNA</i>	1093	2666	1574			+
<i>tRNA-Leu</i>	2668	2742	75			+
<i>ND1</i>	2745	3695	951	ATG	TAA	+
<i>tRNA-Ile</i>	3701	3769	69			+
<i>tRNA-Gln</i>	3767	3838	72			–
<i>tRNA-Met</i>	3841	3909	69			+
<i>ND2</i>	3910	4950	1041	ATA	TAG	+
<i>tRNA-Trp</i>	4952	5018	67			+
<i>tRNA-Ala</i>	5020	5088	69			–
<i>tRNA-Asn</i>	5090	5162	73			–
<i>OL</i>	5163	5194	32			
<i>tRNA-Cys</i>	5195	5262	68			–
<i>tRNA-Tyr</i>	5263	5330	68			–
<i>COX1</i>	5332	6873	1542	ATG	TAA	+
<i>tRNA-Ser</i>	6874	6944	71			–
<i>tRNA-Asp</i>	6950	7017	68			+
<i>COX2</i>	7019	7699	681	ATG	TAA	+
<i>tRNA-Lys</i>	7706	7773	68			+
<i>ATP8</i>	7775	7972	198	ATG	TAA	+
<i>ATP6</i>	7936	8613	678	ATG	TAA	+
<i>COX3</i>	8616	9398	783	ATG	T–	+
<i>tRNA-Gly</i>	9400	9468	69			+
<i>ND3</i>	9469	9813	345	ATA	TA–	+
<i>tRNA-Arg</i>	9816	9884	69			+
<i>ND4L</i>	9885	10,178	294	ATG	TAA	+
<i>ND4</i>	10,175	11,551	1377	ATG	T–	+
<i>tRNA-His</i>	11,553	11,621	69			+
<i>tRNA-Ser</i>	11,622	11,681	60			+
<i>tRNA-Leu</i>	11,683	11,752	70			+
<i>ND5</i>	11,753	13,570	1818	ATA	TAA	+
<i>ND6</i>	13,560	14,087	528	ATG	T–	–
<i>tRNA-Glu</i>	14,085	14,153	69			–
<i>Cyt b</i>	14,158	15,294	1137	ATG	AGA	+
<i>tRNA-Thr</i>	15,301	15,370	70			+
<i>tRNA-Pro</i>	15,370	15,435	66			–
<i>D-loop</i>	15,436	16,615	1180			
Species Names and NCBI Accession Numbers	Genome size (bp)		Base compositions			SNPs (In comparisons with the Texel breed)
<i>O. aries</i> (Texel breed): KJ954145	16,615	A (33.68%)	T (27.36%)	C (25.86%)	G (13.10%)	0
<i>O. aries</i> (Merino breed): HM236174	16,617	A (33.66%)	T (27.36%)	C (25.87%)	G (13.11%)	112
<i>O. aries</i> (Merino landschaf breed): NC001941	16,616	A (33.67%)	T (27.40%)	C (25.81%)	G (13.12%)	28
<i>O. aries</i> (Appenninica breed): KF302450	16,618	A (33.69%)	T (27.39%)	C (25.83%)	G (13.09%)	21
<i>O. aries</i> (Karakas breed): HM236176	16,616	A (33.67%)	T (27.40%)	C (25.82%)	G (13.11%)	15
<i>O. aries</i> (Awassi breed): HM236182	16,620	A (33.65%)	T (27.34%)	C (25.90%)	G (13.11%)	168
<i>O. aries</i> (Tuj breed): HM236183	16,619	A (33.65%)	T (27.36%)	C (25.88%)	G (13.11%)	175
<i>O. aries</i> (Romney breed): HM236175	16,617	A (33.69%)	T (27.39%)	C (25.83%)	G (13.09%)	104
<i>O. vignei</i> : HM236187	16,694	A (33.71%)	T (27.49%)	C (25.85%)	G (13.10%)	383
<i>O. ammon</i> : HM236188	16,613	A (33.67%)	T (27.46%)	C (25.79%)	G (13.08%)	429
<i>O. canadensis</i> : JN181255	16,463	A (33.75%)	T (27.46%)	C (25.86%)	G (12.93%)	795

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## Declaration of interest

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