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The complete mitochondrial genome of eastern lowland gorilla, *Gorilla beringei graueri*, and comparative mitochondrial genomics of *Gorilla* speciesXiao-di Hu¹ and Li-zhi Gao^{1,2}¹Faculty of Life Science and Technology, Kunming University of Science and Technology, Kunming, China and ²Plant Germplasm and Genomics Center, Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China

Abstract

In this study, we determined the complete mitochondrial (mt) genome of eastern lowland gorilla, *Gorilla beringei graueri* for the first time. The total genome was 16,416 bp in length. It contained a total of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and 1 control region (D-loop region). The base composition was A (30.88%), G (13.10%), C (30.89%) and T (25.13%), indicating that the percentage of A+T (56.01%) was higher than G+C (43.99%). Comparisons with the other publicly available *Gorilla* mitogenome showed the conservation of gene order and base compositions but a bunch of nucleotide diversity. This complete mitochondrial genome sequence will provide valuable genetic information for further studies on conservation genetics of eastern lowland gorilla.

Keywords

Eastern lowland gorilla, *G. beringei graueri*, mitochondrial genome

History

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The eastern lowland gorilla, *Gorilla beringei graueri*, has been known as the largest subspecies of eastern gorilla endemic to the mountainous forests of eastern Democratic Republic of the Congo (Robbins et al., 2008). However, over the past years, gorillas have severely been threatened in parts of the country (Vogel, 2000). Currently, five subspecies are recognized in the genus *Gorilla*, including *G. b. beringei*, *G. b. graueri*, *G. gorilla diehli*, *G. g. gorilla* and *G. g. uellensis*. So far, only the mitochondrial genome of *G. g. gorilla* has been reported (Xu & Arnason, 1996). Here, we assembled and characterized complete mitochondrial genome of the eastern lowland gorilla, *G. b. graueri*, using the CLC Genomic Workbench v3.6 (2010). We downloaded the genome raw reads, which were sequenced by Illumina Genome Analyzer II, from NCBI (<http://www.ncbi.nlm.nih.gov/sra/>) (Scully et al., 2012). The complete mitochondrial sequence reported here will add new dimensions to studies on the evolution and conservation genetics of the genus *Gorilla*.

The eastern lowland gorilla mitochondrial genome was 16,416 bp in length (GenBank Accession Number: KM242275) and contained 2 rRNA genes (12S rRNA and 16S rRNA), 22 tRNA genes, 13 protein-coding genes and a control region (Table 1). The synteny of all these genes is well conserved in comparison with typical mitochondrial genomes of *Homininae* subfamily (Anderson et al., 1981; Green et al., 2008; Krause et al., 2010). The total base composition was C (30.89%) > A (30.88%) > T (25.13%) > G (13.10%), suggesting that the percentage of A+T (56.01%) was higher than G+C (43.99%). Most of the genes were

located on the H-strand except for the *ND6* gene and 8 tRNA genes. Nine of the 13 identified protein-coding genes initiated with ATG, *ND1*, *ND3* and *ND5* began with ATA, while *ND2* started with an unusual start codon of ATT. *ND1*, *COX2*, *ATP6*, *ND4L* and *ND5* terminated with TAA, whereas *COX2* and *ATP8* stopped with TAG. Incomplete stop codons (–) were observed in six protein-coding genes.

The total length of 22 tRNA genes, ranging from 59 (*tRNA-Ser*) to 75 bp (*tRNA-Leu*), respectively, were 1511 bp. The L-strand replication origin (*OL*) was 33 bp, which was located between *tRNA-Asn* and *tRNA-Cys*. The control regions (CR) or *D-loop* region was located between *tRNA-Pro* and *tRNA-Phe*, and was 968 bp in length. The *tRNA-Val* intervened between 12S rRNA gene and 16S rRNA gene. The data presented here would facilitate further studies towards a better understanding of the evolution of *Gorilla* mitochondrial genomes.

We then compared the two complete mitochondrial genomes from *G. b. graueri* in this study with *G. g. gorilla* (Xu & Arnason, 1996) (Table 1). Our results show that the gene order and base compositions were well conserved one another; however, a total of 577 SNPs were observed between the two sequenced *Gorilla* mitochondrial genomes.

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Declaration of interest

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Table 1. Features of the *G. b. graueri* mitochondrial genome and comparisons with the mitochondrial genome of *G. g. gorilla*.

Gene	Position		Size (bp)	Codons		Strand
	From	To		Start	End	
<i>tRNA-Phe</i>	1	71	71			H
<i>12S rRNA</i>	72	1021	950			H
<i>tRNA-Val</i>	1022	1090	69			H
<i>16S rRNA</i>	1089	2648	1560			H
<i>tRNA-Leu</i>	2649	2723	75			H
<i>ND1</i>	2726	3676	951	ATA	TAA	H
<i>tRNA-Ile</i>	3682	3750	69			H
<i>tRNA-Gln</i>	3748	3819	72			L
<i>tRNA-Met</i>	3821	3888	68			H
<i>ND2</i>	3889	4926	1038	ATT	TAG	H
<i>tRNA-Trp</i>	4931	4998	68			H
<i>tRNA-Ala</i>	5006	5074	69			L
<i>tRNA-Asn</i>	5076	5148	73			L
<i>OL</i>	5149	5179	31			
<i>tRNA-Cys</i>	5180	5245	66			L
<i>tRNA-Tyr</i>	5246	5310	65			L
<i>COX1</i>	5326	6861	1536	ATG	–	H
<i>tRNA-Ser</i>	6868	6936	69			L
<i>tRNA-Asp</i>	6941	7008	68			H
<i>COX2</i>	7003	7668	666	ATG	TAA	H
<i>tRNA-Lys</i>	7719	7788	70			H
<i>ATP8</i>	7772	7990	219	ATG	TAG	H
<i>ATP6</i>	7945	8625	681	ATG	TAA	H
<i>COX3</i>	8628	9413	786	ATG	T––	H
<i>tRNA-Gly</i>	9415	9482	68			H
<i>ND3</i>	9483	9872	345	ATA	T––	H
<i>tRNA-Arg</i>	9829	9893	65			H
<i>ND4L</i>	9885	10,187	303	ATG	TAA	H
<i>ND4</i>	10,184	11,551	1368	ATG	T––	H
<i>tRNA-His</i>	11,562	11,630	69			H
<i>tRNA-Ser</i>	11,631	11,689	59			H
<i>tRNA-Leu</i>	11,690	11,760	71			H
<i>ND5</i>	11,752	13,563	1812	ATA	TAA	H
<i>ND6</i>	13,579	14,100	522	ATG	–	L
<i>tRNA-Glu</i>	14,098	14,166	69			L
<i>Cyt b</i>	14,171	15,304	1134	ATG	T––	H
<i>tRNA-Thr</i>	15,312	15,377	66			H
<i>tRNA-Pro</i>	15,381	15,448	68			L
<i>D-loop</i>	15,449	16,416	968			
Species Names and GenBank Accession No.	Genome Size (bp)		Base Compositions			SNPs In comparisons with <i>G. b. graueri</i>
<i>G. b. graueri</i> : KM242275	16416	A (30.9%)	T (25.1%)	G (13.1%)	C (30.9%)	0
<i>G. g. gorilla</i> : NC_011120	16412	A (30.9%)	T (25.3%)	G (13.1%)	C (30.7%)	577

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

References

- Anderson S, Bankier AT, Barrell BG, de Bruijn MH, Coulson AR, Drouin J, Eperon IC, et al. (1981). Sequence and organization of the human mitochondrial genome. *Nature* 290:457–65.
- CLC Genomics Workbench v3.6. (2010). Available at: <http://www.clcbio.com/products/clc-genomics-workbench/>
- Green RE, Malaspina AS, Krause J, Briggs AW, Johnson PL, Uhler C, Meyer M, et al. (2008). A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. *Cell* 134:416–26.
- Krause J, Fu Q, Good JM, Viola B, Shunkov MV, Derevianko AP, Paabo S. (2010). The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. *Nature* 464:894–7.
- Robbins M, Hart J, Maisels F, Mehlman P, Nixon S, Williamson L. (2008). *Gorilla beringei graueri*. The IUCN Red List of Threatened Species. Version 2014.2. <http://www.iucnredlist.org/>
- Scally A, Dutheil JY, Hillier LW, Jordan GE, Goodhead I, Herrero J, Lappalainen T, et al. (2012). Insights into hominid evolution from the gorilla genome sequence. *Nature* 483:169–75.
- Vogel G. (2000). Conservation. Conflict in Congo threatens bonobos and rare gorillas. *Science* 287:2386–7.
- Xu X, Arnason U. (1996). A complete sequence of the mitochondrial genome of the western lowland gorilla. *Mol Biol Evol* 13:691–8.