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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of Celebes wild boar, *Sus celebensis* (Cetartiodactyla: Suina: Suidae), and comparative mitochondrial genomics of the *Sus* species

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Abstract

In this study, the complete mitochondrial (mt) genome sequence of *Sus celebensis* was firstly determined. The total genome was 16,481 bp in length and its overall base composition was estimated to be 34.9% for A, 25.8% for T, 26.2% for C, 13.1% for G, respectively, indicating an A-T (60.7%)-rich feature in Celebes wild boar mitogenome. It harbored 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes and a non-coding control region (D-loop region). Comparisons with other publicly available pig mitogenomes revealed abundant nucleotide diversity. This complete mitgenome sequence would accelerate further studies on pig evolution and domestication that will enhance germplasm preservation and breeding programs of the pig gene pool.

Keywords

Celebes wild boar, comparative mitochondrial genomics, mitochondrial genome, *Sus celebensis*

History

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The Celebes wild boar (*Sus celebensis*) is a medium-sized pig which is still found in its abundance in central, east and south-east Sulawesi (MacDonald et al., 1996). Currently, three species for the genus *Sus* had been reported the mitochondrial genome, including *S. cebifrons* (Liu et al., 2014), *S. scrofa* (Lin et al., 1999) and *S. verrucosus* (Fan et al., 2014). Here, the complete mitochondrial genome of the Celebes wild boar was analyzed for the first time. Using the CLC Genomic Workbench v3.6 (2010), we assembled and analyzed the mitochondrial genome of *S. celebensis*, with the Illumina sequencing data from NCBI (http://www.ncbi.nlm.nih.gov/sra/). The complete mitogenomic sequence of Celebes wild boar (*S. celebensis*) would provide new insights into the domestication of the pig and enhance our understanding of the evolution and germplasm conservation of wild boars.

The total length of the mitogenome of the *S. celebensis* (GenBank Accession Number KM203891) was 16,481 bp, which contained two ribosomal RNA genes, 13 protein-coding genes, 22 transfer RNA genes and a major non-coding control region (D-loop region). The distribution of these genes was the same as that found in the pigs (Chen et al., 2013; Xu et al., 2013). The total base composition was 34.9% A, 25.8% T, 26.2% C and 13.1%

Table 1. Features of the *S. celebensis* mitochondrial genome and comparisons with the other three mitochondrial genomes of *Sus* species.

	Position				Base Composition (%)					
Gene	From	To	Intervals	Size (bp)	A	C	G	T	Codons	Strand
D-loop	1	1041	0	1041	35.2	25.5	12.6	26.7		H
$tRNA^{Phe}$	1042	1111	0	70	38.6	21.4	17.1	22.9		H
12S rRNA	1112	2071	1	960	37.4	22.8	17.3	22.5		H
$tRNA^{Val}$	2073	2140	0	68	36.7	22.1	16.2	25		H
16S rRNA	2141	3710	0	1570	39	20.8	16.5	23.7		H
$tRNA^{Leu}$	3711	3785	2	75	30.6	24	18.7	26.7		H
ND1	3788	4744	−2	957	32.4	29.5	12.9	25.2	ATG TAG	H
$tRNA^{Ile}$	4743	4811	−3	69	40.6	11.6	15.9	31.9		H
$tRNA^{Gln}$	4809	4881	1	73	21.9	9.6	27.4	41.1		L
$tRNA^{Met}$	4883	4952	0	70	27.1	28.6	20	24.3		H
ND2	4953	5996	−2	1044	39.3	27.8	9.5	23.4	ATA TAG	H
$tRNA^{Trp}$	5995	6062	6	68	38.2	20.6	17.7	23.5		H
$tRNA^{Ala}$	6069	6137	1	69	24.6	13	24.7	37.7		L

(*continued*)

*These authors contributed equally to this work.

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Table 1. Continued

Gene	Position From	Position To	Intervals	Size (bp)	Base Composition (%) A	C	G	T	Codons	Strand
tRNA^{Asn}	6139	6213	2	75	25.3	16	22.7	36		L
tRNA^{Cys}	6246	6312	0	67	35.8	20.9	17.9	25.4		L
tRNA^{Tyr}	6313	6378	1	66	33.3	18.2	22.7	25.8		L
COX1	6380	7924	3	1545	29.5	24.6	16.4	29.5	ATG TAA	H
tRNA^{Ser}	7928	7996	7	69	24.6	16	29	30.4		L
tRNA^{Asp}	8004	8071	0	68	33.8	13.2	17.7	35.3		H
COX2	8072	8759	0	688	34.3	25	13.4	27.3	ATG T−−	H
tRNA^{Lys}	8760	8826	1	67	31.3	22.4	19.4	26.9		H
ATP8	8828	9031	−43	204	41.7	25	6.4	26.9	ATG TAA	H
ATP6	8989	9669	−1	681	34.5	28.8	9.8	26.9	ATG TAA	H
COX3	9669	10,452	0	784	29.5	28.6	15	26.9	ATG T−−	H
tRNA^{Gly}	10,453	10,521	0	69	36.2	17.4	14.5	31.9		H
ND3	10,522	10,867	1	346	34.4	29.2	11	25.4	ATA T−−	H
tRNA^{Arg}	10,869	10,937	0	69	42	13.1	8.7	36.2		H
ND4L	10,938	11,234	3	297	32.7	25.2	11.5	30.6	GTG TAA	H
ND4	11,228	12,605	0	1378	34.3	39.6	10.1	26	ATG T−−	H
tRNA^{His}	12,606	12,674	0	69	40.6	11.6	13	34.8		H
tRNA^{Ser}	12,675	12,733	0	59	35.6	18.6	15.3	30.5		H
tRNA^{Leu}	12,734	12,803	0	70	38.6	15.7	18.6	27.1		H
ND5	12,804	14,624	−17	1821	35	29	10.5	25.5	ATA TAA	H
ND6	14,608	15,135	0	528	20.8	7.6	27.1	44.5	ATG TAA	L
tRNA^{Glu}	15,136	15,204	4	69	26.1	11.6	23.2	39.1		L
Cyt b	15,209	16,348	0	1140	31.7	29.5	12.8	26	ATT AGA	H
tRNA^{Thr}	16,349	16,417	−1	69	31.9	26.1	17.4	24.6		H
tRNA^{Pro}	16,417	16,481	0	65	20	15.4	29.2	35.4		L

Species	Genbank Accession No.	Genome Size (bp)	Base Compositions				SNPs (In comparisons with *S. celebensis*)
S. celebensis	KM203891	16481	A (34.9%)	T (25.8%)	C (26.2%)	G (13.1%)	0
S. cebifron	KF952600	16473	A (34.9%)	T (25.8%)	C (26.2%)	G (13.1%)	409
S. scrofa	AF034253	16613	A (34.7%)	T (25.8%)	C (26.2%)	G (13.3%)	505
S. verrucosus	KF926379	16479	A (34.9%)	T (25.9%)	C (26.1%)	G (13.1%)	573

G, and a slight A-T (60.7%) bias was detected. The total length of 13 protein-coding genes was 11,413 bp in length. The majority of protein-coding genes used ATG as the start codon except for *ND2*, *ND3* and *ND5* that used the start codon ATA, *Cyt b* that used ATT, and *ND4L* that used GTG. As for stop codons, *COX1*, *ATP6*, *ATP8*, *ND4L*, *ND5* and *ND6* terminated with TAA, whereas *ND1* and *ND2* ended with TAG, and *Cyt b* completed with AGA, respectively. In addition, four genes terminated with incomplete stop codon T−− (*COX2*, *COX3*, *ND3* and *ND4*), which presumptively formed a complete stop codon by posttranscriptional polyadenylation (Boore, 1999).

The 22 tRNA genes of *S. celebensis* were detected based on their respective anticodons and secondary structures, and they ranged in size from 59 bp (*tRNA*^{Ser}) to 75 bp (*tRNA*^{Leu}). The 12S rRNA and 16S rRNA separated by the *tRNA*^{Val} are 960 bp and 1570 bp in length, respectively. The control region of the *S. celebensis* mtDNA was 1041 bp long and located between *tRNA*^{Pro} and *tRNA*^{Phe}.

We then compared the complete *S. celebensis* mitochondrial genome with other three *Sus* species with publicly available sheep mitogenomes, including *S. cebifrons* (Liu et al., 2014), *S. scrofa* (Lin et al., 1999) and *S. verrucosus* (Fan et al., 2014) (Table 1). Our results show that the gene order and base composition were well conserved one another; however, high levels of nucleotide diversity were observed among the four sequenced *Sus* mitochondrial genomes.

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Declaration of interest

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

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