

## MITOGENOME ANNOUNCEMENT

**Mitochondrial genome of bamboo rat *Rhizomys pruinosus***Fang Zhao<sup>1</sup>, Tongzuo Zhang<sup>1</sup>, Jianping Su<sup>1</sup>, Eviatar Nevo<sup>2</sup>, and Gonghua Lin<sup>1</sup><sup>1</sup>Key Laboratory of Adaptation and Evolution of Plateau Biota, Northwest Institute of Plateau Biology, Chinese Academy of Sciences, Xining, China and <sup>2</sup>Institute of Evolution, University of Haifa, Mount Carmel, Haifa, Israel**Abstract**

Bamboo rats are a group of subterranean rodents some of which feed on the roots and shoots of bamboo and other plants. In this study, we sequence the mitochondrial genome of a hoary bamboo rat *Rhizomys pruinosus* from the south of China. The genome is 16,575 bp in length, and had a gene content of 13 protein coding, 22 tRNAs and 2 rRNAs. The overall base composition is 30.94% T, 24.83% C, 32.21% A and 12.02% G, with an A + T bias of 63.15%. The cytochrome genes were the most conservative genes compared with plateau zokor (*Eospalax baileyi*) and blind mole rats (*Spalax carmeli*) in the family Spalacidae. These mitochondrial data are potentially important for the study of molecular evolution, conservation genetics, agricultural technology and epidemiology.

**Keywords**

Bamboo rat, mitochondrial genome, Spalacidae

**History**

Received 5 May 2013

Revised 7 May 2013

Accepted 21 May 2013

Published online 2 July 2013

Bamboo rats are a group of subterranean rodents feed on roots and stems of crude fiber plants such as bamboo. They belong to the Rhizomyinae, Spalacidae (Wilson & Reeder, 2005) and like other species in this family such as zokors (*Eospalax* spp.) and blind mole rats (*Spalax* spp.), bamboo rats inhabit in damp and dark underground tunnel system in most of their lifetime. Due to their cryptic lifestyle, the biology of bamboo rats has long remained unstudied and very few genes have been sequenced. The mutation rate of animal mitochondrial DNA (mtDNA) is higher than that of nuclear DNA. Also, unlike nuclear DNA, which is inherited from both parents and in which genes are rearranged in the process of recombination, there is usually no change in mtDNA from parent to offspring. This makes mtDNA useful for assessing genetic relationships of individuals within a species or among different species which are not too distantly related. It should be mentioned that, the mitochondrial genomes of some zokors (Liu et al., 2011; Su et al., 2013) and blind mole rats (submitted in the GenBank) have been sequenced, while no such data of bamboo rats are available yet.

In this study, we report the complete mitochondrial genome of a hoary bamboo rat *Rhizomys pruinosus* with a GenBank

accession number KC789518. The complete mtDNA was amplified and sequenced through 16 overlapping fragments using specific primers designed in this study. The total length of the genome is 16,575 bp, consisting of 13 protein coding genes, 22 tRNA genes and 2 rRNA genes, and a noncoding displacement loop (D-loop) locus and a replication origin locus of L strand (Table 1). The overall nucleotide composition of the heavy strand is 30.94% T, 24.83% C, 32.21% A, 12.02% G, with A + T > G + C. We also compared our sequence with the mtDNA of plateau zokor (*Eospalax baileyi*, JN540033) and blind mole rat (*Spalax carmeli*, JN571137) to show the variable sites distribution of the 13 protein coding genes. We found that the cytochrome genes (COI, COII, COIII, CYTB) were the most conservative; the ATP6, ATP8 and NADH7 genes were much more variable; especially, the NADH6 which was encoded by L strand is the least conservative. The D-loop region of the *R. pruinosus* is 1145 bp in length, much longer than that of the plateau zokor (933 bp) and the blind mole rat (980 bp).

There are several biological specialties of bamboo rats. First, they live and forage in extensive burrow systems and rarely spend much time above ground, and will hence confront with various environmental stresses (Begall, 2007). Second, most of the bamboo rats are a bamboo specialist, and are well adapted to crude fiber plants (Chen, 2012). Also, bamboo rats are the natural hosts for the disease-causing mold, *Penicillium marneffeii*, which is the third most common opportunistic infection in HIV-positive individuals (Cao et al., 2011; Cooper & Haycocks, 2000). These special traits make the animal an ideal target for researches of evolutionary biology such as hypoxia tolerance, agricultural technology (crude fiber digestion), and medical science (*P. marneffeii* infection control), while the sequenced mitochondrial genome provides a scientific basis for these studies. Moreover, these animals are recognized as valuable food resources, and the mitochondrial genome could also serve as molecular markers for resource utilization and conservation genetics.

Correspondence: G. H. Lin, Key Laboratory of Adaptation and Evolution of Plateau Biota, Northwest Institute of Plateau Biology, Chinese Academy of Sciences, Xining 810008, China. Tel: +86 13897245047. E-mail: lingonghua@gmail.com

Table 1. Characteristics of the mitochondrial genome of *R. pruinosus* and information of variable sites compared with *Eospalax baileyi* and *Spalax carmeli*.

Locus	From	To	Length (bp)	Start	Stop	Variable sites (bp)	Variation percent (%)	Strand
tRNA-Phe	1	66	66					H
12S-rRNA	67	1024	958					H
tRNA-Val	1025	1091	67					H
16S-rRNA	1092	2647	1556					H
tRNA-Leu	2648	2722	75					H
NADH1	2723	3679	957	ATA	TAA	316	33.02	H
tRNA-Ile	3679	3747	69					H
tRNA-Gln	3745	3815	71					L
tRNA-Met	3823	3892	70					H
NADH2	3878	4927	1050	ATC	TAA	375	35.71	H
tRNA-Trp	4930	4996	67					H
tRNA-Ala	4998	5065	68					L
tRNA-Asn	5066	5139	74					L
Rep-origin	5140	5172	33					H
tRNA-Cys	5173	5238	66					L
tRNA-Tyr	5241	5309	69					L
COI	5311	6855	1545	ATG	TAA	384	24.85	H
tRNA-Ser	6853	6921	69					L
tRNA-Asp	6936	7003	68					H
COII	7004	7687	684	ATG	TAA	194	28.36	H
tRNA-Lys	7692	7756	65					H
ATP8	7757	7963	207	ATG	TAG	86	41.55	H
ATP6	7918	8598	681	ATG	TAA	238	34.95	H
COIII	8598	9381	784	ATG	CTT	248	31.63	H
tRNA-Gly	9382	9450	69					H
NADH3	9451	9798	348	ATT	TAA	141	40.52	H
tRNA-Arg	9801	9868	68					H
NADH4L	9869	10,165	297	ATA	TAA	117	39.39	H
NADH4	10,159	11,535	1377	ATG	TAT	501	36.38	H
tRNA-His	11,537	11,602	66					H
tRNA-Ser	11,603	11,662	60					H
tRNA-Leu	11,663	11,732	70					H
NADH5	11,733	13,547	1815	ATT	TAA	670	36.85	H
NADH6	13,544	14,074	531	TTA	CAT	244	45.95	L
tRNA-Glu	14,075	14,143	69					L
CYTB	14,147	15,286	1140	ATG	TAA	350	30.70	H
tRNA-Thr	15,297	15,364	68					H
tRNA-Pro	15,365	15,430	66					L
D-loop	15,431	16,575	1145					H

## Declaration of interest

This work was supported by the Knowledge Innovation Project of the Chinese Academy of Science (KSCX2-EW-J-26). The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

## References

- Begall S, Burda H, Schleich CE. (2007). Subterranean rodents: News from underground. Berlin, Germany: Springer.
- Cao CW, Liang L, Wang WJ, Luo H, Huang SB, Liu DH, Xu JP, et al. (2011). Common reservoirs for *Penicillium marneffeii* infection in humans and rodents, China. *Emerg Infect Dis* 17:209–14.
- Chen GH. (2012). The *Rhizomys sinensis* domesticated research. Master Dissertation in Chinese Academy of Forestry.
- Cooper Jr CR, Haycocks NG. (2000). *Penicillium marneffeii*: An insurgent species among the Penicillia. *J Eukaryot Microbiol* 47:24–8.
- Liu Z, Li Y, Shi F, Lu J, Li M, Wang Z. (2011). Mitochondrial genome of Plateau zokor *Myospalax baileyi*. *Mitochondrial DNA* 22: 174–5.
- Su JH, Wang J, Hua LM, Gleeson D, Ji WH. (2013). Complete mitochondrial genome of the Gansu zokor, *Eospalax cansus* (Rodentia, Spalacidae). *Mitochondrial DNA* DOI: 10.3109/19401736.2013.772166.
- Wilson DE, Reeder DM. (2005). Mammal species of the world: A taxonomic and geographic reference. Washington, DC: Smithsonian Books.