

Complete mitochondrial genome of the feather mite *Ardeacarus ardeae* (Acari, Sarcoptiformes, Pterolichidae)

Yeong-Deok Han and Gi-Sik Min

Department of Biological Sciences, Inha University, Incheon, South Korea

ABSTRACT

In this study, we determined the mitogenome sequence of *Ardeacarus ardeae* (Canestrini, 1878) in the family Pterolichidae (Acari, Sarcoptiformes), which is the first complete mitogenome sequence in feather mite. The mitogenome of *A. ardeae* is 14,069 bp in length and contains 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNAs (rRNAs), and a control region (CR). The phylogenetic tree shows that *A. ardeae* belong to the supercohort Desmonomatides within the order Sarcoptiformes.

ARTICLE HISTORY

Received 27 December 2016
Revised 19 January 2017
Accepted 28 January 2017

KEYWORDS

Ardeacarus ardeae;
complete mitogenome;
feather mite; Pterolichidae;
Sarcoptiformes

Feather mites are referred to as commensal or parasitic species that live on the plumage and skin of birds (Mironov 2003; Proctor 2003). *Ardeacarus ardeae* (Canestrini, 1878) (Acari, Acariformes, Sarcoptiformes, Pterolichidae), which is a monotypic species of the genus *Ardeacarus* Dubinin, 1951, has a worldwide distribution and is mostly observed on wing feathers of the birds in the family Ardeidae (Gaud 1981; Gaud & Atyeo 1996). Here, we present the complete mitogenome sequence of *A. ardeae* in family Pterolichidae, which is the first complete mitogenome from a feather mite.

A single specimen of *A. ardeae* was collected from a wing feathers of little egret *Egretta garzetta* collected from Eumseong-gun, Chungcheongbuk-do Province (36°56'N, 127°41'E). Mitochondrial DNA extraction, sequencing and gene annotation were performed according to the methods described by Song et al. (2016). The extracted mitochondrial DNA (Inhaevodevo-HYD-0030) was deposited in the Inha University, Incheon, South Korea. The phylogenetic tree was constructed based on the analysis of maximum likelihood (GTR+I+G model, PhyML 3.0) and Bayesian inference (GTR+I+G model, MrBayes 3.2.3) methods using the concatenated sequence of 13 protein-coding genes from the related 15 species within the superfamily Acariformes.

The complete mitogenome of *A. ardeae* (GenBank accession no. KY352304) was 14,069 bp in length and contained the typical set of 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), two ribosomal RNAs (rRNAs) and a control region (CR). The overall base composition of the entire

A. ardeae mitogenome consisted of 29.3% A, 45.5% T, 10.8% C, 14.5% G and 74.8% AT. Twelve of the PCGs use an ATN codon (N, any nucleotide), while *atp8* uses TTG. The stop codons of three PCGs are incomplete and use just one T nucleotide.

The gene arrangement of the *A. ardeae* mitogenome, with the exception of tRNAs, was found to be almost identical to those of previously published species in Sarcoptiformes. However, *A. ardeae* has a shorter mitogenome than two closely related species, *Dermatophagoides farinae* (14,266 bp) and *D. pteronyssinus* (14,203 bp). These length differences are mainly due to the CR, which is 214 bp long in *A. ardeae*, while *D. farinae* and *D. pteronyssinus* have CRs composed of 410 and 286 bp, respectively (Dermauw et al. 2009; Klimov & Oconnor 2009).

We inferred the phylogenetic relationship of *A. ardeae* to the Acariformes species. The phylogenetic tree of maximum likelihood and Bayesian inference showed that *A. ardeae* belongs to the supercohort Desmonomatides within the order Sarcoptiformes. Furthermore, *A. ardeae* of the family Pterolichidae showed a sister-group relationship with the family Pyroglyphidae (*D. farinae* and *D. pteronyssinus*) (Figure 1). The phylogenetic relationships found in our study are well-congruent with previous mitogenome studies reported by Lee and Wang (2016) and Xue et al. (2016).

Our study determined the complete mitogenome of *A. ardeae* in the family Pterolichidae for the first time and will be useful for the detailed study of mitogenome evolution

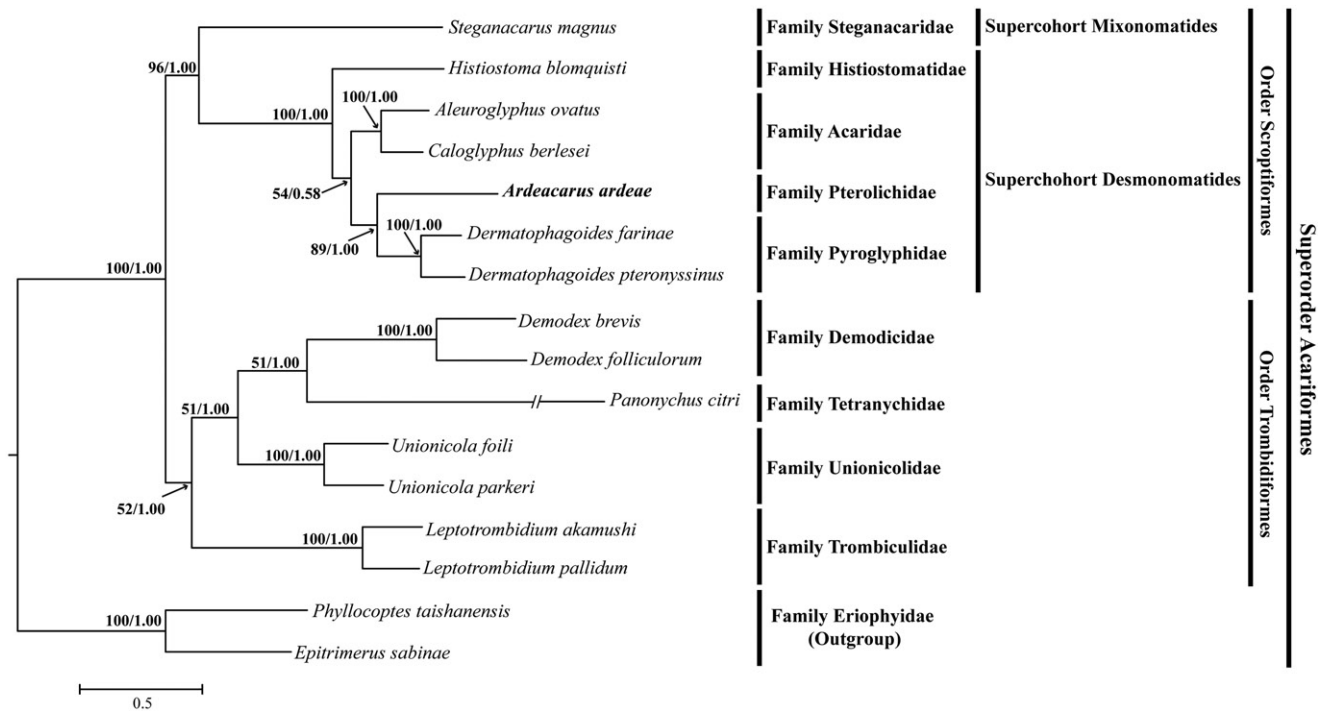


Figure 1. Maximum likelihood and Bayesian inference tree based on the mitogenome sequences of *Ardeacarus ardeae* (KY352304; this study) and 15 other Acariformes species was constructed using PhyML 3.0 and MrBayes 3.2.3, respectively. The following mitogenome were used in this analysis: *Aleuroglyphus ovatus* (KC700022), *Caloglyphus berlesei* (KF499016), *Demodex brevis* (KM114225), *D. folliculorum* (KM114226), *Dermatophagoides pteronyssinus* (EU884425), *D. farinae* (NC013184), *Histiostoma blomquisti* (KX452726), *Leptotrombidium pallidum* (AB180098), *L. akamushi* (AB194045), *Panonychus citri* (HM189212), *Steganacarus magnus* (EU935607), *Unionicola foili* (EU856396) and *U. parkeri* (HQ386015); outgroup: *Eptrimerus sabinae* (KR604966) and *Phyllocoptes taishanensis* (KR604967).

and phylogenetic relationships of the feather mite groups in the order Sarcoptriformes.

Disclosure statement

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

References

- Dermauw W, Van Leeuwen T, Vanholme B, Tirry L. 2009. The complete mitochondrial genome of the house dust mite *Dermatophagoides pteronyssinus* (Trouessart): a novel gene arrangement among arthropods. *BMC Genomics*. 10:107.
- Gaud J. 1981. Acariens Sarcoptriformes plumicoles des oiseaux Ciconiiformes d'Afrique. 1. Introduction et parasites des Ardeidae. *Rev Zool Afr*. 95:806–828. French.
- Gaud J, Atyeo WT. 1996. Feather mites of the World (Acarina, Astigmata): the supraspecific taxa. *Annal Musée Royale Afrique Entrale Sciences Zoologiques*. 277:1–193 (text), 1–436 (illustrations).
- Klimov PB, Oconnor BM. 2009. Improved tRNA prediction in the American house dust mite reveals widespread occurrence of extremely short minimal tRNAs in acariform mites. *BMC Genomics*. 10:598.
- Lee C-C, Wang J. 2016. The complete mitochondrial genome of *Histiostoma blomquisti* (Acari: Histiostomatidae). *Mitochondrial DNA Part B*. 1:671–673.
- Mironov SV. 2003. On some problems in the systematics of feather mites. *Acarina*. 11:29.
- Proctor HC. 2003. Feather mites (Acari: Astigmata): ecology, behavior, and evolution. *Annu Rev Entomol*. 48:185–209.
- Song J-H, Kim S, Shin S, Min G-S. 2016. The complete mitochondrial genome of the mysid shrimp, *Neomysis japonica* (Crustacea, Malacostraca, Mysida). *Mitochondrial DNA A DNA Mapp Seq Anal*. 27:2781–2782.
- Xue X-F, Guo J-F, Dong Y, Hong X-Y, Shao R. 2016. Mitochondrial genome evolution and tRNA truncation in Acariformes mites: new evidence from eriophyoid mites. *Sci Rep*. 6:18920.