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MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of *Acanthosentis cheni* (Acanthocephala: Quadrigyridae)

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ABSTRACT

Acanthosentis cheni is a marine or brackish acanthocephalan found in fish. The complete mitochondrial genome of *A. cheni* (Acanthocephala: Quadrigyridae) is first sequenced. It is a circular molecule of 13,695 bp in size and consists of 12 protein-coding genes (PCGs), 20 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes. Except *tRNA-Gln*, all other mitochondrial genes were encoded on the heavy strand. The gene order and orientation of *A. cheni* mitogenome are basically identical to that of other acanthocephala. This study will facilitate the further research of the population genetics of this species and systematic analyses of the acanthocephala.

Acanthosentis cheni is a marine or brackish acanthocephalan found in fish. The complete mitochondrial genome of *A. cheni* (Acanthocephala: Quadrigyridae) is first sequenced. It is a circular molecule of 13,695 bp in size and consists of 12 protein-coding genes (PCGs), 20 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes. Except *tRNA-Gln*, all other mitochondrial genes were encoded on the heavy strand. The gene order and orientation of *A. cheni* mitogenome are basically identical to that of other acanthocephala. This study will facilitate the further research of the population genetics of this species and systematic analyses of the acanthocephala.

Acanthocephalans (thorny headed worms), which use vertebrates as definitive hosts and arthropods as intermediate hosts, are a small group of obligate endoparasites with a total of about 1200 species in the world (Kennedy 2006). *Acanthosentis cheni* is a marine or brackish acanthocephalan found in the anadromous fish *Coilia nasus* (Li et al. 2011). Despite the osmotic pressure is rather stable in the stomach and intestine of fish, it is difficult for endoparasites to survive for a long time in an environment of increased or decreased salinity (Möller 1978). However, Song et al. (2014) confirmed the samples from marine, brackish and fresh water are the same parasite *A. cheni* using the ITS gene. Here, the complete mitogenome of this species was first determined. *A. cheni* was dissected out under a microscope from intestines of *C. nasus* from Dongting Lake in Yueyang, Hunan province of China, with voucher number ACCN20160122. The accurate annotated mitochondrial genome sequence was submitted to GenBank with accession number KX108947.

The complete mtDNA is 13,695 bp in length and contains 12 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, which is similar to that of other acanthocephala (Gazi et al. 2012), but with only 20 transfer RNA (tRNA) genes while generally there are 22 tRNA in other acanthocephala (Gazi et al. 2012; Pan & Nie 2013; Gazi et al. 2016). The base composition of the complete mitochondrial genome was A (22.38%), C (10.01%), G (24.74%), T (42.87%), with an obvious AT bias (65.25%), as generally shown in other acanthocephalans' mitogenomes (Gazi et al. 2012; Pan & Nie 2013; Gazi et al. 2016). Except *tRNA-Gln*, all other mitochondrial genes were encoded on the heavy strand (H-strand). Six PCGs, *COX1*, *ND6*, *ND3*, *Cytb*, *COX2* and *ND2* start with GTG. Three other PCGs, *NAD4L*, *ND4* and *ND1* start with ATT, *ND5* and *COX3* with ATA, while *ATP6* with ATG as start codon. Six genes use complete stop codons, including four genes with TAG (*ND6*, *ND3*, *NAD4L* and *ND1*), two with TAG (*ATP6* and *Cytb*), whereas other six genes appear to end incomplete stop codons with T (*COX1*, *ND4*, *ND5*, *COX2*, *COX3*, and *ND2*). In 12 PCGs, the shortest one is *NAD4L* gene (249 bp) and the longest one is *ND5* (1,549 bp). The tRNAscan algorithm detected only two tRNA genes within the complete mitochondrial genome sequence. Additional putative tRNA genes were detected by searching by eye for the anticodon sequences and surrounding sequences for secondary structure. The 20 tRNA genes with the size ranging from 51 bp to 72 bp are interspersed along the whole genome. The sequence length of the *rrnL* and *rrnS* rRNA is 876 and 591 bp, respectively. The total length of the non-coding region (NCR) for *A. cheni* is 1,209 bp, which is composed of nine intergenic spacer sequences, ranging from 16 to 711 bp.

Based on the nine published mitogenome sequences of acanthocephala and an outgroup of Rotatoria *Philodina citrine*,
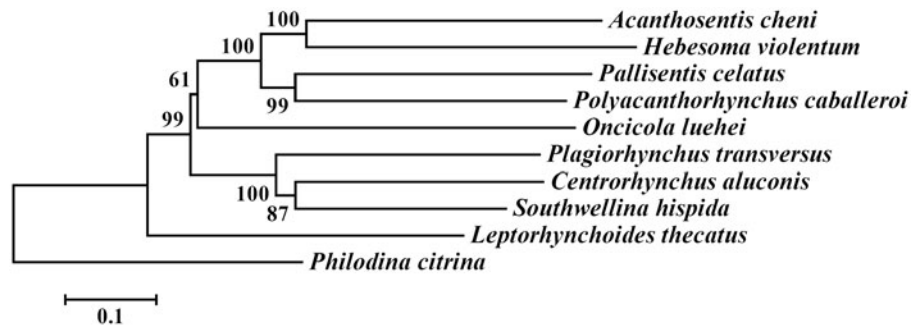
Figure 1. Phylogenetic tree generated using the NJ method based on 12 protein-coding genes for nine acanthocephala and one Rotatoria. *Acanthosentis cheni* (KX108947), *Southwellina hispida* (NC_026516.1), *Pallisentis celatus* (NC_022921.1), *Oncicola luehei* (NC_016754.1), *Plagiorhynchus transverses* (NC_029767.1), *Polyacanthorhynchus caballeroi* (NC_029766.1), *Centrorhynchus aluconis* (NC_029765.1), *Leptorhynchoides thecatus* (NC_006892.1), *Hebesoma violentum* (KC415004.1) and *Philodina citrine* (NC_019806.1).

a phylogenetic tree (Figure 1) was constructed using MEGA 6.0 (Tamura et al. 2013). Mitochondrial genome analyses based on MP, ML and NJ yielded identical phylogenetic trees, indicating a close phylogenetic affinity of nine species of acanthocephala and *P. citrine* (Figure 1). It appeared *A. cheni*, *Hebesoma violentum*, *Pallisentis celatus* which from Eoacanthocephala and *Polyacanthorhynchus caballeroi* formed a monophyletic group with the high bootstrap value (100%). The present study will facilitate the further research of the population genetics of this species and systematic analyses of the acanthocephala.

Disclosure statement

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

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References

Gazi M, Kim J, García-Varela M, Park C, Littlewood DTJ, Park JK. 2016. Mitogenomic phylogeny of acanthocephala reveals novel class relationships. Zool Scr. 45:437–454.

Gazi M, Sultana T, Min GS, Park YC, García-Varela M, Nadler SA, Park JK. 2012. The complete mitochondrial genome sequence of *Oncicola luehei* (Acanthocephala: Archiacanthocephala) and its phylogenetic position within Syndermata. Parasitol Int. 61:307–316.

Kennedy CR. 2006. Ecology of the Acanthocephala. Cambridge: Cambridge University Press. p. 249.

Li WX, Song R, Wu SG, Zou H, Nie P, Wang GT. 2011. Seasonal occurrence of helminths in the anadromous fish *Coilia nasus* (Engraulidae): parasite indicators of fish migratory movements. J Parasitol. 97:192–196.

Möller H. 1978. The effects of salinity and temperature on the development and survival of fish parasites. J Fish Biol. 12:311–323.

Pan TS, Nie P. 2013. The complete mitochondrial genome of *Pallisentis celatus* (Acanthocephala) with phylogenetic analysis of acanthocephalans and rotifers. Folia Parasitol (Praha). 60:181–191.

Song R, Li WX, Wu SG, Zou H, Wang GT. 2014. Population genetic structure of the acanthocephalan *Acanthosentis cheni* in anadromous, freshwater, and landlocked stocks of its fish host, *Coilia nasus*. J Parasitol. 100:193–197.

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol. 30:2725–2729.