Characterization of the complete mitochondrial genome of *Cyclosa japonica* (Araneae: Araneidae)

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**ABSTRACT**

The complete mitogenome of *Cyclosa japonica* (GenBank accession number MK512575) is 14,687 bp in length, containing 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes, and a putative control region. Its gene content and organization are identical with other spider mitogenomes. The overall base composition was as follows: A (35.61%), T (37.35%), C (10.87%), and G (16.18%), with an A + T bias (72.96%). Seven tRNAs (*trnM*, *trnW*, *trnK*, *trnE*, *trnF*, *trnH*, and *trnT*) lacked the TΨC arm stem, while two tRNAs (*trnS1* and *trnS2*) lacked the dihydrouracil (DHU) arm. Phylogenetic tree based on concatenated amino acid sequences of 13 PCGs shows that *C. japonica* is closely related to *Cyclosa argenteoalba*, which accord with morphological classification.

The orb-weaving spider, *Cyclosa japonica* (Araneae: Araneidae), is an important predator of several economical agricultural pests (Wang et al. 1996; Platnick 2015). This species is mainly distributed in China, Russia, Korea and Japan. These spiders weave small webs in paddy fields, trees, and tea bushes. In this study, adult individuals of *C. japonica* were collected from Maolan Nature Reserve in Libo country, Guizhou Province, China (E107°58′, N25°15′), and preserved in the spider specimen room of Guiyang University with an accession number GYU-GZML-14.

The complete mitogenome sequence of *C. japonica* is 14,687 bp in length and is deposited in GenBank under...

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Accession number MK512575. It harbors 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes (rrnL and rrnS), and a putative control region. The gene content and organization of *C. japonica* are identical with other spider mitogenomes (Li et al. 2016; Xu et al. 2019). Twenty-two genes were encoded on the major strand (J-strand), while others were transcribed on the minor strand (N-strand). The overall base composition was as follows: A (35.61%), T (37.35%), C (10.87%), and G (16.18%), with an A + T bias (72.96%). This mitogenome presented a negative AT-skew (-0.024) and a positive GC-skew (0.196).

The *C. japonica* mitogenome displays gene overlap in 28 bp in seven locations. The longest overlap is 16 bp in length and located between *cob* and *trnS2*. The intergenic spacer sequences were spread over 24 regions ranging in size from 1 to 39 bp. The 22 tRNAs had a total of 1297 bp, and their individual lengths ranged from 50 bp (trnC) to 67 bp (trnL2 and trnH). Nine tRNAs appear to be truncated and lack the potential to fold into the cloverleaf secondary structure. Seven of them (trnM, trnW, trnK, trnE, trnF, trnH, and trnT) lacked the TYC arm stem, and two tRNAs (trnS1 and trnS2) lacked the dihydrouracil (DHU) arm.

The *rrnL* and *rrnS* were located between *trnL1* and *trnQ* and separated by the *trnV*, with a length of 1017 and 684 bp, respectively. The control region was located between *trnQ* and *trnM* with a length of 1145 bp, and the A + T content was 69.26%. Three PCGs (cox3, nad6, and nad1) terminate with TAG, two PCGs (nad4 and nad4L) use T and the rest of the genes stop with TAA. Nine PCGs start with typical ATN start codons (ATA, ATT, and ATG), three genes (cox2, cox3, and nad6) use TTG and cox1 is initiated with TTA.

To validated with the phylogenetic position of *C. japonica*, a neighbor-joining phylogenetic tree was constructed using the concatenated amino acid sequences of 13 PCGs with MEGA6 (Tamura et al. 2013). The result showed that *C. japonica* is closely related to *Cyclosa argenteoalba* (Figure 1), which accord well with traditional morphological classification.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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