Complete mitochondrial genome and phylogenetic analysis of *Argiope perforata* (Araneae: Araneidae)

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**ABSTRACT**

The complete mitogenome of *Argiope perforata* (GenBank accession number MK512574) is 14,032 bp in length and contains 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes, and an A+T-rich region. ATT, ATA, TTA, TTG were initiation codons and TAA, TAG, and T were termination codons. Ten tRNAs (*trnD, trnW, trnL2, trnE, trnF, trnR, trnH, trnP, trnT, and trnL1*) lacked the TWC arm stem, while three tRNAs (*trnA, trnS1, and trnS2*) lost the dihydrouracil (DHU) arm. Phylogenetic tree based on 13 PCGs showed that *A. perforata* is closely related to *Neoscona theisi*, and clustered within Araneidae clade.

The orb-weaving spider *Argiope perforata* belongs to the genus of *Argiope*, which includes 81 known species around the world (Wang 1988; Platnick 2015). Most of these spiders often have a strikingly coloured abdomen and are important predators of insect pests (Levi 2004). In this study, adult species of *A. perforata* were collected from Maolan Nature Reserve in Libo country, Guizhou Province, China (N25°18′, E107°52′), and deposited in the spider specimen room of Guiyang University with an accession number GYU-GZML-13.

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(tRNAs), 2 ribosomal RNA genes (rrnL and rrnS), and an A+T-rich region. The gene order and orientation of *A. perforata* are consistent with those of other known spider mitochondomes (Li et al. 2016; Xu et al. 2019). Fifteen genes were transcribed on the minor strand (J-strand), while the others were encoded on the major strand (N-strand). The overall base composition of *A. perforata* is 35.30% for A, 9.65% for C, 38.90% for T, and 16.15% for G, with a high AT bias of 74.20%. The AT-skew and GC-skew of this genome were −0.049 and 0.252, respectively.

A total of 22 bp overlaps have been found at five gene junctions of *A. perforata* mitogenome, and the length of overlaps are ranging from 3 to 7 bp. There are 25 intergenic spacer sequences in a total of 208 bp with length varying from 1 to 26 bp and the largest intergenic spacer is located between *nad3* and *trnL*. The length of 22 tRNAs ranged from 52 bp (*trnA*) to 65 bp (*trnM*), A+T content ranged from 68.52% (*trnR*) to 83.61% (*trnC*). Thirteen tRNAs lack the potential to form the cloverleaf secondary structure. Ten of them (*trnW, trnD, trnL, trnE, trnF, trnR, trnH, trnP, trnT, and trnL*) lacked the TYC arm stem, three tRNAs (*trnA, trnS*, and *trnS*) lost the dihydrouracil (DHU) arm. The *rrnL* and *rrnS* genes are 1022 and 695 bp in length, with the A+T contents of 78.47 and 75.97%, respectively. The A+T-rich region of this mitogenome is 451 bp in length with an A+T content of 79.16% and located between *trnQ* and *trnM*.

Nine PCGs start with a typical ATN (ATT and ATA) codon, three genes (*cox2, cox3*, and *nad6*) start with TTG, and *cox1* uses TTA as initiation codon. Twelve PCGs terminate with conventional stop codons (TAA and TAG), while *nad4* uses incomplete codon (T) as termination codon. Based on the concatenated amino acid sequences of 13 PCGs, the neighbor-joining method was used to construct the phylogenetic relationship of *A. perforata* with 15 other spiders (Kumar et al. 2016). The result showed that *A. perforata* is closely related to *Neoscona theisi*, and clustered within Araneidae clade (Figure 1).

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This study was supported in part by the Special Funding of Guizhou Science and Technology Bureau and Guizhou University [GYU-KYZ-2019-02-08], the Program for First-class university Construction in Guizhou Province [2017158322], the National Natural Science Foundation of China [31760130], the Program for Academician workstation in Guizhou University [20195605], the Training Program for High-level Innovative Talents of Guizhou Province [20164020], and the Program for First-class Discipline Construction in Guizhou Province [201785].

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