Characterization of complete mitochondrial genome of *Evarcha coreana* (Araneae: Salticidae)

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**ABSTRACT**

The complete mitochondrial genome of a hunting spider *Evarcha coreana* was determined. The circular mitogenome is 14,333 bp in length (GenBank accession number MK381265), and contains 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA genes, and a putative control region. The orientation and gene order of *E. coreana* are identical with other spider mitogenomes. The AT content of the overall base composition is 75.86%. Twenty-two genes were in the major strand and 15 genes were in minor strand. Five intergenic regions and 25 reading frame overlaps were found in the mitogenome of *E. coreana*. Seven tRNA genes lost the dihydrouracil (DHU) arm. The control region is 697 bp in length with an A+T content of 81.06%. ATA, ATT, TTA, and TTT were initiation codons, and TAA, TAG, and T were termination codons. Phylogenetic analysis was performed using 13 PCGs with other spiders of the family Salticidae and it was seen that *E. coreana* is closely related to *Telamonia vlijmi* and *Plexippus paykulli*.

The hunting spider *Evarcha coreana* belongs to the genus of *Evarcha*, which includes approximately 85 species distributed across the world. These spiders predate mainly by hunting and are often found on shrubs and short plants in damp areas (Zabka 1985; Maddison and Hedin 2003). In this study, adult specimens of *E. coreana* were collected from Libo county, Guizhou Province, China (N25°20', E107°53'), and were stored in the spider specimen room of Guiyang University with an accession number GYU-GZML-25.

The complete mitogenome of *E. coreana* (GenBank accession number MK381265) is a typical closed-circular molecule of 14,333 bp in length. It contains the entire set of 37 genes, including 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rrnL and rrnS), and a putative control region (Boore 1999). The overall nucleotide composition was 35.02% of A, 15.16% of G, 40.84% of T, and 8.98% of C, with a total A+T content of 75.86% that is heavily biased toward A and T nucleotides. The AT-skew and GC-skew of this mitogenome were −0.077 and 0.256, respectively. Twenty-two genes were coded on the major strand (N-strand), whereas the others were oriented on the minor strand (U-strand). The orientation and gene order of *E. coreana* are identical with other spider mitogenomes (Xu et al. 2019; Yang et al. 2019).

Gene overlaps in the *E. coreana* mitogenome were found at 25 gene junctions and involved a total of 244 bp. The longest overlap is 42 bp in length and situated between *tmW* and *trnY*. There are five intergenic spacer sequences in a total of 87 bp with length varying from 3 to 65 bp and the largest intergenic spacer is located between *trnN* and *trnA*. The length of 22 tRNAs ranged from 51 bp (*trnC*) to 69 bp (*trnY*), and nine of them were encoded on the N-strand. Ten tRNAs lack the potential to form the cloverleaf-shaped secondary structure. Seven of them (*trnC*, *trnD*, *trnG*, *trnR*, *trnF*, *trnP*, and *trnL*), the TΨC arm stems, three tRNAs (*trnA*, *trnS1*, and *trnS2*) lost the dihydrouracil (DHU) arm. Two rRNAs have been identified on the N-strand, the *rrnL* gene locates between *trnL1* and *trnV*, and the *rrnS* gene between *trnV* and *trnQ*. The length of *rrnL* and *rrnS* is 1009 bp and 690 bp, and their A+T content is 79.58% and 78.41%, respectively. The control region of this mitogenome is 697 bp in length with an A+T content of 81.06%, and located between the *trnQ* and *trnM* genes.

In the mitogenome of *E. coreana*, the total length of 13 PCGs is 10,787 bp, which accounts for 75.26% of the total genome. The A+T content of the 13 PCGs ranged from 70.87% (cox3) to 85.90% (atp8). The *cox1* and *cob* initiated with TTA as the start codon, *cox2* and *cox3* began with TTG, *nad2*, *atp6*, *nad4*, *nad4L*, *nad5*, and *nad6* started with ATA, and remaining three PCGs started with ATT. Nine PCGs including *cox1*, *cox2*, *cox3*, *atp6*, *atp8*, *nad3*, *nad5*, *nad6*, and *cob* are terminated with TAA as stop codon, *nad1* and *nad2* end with TAG, *nad4* and *nad4L* end with a single T residue. We analyzed the amino acid sequences of 13 PCGs with
neighbor-joining method to reveal the phylogenetic relationship of *E. coreana* with other spiders in family Salticidae. The result showed that *E. coreana* formed a clade with *Telamonia vlijmi* and *Plexippus paykulli* (Figure 1).

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Figure 1.** The neighbor-joining phylogenetic tree of *Evachra coreana* and other spider in Salticidae. *Tetranychus urticae* was used as an outgroup. GenBank accession numbers of each species were listed in the tree.