

Characterization of the mitochondrial genome of *Arge bella* Wei & Du sp. nov. (Hymenoptera: Argidae)

INTRODUCTION

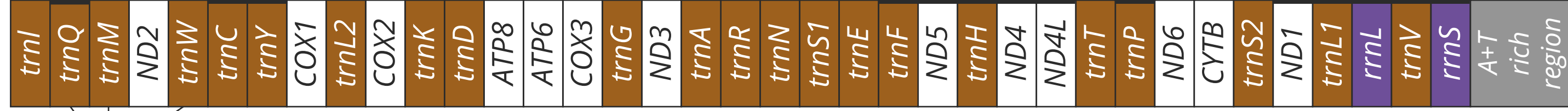
We describe *Arge bella* Wei & Du sp. nov., a large and beautiful species of Argidae from south China, and report its mitochondrial genome based on high-throughput sequencing data. We present the gene order, nucleotide composition of protein-coding genes (PCGs), and the secondary structures of RNA genes.

The nearly complete mitochondrial genome of *A. bella* has a length of 15,576 bp and a typical set of 37 genes (22 tRNAs, 13 PCGs, and 2 rRNAs). Three tRNAs are rearranged in the *A. bella* mitochondrial genome as compared to the ancestral type in insects: *trnM* and *trnQ* are shuffled, while *trnW* is translocated from the *trnW-trnC-trnY* cluster to a location downstream of *trnI*. All PCGs are initiated by ATN codons, and terminated with TAA, TA or T as stop codons.



Mitochondrial genome organisation of *A. bella*

Ancestral type

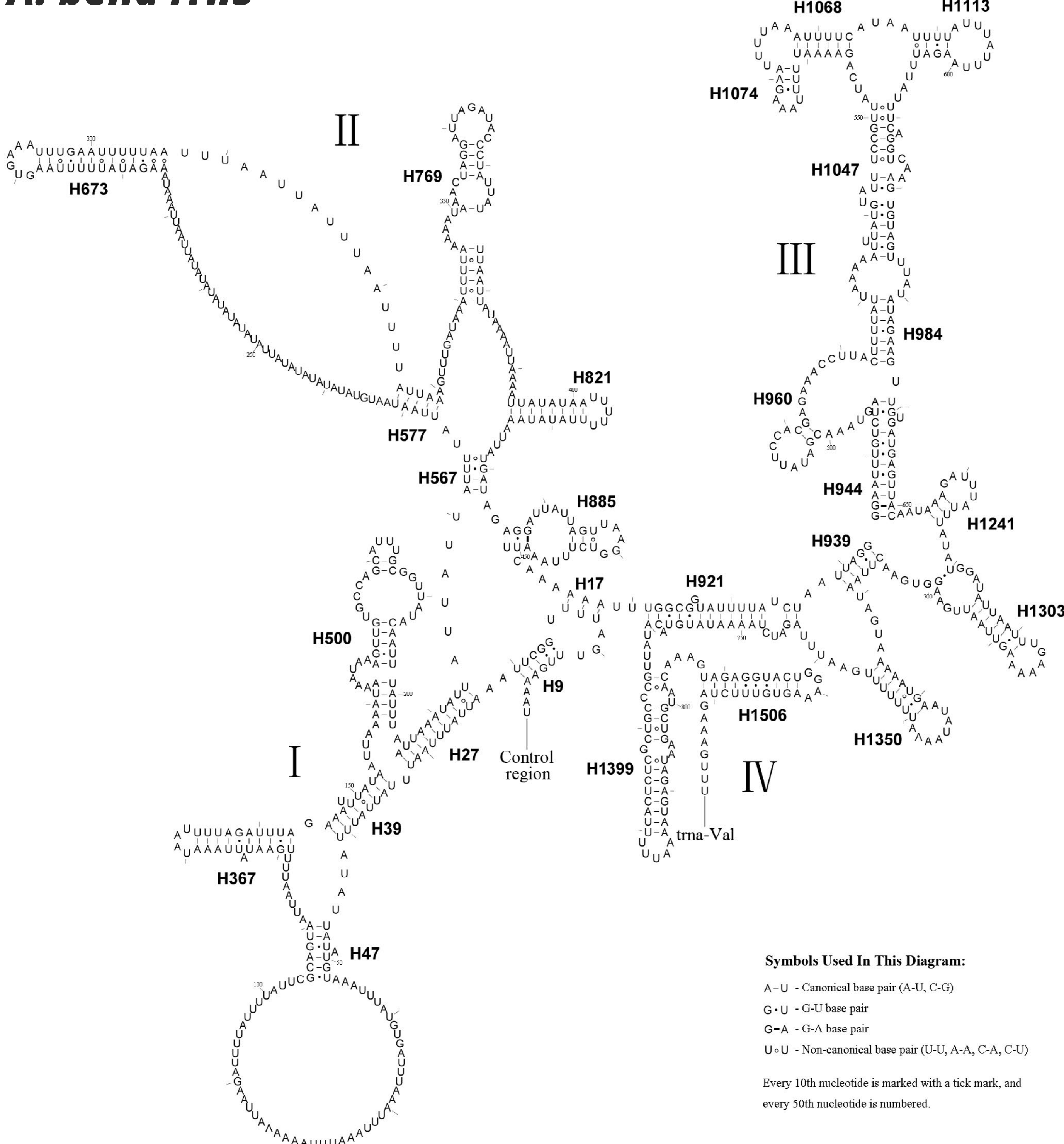


Arge bella



All tRNAs have a typical cloverleaf secondary structure, except for *trnS1*. H821 of *rrnS* and H976 of *rrnL* are redundant.

A. bella *rrnS*

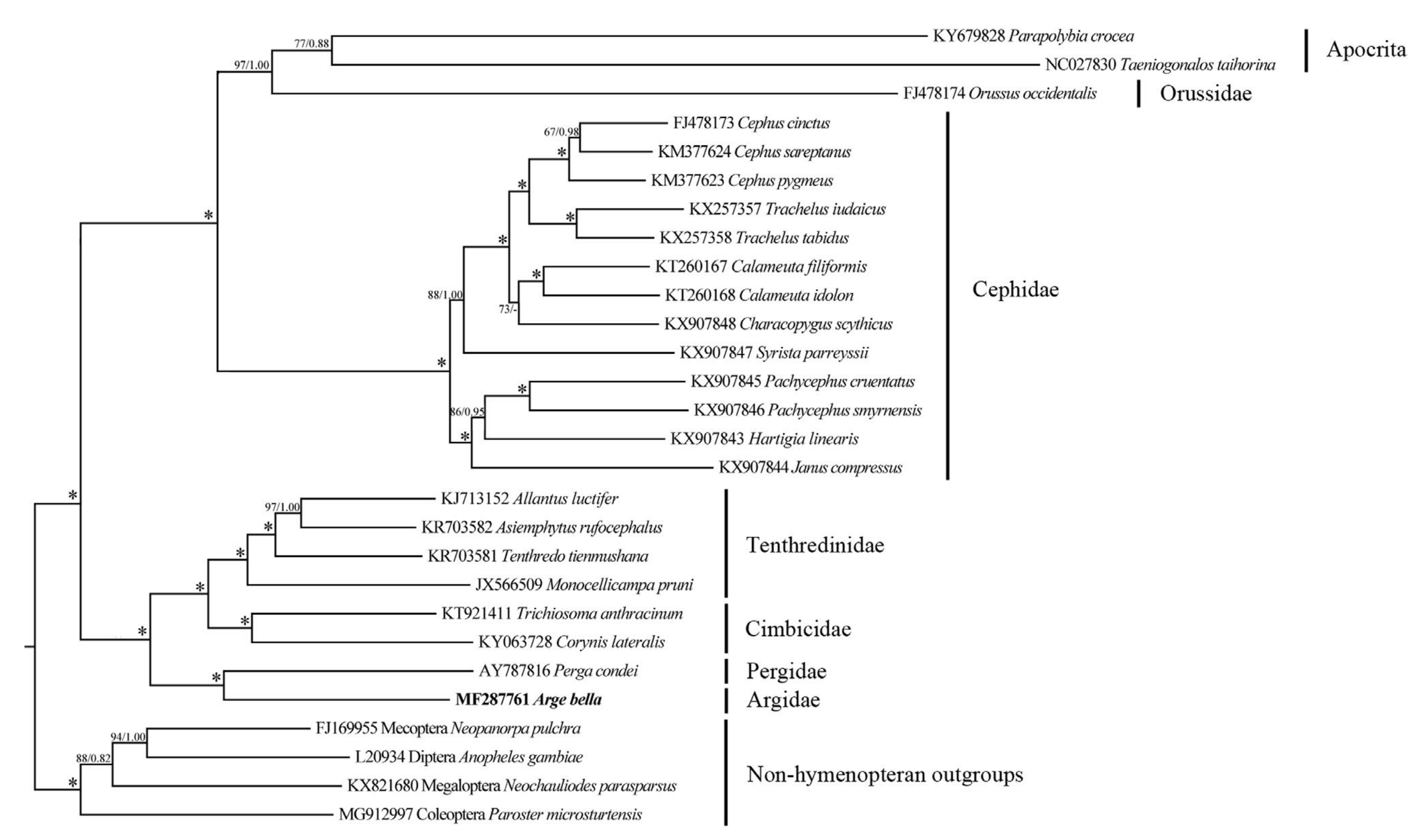


Symbols Used In This Diagram:
 A-U - Canonical base pair (A-U, C-G)
 G-U - G-U base pair
 G-A - G-A base pair
 U-U - Non-canonical base pair (U-U, A-A, C-A, C-U)
 Every 10th nucleotide is marked with a tick mark, and every 50th nucleotide is numbered.

A phylogenetic analysis based on mitochondrial genome sequences of *A. bella*, 21 other symphytan species, two apocritan representatives, and four outgroup taxa supports the placement of Argidae as sister to the Pergidae within the symphytan superfamily Tenthredinoidea.

Phylogenetic tree of Symphyta and selected apocritan and outgroup taxa

based on a Maximum-likelihood analysis of sequence data from 13 PCGs and 2 rRNA genes.



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