

MICRO-INTERNSHIP

The complete mitochondrial genome of the strawberry aphid *Chaetosiphon fragaefolii* Cockerell, 1901 (Hemiptera: Aphididae) from California, USA

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The aphid *Chaetosiphon fragaefolii* Cockerell, 1901 is an agricultural pest and known vector of strawberry viruses. To better understand its biology and systematics, we performed a genomic analysis on *C. fragaefolii* collected from Quinalt strawberry plants from Pacific Grove, Monterey county, California, USA using Oxford Nanopore and Illumina sequencing. The resulting data was used to assemble the aphids complete mitogenome. The mitogenome of *C. fragaefolii* is 16,108 bp

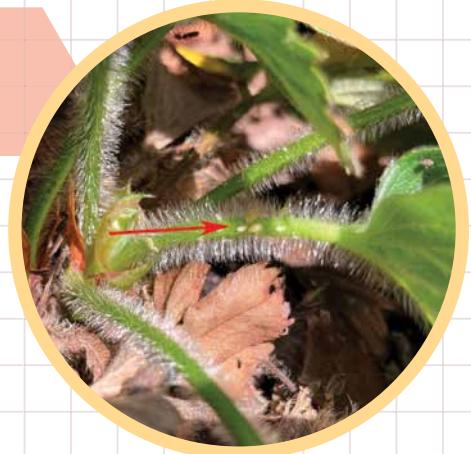
in length and contains 2 rRNA, 13 protein-coding, and 22 tRNA genes. The mitogenome is similar in content and organization to other Aphididae. Phylogenetic analysis of the *C. fragaefolii* mitogenome resolved it in a fully supported clade in the tribe Macrosiphini. Analysis of the cox1 barcode sequence of *C. fragaefolii* from California found exact and nearly identical sequences to *C. fragaefolii* and *C. thomasi* Hille Ris Lambers, 1953, suggesting the two species are conspecific.

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Chaetosiphon fragaefolii growing on a strawberry plant. The arrow indicates the specimens analyzed in this study.

