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MITOGENOME ANNOUNCEMENT



The complete mitochondrial genome of the kelp fly *Fucellia costalis* (Diptera: Anthomyiidae) from Pacific Grove, California

Hartnell College Genomics Group^{*}, Ivan D. Agudelo^a, Karina Almanza^a, Maria Guadalupe Altamirano Manriquez^a, Paulina Andrade^a, Eduardo Anguiano^a, Sandra Ayala^a, Dominic Barrios^a, Lyric Batistiana^a, Kruthi Battar^a, Daisy Noemi Benavides^a, Rafaela Chavez^a, Yosselin Cuevas^a, Neovid C. Cuevas^a, Rogelio De Jesus Garcia^a, Maria E. Diaz^a, Jamileth Figueroa^a, Martin Flores^a, Aaron Galvan^a, Yazmin Garcia^a, Christian Gonzalez Balcazar^a, Gabriel Guerrero^a, Maiya R. Harper^a, Tania Hernandez^a, Jeffrey Y. Honda^b, Jeffery R. Hughey^a, Victoria N. Hutchins^a, Raul Rodrigo Lazaro Olivera^a, Evelyn Macias Reyes^a, Isela M. Magallon^a, Adrian J. Maldonado^a, Dayana Maravillo Sanchez^a, Lauryn Martinez^a, Christian Mendoza^a, Antonio Mendoza^a, Jason Montoya^a, Prashant P. Naidu^a, Alexis Novoa^a, Natalie M. Ortega^a, David Ortiz^a, Anastacia M. Paredes^a, Eduardo Perez Solis^a, Abbey A. Plascencia^a, Alejandra N. Ponce^a, Alicia E. Ramirez^a, Maria F. Ramirez^a, Sergio Rodriguez^a, Rosa A. Sanchez^a, Nia N. Serrano^a, Francisco D. Solano^a, Daniel Soto^a, Alicia Steinhardt^a, Maria O. Taveras Dina^a, Alejandra L. Tong^a, Brenda J. Torresillas^a, Rolando Valdez^a, Paola Vidales Villicana^a, Adrian Zamora^a and Frances L. Wong^a

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ABSTRACT

Genomic analysis of the kelp fly *Fucellia costalis* (Family Anthomyiidae) from Asilomar beach, Pacific Grove, California, resulted in the assembly of its complete mitogenome. The mitogenome is 16,175 bp in length, A + T biased (78.1%), contains 37 genes, a large 1356 bp control region, and has a high-level of gene synteny to other Muscoidea. Phylogenetic analysis of *F. costalis* fully resolves it in a clade with two members of the Anthomyiidae, *Delia platura* (8.2% pairwise genetic distance) and *D. antiqua* (9.2% distance), in a sister position to *Scathophaga stercoraria* (7.8% distance) from the Scathophagidae. The phylogenetic position and genetic distances of *F. costalis* support the continued recognition of the subfamily Fucellinae. This identification and data extends the distributional range of *F. costalis* northward from California to Vancouver Island, Canada.

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The Dipteran family Anthomyiidae consists of approximately 1100 species that occur worldwide and inhabit a diversity of habitats including seashores, gardens, woods, open fields, and alpine meadows (Huckett 1971; Couri and Rodrigues-Júnior 2012). A single complete mitogenome was published for the family of *Delia antiqua*, subfamily Anthomyiinae (Zhang et al. 2015). Here, we describe the mitogenome of a kelp fly collected from Asilomar beach, Pacific Grove, California (36°37'43.2"N, -121°55'17.5"W), *Fucellia costalis*, an abundant swarming Dipteran and the largest of 26 species in *Fucellia*, subfamily Fucellinae (Aldrich 1918; Cole 1969).

DNA was extracted from *F. costalis* (Specimen Voucher-Hughey, 17 September 2016, J. Gordon Edwards Museum, San Jose State University) following the protocol of Lindstrom et al. (2011). The 76 and 150 bp paired-end Illumina library constructions and sequencing were performed by myGenomics, LLC (Alpharetta, GA). The mitogenome was assembled using default de novo settings in MEGAHIT (Li et al. 2015). The single gap that resulted was

closed using standard PCR and Sanger sequencing methods (Lindstrom et al. 2011) with the following primers: F/d-loop 5'-GTTCACTAATAAGATTAATAGATATC-3' and R/trnMet 5'-GATTAGAACCTTTATAAATGGGG-3'. The genes were annotated manually by aligning the *F. costalis* mitogenome to *Scathophaga stercoraria* (GenBank accession KM200724) in Geneious R11 (Biomatters Limited, Auckland, New Zealand). Alignment of *F. costalis* to other complete Muscoidea mitogenomes was accomplished with MAFFT (Katoh and Standley 2013). The Maximum-likelihood analysis was executed using RaxML in Trex-online (Boc et al. 2012) with the GTR + gamma model and 1000 bootstraps. The tree was visualized with TreeDyn 198.3 at Phylogeny.fr (Dereeper et al. 2008).

The mitogenome of *F. costalis* (GenBank accession number MH823369) is 16,175 bp in length and A + T rich with base a composition of 40.0% A, 38.1% T, 9.4% G, and 12.5% C. It is similar in length, content, and gene organization to other Muscoidea (Ding et al. 2015; Zhang et al. 2015; Li et al. 2016). The mitogenome contains 22 tRNA (*trnL* and *trnS* are

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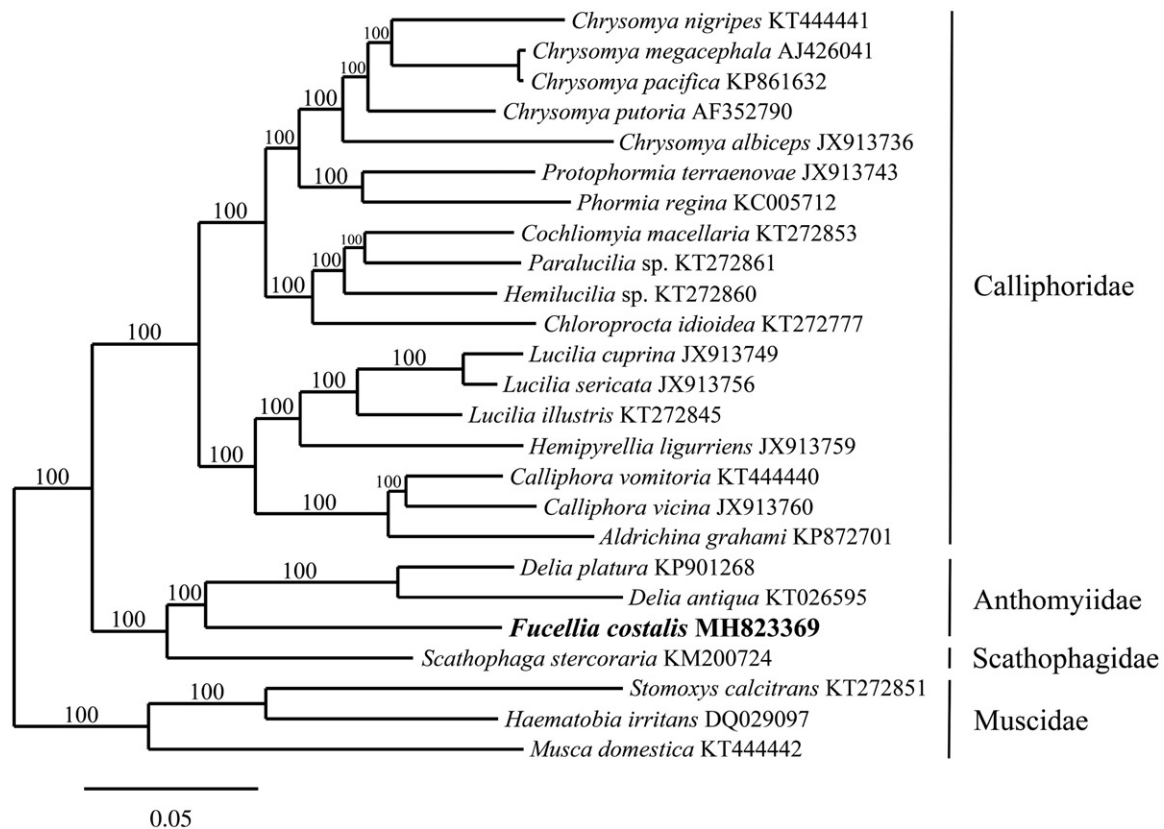


Figure 1. Maximum-likelihood phylogram of *Fucellia costalis* and related Diptera. Numbers along branches are RaxML bootstrap supports based on 1000 replicates. The legend below represents the scale for nucleotide substitutions.

duplicated), two rRNA (*rrnL*, *rrnS*), 13 genes involved in electron transport and oxidative phosphorylation, and a control region that is 1356 bp in length. Six of the coding genes are initiated with the ATG codon (*ATP6*, *COII*, *COIII*, *CytB*, *ND4*, *ND4L*), four with ATT (*ATP8*, *ND2*, *ND5*, *ND6*), two with ATA (*ND1*, *ND3*), and one with ATC (*COI*). Nine of the coding genes terminate with the stop codon TAA, however *COI*, *COII*, *ND4*, and *ND5* terminate with the incomplete codon T. Eight tRNAs, *ND1*, *ND4*, *ND4L*, *ND5*, and the two rRNAs encode on the light-strand, with the remaining genes encoding on the heavy-strand. Phylogenetic analysis of the *F. costalis* mitogenome resolves it in a fully supported clade with *Delia platura* (8.2% pairwise genetic distance) and *D. antiqua* (9.2% distance) (subfamily Anthomyiidae), sister in position to *Scathophaga stercoraria* (7.8% distance) (Figure 1). A BLAST search of the *F. costalis* mitogenome found a single genetic match of an unidentified Anthomyiid from Vancouver Island (COI GenBank accession JF867328), extending the known distribution of *F. costalis* from California to Canada.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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