Full Mitochondrial Genome Sequence of the Sugar Beet Wireworm *Limonius californicus* (Coleoptera: Elateridae), a Common Agricultural Pest

Alida T. Gerritsen, a, Daniel D. New, a Barrie D. Robison, a, b Arash Rashed, a, b Paul Hohenlohe, a, b Larry Forney, a, b Mahnaz Rashidi, c Cathy M. Wilson, d Matthew L. Settles **a**

Institute for Bioinformatics and Evolutionary Studies (IBEST), University of Idaho, Moscow, Idaho, USA; Department of Biological Sciences, University of Idaho, Moscow, Idaho, USA; Department of Plant, Soil and Entomological Sciences, University of Idaho Aberdeen R&E Center, Aberdeen, Idaho, USA; Idaho Wheat Commission, Boise, Idaho, USA.

* Present address: Matthew L. Settles, University of California Davis, Davis, California, USA.

We report here the full mitochondrial genome sequence of *Limonius californicus*, a species of click beetle that is an agricultural pest in its larval form. The circular genome is 16.5 kb and contains 13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes.

**Received 25 November 2015. Accepted 28 November 2015. Published 21 January 2016.**

**Citation** Gerritsen AT, New DD, Robison BD, Rashed A, Hohenlohe P, Forney L, Rashidi M, Wilson CM, Settles ML. 2016. Full mitochondrial genome sequence of the sugar beet wireworm *Limonius californicus* (Coleoptera: Elateridae), a common agricultural pest. Genome Announc 4(1):e01628-15. doi:10.1128/genomeA01628-15.

**Copyright** © 2016 Gerritsen et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

**Address correspondence to Alida T. Gerritsen, alida@uidaho.edu.**

Wireworms are the larval stage of click beetles (Coleoptera: Elateridae), of which several species are serious pests due to their damage to the seedlings, roots, and stem tissues of economically important crops (1, 2). The sugar beet wireworm *Limonius californicus* (Mannerheim) is a significant threat to cereal and potato production in the Pacific Northwest region of the United States. Control methods for larvae were developed in the 1950s and involved the widespread application of environmentally persistent chemicals, such as dichlorodiphenyltrichloroethane (DDT) and γ-hexachlorocyclohexane (Lindane) (3), both of which were later banned for use and are not used on crops today due to health and environmental risks. Although current broad-spectrum insecticides, such as neonicotinoids, induce morbidity, wherein the larvae become sick and stop feeding for a period, they subsequently survive to feed and eventually reproduce (3, 4). Constructing a genetic reference for this pest is not only the first step in creating more targeted control methods but also essential in understanding how populations evolve resistance in response to pesticides.

A single specimen of *L. californicus* was collected on 10 December 2014 from a farmer’s field in Aberdeen, ID, at a 6-inch depth into the soil. The specimen species was confirmed on site, and DNA extraction was conducted using cetyltrimethylammonium bromide (CTAB) methodology. The DNA was sheared to 800-bp average fragment length, and library preparation was performed on the Apollo 324 platform. Reads were sequenced on an Illumina MiSeq with paired-end 300-bp lengths at the University of Idaho’s IBEST Genomics Resources Core; sequencing of the library resulted in 160× coverage of the mitochondrial genome.

Following sequencing, reads were processed using a custom bioinformatics pipeline to remove duplicate reads, trim off low-quality bases and sequence adapters from the read ends, and overlap pairs using FLASH (GitHub) (3). The mitochondrial genome was then assembled using the ARC software package (GitHub), which uses a mapping reference to seed for iterative assemblies. The *Elateridae* species (Coleoptera: Elateridae; accession number KF961574) mitochondrial genome sequence was used to initially seed the ARC assembly.

Following assembly, NCBI BLAST was used to identify a large set of related mitochondrial sequences from coleopteran species and assemble a tree using FastTree (6). Gene annotations were predicted from the MITOS Web server (7); annotations and open reading frames (ORFs) were later refined and confirmed by constructing a custom BLAST database in Geneious 8.0 (8) from the reference species list. A total of 51 species were compared to the *L. californicus* assembly, with *Chaetosoma scaritides* (Coleoptera: Chaetosomidae; accession no. NC_011324) identified as the closest sequence.

The mitochondrial DNA (mtDNA) genome of *L. californicus* is a circular DNA molecule of 16,783 bp, with a G+C content of 29.5%. Predicted annotations from both Geneious and the MITOS server include common respiratory genes (*atp6, atp8, cob, cox1, cox2, cox3, nad1, nad2, nad3, nad4, nad4l, nad5, and nad6*), 2 rRNA genes (large and small subunits), and 22 tRNA genes. This full mtDNA genome sequence is an important first step in assessing the genetic variation within this pest species and developing targeted control methods.

**Nucleotide sequence accession number.** The mtDNA genome sequence is deposited in GenBank with accession number KT852377.

**ACKNOWLEDGMENTS**

This work was supported by NIH grants to Larry Forney for COBRE III PAR-10-196 and RFA-RR-09-005.

We thank the Idaho Wheat Commission for their support and interest in the project and David Streett for work on bioinformatics applications.
REFERENCES

1. Toba HH, Campbell JD. 1992. Wireworm (Coleoptera: Elateridae) survey in wheat-growing areas of northcentral and northeastern Oregon. J Entomol Soc Brit Columbia 89:25–30.

2. Benefer CM, van Herk WG, Ellis JS, Blackshaw RP, Vernon RS, Knight ME. 2012. The molecular identification and genetic diversity of economically important wireworm species (Coleoptera: Elateridae) in Canada. J Pest Sci 86:19–27.

3. Morales-Rodriguez A, Wanner KW. 2015. Efficacy of thiamethoxam and fipronil, applied alone and in combination, to control Limonius californicus and Hypnoidus bicolor (Coleoptera: Elateridae). Pest Manag Sci 71:584–591. http://dx.doi.org/10.1002/ps.3877.

4. Van Herk WG, Vernon RS, Tolman JH, Saavedra HO. 2008. Mortality of a wireworm, Agriotes obscurus (Coleoptera: Elateridae), after topical application of various insecticides. J Econ Entomol 102:375–383.

5. Magoč T, Salzberg SL. 2011. FLASH: fast length adjustment of short reads to improve genome assemblies. Bioinformatics 27:2957–2963. http://dx.doi.org/10.1093/bioinformatics/btr507.

6. Price MN, Dehal PS, Arkin AP. 2010. FastTree 2–approximately maximum-likelihood trees for large alignments. PLoS One 5:e9490. http://dx.doi.org/10.1371/journal.pone.0009490.

7. Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol 69:313–319. http://dx.doi.org/10.1016/j.ympev.2012.08.023.

8. Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647–1649. http://dx.doi.org/10.1093/bioinformatics/bts199.