The complete mitochondrial genome of the New Zealand parasitic blowfly *Lucilia sericata* (Insecta: Diptera: Calliphoridae).

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ABSTRACT

In the present study, the complete mitochondrial genome of the New Zealand parasitic blowfly *Lucilia sericata* (green bottle blowfly) field strain NZ_LucSer_NP was generated using next-generation sequencing technology. The length of complete the mitochondrial genome is 15,938 bp, with 39.4% A, 13.0% C, 9.3% G, and 38.2% T nucleotide distribution. The complete mitochondrial genome consists of 13 protein-coding genes, two ribosomal RNAs, 22 transfer RNAs, and a and a 1,124 bp non-coding region, similar to most metazoan mitochondrial genomes. Phylogenetic analysis showed that *L. sericata* NZ_LucSer_NP forms a monophyletic cluster with the remaining six *Lucilia* species and the Calliphoridae are polyphyletic. This study provides the first complete mitochondrial genome sequence for a *L. sericata* blowfly species derived from New Zealand to facilitate species identification and phylogenetic analysis.

KEYWORDS: Diptera, Calliphoridae, Luciliinae, complete mitochondrial genome, *Lucilia sericata*.

Members of the Calliphoridae (blowflies) are important for medical and veterinary management. The large and highly variable mitochondrial (mt) genomes of blowflies are ideal sources of molecular markers suitable for studying population genetic structures and evolution.

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Lucilia sericata NZ_LucSer_NP was selected for genome sequencing as a representative of an NZ field strain of *L. sericata*.

The *L. sericata* specimen was collected from the Palmerston North area (40°21.3′ S, 175°36.7′ E), and is stored and available upon request from AgResearch Ltd., Grasslands Research Centre (accession number: NPY120886). High molecular weight genomic DNA was isolated from entire *L. sericata* adult males using a modified phenol:chloroform protocol explained in our previous articles (Palevich et al. 2019a; Palevich et al. 2019b; Palevich et al. 2019d). The Illumina NovaSeq™ 6000 (PE150, Novogene, China) platform was used to amplify the entire mitochondrial genome sequence (BioProject ID: PRJNA667961, GenBank accession number: MW123004). The mitochondrial genome was assembled and annotated and previously described (Palevich et al. 2019c; Palevich et al. 2019e; Palevich et al. 2020).

The mitogenome (15,938 bp) is standard in size and comparable to other *L. sericata* strains and isolates (Nelson et al. 2012). For example: genes are transcribed in both directions, it contains 13 protein-coding genes (PCGs), two rRNAs, 22 tRNAs and an AT-rich region (1,124 bp). Among these 23 are located on the heavy strand with the remaining 14 genes located on the light strand, consistent with other *Lucilia* species AJ422212, JX913758, and JX913744 (Stevens JR et al. 2008; Nelson et al. 2012) and isolates. The studied genome has a high T content (38.2 %) and a low G content (9.3 %), resulting in a very strong A+T bias (77.7 %) and in particular the AT-rich region (90.1 %). Gene order, sizes and all common organization features are relatively conserved among the blowfly and fly mitogenomes (usually 14.5-19.6 kb) (Stevens J et al. 2001; Stevens JR 2003; Stevens JR et al. 2006).

The phylogenetic position of *L. sericata* NZ_LucSer_NP was estimated using maximum-likelihood, implemented in RAxML version 8.2.11 (1,000 bootstrap replications) (Stamatakis 2014), and the Bayesian inference (BI), implemented in MrBayes version 3.2.6 (default settings, four MCMC chains) (Huelsenbeck et al. 2001) approaches. Complete mitogenome

sequences of 27 available blowfly species were retrieved from GenBank and phylogenetic analyses performed on the concatenated mitochondrial PCGs and rRNA genes (Figure 1). Within the Calliphoridae, *L. sericata* NZ_LucSer_NP formed a monophyletic cluster with the remaining Luciliinae species, there was also strong support for the sister-grouping of Calliphorinae with Luciliinae. Overall, the dendrogram topology is highly congruent with the previous results of Nelson et al. (2012). In the pursuit of improving the phylogenetic resolution within the phylum Calliphoridae, future efforts should focus on the availability of more complete mitogenomes across all blowfly species, and especially for different strains/isolates.

Disclosure statement

No potential conflict of interest was reported by the authors.

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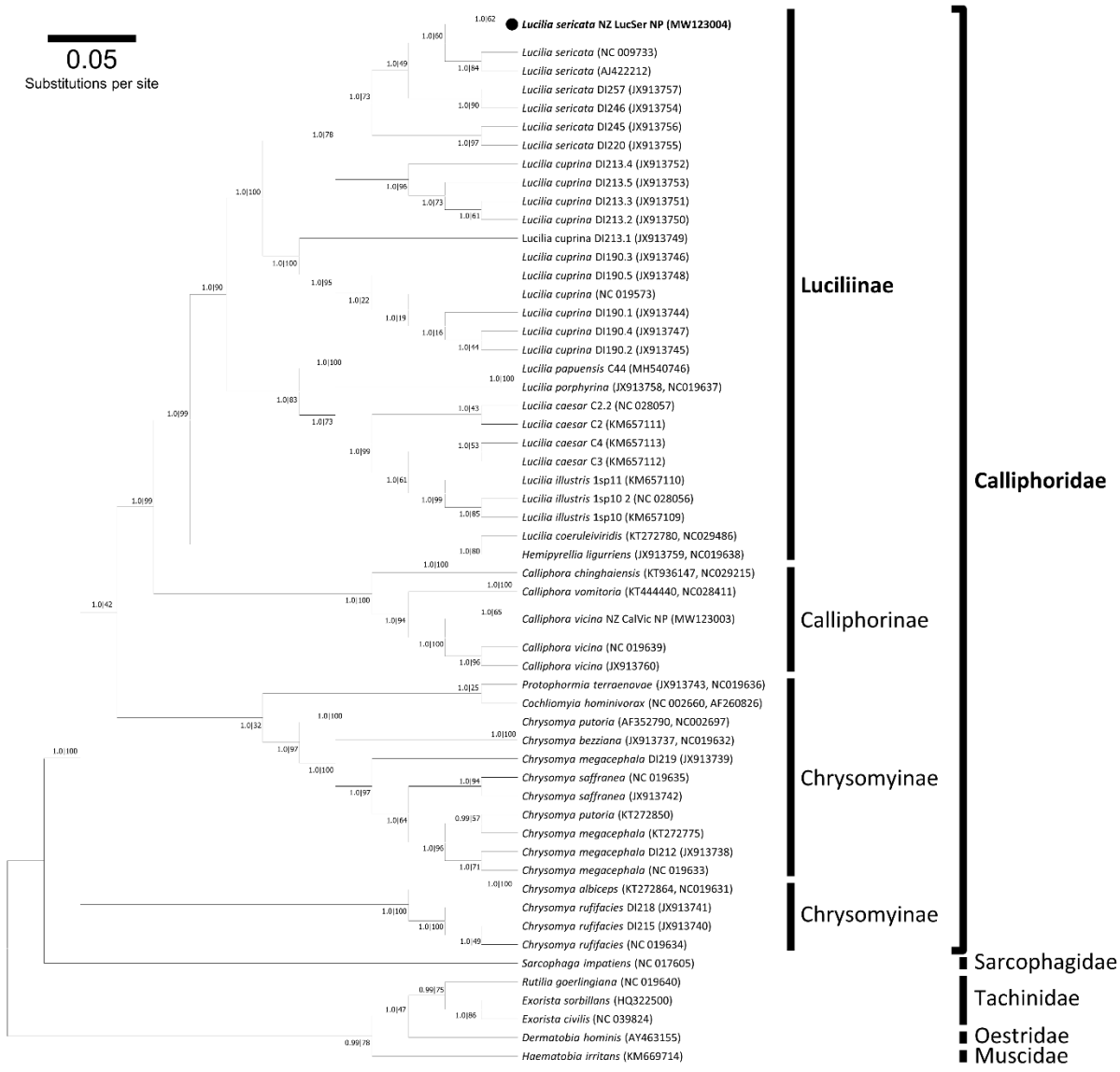

Figure 1. A summary of the molecular phylogeny of the Calliphoridae complete mitochondrial genomes. The evolutionary relationship of *Lucilia sericata* field strain NZ_LucSer_NP (black circle) was compared to the complete mitochondrial genomes of 67 blowfly species or isolates retrieved from GenBank (accession numbers in parentheses) and nucleotide sequences of all protein-coding genes were used for analysis. Phylogenetic analysis was conducted using the Bayesian approach implemented in MrBayes version 3.2.6 (Huelsenbeck et al. 2001) and maximum likelihood (ML) using RAxML version 8.2.11 (Stamatakis 2014). The mtREV with Freqs. (+F) model was used for amino acid substitution and four independent runs were performed for 10 million generations and sampled every 1,000 generations. For reconstruction, the first 25% of the sample was discarded as burnin and visualized using Geneious Prime (Kearse et al. 2012). Nodal support is given: Bayes posterior probabilities|RAxML bootstrap percentage. The phylogram provided is presented to scale (scale bar = 0.05 estimated number of substitutions per site) with the species *Haematobia irritans* from the family Muscidae used as the outgroup.