


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

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### ABSTRACT

In this study, the complete mitochondrial (mt) 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 mt genome is 15,938 bp, with 39.4% A, 13.0% C, 9.3% G, and 38.2% T nucleotide distribution. The complete mt genome consists of 13 protein-coding genes (PCGs), two ribosomal RNAs, 22 transfer RNAs, and a 1124 bp non-coding region, similar to most metazoan mt 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 mt genome sequence for a *L. sericata* blowfly species derived from New Zealand to facilitate species identification and phylogenetic analysis.

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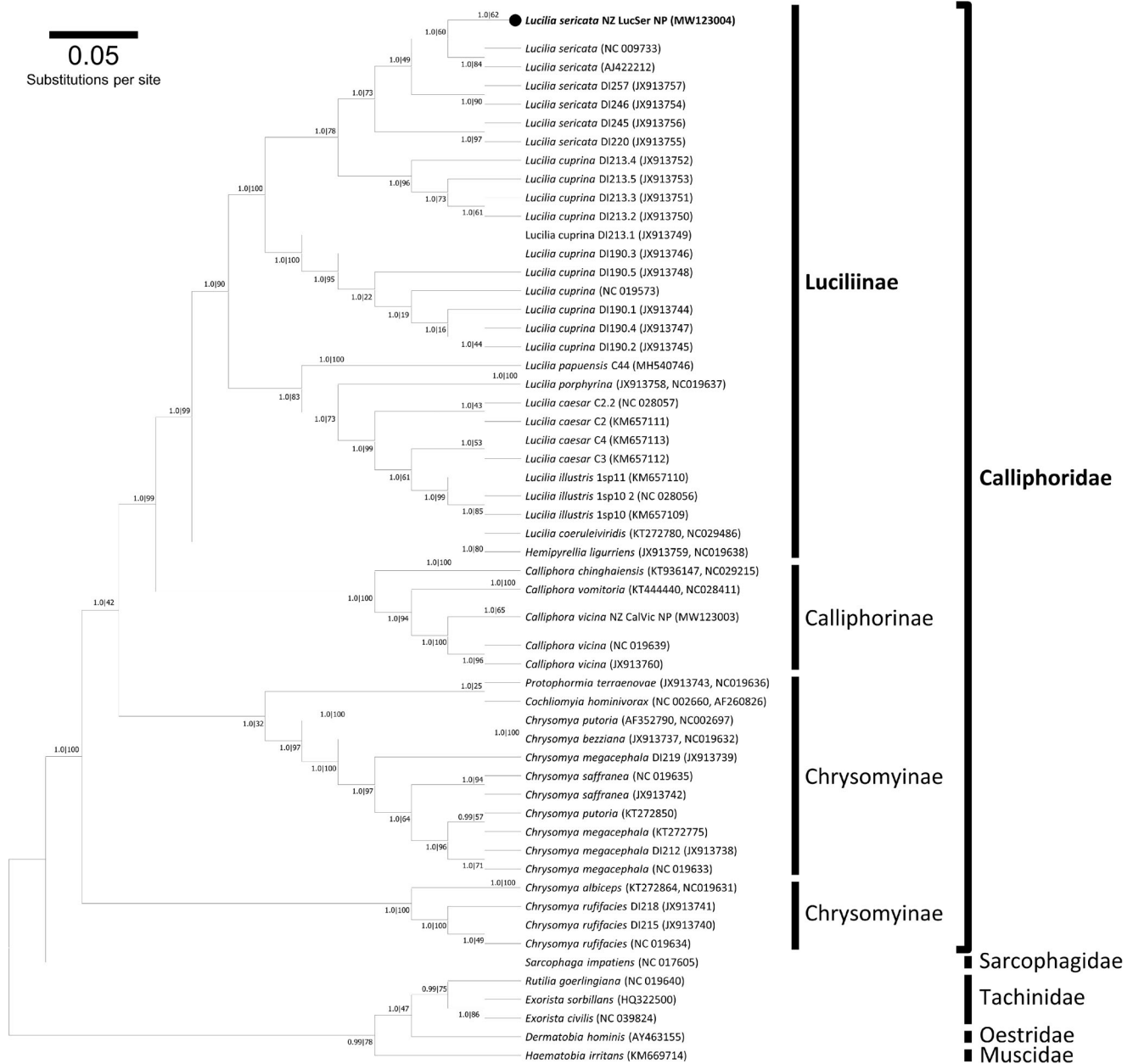
Members of the Calliphoridae (blowflies) are important for medical and veterinary management. The large and highly variable mitochondrial (mt) genomes of blowflies are ideal sources of molecular markers suitable for studying population genetic structures and evolution. *Lucilia sericata* (Meigen) NZ\_LucSer\_NP was selected for genome sequencing as a representative of an NZ field strain of *L. sericata*. The *L. sericata* NZ\_LucSer\_NP mitogenome resource will facilitate investigation of phylogenomic relationships of both species- and strain-level diversity among Calliphoridae. In addition, future comparative studies exploring the features of other available representative mitogenomes derived from Australia may shed light on the evolutionary provenance 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 Center (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, Kelly, Ganesh, et al. 2019; Palevich, Kelly, Leahy, et al. 2019; Palevich et al. 2019b). Genomic DNA was prepared for whole-genome sequencing using an Illumina TruSeq Nano library preparation kit (Illumina, Inc., San Diego, CA) according to the manufacturer's instructions. The Illumina NovaSeq™ 6000 (PE150, Novogene, Beijing, China) platform was used to amplify the entire mt genome sequence (BioProject ID: PRJNA667961, GenBank accession number: MW266393). The mt genome was assembled and annotated using the NOVOPlasty pipeline version 3.1 with default parameters (Dierckxsens et al. 2016), as previously described (Palevich

et al. 2019a; Palevich, Maclean, Mitreva, et al. 2019; Palevich et al. 2020, Palevich and Maclean 2021).

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 (1124 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 J 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 sizes and all common organization features are relatively conserved among the blowfly and fly mitogenomes (usually 14.5–19.6 kb) (Stevens J and Wall 2001; Stevens JR 2003; Stevens JR and Wallman 2006).

The phylogenetic position of *L. sericata* NZ\_LucSer\_NP was estimated using maximum-likelihood, implemented in RAxML version 8.2.11 (1000 bootstrap replications) (Stamatakis 2014), and the Bayesian inference (BI), implemented in MrBayes version 3.2.6 (default settings, four MCMC chains) (Huelsenbeck and Ronquist 2001) approaches. Complete mitogenome sequences of 27 available blowfly species were retrieved from GenBank and phylogenetic analyses performed on the concatenated mt PCGs (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



**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 and Ronquist 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 1000 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.

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 mitochondrial genomes across all blowfly species, and especially for different strains/isolates.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

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## Data availability statement

Mitogenome data supporting this study are openly available in GenBank at: <https://www.ncbi.nlm.nih.gov/nuccore/MW266393>. Associated BioProject, SRA, and BioSample accession numbers are <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA667961>, SRR13038366, and SAMN16745530, respectively.

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