

Tristan Dennis  
Postdoctoral Research Associate  
Department of Vector Biology  
Liverpool School of Tropical Medicine  
Liverpool, UK

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Dear Editor at *Proceedings of the Royal Society B: Biological Sciences*,

We wish to submit an original Research Article entitled “*Estimating family structure from helminth larvae with genomic data.*” for consideration by *Proceedings of the Royal Society B: Biological Sciences*. The authors have approved the manuscript, and approve of submission to *Proceedings of the Royal Society B: Biological Sciences*. We confirm that this is an original piece of work, and is not published, nor under consideration for publication, elsewhere.

In this Article, we use modern genomic techniques to estimate helminth family structure. Estimating family structure (kin-ship, and parent-offspring relationships) enables the direct observation of helminth fecundity rates, density-dependence, and parasite load, as well as an understanding of whether new infection following treatment is a result of incomplete clearance, or complete clearance followed by reinfection. This information is key for identifying trial endpoints, and for informing disease modeling. Often, direct observation of these parameters is impossible given the inaccessibility of many adult helminths (e.g. in the liver in *Schistosoma mansoni*, or deep in the skin in *Onchocerca volvulus*). The use of helminth larvae for family structure identification is problematic for taxa that lack established marker panels, and often have small quantities of DNA for analysis. Here, we trial low-coverage whole-genome sequencing and mitochondrial genome sequencing, techniques that can overcome these issues, to identify family structure in *Onchocerca volvulus*, agent of river blindness and onchocerca-associated epilepsy. We find that these two techniques offer promise in affordably resolving relationships between *O. volvulus* larvae, and may be generalised to other helminth systems as a way to further elucidate helminth breeding dynamics and establish whether trial endpoints have been reached.

We believe this work is of interest to the readership of *Proceedings of the Royal Society B: Biological Sciences* because of its general interest to the biological community - particularly disease ecologists, tropical medicine practitioners, and parasitologists. Moreover, our findings are particularly relevant to the journal's readership as they offer promising techniques toward further understanding helminth infection dynamics, as discussed in recent individual articles<sup>1</sup> and a special issue concerned with parasite dynamics and helminthology<sup>2</sup>.

We thank the editor for consideration of our Article, and look forward to hearing your decision at your earliest convenience.

Yours sincerely,

Tristan Dennis

Correspondence to: [Tristan.Dennis@lstmed.ac.uk](mailto:Tristan.Dennis@lstmed.ac.uk)

And: [Poppy.Lamberton@glasgow.ac.uk](mailto:Poppy.Lamberton@glasgow.ac.uk)