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FIRST PERSON

First person – Guy Oldrieve

First Person is a series of interviews with the first authors of a selection of papers published in Biology Open, helping early-career researchers promote themselves alongside their papers. Guy Oldrieve is first author on 'The genomic basis of host and vector specificity in non-pathogenic trypanosomatids', published in BiO. He is a PhD student in the lab of Keith Matthews at the Institute for Immunology and Infection Research, in the School of Biological Sciences at the University of Edinburgh, investigating the genetic basis of parasitism, informed by computational and molecular approaches.

Guy Oldrieve

What is your scientific background and the general focus of your lab?

I studied Zoology at Cardiff University, where I developed an interest in parasitology and computational biology. I combined these interests during my master's project, 'transcriptomic insights into avirulence and host manipulation', with Pete Kille at Cardiff University. The experience and mentorship I gained in Cardiff led to my PhD as part of the Wellcome Trust 'Hosts, Pathogens and Global Health' program at the University of Edinburgh. I chose a PhD that embraced both computational and molecular parasitology in Keith Matthews' lab. My project focuses on *Trypanosoma brucei*, a single-celled parasite and the causative agent of human and animal trypanosomiasis. However, the pandemic put a stop to my lab work, and I went in search of something to keep me busy during the long lockdowns!

Javier López-Vidal (another member of the Matthews lab) works with the closely related non-pathogenic species *Trypanosoma theileri,* which infects cattle and is transmitted by tabanid flies, and *Trypanosoma melophagium*, which infects sheep and is transmitted by the sheep ked. The *T. theileri* genome was published in 2017 and we decided to sequence and assemble the *T. melophagium* genome to identify the genomic basis of the host and vector specificity exhibited by these closely related species. Whilst our main motive was to answer this fascinating biological question, the project could be completed almost entirely from home and provided a remote undergraduate honours project for Beatrice Malacart, who helped assemble and analyse the *T. melophagium* genome during her time in the Matthews lab.

"… the pandemic put a stop to my lab work, and I went in search of something to keep me busy during the long lockdowns!"

How would you explain the main findings of your paper to non-scientific family and friends?

Trypanosoma theileri (*T. theileri*) is a parasite which infects cattle and is transmitted by tabanid flies. *T. theileri* does not harm its host and apparently avoids the host's immune system via a group of proteins which coat the surface of the parasite cell. As the tabanid fly only intermittently feeds on cattle, it is possible that the protein-covered cell surface coat enables a longer infection time in cattle which would increase the chance of *T. theileri* being transmitted between cattle. *Trypanosoma melophagium* is closely related to *T. theileri* but infects sheep and is transmitted by the sheep ked, which resembles a tick but is actually a wingless fly. Keds spend their whole life attached to sheep, providing many opportunities to transmit *T. melophagium*. We compared the genetic components of *T. theileri* and *T. melophagium* to look at the genetic basis of their host and vector specificity. We found that *T. melophagium* appears to use a different protein cell surface coat to that used by *T. theileri* to evade the host immune system. We tentatively link this differential investment to the biology of the insect vectors (tabanid fly/ sheep ked) which spend vastly different lengths of time in contact with their mammalian hosts.

What are the potential implications of these results for your field of research?

The potential causes of host and vector specificity has intriguing evolutionary implications, whilst the comparison between these species and the highly pathogenic relatives, such as the African trypanosome, *T. brucei*, could facilitate identification of pathogenicity hallmarks at the genome level. Our *T. melophagium* genome assembly also broadens the diversity of publicly available

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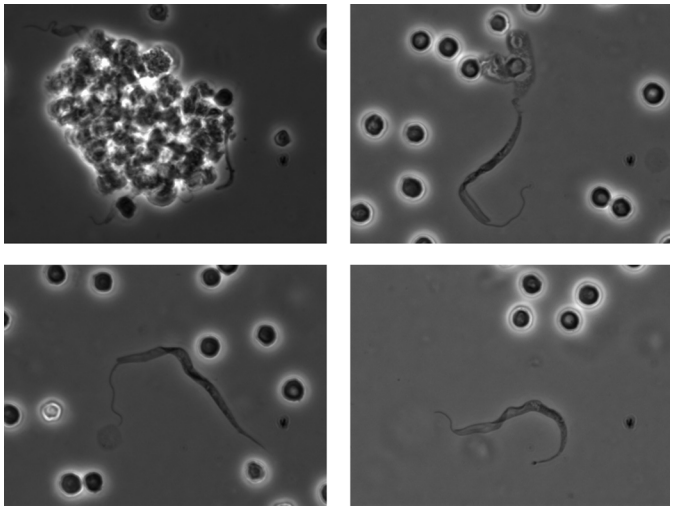

***Trypanosoma melophagium* growing in conditioned media.** The parasites were isolated from Soay sheep on the island of St. Kilda, Scotland, flown to Edinburgh via helicopter and cultured at the University of Edinburgh. Photo credit: Javier López-Vidal.

trypanosome genome sequences, improving our understanding of the diversity and conservation within this group.

What has surprised you the most while conducting your research?

Whilst phylogenetic analysis confirms these species are closely related, the apparent lack of the dominant proteins which likely coat the cell surface of *T. theileri* in *T. melophagium* was a surprise.

What, in your opinion, are some of the greatest achievements in your field and how has this influenced your research?

Trypanosome biology has enjoyed many groundbreaking advances, such as the identification of many biochemical and cytological peculiarities, which allowed us to draw parallels with the organisms studied in this work. Also, portable sequencing devices, such as the Oxford Nanopore minION we used, have revolutionised the quality and speed at which genomic data can be produced. During this study we were able to produce a rough draft of the genome assembly from live cells in ∼2 days. The data was produced in-house which opens the possibility of real-time analysis of genomic data without the need for investment in traditional sequencing equipment.

“During this study we were able to produce a rough draft of the genome assembly from live cells in ∼2 days.”

What changes do you think could improve the professional lives of early-career scientists?

Long term job security. As a PhD student looking at potential career paths, it seems early-career scientists are often flung from university to university on the hunt for short-term contracts. I believe this prevents early-career scientists from settling down, which would not only improve their research but also promote a more sustainable work–life balance.

What's next for you?

Back to the lab! Now restrictions have been lifted in the lab, I need to focus on my original PhD project – developmental incompetence in *Trypanosoma brucei*.

Reference

Oldrieve, G. R., Malacart, B., López-Vidal, J. and Matthews, K. R. (2022). The genomic basis of host and vector specificity in non-pathogenic trypanosomatids. *Biology Open* **11** bio059237.