CHIEF SCIENTIST OFFICE

CODE: TCS/18/22

RESEARCH PROJECT BRIEFING

INVESTIGATING GIARDIA IN SCOTLAND FROM A ‘ONE HEALTH’ PERSPECTIVE

AIMS

Giardia is a single-celled intestinal parasite which causes clinical disease in humans, livestock and companion animals and there is growing evidence of an endemic cycle of disease in Scotland. This study was aimed at developing and deploying novel molecular methods for genetically characterising *Giardia* isolated from humans and animals, to help quantify the public health importance of animal-derived strains of the parasite.

KEY FINDINGS

- The endemic population of *Giardia* in Scotland has largely been overlooked due to a long-standing presumed association with human travel. Contaminated water was found to be the most frequently identified route of *Giardia* transmission in developed countries.
- A new molecular marker for *Giardia* was developed based on PCR amplification of the *triosephosphate isomerase* gene. This was found to improve the genotyping success rate of isolates from both human and companion animal sources.
- While the routine sequencing of clinical isolates in the public health sphere would allow a genomics-led approach to outbreak detection, there exists logistical obstacles to the application of this technology which have yet to be overcome.
- Potentially human-infective genotypes have been detected circulating in the UK companion animal population, with with 17.4% of feline-derived *Giardia* isolates potentially being zoonotic.
- Domestic pets may be involved in the endemic transmission of giardiasis in the UK and therefore appropriate hygiene measures should be observed when interacting with both symptomatic and asymptomatic animals.

WHAT DID THE STUDY INVOLVE?

This study involved a close collaboration of veterinary and NHS-based researchers, and was prompted by work of the **Diagnostic and Reference Parasitology Service, which detected an endemic cycle of human giardiasis in Scotland. Three main objectives were defined:**

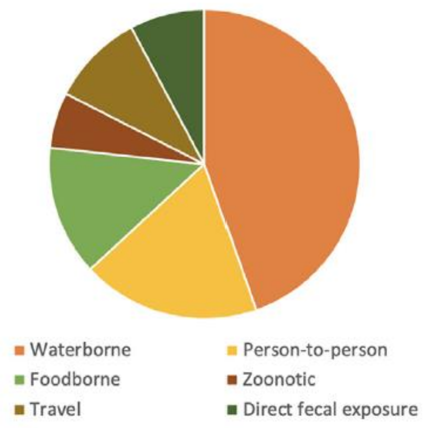
1. To develop an improved marker-based *Giardia* genotyping assay, which could overcome the limitations of current methods

2. To characterise a panel of feline and canine *Giardia* isolates to determine the prevalence of potential zoonotic genotypes in the UK companion animal population

3. To investigate the potential for applying whole-genome sequencing to the characterisation of clinical isolates of *Giardia*

WHAT WERE THE RESULTS AND WHAT DO THEY MEAN?

- A novel qPCR assay was developed based on the parasite's *tpi* gene. All available allelic sequences were collected from online databases and bioinformatic analysis performed. Previously unrecognised polymorphisms were detected, allowing novel primers to be designed, tested and validated. This allowed creation of a more sensitive assay.
- 174 *Giardia* positive faecal samples from UK companion animals were obtained together with 79 anonymised human samples. 37 human and 65 cat and dog samples were successfully genotyped using the new method and the results are shown below.
- A targeted enrichment method was attempted to isolate *Giardia* nucleic acid from faecal samples for genomic sequencing. Although the parasite DNA could be enriched, this could not be achieved to a sufficient level to construct libraries for sequencing.
- A systematic review of the world literature on *Giardia* outbreaks in developed countries was undertaken. 75 articles meeting strict criteria were statistically analysed and a number of different transmission routes were identified and catalogued, shown below.



Outbreaks by transmission route

The majority of reported outbreaks were waterborne in nature.

Assemblage	Human (n=37)	Canine (n=19)	Feline (n=46)
A (human/zoonotic)	12	1	4
B (human/zoonotic)	25	0	4
C (canine)	0	10	0
F (feline)	0	8	38

***Giardia* strains found in UK humans, dogs & cats**

All human samples were found to contain either strains 'A' or 'B', which are recognised as being human-infective. These strains were also identified in nine of the companion animal faecal samples, principally from cats, although the majority of cats and dogs harboured host-species specific strains.

WHAT IMPACT COULD THE FINDINGS HAVE?

The finding of human-infective strains of *Giardia* in companion animals underlines the importance of pet owner hygiene when handling cats and dogs and their waste products. The findings of the molecular survey together with the scoping literature review highlights the requirement for further studies to assess the zoonotic risk of *Giardia* associated with companion animals in high-income countries such as Scotland. In particular, the novel genotyping *Giardia* assay developed strengthens capacity to characterise parasite genotypes from human and animal sources and so may be utilised to facilitate such studies and provide quantitative data on the risk of *Giardia* from different environmental compartments.

HOW WILL THE OUTCOMES BE DISSEMINATED?

The results of this study have been published in peer-reviewed international journals and in theses/dissertations deposited at the University of Glasgow. This includes articles on ‘A novel *Giardia* genotyping method and its application’ (https://doi.org/10.1016/j.crpvbd.2022.100105), ‘The molecular epidemiology of giardiasis’ (https://doi.org/10.1016/j.pt.2020.09.013) together with ‘Transmission sources of *Giardia* in developed countries’ (https://doi.org/10.1016/j.crpvbd.2022.100084). The work supported undergraduate and postgraduate research projects (http://theses.gla.ac.uk/83312/) with findings being presented at international conferences, including those of the European College of Veterinary Public Health in 2021 and the British Society of Parasitology in 2023.

CONCLUSION

Giardiasis is a neglected pathogen of ‘One Health’ importance. The potential of companion animals to contribute to the endemic cycle of disease in Scotland has been established, however further studies are required to determine the relative importance of domestic pets in the transmission of *Giardia* to humans in comparison to other environmental sources.

The findings of this project not only provide the incentive for further work but also the molecular tools necessary to perform such investigations.

RESEARCH TEAM & CONTACT

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Additional Information

The project was completed on the 30th September 2024.