TCS/18/22 – Investigating the epidemiology of endemic *Giardia* in Scotland using a whole genome sequencing approach

The Scottish Parasite Diagnostic and Reference Laboratory and Health Protection Scotland have established that the majority of Scottish cases of the gastrointestinal parasite Giardia duodenalis are acquired locally rather than being travel-related; the source of infection in most cases is unknown. We will investigate molecular diversity and epidemiology of Giardia in Scotland using whole genome sequencing (WGS). We will develop a novel WGS-based parasite genotyping system, applying it to a large collection of human isolates collected in Scotland, to determine molecular types and to identify genetically-linked clusters of cases. Information will be integrated with metadata from Health Protection Scotland to improve understanding of Giardia epidemiology. We intend to improve healthcare in Scotland through (a) increasing capacity to characterise parasites at a molecular level, (b) determining the presence and distribution of zoonotic strains and (c) developing molecular/bioinformatic tools to underpin disease surveillance and control, allowing evidence led changes to laboratory testing policies. The tools developed in this project will permit the identification of genetically-linked clusters of cases, allowing for the detection and management of outbreaks. These tools can also be used to trace transmission routes in order to provide evidence for risk assessment.