

Student Project: Systematic literature review on anthelmintic resistance genes in human and veterinary parasites

Fields of interest

Parasitology, Drug Resistance, Population Genetics, Neglected Tropical Diseases

Background

Soil-transmitted helminth parasites affect both humans and livestock species, causing a range of health problems in their hosts. In areas with high endemicity, regular mass deworming is administered to curb parasite infection and transmission. As parasites produce large quantities of eggs that are released into the environment through stool of infected individuals, reinfection via the environment is common. Unfortunately, regular anthelmintic treatment poses a risk for resistance evolution in parasite populations. While rapid resistance evolution to deworming treatments has been observed in livestock parasites, there is no firm evidence for anthelmintic resistance in human parasites. This could partly be explained by different treatment regimens: young livestock animals are dewormed monthly in some areas to boost growth, whereas mass deworming in humans typically is not administered more than twice per year and targeted to children only. Thus, there has been greater evolutionary pressure on livestock parasites. However, preliminary analysis suggest that observed differences in resistance evolution in human and helminth parasites may also be caused by differences in parasite and host biology. New plans for eliminating human soil-transmitted helminth diseases consider expansion of mass deworming to adults which will increase evolutionary pressure on parasites. Therefore, understanding what factors and mechanisms contribute to anthelmintic resistance evolution is important both for human health and for veterinary health and food security.

Problem statement

Mathematical population genetic models can help to understand how much different treatment strategies and parasite- and host-specific factors contribute to eco-evolutionary processes that drive or hinder the emergence and spread of anthelmintic resistance. To parameterise these models an overview of genes conferring resistance to different anthelmintic treatments in human and livestock parasites is needed. In addition, quantitative data on fitness benefits and costs of different resistance mutations is required.

Objective

The objective of this project is to produce a dataset of genes and mutations involved in anthelmintic resistance in human and livestock parasites, their prevalence in different populations, and their fitness benefits and costs. The dataset will be used as input for mathematical population genetic models of the evolution of anthelmintic resistance with the larger goal of developing effective strategies for disease control and management.

Key activities / Tasks

- Conduct a systematic literature review including peer-reviewed and grey literature on anthelmintic resistance genes and mutations in human and livestock parasites and model organisms (e.g. *C. elegans*).
- Compile a dataset of the prevalence of resistance mutations in different species and populations, estimated fitness benefits and costs, prevalence of coinfections with different

parasites and, where available, evidence for interspecies interactions (e.g. competition) from population-based and/or experimental studies.

- Based on the review and extracted data develop suitable model structures to investigate the evolution of anthelmintic resistance (conceptual model structures, no advanced maths or coding required at this stage of the project).

Additional information

This project will be jointly supervised by Dr Federica Giardina (Biostatistics, Radboud UMC) and Dr Carolin Vegvari (Imperial College London / Oriole Global Health Ltd) and supported by Dr Swati Patel (Mathematics dept, Oregon State University) and Dr Kelsey Pano Lyberger (Biology dept, Stanford University) who will take on tasks of the systematic review, e.g. second reviewers for study selection and data extraction.