

# Advancing Parasitology through Molecular Tools

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Throughout human history, parasites have always incited a dichotomy of fascination and repulsion. From ancient observations with the naked eye, to modern examinations under sophisticated microscopes, parasitology has traditionally relied on studying parasites from fecal matter, body fluids and dissected animals documenting their morphology and lifecycles. The development of molecular methods has revolutionized our understanding of parasites. Genetic analyses can now be combined with morphological observations, allowing for more accurate classification and species identification - even on cryptic parasite species or eggs that appear identical under a microscope. Molecular parasitology leverages DNA sequencing of known reference specimens to enable non-invasive parasite detection and classification using small samples like feces, blood or other tissues.

Metabarcoding, the study of a specific DNA sequences like the ITS2 region, allows simultaneous identification of multiple parasite species. Coupled with next-generation sequencing, metabarcoding has improved the ability to detect mixed infections that would be difficult through microscopy alone, providing rapid and accurate species-level identification without extensive taxonomic expertise under the assumption that the sequences for all species are available.

All grazing animals will be subjected to strongyle nematode infections during their lifetime. The intense use of anthelmintic drugs in modern animal husbandry has led to increasing drug resistance in many nematode species. Molecular tools can be used to identify and evaluate genetic markers associated with resistance, enabling more targeted and effective treatment strategies to retain drug efficacy. From a One Health perspective, monitoring anthelmintic resistance is crucial because it affects animal welfare, food security and sustainable farming.

In my research at SLU, I have focused on three key areas

- A) Using metabarcoding to investigate nematode community compositions (nemabiomes) in livestock (sheep and horses) and wild ungulates in Sweden. This research provides detailed insights into the interactions between different parasitic species, their relative abundances and the overall parasite diversity.
- B) Exploring how the nemabiome responds to anthelmintic treatment in sheep and horses, to guide effective treatment strategies and retain drug efficacy for the future. A key feature of this research is to monitor how the relative frequencies for each species change after treatment.
- C) Investigating the relevance of candidate genes and single nucleotide polymorphisms thought to be involved in anthelmintic treatment. As we currently face problems with increasing anthelmintic drug resistance, genetic could offer new tools to enable early detection.

Moving forward, I have secured research funding to continue my research. FORMAS funds two projects for investigating 1) Horizontal transmission of gastrointestinal nematodes between farmed animals and wildlife, to gain knowledge on how parasites spread between locations and host species. 2) How reindeer herding can adapt to climate change by linking reindeer genetics to diseases (parasites, viruses, bacteria) and traditional knowledge.

A third project is funded by SLF and focuses on investigating the prevalence of anthelmintic drug resistance in nematodes on cattle farms in Sweden. This research will also analyze which preventive measures taken by cattle owners has the best effect for mitigating parasite infections and anthelmintic resistance.