

Application of ‘Nemabiome’ deep amplicon sequencing together with other ‘omics approaches to investigate anthelmintic resistance in livestock gastrointestinal nematodes across Europe and Anatolia

Archer, J¹, Neveu, C²., Guegnard, F²., Chereau, A²., Vernudachi, A.³., Mwangi, H⁴., Charlier, J⁴., Antonopoulos, A⁴., Claerebout, E⁵., Goes, J⁵., Kozan E⁶., Erez, S⁶., Sotiraki, S⁷., Ligda, P⁷., Ligdas, A⁷., McElligot, T⁸., Duffy, K⁸., Samson-Himmelstjerna, Gv⁹., Krucken, J⁹., Cotton, J¹., **Laing, R¹**

1. School of Biodiversity, One Health and Veterinary Medicine. College of Medical, Veterinary and Life Sciences, Garscube Campus, University of Glasgow, UK
2. National Research Institute for Agriculture, Food and Environment, Paris, France
3. Invenesis Biosciences, Saint-Blaise, Switzerland
4. Kreavet, Kruibeke, Belgium
5. Faculty of Veterinary Medicine, Department of Translational Physiology, Infectiology and Public Health, University of Ghent, Belgium
6. Afyon Kocatepe University, Afyonjarahisar, Türkiye
7. Institute of Veterinary Research, Elgo-Dimitra. Athens, Greece
8. Micron Agritech. Dublin, Ireland
9. Department of Veterinary Medicine, Institute of Parasitology and Tropical Veterinary Medicine, Freie University, Berlin, Germany

Abstract

Parasitic gastrointestinal nematodes (GINs) cause significant morbidity in livestock as well as substantial economic losses to agricultural workers. Controlling livestock GINs relies heavily on the use of anthelmintics such as benzimidazoles (e.g., albendazole), macrocyclic lactones (e.g., ivermectin/moxidectin) and levamisole. However, indiscriminate use of these broad-spectrum drugs over many years has contributed to the wide-spread development of anthelmintic resistance (AR). Detecting and monitoring the development and spread of AR in GINs of livestock is typically done using the faecal egg count reduction test (FECRT), which involves measuring the percentage reduction of nematode eggs passed in faeces pre- and post-treatment. This approach, however, is arduous, time consuming and insensitive.

The ANTHELMOGRAM consortium introduces a novel decision-support tool that aims to overcome the current limitations in diagnosing AR in livestock GINs. Taking advantage of a newly developed high-throughput automated larval motility assay, the ANTHELMOGRAM platform can phenotype up to 4,000 samples per week and accurately determine the resistance/susceptibility status of up to 10 different compounds per parasite population. The assay will be applied to GINs of cattle, sheep and goats from six countries across Europe and Anatolia where AR is a major concern. In addition, all GIN samples will be genotyped using a highly sensitive ‘Nemabiome’ approach (analogous to microbiome metabarcoding) to reveal GIN species composition/abundance within each sample. As

well as this, whole-genome and transcriptomic data will be generated from phenotyped isolates of interest. This will allow further scrutiny of known/suspected anthelmintic resistance markers, as well as the potential discovery of new resistance markers, and will thus be the first large scale anthelmintic 'resistome' study.