

Discovery Omics to Support *Nematodirus helvetianus* Control

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N. helvetianus is a GI nematode of the small intestines infecting young, immunosuppressed cattle, often as part of a coinfection [1]. Infection leads to diarrhoea, weight loss, and dehydration negatively impacting animal welfare and economic production [3]. Control is challenging and new solutions are required. However, molecular research into *N. helvetianus* has been limited. Therefore, the aim of this project is to produce the first discovery transcriptome for *N. helvetianus* to support future functional genomics.

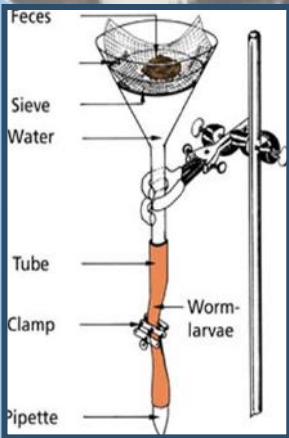
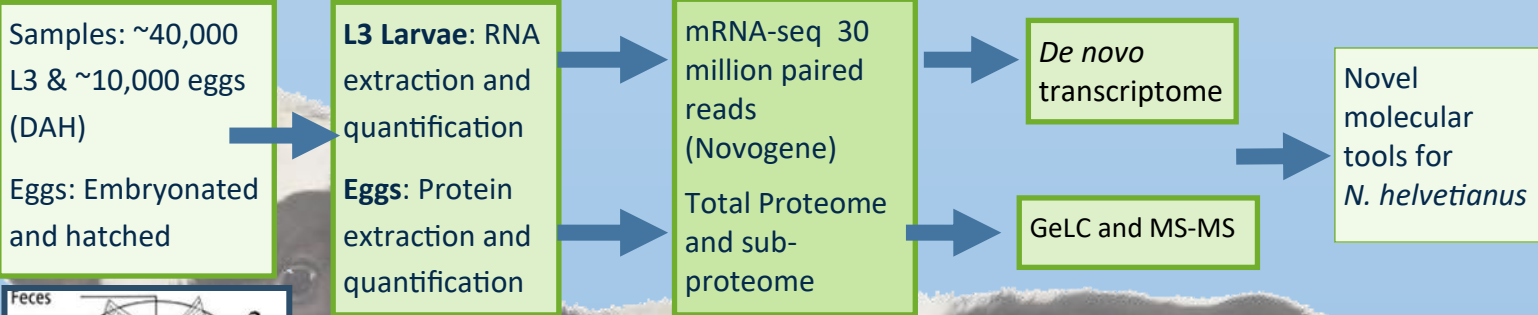


Figure 1. Baermann Funnel.

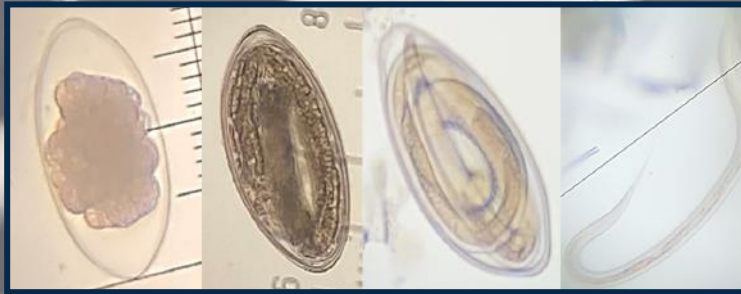


Figure 2. Documentation of egg development from embryo to L3 larvae. Embryo, L1 and L2 within the egg and the hatched L3. Larvae will be filtered using a Baermann funnel and used for protein analysis.

Transcriptomics

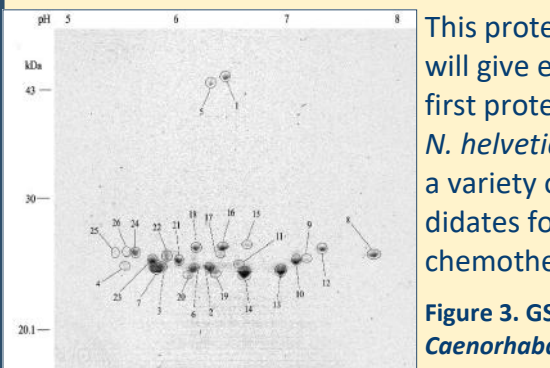
At present, no nucleotide databases exist for *N. helvetianus*. We have extracted tRNA from L3 larvae using a Zymo extraction kit. *De novo* transcriptome assembly through Novogene. This discovery transcriptome will be put to work to uncover potential control targets including the glutathione transferase superfamily.



Transcriptomics coupled with proteomics are powerful tools.

Proteomics

With the support of the first *N. helvetianus* transcriptome we are uncovering the global proteome using a GeLC proteomics approach. Global proteomics will be supported with targeted sub-proteomics of isolated protein super-families including the glutathione transferases (GSTs) [5].



This proteomic research will give evidence to the first proteome for *N. helvetianus* opening up a variety of potential candidates for immuno- or chemotherapy.

Figure 3. GST purification gel in *Caenorhabditis elegans* [6].

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