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FACULTY OF HEALTH AND MEDICAL SCIENCE
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Gluck Equine Research Center

Profiling microRNAs from the Equine Bloodworm (*Strongylus vulgaris*)

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AIMS

1) Establish the microRNA (miRNA) complement of *S. vulgaris*
2) Explore miRNAs excreted from *S. vulgaris*
3) Investigate the presence of *S. vulgaris* miRNAs in blood samples from infected horses

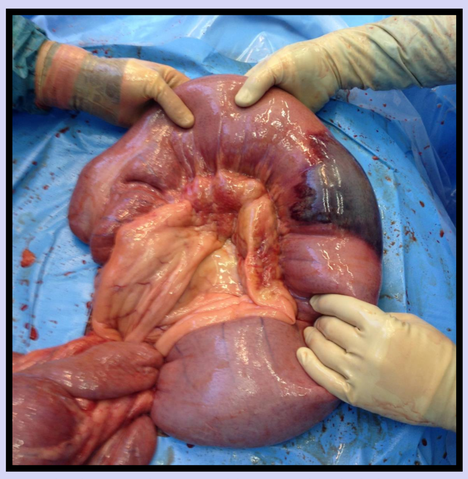
HIGHLIGHTS

- A total of 149 mature (36 novel) *S. vulgaris* miRNAs were identified
- *Strongylus vulgaris* larvae were found to excrete miRNAs to their host
- Parasite-derived miRNAs were detectable in plasma samples from infected horses

BACKGROUND

Strongylus vulgaris

- *Strongylus vulgaris* is a relatively common intestinal parasite of horses
- The migrating larval stages reside in the horse's Cranial Mesenteric Artery for several months, leading to endarteritis and risk of fatal intestinal necrosis
- The currently available methods for detection of *S. vulgaris* infection, are not effective in diagnosing the highly pathological pre-patent stages
- The miRNA complement of *S. vulgaris* has not yet been annotated

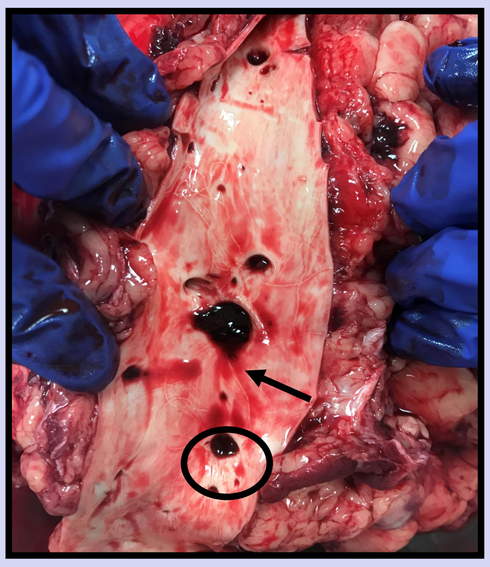


Intestinal necrosis caused by *S. vulgaris infection*

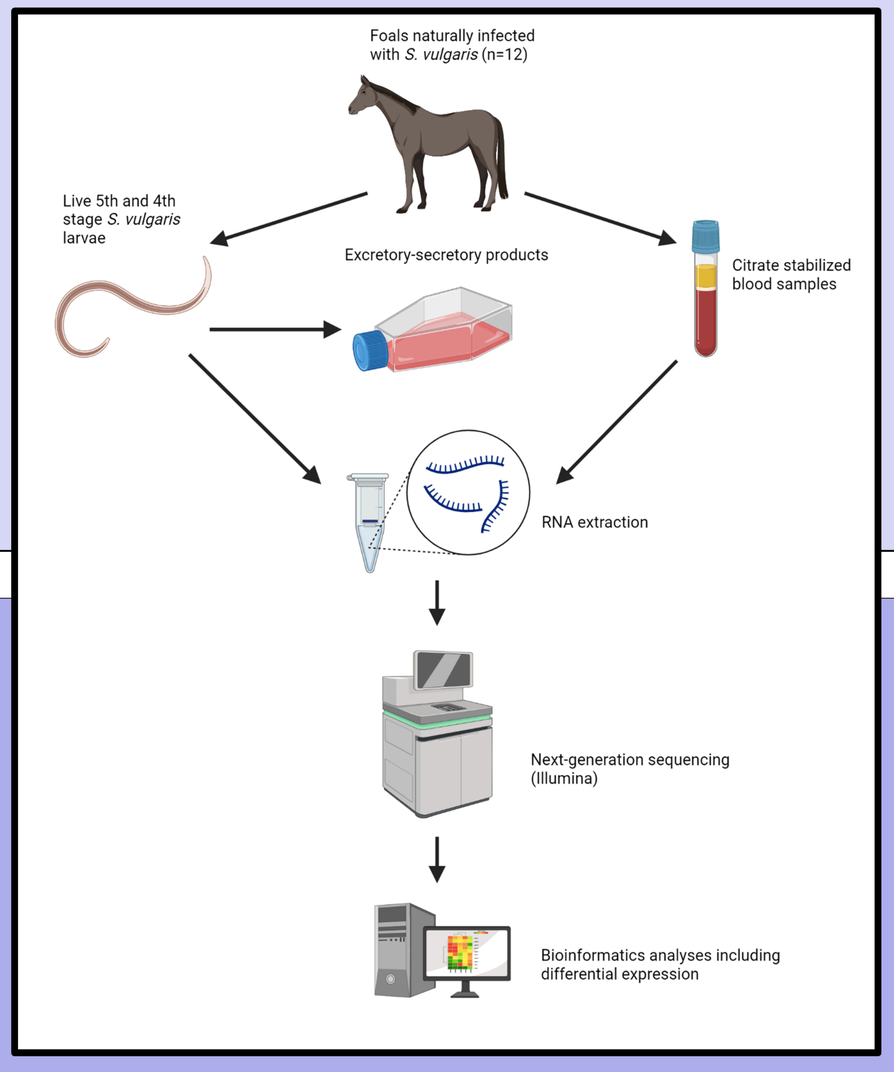
MicroRNAs

- microRNAs are short RNA molecules acting as post-transcriptional gene regulators
- Parasites excrete miRNAs to their host, possibly to modulate host immunity
- Profiling of miRNAs from parasites improves knowledge of host-parasite interactions
- miRNAs can possibly serve as drug targets or diagnostic biomarkers of infection

METHODS



Larvae were collected from the Cranial Mesenteric Artery (arrow) and the Celiac Artery (circle)



Larvae were incubated for up to 72 hours for collection of excretory-secretory products

RESULTS

- Overall 149 *S. vulgaris* miRNAs were detected in the larval samples, hereof, 36 novel miRNAs
- All 149 *S. vulgaris* miRNAs were also detected in the excretory-secretory products
- In the plasma samples 145 of the parasite-derived miRNAs were detectable
- Significant differences in miRNA expression were found between, sample types (larvae, excretory-secretory products and plasma)
- Significant differences in miRNA expression were found between larval stages (L4/L5) and sexes (male/female)

Clustering was observed between the different sample types; larvae (L), excretory-secretory products (ES) and plasma (P). Likewise, partial clustering was observed for stage (L4/L5) and sexes (female/male).

DISCUSSION

- In this study 149 miRNAs were annotated to the *S. vulgaris* miRNA complement, which is comparable to the number of miRNAs found in other nematodes
- Differences in miRNA expression between sample types, suggests that specific miRNAs are excreted to the host, while others are used for internal regulation in the worm
- Parasite-derived miRNAs were detectable in host blood samples, but samples from uninfected horses needs to be evaluated before conclusions can be made on the diagnostic potential of circulating miRNAs
- RT-qPCR validation of selected miRNAs needs to be carried out before final annotation of miRNAs found in this study

PERSPECTIVES

- Target prediction can help elucidate the biological functions of the miRNAs found in this study. This will provide further insight into the parasite-host interaction
- Knowledge about miRNA function, both in parasite and host, can be important in search for new drug targets
- Future studies should be conducted to support or reject a diagnostic potential of circulating *S. vulgaris* miRNAs in horses

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