Novel environmental biomarkers for liver fluke control.

Fasciola hepatica is a species of parasitic flatworm of global concern, due to its ability to cause fascioliasis in both humans and animals with a significant impact on livestock species. An estimated 90 million humans and 700 million ruminants are at risk of liver fluke infection, with economic losses considered a serious issue for farming communities. Infection risk is highly dependent on the presence of the intermediate snail host *Galba truncatula* in the environment. At present, detection of snail hosts is limited to physical identification or through novel environmental DNA (eDNA) methodologies. This study intends to uncover alternative novel environmental biomarkers for *G. truncatula* supporting liver fluke control to improve field diagnostics and subsequently highlight risk areas for *F. hepatica* infection. In the absence of *G. trunctatula* genome or transcriptome support we have generated the first discovery transcriptome for *G. truncatula* supported with transcriptomes from the closely related *Galba cubensis*. The transcriptomes for *G. truncatula* and *G. cubensis* were generated using tRNA harvested from snails at three different time points: day 0 (uninfected), 10 days post infection, and 42 days post infection. These discovery transcriptomes are now supporting metaproteomic approaches for the detection of environmental proteins (eProteins) from *G. truncatula* and *F. hepatica*. To identify eProteins, water sample collection has been performed on *G. truncatula* and *F. hepatica* isolates across life stages (including embryonating eggs, hatching miracidia, and their subsequent decay). All water samples have been analysed through a GeLC metaproteomic approach to identify eProteins detected in experimental water samples.