Developmental and secretory regulation of microRNAs in an expanded *Fasciola hepatica* dataset

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Fasciola hepatica is a ubiquitous veterinary parasite that costs the UK agriculture industry over £20 million annually, and a Neglected Tropical Disease pathogen in humans with over 90 million people at risk worldwide. Fluke control is threatened by resistance to four of the five available flukicides; improved understanding of fluke biology could lead to new therapies. Micro (mi)RNAs are non-coding RNAs proposed as therapeutic and diagnostic targets in biomedicine. While parasite miRNAs have attracted interest, in general, parasite miRNA complements remain poorly profiled. Here we describe an expanded set of *F. hepatica* miRNAs, and the first developmental profile of miRNAs in this species. Small RNA sequencing of fluke life stages, coupled with published data, identified a total of 151 mature miRNAs. We have used Locked Nucleic Acid based qPCR assays to profile expression of all of these across metacercariae, juvenile and adult tissue samples, as well as adult- and juvenile-derived extracellular vesicles (EVs). A total of 144 miRNAs were validated by qPCR, with 57 present in all life stages. Several miRNA were restricted to individual life stages including 11 specific to metacercariae and 13 specific to adults. These are the first data demonstrating the developmental importance of individual fluke miRNAs. 58 miRNAs were detected in EVs; we are currently establishing whether these are detectable in *in vivo* samples and performing in silico predictions of their potential host mRNA binding partners. These data will contribute to understanding of host parasite interactions and may lead to new diagnostic and therapeutic avenues for fasciolosis.