Can many biomarkers make light work of liver fluke parasite diagnostics?

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Project Description: Liver fluke parasites are a pervasive economic threat on UK sheep and cattle farms. Control of fluke infections is achieved primarily by treating animals with flukicide drugs, although this approach is becoming limited by developing drug resistance and consumer pressure for organic, drug residue-free produce. There is therefore a need to reduce flukicide use. One way to do this is by employing diagnostically led, selectively targeted treatment regimes (instead of blanket treatments of entire herds), but existing diagnostic tools have drawbacks meaning they are of limited value in supporting such an approach. The aim of this project is to identify new molecular biomarkers to support the development of improved diagnostic tools. Our approach will be to use state-of-the-art omics methods, combining proteomic, peptidomic and transcriptomic analysis of blood sera from fluke infected sheep. We will then analyse these 'big data' datasets using a computational method called network analysis to identify patterns indicative of fluke infection. This will be the first study to perform these omics methods in such depth in any host-parasite system, the first to analyse them as a single combined polyomic dataset, and the first to use network analysis to identify biomarker patterns in a parasite infection dataset. Our ultimate goal is to identify biomarker patterns that provide earlier and more sensitive diagnosis of fluke infection than is possible with existing tools. This will enable reduced flukicide use, and efficiency savings for farmers, through targeted, early intervention treatment of infected animals.