

Publication

Advances in metabolic profiling of experimental nematode and trematode infections

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**ID** 524384**Author(s)** Wang, Yulan; Li, Jia V; Saric, Jasmina; Keiser, Jennifer; Wu, Junfang; Utzinger, Jürg; Holmes, Elaine**Author(s) at UniBasel** [Keiser, Jennifer](#) ; [Utzinger, Jürg](#) ;**Year** 2010**Title** Advances in metabolic profiling of experimental nematode and trematode infections**Journal** Advances in parasitology**Volume** 73**Pages / Article-Number** 373-404

Metabonomics, which is the combination of metabolic profiling of biological samples using spectroscopic methods, together with multivariate data analysis, is a powerful approach for biomarker recovery. Moreover, metabonomics holds promise to enhance our understanding of host-parasite interactions at the metabolic level, and therefore provides a framework for discovery of novel targets for diagnostics, drugs and vaccines. In this review, we summarise progress made to date with metabolic profiling strategies applied to different host-parasite models in the laboratory. First, we emphasise the application of two parasitic worm infections that are particularly relevant for Southeast Asia and the People's Republic of China, namely the trematode *Schistosoma japonicum* causing schistosomiasis, and the nematode *Necator americanus* causing hookworm disease. Next, we review metabolic profiling studies on the liver fluke *Fasciola hepatica* in the rat model, the intestinal fluke *Echinostoma caproni* harboured in mice and characterise the metabolic responses in the hamster to a *S. japonicum*-*N. americanus* co-infection. We extract parasite-specific biomarkers and distinguish them from a more general response to an infection at the biochemical level. For example, suppression of tricarboxylic acid cycle metabolites is only noted for a *Schistosoma* spp. infection, whereas alterations in metabolites derived from the gut microbiota are common for all the parasitic infections investigated thus far. Finally, we explore how the insight gained with experimental infections could be transferred to human populations and conclude with a section on research needs with regard to molecular diagnostics in parasitology

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