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Vaccine development against parasites has been greatly facilitated by the advancement of -omics tools that have identified many candidate target molecules by exploring their stage- and tissue-specific expression. While ‘traditional’ vaccines have been manufactured as either live, attenuated or more recently as recombinant proteins, an area of prime importance that has been largely neglected is the characterisation of parasites-derived glycans.

Glycans are highly immunogenic and often play roles in protecting parasites against immune attack and/or direct evasion of host responses by impairing immune functions; thus, they can present a major target for disrupting parasite-host interaction. We focus on an important zoonotic parasite, *Fasciola hepatica*, a worm that causes detrimental One Health consequences because it infects up to 17 million people and results in annual losses >€2.5 billion to livestock and food industries worldwide. Mass drug treatment campaigns in high-endemic areas have been undertaken, but the global emergence of anti-helminthic resistance, principally to triclabendazole, poses challenges to these efforts.

To address this gap, we utilized glycan and glycopeptide analyses, along with bioinformatics tools, to characterize the glycosylation of individual *F. hepatica* proteins. We found huge heterogeneity in glycosylation exerted by the 1727 N- and O-glycoforms we characterized, resulting in great protein variability in the fluke extracts, which are far more complex than anticipated by proteomic analysis.

Altogether, we glyco-mapped 123 glycoproteins associated with the parasite’s invasive state, 71 of which are excreted-secreted proteins regarded as promising vaccine targets.

Our data provide a sounder foundation for improving future vaccine development to control fascioliasis.

World Federation of Parasitologists (WFP) and International Federation for Tropical Medicine (IFTM) Symposium: Exploring the One Health and Planetary Health Dimensions of Helminth Diseases

Track 2: Infectious diseases and (neglected) tropical diseases

### Old hosts as treasure troves of worms, worms as tags for new hosts: The overlooked potential of helminthology in invasion biology

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Introduced alien species are major threats to biodiversity. Reasons may include parasite co-introduction and transmission, but this parasitological impact on local hosts and ecosystems is understudied. Moreover, origins and identity

of introduced species/strains are often unknown, let alone of their parasite fauna. Monitoring only provides partial answers for want of baseline data: especially in the Global South, native parasite biodiversity is poorly known.

We studied introduced hosts (cichlids, sardines, frogs) in Central and Southern African inland waters, and the monogenean flatworms infecting them. Given their one-host life-style, these are hypothesized to be easily co-introduced with their hosts, and to be “tags” for host populations.

Monogeneans were collected from hosts retrieved from biodiversity collections and recent fieldwork. Parasites were morphologically identified to species level, and characterised using nuclear and mitochondrial markers, including some mitogenomes.

We showcase the potential of historical fish collections to establish pre-translocation baselines for parasite communities, allowing to distinguish native from co-introduced parasite species. Monogeneans can help trace origins and pathways of aquatic invasions. For the notoriously invasive Nile tilapia and African clawed frog, parasite mitochondrial markers provide higher resolution than host genetics.

“We offer a proof-of-concept of biodiversity infrastructure and helminths as sources of information in a One Health context. This contributed to media interest for using natural history collections in infectious disease research. However, a closer look at the parasitology of Nile tilapia, a fish of global economic and ecological importance, indicated that a One Health approach is mostly lacking.

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### From local to global: Exploring the impact of schistosomiasis and helminth diseases on one health

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Helminths (*Schistosoma*, soil-transmitted helminths, etc.) affect around 25% of the world’s population. They constitute a significant public health challenge, particularly in tropical and subtropical regions, where they affect millions of individuals. These neglected tropical diseases exert a profound impact on both human and animal health, highlighting the interconnectedness of ecosystems, human communities and animal populations.

Vaccine development emerges as a promising avenue for addressing helminth infections. We explore the challenges and advancements in vaccine research, including the