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Improving diagnostics for *Schistosoma bovis* infections in cattle across Africa.

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The platyhelminth *Schistosoma bovis* is responsible for significant pathology and reduction in productivity in cattle across large regions of Africa. In addition to its veterinary importance, *S. bovis* has been identified as a potential zoonotic threat, through hybridisation with *S. haematobium*. Diagnostics techniques for many helminth parasites currently rely on low sensitivity, low throughput, microscopic methods. To improve on these limitations, new diagnostic tools such as lateral flow assays (LFA) are available. Molecular tests such as LFAs represent a medium throughput technology, with excellent sensitivity for the detection of active disease.

Using a framework of technologies originally developed for the detection of *Schistosoma japonicum* specific antibodies in humans, we aim to provide enhanced detection of *S. bovis* in cattle across Africa. We have shortlisted protein targets from *S. bovis* by identifying homologues of *S. japonicum* proteins with the highest diagnostic potential. So far, several proteins have been identified as diagnostic targets and have been recombinantly produced in *E. coli*. These diagnostic targets are involved in various biological processes within the parasite, including metabolic pathways, transcriptional regulation, glycolysis, phosphorylation, and cell signalling. Alongside these targets are a number of potential diagnostic candidates with currently incomplete coding sequence predictions. We intend to clarify these transcript sequences using cDNA derived from *S. bovis* worms originating from natural infections and include them in the recombinant production pipeline.

We aim to screen this small library of *S. bovis* proteins with infected cattle serum, incorporating any candidates with diagnostic potential into lateral flow technologies for point-of-care detection of *S. bovis* infection.