Unravelling the Genetic Diversity and Hybridisation of *Schistosoma* and *Fasciola* species in Cattle Across Uganda's Cattle Corridor

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Schistosoma and *Fasciola* species infect humans but also cause significant economic losses in livestock. Detection of these parasites remains challenging due to limited field-adapted diagnostic tools. Additionally, the increasing reports of hybridisation between human (*S. haematobium*) and animal (*S. bovis*) infecting *Schistosoma* species and between *F. gigantica* and *F. hepatica* may complicate their detection and control. Therefore, our study aims to determine the genetic diversity of *Schistosoma* and *Fasciola*, and their hybrid forms, and to determine the prevalence of *Schistosoma* infections in cattle. The study was conducted across five districts within the *"cattle-corridor"* of Uganda. From each, one subcounty was chosen from which 10 farms or herds were randomly selected, and serum samples were obtained from cattle. Additionally, an abattoir from each district was visited to collect worms. Schistosomes were collected from mesenteric veins of the small intestine while liver flukes were obtained by making incisions in the bile ducts of the liver and stored in 70% ethanol. A new ELISA test, based on the Conserved Oligomeric Golgi complex subunit 4 (COG4) protein developed in our lab, will be used to detect *S. bovis* infection in serum. Schistosomes and liver flukes will be confirmed using HRM qPCR and cPCR using nuclear phosphoenolpyruvate carboxykinase (PEPCK) gene primers. PCR protocols were optimized through evaluation of primer sets, adjustment of annealing temperatures, and refinement of reagent concentrations. Initial analysis of worms obtained from Uganda in 2024 confirmed 70 liver flukes as *F. gigantica*, whereas, of the two pairs of *Schistosoma* worms speciated, one pairing was between *S. curassoni* and *S. bovis* and the other between a hybrid of *S. mattheei* and *S. curassoni*, and *S. bovis*. Further field work was conducted between October - December 2025 and yielded 430 cattle serum samples, 170 *Schistosoma* and 348 *Fasciola* worms. Preliminary results underscore the need for expanded genomic surveillance to clarify transmission dynamics and guide effective control strategies

Key words: Hybridisation, Schistosoma, Fasciola, Cattle corridor, Uganda