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200 years Theodor Bilharz
Schistosomiasis Research in Germany and Beyond

Abstract Book

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ORAL PRESENTATIONS

Session I - History and Global Health

Date / Time: Wednesday, October 8th, 2:15 PM - 4:05 PM

The fight against schistosomiasis from Theodor Bilharz to the second half of the 20th century: a critical historical reflection

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Theodor Bilharz - The role of the scientist in Egypt

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Schistosomiasis, a parasitic disease first identified in Egypt in the 1850s by the German physician Theodor Bilharz, became a major endemic health problem, with an accelerated spread due to irrigation changes by the 20th century in Egypt. Many efforts were done at early times to control and manage the disease but the results were always not satisfactory. In response, in 1988, Egypt launched a large-scale control program that included molluscicide, surveillance, and eventually mass praziquantel therapy. These efforts dramatically reduced the national prevalence of the disease from 40% in the mid-20th century to less than 0.5% by 2016.

Central to this success has been Theodor Bilharz Research Institute (TBRI), founded in 1964 and inaugurated in 1978 through a collaboration between Egypt and Germany. Named after the German physician who first described the urinary blood fluke, TBRI has been a cornerstone of the nation's fight against the disease. The institute developed research and clinical capacity in parasitology, medical malacology, public health, urology and hepato-gastroenterology trying to manage the disease and its most common complications. TBRI also trained thousands of clinicians and technicians and also established key resources, like the Schistosome Biological Supply Centre which supplied biological materials to more than 30 countries all over the world.

Today, TBRI continues to lead the way in schistosomiasis elimination. Its work focuses on developing field-adapted diagnostics, utilizing molecular and nano-biotechnology platforms, and providing continuous training to the workforce in addition to offering medical and surgical services to thousands of Egyptian citizens as part of the Egyptian Government strategy.

As Egypt shifts its focus from disease control to the interruption of transmission, TBRI is positioned to lead future priorities, including advanced clinical management of the diseases and its complications, sensitive surveillance to detect any remaining areas of the disease, innovation in snail control, vigilance against drug resistance and development of scalable point-of-care tests.

This is a powerful story of how sustained public health action, combined with the dedicated work of an institute like the TBRI, can translate scientific knowledge into the elimination of a major national health burden.

Global elimination of schistosomiasis: updates, progress and challenges

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Schistosomiasis is a parasitic infection that can be acute or chronic, with debilitating effects such as anaemia, periportal fibrosis, hydronephrosis, complications of the genital tract, and an increased risk of HIV transmission. The WHO strategy to control and eliminate schistosomiasis relies on preventive chemotherapy for at-risk groups, health education and behaviour change, access to safe drinking water and sanitation, environmental management, and snail control.

The World Health Organization's 2021-2030 Roadmap for Neglected Tropical Diseases (NTDs) reiterates the goal of eliminating schistosomiasis as a public health problem globally and eliminating transmission in selected countries, in accordance with World Health Assembly Resolution 65.21.

Schistosomiasis is endemic in 79 countries and territories, with 254 million people requiring preventive chemotherapy in 51 countries with moderate to high transmission. The African region bears the heaviest burden, accounting for 91% of the global population requiring preventive chemotherapy for schistosomiasis.

Between 2006 to 2023, endemic countries reported a cumulative 1.1 billion people receiving preventive chemotherapy for schistosomiasis, of whom 75.8% were school-age children and 24.2% were adults. This has led to a significant reduction in the prevalence of the disease. However, as a result of global challenges such as climate change and migration, schistosomiasis is emerging in new areas where the disease was previously absent.

The elimination of schistosomiasis requires the sustained implementation of programmes to consolidate achievements and prevent any resurgence of transmission. This can be made possible by firm country ownership and a steady flow of financial resources that would also allow developing new tools, such as new diagnostics, medicines and vaccines, and scaling up innovative strategic approaches such as test-and-treat and the management of genital schistosomiasis.

Key words: Schistosomiasis elimination, public health problem, progress, challenges

A century of schistosomiasis history in the Democratic Republic of Congo: origins, current challenges, and a call for renewed research partnerships

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The Democratic Republic of Congo (DRC) carries one of the heaviest burdens of schistosomiasis in sub-Saharan Africa, yet national control efforts face persistent structural, security, and operational challenges. This review synthesizes published and unpublished data, expert insights, and national reports to analyze the disease's complex century-long trajectory.

While schistosomiasis cases were already sporadically noted in the 19th century, the 1923 Lemfu Mission outbreak marked a turning point, prompting sustained attention. We identify three critical phases: (1) *Pre-independence* (1885–1960), characterized by active research but no coordinated control; (2) *Post-independence* (1960–2012), where mapping expanded, transmission drivers such as mining, agriculture, population movement, artificial lakes and dam construction were progressively understood, but control relied on non-state actors. Research progressively declined amid political instability; and (3) *Post-2012 London Declaration*, during which the DRC reformed its health system, began national mapping and mass drug administration despite facing major governance and insecurity constraints. Scientific research, however, has remained limited in both output and institutional integration. Current barriers include fragmented health-research linkages, funding shortages, logistical hurdles due to the DRC's size and insecurity, and workforce gaps.

Early 2025, a new national consortium of researchers from eight Congolese institutions was formed to redefine research priorities in line with control goals and to build capacity for the next generation of schistosomiasis specialists. This calls for renewed partnerships to support locally grounded, evidence-based strategies to address this neglected but persistent disease in the DRC.

Control of schistosomiasis: Where are we?

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Schistosomiasis is a neglected tropical disease caused by parasitic trematodes of the genus Schistosoma, which continues to affect over 250 million people globally, and predominantly in sub-Saharan Africa. Control efforts have relied on preventive chemotherapy with praziquantel, delivered through mass drug administration (MDA) targeting school-aged children and high-risk populations. Despite its beneficial effect on reduced morbidity, reinfection remains a big challenge for effective schistosomiasis control.

To overcome this challenge, integrated control strategies have increasingly emphasized snail control, water, sanitation, and hygiene (WASH) improvements, health education, and surveillance systems. The WHO 2021–2030 NTD Roadmap set ambitious targets, including the elimination of schistosomiasis as a public health problem in all endemic countries by 2030. Advances in diagnostic tools, renewed investments in WASH infrastructure, and vaccine development are among other actions to improved control outcomes. However, challenges persist, including logistical difficulties in delivering MDA to remote populations, inadequate WASH coverage, limited resources for snail control, and the need for more sensitive diagnostic methods in low-endemicity settings, as well as an effective vaccine. Sustained political commitment, fund mobilization, cross-sector collaboration, and community engagement are essential for achieving long-term elimination.

Key words: Schistosomiasis, Reinfection, Control-tools.

Schistosomiasis through the ages – the pharma perspective

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The most ancient evidence of schistosomiasis dates back to more than 6,000 years ago in Northern Syria; though, schistosomiasis spread to Egypt as a result of the importation of monkeys and slaves under the dynasty of the Pharaohs and has been in active state of evolution in the African Great Lakes region where, still today, the vast majority of the over 250 million people affected by this disease live.

Schistosomiasis is also known as bilharzia, after German physician Theodor Bilharz, who first described the cause of urinary schistosomiasis in 1851. It is one of the 21 Neglected Tropical Diseases (NTDs).

After so many years, elimination of this disease represents still a global ambition. Pharma has played a significant role in this endeavor with the current standard-of-care treatment developed in the laboratories for parasitological research of Bayer and Merck in Germany in the 1970s.

Merck initiated its 'Schistosomiasis Elimination Program' in cooperation with WHO back in 2007. Through this initiative, Merck supports the requirements of the WHO's 2021-2030 Roadmap for NTDs, leading the global collaborative efforts to eliminate schistosomiasis as a public health problem. Each year, Merck provides up to 250 million tablets; more than 2 billion tablets have been donated so far, enabling the treatment of almost 900 million people, school-aged children and adults in sub-Saharan Africa. Latest results showed disease prevalence in sub-Saharan Africa decreased by 53%-67% over the last 10 years.

Collaborative efforts continue. Within a Consortium of partners, a new drug tailored for preschoolers has been introduced. Treatments for schistosomiasis are now available for all age groups. In addition, through its continuous investments into R&D for a next generation of drugs, health education, advocacy, Merck implements, together with its partners, a comprehensive approach towards the elimination of such a dangerous parasitic disease, second only to malaria.

Shedding new light on the reproductive development of female Schistosoma mansoni: how schistosome males and final hosts team up to turn "girls into women"

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In contrast to other platyhelminths, schistosomes have evolved separate sexes. Remarkably, egg production depends on the pairing-dependent maturation of female gonads – a unique feature of schistosome biology. While the molecular principles controlling female gonad differentiation remain largely unknown, transcriptomics research of recent years provided data sets helping to unravel developmental aspects. To this end, we performed bulk RNA-seq analyses and, for the first time, single-cell transcriptomics of gonads to discover genetic networks controlling the reproductive biology of female *Schistosoma mansoni*.

We extracted ovaries of paired females for single-cell RNA-seq with disassociated oocytes; 1,967 oocytes expressing 7,872 genes passed quality controls, and bioinformatics revealed four cell clusters: somatic cells, germ cells/progeny, intermediate-stage (IntO), and late germ cells. In IntO, we detected a highly transcribed transcription factor of the retinoic acid (RA) nuclear receptor (RAR) family, SmRAR, which is strongly regulated: stage-preferentially transcribed in adults, sex-preferentially in females, high abundantly in the ovary, and pairing-dependently in females and ovaries. RNAi demonstrated the decisive role of Smrar for oocyte differentiation and meiosis in paired females. In vitro, the addition of 9-cis RA led to elevated egg production of *S. mansoni* couples *in vitro*, while blocking RA signaling caused the opposite. This strongly suggests an additive influence of RA, and thus the host environment, for oocyte differentiation.

Based on our findings, we suggest a new role for the schistosome male. It may serve as a "biological technical assistant" for the female, which depends on pairing for SmRAR expression as prerequisite to "correctly interpret" the host environment for its development. This is a novel aspect of the reproductive biology of schistosomes and may be stimulating for young researchers to delve into this novel research subject.

Metabolic reprogramming and redox imbalance in host–parasite interactions

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Background & Aims: *Schistosoma mansoni* affects over 200 million people worldwide. While eggs are the primary mediators of liver pathology, the mechanisms linking parasite-induced metabolic changes and hepatocellular responses remain poorly understood. This study investigates how *S. mansoni* infection and egg presence alter host metabolism and provoke hepatocellular damage and proliferation through oxidative stress.

Methods: We employed a multi-modal approach in *S. mansoni*-infected hamster models and human hepatoma cells, including mass spectrometry imaging, metabolite profiling, live-cell imaging, gene/protein expression analyses, and histopathology. Functional experiments assessed the roles of oxidative stress and metabolic reprogramming. Key findings were validated in human liver biopsies from infected patients.

Results: *S. mansoni* infection led to hepatic depletion of neutral lipids and glycogen, accompanied by altered lipid species distribution and dysregulation of metabolic enzymes. Eggs actively incorporated host lipids, contributing to metabolic exhaustion in surrounding parenchyma. These changes induced oxidative stress, triggering a DNA damage response and the upregulation of replication licensing factors and cell-cycle regulators in hepatocytes. In vitro, soluble egg antigens stimulated hepatoma cell proliferation, which was reversed by antioxidants such as reduced glutathione.

Conclusion: *S. mansoni* infection and egg-induced metabolic reprogramming lead to redox imbalance and DNA damage, promoting hepatocellular proliferation. These findings reveal a mechanistic link between parasite metabolism and host liver pathology, highlighting oxidative stress as a potential therapeutic target in schistosomiasis-associated liver disease.

From Bilharz's twig to thriving tree: revealing the diversity of blood flukes

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Bilharz's discovery in 1851 of the first fluke formally known to live within blood vessels initiated a very much ongoing process of discovery involving many investigators that today recognizes a blood fluke Superfamily Schistosomatoidea containing 13 families and about 89 genera. Feeding on vertebrate blood is a trait they likely inherited from common ancestors with polyopisthocotylean monogeneans, recently recognized as the sister group to the trematodes. A case has been made for considering the blood flukes to be the primordial digeneans, not only because of pre-adaptations acquired from polyopisthocotylean-like ancestors, but for other reasons as well, including their 2-host life cycles and broad patterns of host usage. Blood fluke adults are found in an unparalleled spectrum of definitive hosts, ranging from chondrichthyans, acipenseriforms, teleosts, turtles, crocodilians, and birds and mammals. Eggs produced by adult blood flukes are striking in their diverse shapes and collectively vary over an order of magnitude in size. Blood flukes also infect a greater diversity of first intermediate hosts – marine polychaete annelids, marine bivalves and a broad variety of gastropods - than any other digenean group. Their larval stages are also diverse, ranging from small, ovoid daughter sporocysts or rediae producing few cercariae, to amorphous daughter sporocysts that produce prodigious numbers of cercariae. Blood fluke cercariae range from nearly tailless non-swimming forms to forms with partially forked tails to cercariae with long forked tails well-adapted to penetrate host skin. Additionally, members of the Schistosomatidae exhibit dioecy, and have subsequently evolved a variety of alternative egg-laying strategies, bringing us back to Bilharz's seminal discovery, a schistosome unique or nearly so among the entire superfamily for predictably ovipositing in the bladder wall. Additional discoveries and surprises await. Supported by NIH R37AI101438 and P30GM110907.

Molecular characterization of Bulinus spp. from Lambaréné and surroundings, Gabon

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Background: Schistosomiasis is a parasitic disease that can be acute and chronic, caused by blood flukes of the genus *Schistosoma*. These parasites have a complex life cycle involving freshwater snails as intermediate hosts. The geographical distribution of schistosomiasis depends on the presence of specific snail vectors, which vary by *Schistosoma* species and region. In Africa, snails of the genus *Biomphalaria* serve as intermediate hosts for *S. mansoni*, while *Bulinus* species transmit *S. haematobium*, *S. intercalatum*, and *S. guineensis*. In Gabon, where schistosomiasis remains endemic, previous reports have documented the presence of *Bulinus globosus* and *Bulinus forskalii*. However, reliable identification and classification of *Bulinus* species remain a challenge, particularly in field settings. To address this, we conducted molecular characterization of *Bulinus* snails collected in Lambaréné, Gabon.

Methods: Snail samples were collected from four sites in Lambaréné and its surrounding areas. DNA was extracted from individual snails, and several primer sets targeting the mitochondrial cytochrome oxidase subunit 1 (cox1) gene were tested for PCR amplification. The most effective primer set was used for Sanger sequencing. Sequence data were then analyzed to support species identification. This is also important for the EVASAB project.

Results: The results of the molecular analysis, along with morphological and molecular identification of the collected *Bulinus* species, will be presented at the meeting.

Modelling regulation of *Schistosoma* infection rates in snail populations

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Background: Much remains unknown about how biological interactions between human *Schistosoma* species and their snail host shape infection dynamics in natural snail populations. Field surveys in endemic regions show that snail infection rates are generally low and unassociated with prevalence in humans from the same focus, unless *Schistosoma* was recently introduced. This suggests self-limiting regulation of infection rates in snail populations, which could hamper schistosomiasis control efforts based on mass drug administration (MDA) in humans. Through mathematical modelling, we investigated whether genetically encoded resistance to *Schistosoma* infection in snails can describe the patterns in snail infection prevalences observed in nature.

Methods: We designed a deterministic model of *Schistosoma* transmission in snails. Infection susceptibility was modelled as a monogenic trait, with resistance being conferred by a dominant allele. To mimic the reduced fecundity often observed in laboratory-bred resistant snails, resistant allele homozygosity was assumed to be non-viable. For varying transmission rates between humans and snails, we studied snail infection dynamics after *Schistosoma* introduction, infection prevalence at equilibrium, and the effect of schistosomiasis control interventions.

Results: Simulating introduction of *Schistosoma* in a naïve snail population lead to a transient peak in infection prevalence, followed by a decrease to 11% in endemic equilibrium. If set sufficiently high, transmission rate did not affect the equilibrium state. Accordingly, MDA (i.e., reducing human-to-snail transmission) had no effect on snail infection prevalence.

Conclusion: Genetically encoded resistance with a reproductive trade-off can explain both outbreak dynamics and stable low endemic infection rates in snails. Including such snail traits in individual-based schistosomiasis models may improve predictions of snail-to-human transmission under declining human prevalence.

100 years of neglect in paediatric and genital schistosomiasis

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Updating standardized WHO assessment of schistosomiasis-related pathology with focused point-of-care ultrasonography

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Ultrasonography is used as a safe, fast, non-invasive, and relatively inexpensive technique for assessing chronic schistosomiasis-related pathology in clinical and field settings. A first standardized ultrasound protocol had been established by experts at a WHO-chaired meeting in Cairo, Egypt, in 1990. A reviewed protocol was later published in 2000. Scientific studies using the WHO-protocols showed that further amendments are necessary, and that sonomorphologic abnormalities due to Asian schistosomiasis (*Schistosoma japonicum* and *S. mekongi*) had not been addressed before.

A WHO-chaired expert group now reviewed the existing literature and established a standardized ultrasound protocol focusing on relevant and reproducible ultrasound findings caused by all *Schistosoma* species pathogenic to humans. A special focus on Asian schistosomiasis pathology summarizes the key elements of active and post-infectious lesions due to *S. japonicum*, such as liver lesions and danger signs, predicting severe outcome of the disease.

We present the "Basel protocol", supported by the latest research data, and discuss the rationale behind important protocol updates.

New insights on pulmonary schistosomiasis

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A precise timeframe to differentiate acute schistosomiasis (AS) and chronic schistosomiasis (CS) is not well defined. Based on recent published literature, lung nodular lesions in AS and CS seem to have the same pathophysiology, that is, eggs laid in situ by adult worms, during an ectopic migration. Moreover, the occurrence of lung nodules due to clusters of eggs and the systemic immunoallergic reaction of AS (Katayama syndrome) may be two separate clinical entities, which may overlap during the early phase of infection. Consequently, the classical distinction between AS and CS loses much of its conceptual validity. If adult worms play a more important role in the early phase of the disease the clinical management of AS should probably be revised.

Keypoints:

- The proportion of patients with chronic schistosomiasis diagnosed with pulmonary nodules seems much higher than previously described in the literature.
- Nodular lesions in chronic schistosomiasis are very similar to those described in acute schistosomiasis; both should be caused by clusters of eggs, and both may be unrelated to the presence of pulmonary symptoms.
- Katayama syndrome, which occurs also in patients infected by male parasites only, seems therefore not to be related to egg deposition.
- Adult worms can be found all over the body and 'ectopic' sites are more frequent than previously described.
- Focal lung lesions incidentally observed during chronic schistosomiasis seem to disappear spontaneously (or clearance may be accelerated by praziquantel), similar to what is known for pulmonary lesions observed during early infection.

Evaluation of the efficacy of alternative praziquantel treatment regimens in an endemic area for Schistosoma mansoni in Northeastern Brazil

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Introduction: Praziquantel (PZQ) treatment is the main strategy for controlling the morbidity and mortality caused by *Schistosoma mansoni* infection in endemic areas. However, its administration in a single dose appears to be insufficient to eradicate schistosomiasis, highlighting the importance of investigating new therapeutic regimens to improve efficacy.

Objective: To evaluate the efficacy of different PZQ regimens in combating *S. mansoni* infection in a highly endemic area of the state of Sergipe, northeastern Brazil.

Method: Participants with confirmed *S. mansoni* infection were randomized and treated with a standard single dose of PZQ (Group 1); or with two doses 24 hours apart (Group 2); or with two doses 30 days apart (Group 3). Efficacy was assessed 60 days (D60) after the completion of each treatment regimen, based on the detection of CAA in urine using the UCP-LF assay and the detection of eggs in stool using the Kato-Katz (KK) method.

Results: A total of 88 participants who tested positive for infection by both KK and UCP-LF CAA at baseline were included in this study. On D60, all three study groups achieved 100% cure rates (CR) according to KK. Lower CRs were revealed by UCP-LF CAA: 80.4% in Group 2, 57.7% in Group 3, and 56.3% in Group 1. The egg reduction rates (ERR) and infection reduction rates (IRR) observed via KK and UCP-LF CAA were 100% and >98%, respectively.

Conclusion: More sensitive antigen diagnostics showed that PZQ treatment with two repeated doses spaced over a shorter period (24 hours) led to the highest CR. A reduction in *S. mansoni* burden was observed over time, with ERR/IRR values in all groups exceeding the efficacy threshold established by the WHO (>90%). Cure rates varied according to the diagnostic method used, being overestimated when based on egg quantification, which highlights the importance of using more sensitive tools for detecting active infections and monitoring PZQ efficacy.

Keywords: Efficacy, Safety, Praziquantel, Schistosomiasis, *Schistosoma mansoni*, Brazil.

S. mansoni infection of HBsAg-transgenic mice elicits hepatocellular damage, hepatic decompensation and carcinogenesis

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Background: Schistosomiasis, one of the most prevalent neglected tropical diseases (NTDs), affects over 250 million people worldwide. Blood-borne *S. mansoni* eggs either penetrate the gut wall to migrate into the lumen, or become trapped in blood capillaries such as liver sinusoids.

Chronic infection with Hepatitis-B-Virus (HBV) causes hepatic inflammation and necrosis, ultimately leading to hepatocellular carcinoma (HCC) formation. HBV entry into hepatocytes is facilitated through three viral surface proteins collectively labeled HBV surface antigens (HBsAg). In a murine model, the postnatal expression of these surface antigens in hepatocytes leads to chronic liver injury, regenerative hyperplasia, adenomas and HCC.

Coinfections of *S. mansoni* and HBV occur disproportionally often in endemic areas and lead to a more rapid progression of liver pathology, increasing the incidence and mortality of HCC.

This project aimed to investigate their combined effects on hepatic carcinogenesis and metabolism.

Methods: Transgenic (tg) mice expressing all three forms of HBsAg were infected with *S. mansoni* at the age of 43 weeks. After nine weeks of infection, the animals were sacrificed. Liver-to-body weight ratios, ALT, glucose, and albumin levels, hepatic tumor numbers and sizes were determined and compared to infected wt-mice, as well as non-infected wt- and tg-control animals.

Results: *S. mansoni*-infected mice showed larger liver-to-bodyweight ratios than non-infected animals, while also exhibiting higher serum ALT levels. Glucose levels of infected tg-mice were significantly lower compared to both infected wt- and non-infected tg-animals. Additionally, infected tg-mice show lower albumin levels than wt- and tg-mice. Furthermore, infected tg-animals presented larger liver tumors and increased numbers of atypical nucleoli.

Conclusion: The observed increase in liver-to-bodyweight ratios and ALT levels suggest an additive effect on hepatocellular damage in HBsAg-tg-*S. mansoni*-infected mice compared to the individual disease models. Furthermore, decreases in serum glucose and albumin levels indicate hepatic decompensation. Tumor size and atypical nucleoli strongly suggest enhanced carcinogenesis in this co-infection model.

Prevalence of placental schistosomiasis and associations with adverse birth outcomes among pregnant women in Agogo, Ghana – Schisto-SGA/Agogo-2000

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Background: Schistosomiasis during pregnancy is associated with increased risk of adverse birth outcomes (ABO) such as low birth weight (LBW) or small for gestational age (SGA) [1]. Possible underlying pathophysiological mechanisms include placental inflammation, which can be induced by placental schistosomiasis (PS) [2]. Reliable data on the prevalence of PS and its association with ABO are sparse. One study from 1972 showed a prevalence of 20% based on a tissue maceration technique [3], which was confirmed in a newer study using polymerase chain reaction [4].

Methods: The design of the initial project was a cross-sectional study carried out between 2000 and 2001 in Agogo (Ghana) with the purpose to analyse associations of maternal malaria with ABO. Detailed data on the cohort (n=839) and residual samples (extracted DNA from peripheral maternal and placental blood) are still available. Samples are tested for the presence of schistosomiasis using a PCR protocol targeting Dra1. Prevalence of maternal and placental schistosomiasis will be assessed and its impact on prematurity, SGA and LBW calculated using multivariate analysis. Ethical approval for the original study was approved by the University of Science and Technology Kumasi and for the current retrospective analysis by the Kwame Nkrumah University in Kumasi (Ghana).

Results: Preliminary data will be presented at the conference.

Discussion: Assessing the prevalence of PS in endemic regions is a challenge and epidemiological data remain scarce. Meanwhile, maternal schistosomiasis poses a threat to maternal and newborn health. Better understanding of the relationship between maternal schistosomiasis and ABO would underline the importance of the urgently needed treatment of schistosomiasis in pregnant women and young women of reproductive age and provide further rationale for treatment recommendations.

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Session IV - Drugs and Diagnostics

Date / Time: Thursday, October 9th, 11:20 AM - 12:55 PM

Novel drugs for schistosomiasis

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Schistosomiasis is a debilitating parasitic disease responsible for a huge public health burden. Female genital schistosomiasis (FGS) affects up to 56 million women in sub-Saharan Africa, causing infertility, ectopic pregnancy, miscarriages, and an increased risk of HIV infection in girls and women across the continent. Treatment and control relie on a single drug, praziquantel. Yet with concerns of drug resistance, along with the drug's other drawbacks, the scientific community has recognized an urgent need for the development of new treatments. Moreover, there is currently no treatment for the morbidity of FGS. Hence, this is a key moment to expand antischistosomal drug discovery efforts. Drug repurposing is a widely used strategy in drug discovery for underfunded diseases and might help to quickly advance novel antischistosomal lead compounds. In this presentation, I will summarize results from *in vitro* and *in vivo* evaluation of antimalarials and antimalarial-praziquantel combinations on *Schistosoma mansoni* including pharmacokinetic studies. I will give an update on our work with derivatives from a former Hofmann La-Roche lead compound Ro- 13-3978. Lastly, I will provide insights on our work to contribute towards a treatment for FGS morbidity, by establishing preclinical models to evaluate pharmaceutical treatment options.

A decade of learnings in schistosomiasis drug discovery and beyond

Thomas Spangenberg[1].

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Schistosomiasis, a neglected tropical disease caused by parasitic blood flukes of the genus *Schistosoma*, affects approximately 240 million people globally, with significant morbidity and mortality in endemic regions. The current treatment, praziquantel (PZQ), has been the cornerstone of schistosomiasis management since its approval in 1980. However, imperfect cure rates with limited activity beyond adult worms as well as rising concerns regarding drug resistance have prompted the need alternatives to PZQ.

To achieve this goal, it is essential to have a deep understanding of PZQ. Hence an overview of a decade of research is given starting with some historical considerations of the drug. The status of our knowledge will be provided such as its the mode of action, the pharmacodynamic and pharmacodynamic relationship as well as the contribution of the metabolite to the overall clinical activity and potential drug resistance.

Next a repertoire of activities will be discussed focusing on the discovery of new therapeutic interventions to combat this neglected tropical disease as well as highlighting research gaps and open innovation initiatives.

Instrument-free bead-based method for capturing and concentrating Schistosoma antigen (CAA) for use with lateral-flow diagnostic tests

Danielle de Jong[1], Andy Wende[2], Pytsje T. Hoekstra[1], Govert J. van Dam[1], Paul L.A.M. Corstjens[1].

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Detection of circulating anodic antigen (CAA) is well-known as an effective means to diagnose active *Schistosoma* infections. The Lateral Flow (LF) based CAA assay with high sensitivity luminescent Up-Converting reporter Particles (UCP), is an effective way to detect the antigen in serum and urine. However, for the preferred non-invasive specimen urine, detection requires concentration of CAA as well as removal of proteinaceous material. The current preanalytical workflow comprises TCA extraction followed by ultrafiltration of urine, a workflow difficult to deploy in Point-Of-Care settings.

This work aimed at advancing the preanalytical part of CAA testing from urine specimens in a multitude of aspects: time, complexity, instrumentation, and cost. Ideally, all that is improved without compromising on the analytical performance of the overall workflow. The final goal is to deploy such preanalytical module together with the UCP-LF CAA assay in endemic countries to equip health workers with a true POC solution strengthening their toolset for tackling Schistosoma infections.

We have developed a method based on the use of paramagnetic microparticles employing a simple "bind & elute" scheme to concentrate and purify the CAA from urine specimens. The eluate can directly be applied to the UCP-LF CAA assay. This advanced preanalytical workflow takes only 10 minutes and requires no instruments such as a high-speed centrifuge. The procedure's input volume as well as its analytical sensitivity is equivalent to the established ultrafiltration-based protocol. First data with clinical specimens indicate consistent clinical performance.

We established a preanalytical workflow that streamlines the diagnosis of *Schistosoma* infections by the UCP-LF CAA assay. It reduces sample preparation time from 45 to 10 min. The use of magnetic beads versus ultrafiltration columns allows a cost-efficient preanalytical step that can be optimized for field-deployment in low-resource settings.

Identification of a circulating carbohydrate antigen as a highly specific and sensitive target for schistosomiasis serology

Anna O. Kildemoes[1], Tom Veldhuizen[1], Lisette van Lieshout[1], Taniawati Supali[2], Daniel Camprubí-Ferrer[3], Jose Munoz[3], Leo Visser[1], Sammy M. Njenga[4], Meta Roestenberg[1], Angela van Diepen[1], Cornelis H. Hokke[1].

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The World Health Organization (WHO) 2030 roadmap for schistosomiasis calls for development of highly sensitive and specific diagnostic tools to continue and sustain progress towards elimination. Serological assays are excellent for sensitive detection of primary schistosome infections and for schistosomiasis surveillance in near- and post-elimination settings. To develop accurate assay formats, it is necessary to identify defined antibody targets with low cross-reactivity and potential for standardized production. We aim to identify such target(s) with focus on defined schistosome glycan antigens. Target identification was performed by assessing antibody responses in well-characterized cross-sectional and cohort sample sets (n = 366 individuals) on tailor-made antigen microarrays. IgM and IgG binding to candidate diagnostic targets was measured for serum/plasma samples from controlled human schistosome infection models, schistosome-infected travelers, soil-transmitted helminth-infected individuals, and non-infected individuals. We found that antibodies to a schistosome gut-associated glycan, the circulating anodic antigen (CAA), identify schistosome infection with high sensitivity (IgM ≥100%, IgG ≥97%) and specificity (IgM ≥93%, IgG ≥97%) in the test samples. Infection dose affected timing of anti-CAA antibody isotype switch. Furthermore, we demonstrate that other non-specific glycan epitopes in crude schistosome cercarial and egg antigen preparations can contribute to generation of false schistosomiasis positives, which is relevant for current serological assays based on these antigen mixtures. In conclusion, CAA is an excellent single glycan antigen target for development of highly sensitive and specific tools for schistosomiasis serology with use cases for travelers and surveillance in near- and post-elimination settings, as well as emerging transmission zones.

Diagnostics for male genital schistosomiasis: preliminary findings from a cross-sectional study of Zambian men

Bronwyn Neufeld[1], Sergio España-Cueto[2,3], Rhoda Ndubani[4], Lisette van Lieshout[5], Bonnie L. Webster[6], Maina Cheeba[4], Isaac Mshanga[4], Lucas Cunningham[7], Sekeleghe Kayuni[7,8], J. Russell Stothard[7], Kwame Shanaube[4], Amaya L. Bustinduy[1].

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Male genital schistosomiasis (MGS), a gender-specific manifestation of urogenital schistosomiasis, typically results from the entrapment of *Schistosoma haematobium* eggs within the male genital tract. There are no current and accurate estimates of the burden of MGS, due to disease underreporting primarily from diagnostic challenges and a lack of general awareness within the health system. Semen microscopy for *Schistosoma sp. ova* is typically used for diagnosis though this technique suffers from low sensitivity and lacks protocol standardization. The introduction of molecular diagnostics, such as polymerase chain reaction (PCR), has partly helped overcome the challenge of low sensitivity, but has limited applicability in resource-constrained settings. This cross-sectional study seeks to recruit 300 men over 18 years of age from households of women who are enrolled in an ongoing study on female genital schistosomiasis across three sites of varying endemicity in Zambia. The aim of the study is to investigate the prevalence of MGS by different diagnostic assays and evaluate their performance. After informed consent and a symptom questionnaire, participants provide biological samples including semen, urine, and finger prick blood. Participants also undergo examination with a portable ultrasound to assess urogenital morbidity. Parasitological methods on semen and urine are used for *S. haematobium* egg detection and qPCR for the detection of Schistosoma sp. DNA in semen. The performance of each diagnostic test (microscopy, qPCR) will be assessed using a composite reference standard of any positive test for infection. Data collection is currently ongoing and preliminary results will be presented.

Developing machine learning tools for the enhanced detection of female genital schistosomiasis in cervical images

Morgan E Lemin[1], Amaya L Bustinduy[1] & Chrissy h Roberts[1].

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The exponential growth in machine learning has led to significant developments in how the medical community diagnoses disease, particularly through computer vision applications. One promising application of this technology is the enhanced detection of female genital schistosomiasis (FGS), a neglected tropical disease that causes significant morbidity in up to an estimated 56 million women and girls, mostly within Sub-Saharan Africa. However, sufficiently annotated FGS images remain scarce, which is hampering the progress of computer vision.

Results from a preliminary binary classification computer vision tool will be briefly presented. This model used a supervised convolutional neural network architecture to classify cervical images as either FGS-positive or FGS-negative. The model yielded a specificity of 76.9% (95% CI 57.9%-89.0%) but low sensitivity (56.2%, 95% CI 33.2%-76.9%), demonstrating challenges related to poor training data. These results provide an encouraging baseline for the ongoing development of more complex models.

Work is now underway to develop more complex models, including the application of unsupervised machine learning and the use of over 20,000 colposcope images taken across three FGS field studies in Zambia and Malawi. Ongoing work focuses on addressing key obstacles such as poor ground truth definition and image annotations of variable quality and granularity. Despite these challenges, computer vision holds considerable promise for deployment in the low-resource settings, where FGS is endemic and where machine learning tools could significantly enhance diagnostic capacity.

Session V - Immunology, Metabolomics and Microbiome

Date / Time: Thursday, October 9th, 2:45 PM - 4:40 PM

Immunological consequences of maternal schistosomiasis

Clarissa Prazeres da Costa[1].

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Schistosomiasis, a major parasitic disease affecting over 200 million people worldwide, poses unique challenges for women of reproductive age, of whom an estimated 40 million are chronically infected. Increasing evidence demonstrates that maternal helminth infection profoundly influences offspring immunity through fetomaternal immune cross-talk, altering T cell priming, dendritic cell function, and B cell development. These effects extend into adulthood, shaping susceptibility to allergies, infections, and vaccine responses. Murine models show that maternal schistosomiasis imprints long-lasting immune modulation, with altered CD4+ and CD8+ T cell responses, alongside dendritic cell reprogramming. Beyond direct immunological effects, maternal infection modifies the microbiota and bile acid metabolism, although these changes are not directly transferred to offspring, suggesting complex prenatal and postnatal influences. Importantly, treatment with praziquantel (PZQ) during pregnancy not only reduces maternal morbidity but also reawakens anti-parasite immunity, enhancing cytokine responses and improving resilience to pregnancy-associated stress. Offspring of PZQ-treated mothers exhibit reduced worm burdens, restored protective IgE responses, and enhanced cytokine production upon infection, indicating transgenerational immune priming. High-dimensional immune profiling reveals that PZQ modifies B cell and dendritic cell subsets, shifting offspring immune responses from tolerance toward effective parasite clearance. Collectively, these findings highlight maternal schistosomiasis as a critical determinant of immune system development and demonstrate that prenatal anthelminthic treatment can counteract parasite-induced immune suppression. These results provide mechanistic support for the World Health Organization's recommendation of PZQ treatment during pregnancy, emphasizing its potential to improve both maternal health and offspring immune competence in endemic regions.

Regulation of schistosomiasis by the host gut microbiome

Thabo Mpotje[1,2,3], Martin Gael Oyono[4], Leonel Meyo Kamguia[4,5], Leonel Javeres Mbah Ntepe[4], Moise Wokam[4], Bernard Marie Zambo Bitye[4], Ornella Alactio[4], Severin Donald Kamdem[1], Paballo Mosala[1,2], Nada Abdel Aziz[1,2,6], Donald D. Nyangahu[2,7], Fungai Musaigwa[1,2,8], Erve Martial Kuemkon[9], Francis Konhawa[9], Gladys K. Tchanana[9], Frungwa Nche[10], Alim Oumarou[11], René Ghislain Essomba[9,10,11], Michel Kengne[9], Marie Claire Okomo Assoumou[11], Katie Lennard[12], Claudia Demarta-Gatsi[13], Thomas Spangenberg[13], Frank Brombacher[1,2], Justin Komguep Nono[1,2,4,*#].

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Schistosomiasis continues to afflict mankind globally. Owing to its clear efficacy in killing adult worms, treatment with praziquantel is the current most cost-effective approach to therapeutically control the infection and limit the associated morbidity. However, treatment does not prevent reinfection and is not effective against non-adult forms of the parasite and poorly, if at all, directly resolve pathology. This is further compounded by the absence of effective vaccines, early detection and morbidity monitoring tools for the sustainable control of the infection and associated disease.

The host gut microbiome has recently gathered an increasing amount of interest from infectious disease specialists and non-communicable diseases researchers alike. In fact, it is well recognized now that the host gut microbiome constitutes a potential exploitable tool to monitor and perhaps influence the progression several diseases but its role during schistosomiasis is still superficially known.

Here, we show comprehensive gut metagenomic signatures of school-aged children from *S. mansoni* endemic areas and report on differential gut microbes that robustly associate with either infection and/or pathology, independently from underlying diverse host genetic profiles. A regulatory role of the gut microbiome at the clinical level is hereby suggested. Mechanistically, we explore such a possible regulatory role and demonstrate that fecal microbiota transfer (FMT) between mice by coprophagy is sufficient to transfer resistance to disease during chronic schistosomiasis and rescue from morbid death.

Taken together, a case for the central regulation of the host susceptibility to schistosomiasis by gut microbes, independently from the host genetic background and environmental influence, is hereby unprecedentedly suggested.

Effects of the prenatal maternal environment on the foetal immune system at birth

Juliet Karger[1,2,3], Achala Kamaladasa[1,3], Ulrich F. Prodjinotho[1,3], Sèyigbena P. Déo-Gracias Berry[1,3], Esther Ludwig[1,4], Meral Esen[5], J. Honkpehedji[4], Ayola Akim Adegnika[4,5], Silvia Lobmaier[2,6], Clarissa Prazeres da Costa[1,3,7].

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Background: The effect of the environment on the immune system is increasingly appreciated as studies indicate that differences in immune response between geographically and economically distinct regions are identified. The mother provides the growing baby with its first environment. The main objective of this study is to identify potential differences in cord blood immune cell types based on the distinct geographical locations where the mother resided during the pregnancy.

Methods: Mothers' peripheral blood (PBMC) and foetal cord blood (CBMC) were collected from healthy mother-child dyads in Germany and Gabon at birth. The phenotype and functionality of immune cells in both PBMC and CBMC fractions were identified with full-spectrum flow cytometry using two panels with 28 markers each. The protein profile of the samples collected was measured with the OLINK inflammatory panel.

Results: There are three study populations in this study: German mothers in Germany, recent Immigrant African mothers living in Germany, and Gabonese mothers in Gabon. High-dimensional analysis, including FlowSOM and UMAP, revealed significant differences in T and B cell subset distributions among the three populations. Accordingly, Gabonese mothers showed a more differentiated and chronically activated immune profile compared to German mothers. Interestingly, the newly immigrated African mothers followed the same trends as the German mothers. Ongoing analyses will provide further insights into these population-specific immune landscapes. Further initial analysis of 92 proteins in this cohort shows a distinct protein profile between mothers and cord dyads from Germany compared to Gabon.

Conclusion: This research advances understanding of how environmental factors shape precursor and immune cell development, contributing to the developmental origins of health and disease theory.

Individually or as a team - The immunological milieu in the lung caused by migrating single-sex or mixed-sex larvae of *Schistosoma mansoni*

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While the lung is considered an efficient site for stopping the larvae of the acute. Infection phase from migrating through extensive inflammatory responses in the surrounding tissues, little is known about these processes. To date, the highest resistance to infection has been achieved in experimental studies with radiation-attenuated cercariae immunization, which elicits a strong Th1/Th2 response in the lung and results in up to 80% protection. Based on our own studies demonstrating a systemic, unpolarized Th1/Th2 response resulting from infection with male or female *Schistosoma mansoni*, we hypothesize that this atypical immune response is already detectable during the pulmonary passage of parasite larvae. Therefore, we examined the immune milieu in the lungs of mice caused by migrating schistosome larvae, either male or female (single-sex groups) or male + female (bisexual control), 4 and 16 days after infection in bronchoalveolar lavage and lung tissue by flow cytometry, qPCR, and multiplex analyses. Our results show only minor differences in the inflammatory profile between the single-sex groups but significant differences compared with the bisexual control group. Both single-sex infected groups have increased expression of inflammatory markers in lung tissue, higher numbers of cytotoxic T cells (day 4 post-infection) and more T helper cells (day16 post-infection), compared with the bisexual control group. A single-sex infection, regardless of whether it is an infection with male or female cercariae, causes an immune milieu in the lung that is clearly different from an infection with both sexes. In terms of identifying therapeutic targets to achieve resistance to re-infection, it is of great scientific interest to identify the differences in the inflammatory potential of male or female and male +female parasites.

Is IPSE from *Schistosoma mansoni* eggs a light chain-selective IgE-binding factor?

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Schistosoma mansoni eggs are immature after oviposition, but achieve a remarkable maturation and size increase while migrating through the tissues before reaching the gut lumen about a week later. During maturation, a distinct, biosynthetically active multi-layered structure develops underneath the egg shell. Schistosome eggs have been likened to slow release capsules, which mature and release proteins as they migrate through the tissues, ultimately ensuring that only mature eggs reach the lumen of the gut. One prominent secreted protein, identified in 2003, called IPSE (for Interleukin-4 Inducing Principle from Schistosome Eggs), was shown to be an IgE-binding factor, capable of activating basophils purified from peripheral blood of immunologically naïve donors, by inducing IL-4 and IL-13 release.

We were interested in understanding the mechanisms behind binding of IgE by IPSE, which is mediated via the constant region of the IgE, independently of its specificity. We created six different IPSE single and double mutants by swapping suspected critical residues to Alanine or Leucine, expressed them recombinantly in HEK293-6E cells grown in suspension, and assessed their ability to induce activation of a luciferase-based IgE reporter system. Two mutants almost completely ablated the ability of IPSE to activate the IgE reporter system: C132A, a cysteine residue known to be involved in homodimer formation, and T92Y/R127L, while T92Y/R127A, R127A and R127L showed a moderate reduction in functional activity.

By expressing various truncated IgE molecules, ranging from an IgE only consisting of Cε3-Cε4 Cε2-Cε4 as well as a full length IgE-motavizumab (Cε1-Cε4 with κ-light) chains, we were able to show that IPSE requires a full-length constant chain Cε1-Cε4 of IgE. Our preliminary data also points to a strong preference of IPSE for IgE-λ compared with IgE-κ. We are currently attempting to verify and quantify this binding preference using isothermal titration calorimetry.

Session VI - Multidisciplinary perspectives including implementation science

Date / Time: Thursday, October 9th, 5:10 PM - 7:05 PM

Beyond the parasite: a multidisciplinary lens on accelerating schistosomiasis control and elimination

Ghyslain Mombo-Ngoma[1].

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Despite decades of interventions, schistosomiasis remains a major public health burden. This keynote will explore how multidisciplinary approaches—including epidemiology, behavioral science, environmental engineering, genomics, and policy—can converge to accelerate elimination efforts. Through the lens of implementation science, we will examine how real-world constraints, stakeholder engagement, and systems thinking shape the effectiveness and scalability of interventions. The talk will highlight case studies from endemic regions, and propose a framework for embedding implementation research into national programs and cross-sector partnerships.

Triggering shifts in the management of schistosomiasis through implementation research: lessons learnt from Madagascar

Daniela Fusco[1].

[1] Implementation Research group at the Bernhard Nocht Institute for Tropical Medicine

The World Health Organization (WHO) set the goal of eliminating schistosomiasis as a public health problem by 2030. Yet, the majority of endemic countries are far from achieving this ambitious goal. Among those, Madagascar ranks fifth in terms of prevalence with peaks of 60% among adult populations that are systematically excluded from control programs.

Since 2018 the BNITM has established a stable partnership in Madagascar aimed at implementing and testing the effectiveness and feasibility of innovative control programs for schistosomiasis. Vulnerable populations such as small children and pregnant women, so as adult populations at high risk of exposure and of developing chronic conditions were targeted for our interventions. Different implementation research frameworks were adopted on the basis of the specific program and the different stakeholders involved in the project.

Our studies contributed to the establishment of a direct collaboration with the national program for the fight against schistosomiasis setting new priorities for the country in order to push forward the WHO target of elimination. With our studies we managed to provide proofs of principle for the establishment of (i) treatment programs for pre-school aged children, (ii) integrated services at the primary level of care for the management of women's health (iii) adapted strategies for the ante-natal care services. Additionally, our studies contributed to prove very high safety for the treatment with Praziquantel of vulnerable groups such as pregnant women and toddlers. Furthermore, many of the lessons learnt in Madagascar are being now translated to other countries in order to generalise the findings and increase their impact towards a global change in schistosomiasis control strategies. Last but not least, over the course of the years we offered free of charge treatment and medical care assistance to more than 20.000 individuals proving the direct impact of implementation research on the overall well-being of the populations included in the studies.

Scanning shells to support research - Creating a digital collection of schistosomiasis host snails for science and education

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Schistosomiasis is a parasitic disease caused by schistosomes and transmitted by freshwater snails. It is one of the most significant neglected tropical diseases, responsible for approximately 300,000 deaths annually, primarily in sub-Saharan Africa. Many schistosomiasis control programmes focus on mapping host snail populations and eradicating them in endemic areas. These efforts depend on the accurate identification of snail host species, often requiring assistance from individuals who lack formal training in malacology.

Our project aims to support malacological education and disseminate knowledge about schistosome-transmitting snails. The Natural History Museum in London houses one of the world's largest and most important collections of gastropod shells. Many of these specimens hold scientific value not only from a taxonomic perspective but also because some are known intermediate hosts of schistosomes.

We digitised a portion of the museum's African snail collection known to transmit schistosomes. Each shell was photographed, and micro-computed tomography (micro-CT) was used to create high-resolution 3D mesh models. These models were further optimised for 3D printing. All digital 3D models have been uploaded to the open-access platform Sketchfab, where they are freely available for download. Additionally, we demonstrate a method for producing large-scale 3D-printed replicas, which, when painted, serve as highly accurate representations of the original shells.

This online catalogue of digital 3D models represents a valuable tool for teaching shell morphology and raising awareness about schistosomiasis, particularly in endemic regions. Moreover, the methodology presented here can be easily applied to similar collections in other museums, allowing for the digital preservation of scientifically important and fragile specimens and their use in education, research, and public outreach.

Closing the treatment gap: social science perspectives on introducing new pediatric schistosomiasis treatment for preschoolers in Uganda

Isabelle Lange, Stella Neema, Dianne Verhoeven, Laura Roth, Lisa Riegl, Joseph Kimera, Andrea Winkler.

Despite growing global efforts to control schistosomiasis, a significant treatment gap remains for children under six. Of the estimated 250 million people affected by the disease, approximately 50 million are preschool-aged children (PSAC), a group historically excluded from mass drug administration. In response, the public-private Pediatric Praziquantel Consortium has developed a new pediatric treatment option which is suitable for preschool-aged children (3 months to 6 years of age). This new 150mg tablet – palatable, small in size, easier to dose, and water-dispersible – aims to improve acceptability among very young children and their parents.

In 2025, following the positive scientific opinion by EMA on the new medication, the ADOPT project piloted its distribution in Uganda and Côte d'Ivoire, with Kenya to follow, testing two approaches under conditions simulating real-world practice (fixed-point and door-to-door distribution). This paper presents preliminary social science results evaluating the pilot in Uganda, for which we employed a multimethod, participatory approach. We conducted in-depth interviews, focus group discussions, observations and transect walks with parents of PSAC, community health workers, healthcare providers, local leaders, and district health authorities. We also administered a survey with parents of PSAC to gather quantitative data on awareness, preferences, and experiences with the intervention.

Findings underscore how community histories, lived experiences, and local priorities critically shape the reception of this health intervention. Key factors influencing the delivery and uptake included trusted sources of information, convenience of delivery, incentives for distributors, and the legacies of previous health campaigns. Drawing on cross-country comparisons, we reflect on practical considerations for introducing this new drug and offer critical insights for future schistosomiasis campaigns targeting preschoolers.

Enhanced preventive antiparasitic treatment for better health of African pregnants and their babies

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Pregnant women in Africa are exposed to considerable health risks, with parasitic infections being a major threat. Schistosomes, soil transmitted helminths, and malaria parasites are highly prevalent and polyparasite infections are common. In pregnancy, besides iron deficiency parasites are a key factor causing anaemia associated with an increased risk of maternal and infant morbidity and mortality. More than 50% of the pregnant women are affected by anaemia and an estimated 0.8 million pregnant women globally have severe anaemia.

Antenatal care is a health program to regularly deliver health services including preventive measures with the aim of improving maternal and newborn health. In terms of fighting parasitic diseases, WHO recommends to preventively treat soil-transmitted helminths, schistosomes and malaria parasites. In many endemic sub-Saharan African countries, however, these recommendations are often only partially implemented and not consistently applied in daily antenatal care. Reasons are multifactorial but hesitation in administering multiple drugs this vulnerable population and the complexity of integrating the use of multiple drugs into the antenatal care schedule. On the other hand, data is accumulating that outweighs the potential risk of antiparasitic drug intake versus health benefits.

The project aims to increase the uptake and integration of presumptive antiparasitic treatment during pregnancy to combat anaemia and improve health outcomes for pregnant women and their babies in sub-Saharan Africa. To this end, a multi-country trial will assess the safety, tolerability and efficacy of co-administered antiparasitic drugs. Pharmacokinetic data, cost-effectiveness analysis and public health stakeholder's involvement will further strengthen the case for future implementation of co-administered antiparasitic drugs in antenatal care schedules. Training in African scientific leadership will contribute to a critical mass of highly trained professionals.

Session VII - Epidemiology and Prevention

Date / Time: Freitag, October 10th, 9:00 AM - 10:50 AM

Schistosomiasis control revisited: insights from the Corsican outbreak and emerging epigenetic and genetic strategies

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Despite 200 years of research, breaking the schistosome life cycle remains a persistent challenge. Core interventions—limiting water contact, controlling snail vectors, and treating infected individuals with praziquantel—have yielded substantial progress in many endemic regions. Yet, true eradication remains distant, with the WHO's targets appearing increasingly optimistic.

The autochthonous schistosomiasis outbreak in Corsica (2013–2019) illustrates both the success and fragility of current control frameworks. Genomic analyses identified a *Schistosoma haematobium* × *S. bovis* hybrid, likely introduced from Senegal. No infected intermediate hosts were found despite intensive surveys, and potential animal reservoirs remained unidentified. Human transmission persisted at low levels, possibly sustained by undetected local reservoirs and limited compliance with non-pharmaceutical measures. Notably, transmission may have been interrupted by COVID-19-related travel restrictions rather than by active control.

This case underscores the need for more robust, resilient interventions. Our lab is exploring next-generation strategies, including epigenetically modified *Biomphalaria spp*. with altered susceptibility to infection and CRISPR-based gene drives targeting schistosome reproductive success. These molecular approaches aim to supplement conventional measures and provide long-term disruption of transmission by focal treatment.

Prevalence of *Schistosoma haematobium* infection and associated factors among children aged 3 to 14 years in Klouekanme District, Southern Benin

Francis Bohissou[1,5,6], Lazare Hounsou[1], Nicaise Denis C. Djegbe[1,3,4], Robinson Woli[1], Diolinda Nahum[1], Salomon Dossou[1], Charlotte Kpohonnou[1], Rodrigue Sondjo[a], Germain G. Padonou[1,2], Jana Held[5], Martin Akogbeto[1].

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Background: Urinary schistosomiasis remains a public health concern, particularly among young children in sub-Saharan Africa. Despite the ongoing nationwide mass drug administration campaign, sporadic outbreaks have been reported in certain districts of southern Benin. This study aimed to evaluate the prevalence of *Schistosoma haematobium* infection and identify associated risk factors among children aged 3 to 14 years in Klouekanme, a rural area in southern Benin.

Methods: A cross-sectional study was carried out in August 2024 involving 502 children aged 3 to 14 years from the communities of Lanta and Ahogbeya in the Klouekanme district. Urine samples were collected and centrifuged, with microscopy employed to identify *Schistosoma haematobium* eggs. Information on potential risk factors for schistosomiasis was gathered using a semi-structured questionnaire. Bivariate and multivariate logistic regression analyses were conducted to determine significant risk factors for infection.

Results: The prevalence of *Schistosoma haematobium* infection was 24.3% (122/502; 95% CI: 13.0–19.0). Statistically significant associations were observed for residing in Lanta compared to Ahogbeya (OR = 2.62; 95% CI: 1.48–4.59), frequent contact with swamps (OR = 9.29; 95% CI: 3.77–30.91), use of unprotected water sources (OR = 2.00; 95% CI: 1.25–3.22), and being older than five years compared to children under five (OR = 4.00; 95% CI: 2.11–8.43).

Conclusions: Despite the widespread use of Praziquantel to reduce the morbidity of schistosomiasis in this area, the disease remains highly prevalent. Its persistence is associated with exposure to unprotected water sources and swamps, underscoring the importance of strengthening Water, Sanitation, and Hygiene (WASH) initiatives within the community. Nonetheless, further research is needed to gain deeper insights into the molecular distribution of the parasite and to reassess the current efficacy of Praziquantel.

Keywords: *Schistosoma haematobium*, prevalence, associated factors, Benin

Declining prevalence of *S. mansoni* infection and periportal fibrosis after four rounds of mass drug administration with praziquantel among adult population on Ukerewe island, north-western Tanzania

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Background: In Tanzania, control and elimination of intestinal schistosomiasis relies on mass drug administration (MDA) with praziquantel (PZQ), targeting high-risk communities. Over four years, adult residents in 20 villages on Ukerewe Island received repeated MDA. Here, we report changes in *S. mansoni* infection prevalence and periportal fibrosis after four treatment rounds.

Methods: After four PZQ rounds, a cross-sectional survey included 3,639 adults (≥18 years) from 20 villages. Each participant provided a stool sample screened for *S. mansoni* using the Kato-Katz technique. Among them, 1,992 underwent abdominal ultrasonography (Niamey protocol) to detect *S. mansoni*-related hepatosplenic morbidity. Demographic and clinical data were collected via questionnaire.

Results: The overall prevalence of *S. mansoni* infections was 12.6% (95% CI: 11.6-13.7), representing a 58.6% decline from the baseline prevalence of 30.4%. Most infections had low (38.4%) or moderate (48.9%) intensity. Six villages maintained prevalence below 10%, while 14 remained above 10% but still below baseline. The prevalence of periportal fibrosis (PPF) was 12.9% (95% CI: 11.5–14.5), a 73.2% decline from baseline (48.1%). However, splenomegaly, hepatomegaly, and portal vein dilatation increased by 24.9% (from 40.5% to 50.6%), 21.7% (from 66.2% to 84.6%), and 1.9% (from 67.7% to 69%), respectively.

Conclusion: Four years of mass drug administration have successfully reduced the prevalence of *S. mansoni* infection and related periportal fibrosis. However, these findings indicate that more than four rounds of treatment are necessary to further reduce the prevalence of hepatosplenic morbidities associated with *S. mansoni* infection. Additionally, treatment should be complemented by improvements in clean water supply, sanitation, and hygiene interventions to halt or further reduce the transmission intensity of *S. mansoni* infection.

Co-infections galore: *Schistosoma haematobium* and species interactions in Malawi

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Schistosomiasis was first described in Egypt by Bilharz but the 'same' disease was likely present in the southern cone of Africa although being caused perhaps by different species. Though outside this talk's remit to debate the existence of *Schistosoma capense*, today I elaborate on Bilharz's original and understandable oversight - the importance of mixed species infections. In so doing, I present key epidemiological and clinical findings from our four year multi-disciplinary study entitled HUGS (Hybridisation in UroGenital Schistosomiasis). Starting in 2021, the HUGS study took place in southern Malawi where I spotlight the public health importance of *Schistosoma mattheei*, together with *Schistosoma haematobium* and *Schistosoma mansoni* co-infections. Previously, *S. mattheei* was considered a common parasite of livestock in southern Africa but now has a growing reputation for its ability to infect people, either in pure or in hybrid forms. Indeed, *S. mattheei* has been recently incriminated in both female and male genital schistosomiasis and its transmission does not appear to respond well to current preventive chemotherapy; we can even speculate upon a cryptic historical connection back to *S. capense* by ancestral hybridisation(s) with other sympatric schistosomes locally. As we celebrate Bilharz's legacy, we can now better frame the One Health intervention needed and future control efforts required to move towards WHO's ambitious 2030 public health targets and beyond.

Advancing schistosomiasis control: integrative modelling with SchiSTOP

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Mathematical modelling has become a crucial tool for informing control and elimination strategies for schistosomiasis. Building upon SchiSTOP, a new individual-based modelling framework, we have addressed several critical aspects to enhance schistosomiasis control efforts. We showcase multiple studies illustrating how SchiSTOP modelling effectively answers epidemiological questions and informs public health strategies.

First, we underscore the necessity of integrating a refined representation of immunity and intermediate host dynamics into models. This improved understanding is pivotal for accurately predicting long-term transmission trends and assessing intervention effectiveness. Further, SchiSTOP was extended to inform optimal field data collection strategies by modelling different sampling processes, including frequency, diagnostic tests (such as Circulating Anodic/Cathodic Antigen (CAA/CCA) assays), and targeted age groups. Enhanced algorithm efficiency has significantly accelerated model calibration and prediction, increasing the practicality of these models in real-world scenarios.

Furthermore, we explored the impact of treating pre-school age children (pre-SAC) using newly available paediatric praziquantel l formulations. Incorporating a morbidity module into SchiSTOP allowed comprehensive health outcome assessments, demonstrating potential disease burden reductions through early intervention. Additionally, cost-effectiveness analyses of treatment delivery platforms were conducted in two Ugandan parishes, guiding resource allocation and policy decisions.

Currently, efforts are ongoing to calibrate SchiSTOP for *S. haematobium*, further broadening its applicability and relevance across diverse epidemiological contexts. This comprehensive modelling approach provides essential insights for guiding future schistosomiasis elimination strategies.

Resistance Evaluation and Surveillance Initiative for Schistosomiasis Treatment (RESIST)

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Zanzibar (Tanzania) has been implementing mass drug administration (MDA) with praziquantel (PZQ) against *Schistosoma haematobium* infections since the 1980s, achieving elimination of schistosomiasis as a public health problem in most areas. However, hotspots with high prevalence of infection (5-10%) remain. The RESIST project, integrates parasitological surveillance, genomic analyses, and mathematical modelling to investigate whether MDA-driven selection for drug-resistant parasites contributes to these persistent hotspots. With the recent discovery of the molecular target of PZQ and the development of a pipeline for *miracidia* whole genome amplification and sequencing (WGS), we can now screen *S. haematobium* populations for variants associated with PZQ sensitivity. In 2024–2025, quintuple urine filtrations over five days were conducted before and after mass drug administration (MDA) among >1000 children from two hotspot schools. Single pre-treatment urine filtrations were also conducted in 15 non-hotspot schools (~800 children per school). In hotspot schools, prevalence based on quintuple sampling was twice that based on a single sample, with one school reaching 35% prevalence over five days. Individual *miracidia* from infected children collected in 2024-25 were preserved on FTA cards for subsequent WGS, which will be compared to archived samples collected from the same 17 schools in 2012 and 2017. In the hotspot schools, genomic variants of S. haematobium from 234 children pre-treatment will be compared to those from 16 children who remained positive post-treatment, to identify alleles potentially linked to reduced drug efficacy.

RESIST is establishing the foundations for population-based genomic surveillance of drug resistance in Schistosoma, and will have important implications for PZQ resistance monitoring and the deployment of novel drugs.

Session VIII - Vaccines and other future perspectives

Date / Time: Freitag, October 10th, 11:20 AM - 12:20 PM

Insights from controlled human schistosome infection

Emma L. Houlder[1], Meta Roestenberg[1], Jan Pieter R. Koopman[1], Marijke C. C. Langenberg[1], Marie-Astrid Hoogerwerf[1], Jacqueline J. Janse[1], Koen A. Stam[1], Cornelis H. Hokke[1], Maria Yazdanbakhsh[1], Leo G. Visser[1], Emmanuella Driciru[1,2], Jeroen Sijtsma[1], Govert J. van Dam[1], Paul L. A. M. Corstjens[1], Friederike Sonnet[1], Stan T. Hilt[1], Alison M. Elliott[2], Angela van Diepen[1], Lisette van Lieshout[1], Claudia J. de Dood[1], Arifa Ozir-Fazalalikhan[1], M Y Eileen C van der Stoep[1], Pauline Meij[1] and the wider schistosomiasis controlled infection team.

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Novel chemotherapeutics and vaccines are urgently needed in schistosomiasis. Moreover, our understanding of clinical and immunological outcomes in natural endemic infection is limited by inherently heterogenous and obscure exposure histories. To provide clarity, a controlled human *Schistosoma mansoni* infection model was developed at LUMC, Netherlands. Initial single-sex dose escalation studies were performed using male or female cercariae. In these studies, dose-dependent clinical acute schistosomiasis (Katayama) was observed. A 20-cercariae dose was chosen to balance infection rate (over 60%) with acceptable adverse events. Notably, resistance to praziquantel treatment was observed in the female-only model, a finding that has global health implications as well as limiting further use of this model. Immunologically, similar responses were seen in male and female cercariae infection, with early Th1 responses changing to Th2 by week 8 post-infection. To extend this model, and ask if partial immunity develops with multiple infections, a repeat (3x) infection model was performed. Notably, no development of protection from infection was observed. However, clinical symptoms as well as innate cytokines were maximal in the primary infection, and reduced after repeat exposure, suggesting a level of tolerance develops. Mixed Th1/Th2/regulatory worm-specific T cell responses peaked in the secondary infection cycle, remaining elevated until final treatment. In the second infection cycle, a minority of participants were accidentally exposed to female cercariae, with potential egg-production and higher Th2 responses observed during the third infection cycle. Together, the controlled human infection model has provided significant insights into the clinical and immunological aspects of *S. mansoni* infection. Current/future work is focused on transferring this model to the endemic area (Uganda), deeper immune phenotyping, and vaccine and therapeutic testing.

New antischistosomal strategies: from insects as drug source to an RNAi therapy concept

Tobias Schmitt[1], Tom L. Gallinger[2], Saranya Geetha[1], Miray Tonk[3], Andreas Vilcinskas[3], Carlo Unverzagt[4], Martin Schlitzer[2], Christoph G. Grevelding[1], Simone Haeberlein[1].

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Using *in silico* approaches, worm *in vitro*-culture systems, animal models, and post-genomics tools, we explore novel strategies to identify antischistosomal molecules. RNA interference (RNAi) is a highly specific approach for gene silencing and promises tremendous potential as novel therapeutic concepts for pathologic conditions. This includes infectious diseases, when genes of the pathogen are targeted. To explore siRNA therapy against *Schistosoma mansoni*, we prioritized genes known to be vital for the parasite. Efficacy of modified siRNAs with extended half-life was confirmed against worms *in vitro*. This way, we selected siRNAs against six target genes to be tested in a mouse model. We achieved worm burden reduction of up to 60% using siRNAs targeting ATPases or a GPCR. Future work will further optimize the protocol and test efficacy against juvenile parasites.

Next to this target-focused approach, we explore insects as source for antischistosomal drug discovery, which represent the most species-rich class of animals on earth with a wide spectrum of biologically active molecules. To this end, we made use of in vitro screenings and molecular docking-based in silico screenings (PMIDs: 30870428, 33019687, 35215232). We found *in vitro* activity for a ladybird-derived alkaloid (harmonine) and venom from an assassin bug. Both inhibited motility and egg production of schistosomes at low micromolar concentrations. Also, we observed pleiotropic effects on cells essential for parasite survival, including an arrest of stem-cell proliferation. In another approach, we created a virtual library of over 1000 insect molecules that were docked against a known druggable target of *S. mansoni*, thioredoxin glutathione reductase (SmTGR). For one of the potential SmTGR inhibitors identified, buprestin H from jewel beetles, we confirmed activity against *S. mansoni in vitro*. Our studies highlight the potential of siRNA as well as insect-derived molecules in antischistosomal drug discovery.

Are GPCRs viable drug targets in *Schistosoma mansoni*? Insights from RNAi and neuropeptide interaction studies

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Schistosomiasis, a neglected tropical disease affecting millions of people and animals, is caused by parasitic flatworms of the genus Schistosoma. In schistosomes, female sexual maturation and egg production depend on constant pairing with a male. The eggs, finally, cause the pathology associated with schistosomiasis.

Praziquantel (PZQ) is the only available drug and is effective mainly against adult worms, not juveniles or eggs. The reliance on a single drug and the lack of a vaccine highlight the urgent need for new therapeutic targets. Given their key roles in cell biology and druggability, G protein-coupled receptors (GPCRs) are promising drug candidates. We focused on GPCRs that are pairing-dependently expressed in *S. mansoni* (1,2). Using a novel RNAi approach with two non-overlapping dsRNA, we achieved high knockdown efficiencies (92–99%), compared to single dsRNAs (40–60%). After 21 days of GPCR knockdowns *in vitro*, we observed shrunken testicular lobes, empty seminal vesicles, body curling, tegument damage, reduced motility/vitality, and complete loss of egg production. EdU assays showed decreased neoblast proliferation in somatic and gonadal tissues, and fewer mature oocytes, confirming roles of the selected GPCRs in parasite vitality and reproduction. To deorphanize these GPCRs, we tested interactions with neuropeptides (NPPs) using the MALAR-Y2H system and Bioluminescence Resonance Energy Transfer (BRET). For one representative receptor, GPCR9, MALAR-Y2H and BRET assays indicated interactions with NPPs 26 and 41. RNAi of these NPPs showed similar phenotypes as for GPCR9.

In summary, we present an improved protocol for GPCR RNAi, identified ligands of orphan GPCRs, and highlight the crucial roles of specific GPCRs in *S. mansoni* reproduction and survival. These GPCRs are promising targets for drug design, which offers potential for new strategies controlling schistosomiasis.

References:

1.PMID: 29346437
2.PMID: 38047698

POSTER PRESENTATIONS

Session I - Wednesday, October 8th, 3:40 PM - 5:10 PM

Category I - The Parasite and Its Hosts - Posters n°1 to n°8

Poster n°1

200th anniversary of Theodor Bilharz´ birthday

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When you end up in a small town in the Danube valley in Southwest Germany you hardly imagine that an internationally well-known scientist grew up here: 200 years ago, Theodor Maximilian Bilharz was born in the town of Sigmaringen. He qualified in Medicine 1849 at the near University of Tübingen. The former lecturer of Tübingen University, Wilhelm Griesinger asked him to come with him to Cairo. Later, he was appointed head of the medical Department of the Qasr el Einy hospital of Cairo and of the Cairo Medical school. Bilharz started to perform autopsies on corpses of patients who had died from "endemic hematuria". Between 1851 and 1853, in a series of autopsies Bilharz found male and female adult trematode worms, in the bladder wall and in the mesenteric veins and named the new species: "*Distoma haematobium*". Later the genus Bilharzia was generated but eventually it took the name *Schistosoma haematobium*. Bilharz also discovered other worm species, now known as Hymenolepis nana and Heterophyes heterophyes and described the electric organ of Nile-electric catfish (*Malapterurus electricus*) as well as another Nile fish (*Brycinus macrolepidotus*). Theodor Bilharz tragically passed away in Cairo 1862 of an epidemic febrile infection only 37 years old.

Poster n°2

Prednisolone modulates hepatosplenic pathology and systemic biomarkers in murine *Schistosoma haematobium* infection: a complex immunomodulation

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Schistosoma haematobium is a parasitic flatworm that causes urogenital schistosomiasis; however, studying its pathogenesis is challenging due to the absence of an appropriate small animal model. Murine models often show egg localization in hepatic and intestinal tissues, making it difficult to assess urogenital effects. This study evaluated the impacts of prednisolone, an immunosuppressant, on *S. haematobium*-infected mice. Albino mice were divided into four groups: normal, infected, and prednisolone controls, and infected+prednisolone. At 12 weeks post-infection (pi), mice received 0.5 mg/kg of prednisolone for 7 days. At 16 weeks pi, assessments were made for worm burden, organ pathology, and biomarkers. Results showed no significant difference in worm burden between treatment groups. While untreated infected mice had decreased WBC counts and elevated ALT and AST levels, prednisolone improved WBC counts and partially addressed hypoalbuminemia. The hepatic pathology of the infected mice showed widespread hepatocyte necrosis, Kupffer cell hypertrophy, and significant infiltration of mononuclear (MNL) and polymorphonuclear leukocytes (PMN) into the periportal areas. In the infected+prednisolone group, there was a reduction in the severity of hepatocyte necrosis, but localized intralobular areas of pseudotubercules with severe PMN and MN leucocytes, along with fibrous connective tissue formation. The spleen of the infected control was hyperactive, showing moderate deposition of hemosiderin pigments in the red pulp and a white pulp that was significantly populated by mononuclear and macrophage proliferation. In contrast, the spleen sections of the infected+prednisolone group revealed a large amount of thrombocyte sequestration within the red pulp and a white pulp that was moderately to severely reactive. Overall, prednisolone did not eliminate liver pathology but altered the inflammatory response, with adverse splenic consequences.

Poster n°3

The Schistosome and Snail Resource (SSR): enabling access to live schistosome and snail resources for translational research

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The Schistosome Snail Resource (SSR) is a Wellcome Trust-funded biomedical resource jointly managed by the London School of Hygiene and Tropical Medicine (LSHTM) and the Natural History Museum (NHM). SSR supports global schistosomiasis research by maintaining and distributing live Schistosoma life-cycles and their snail hosts, an essential but technically demanding task requiring infrastructure and expertise. Most laboratories rely on centralized resources, particularly the Schistosomiasis Resource Center at the Biomedical Research Institute (BRI) in the USA, the largest and most widely used provider. However, regulatory and logistical challenges often limit access from Europe. Facilities as Moluscario Lobato Paraense - Fiocruz (Brazil), Université de Perpignan (France) can support with specific schistosome strains, and a few smaller facilities are spread worldwide, maintaining life-cycles mainly for internal use. The SSR offers an open-access, UK-based alternative. We currently maintain life-cycles of *S. mansoni*, *S. haematobium*, and *S. rodhaini*, as well as several snail species: *Biomphalaria glabrata* (multiple strains), *Bulinus truncatus*, *B. t. truncatus*, *B. wrighti*, *B. africanus*, and *Radix (Lymnaea) natalensis*. Future plans include acquiring field-derived strains and veterinary Schistosoma species of zoonotic relevance. We provide diverse materials: live and preserved parasites (cercariae, miracidia, adults, eggs), infected/uninfected snails, molecular-grade DNA, and reagents like Soluble Egg Antigen (SEA). SSR also supports labs establishing life-cycles through protocol sharing and training. As demand grows for diverse, well-characterized strains, the SSR plays a key role in enabling ethical, high-impact research. By refining methods, like using inbred snail strains to increase infection success and reduce animal use, we strengthen global efforts in parasite biology, vaccine development, diagnostics, and schistosomiasis control.

Poster n°4

Intra-specific variations in *Schistosoma mansoni* and their possible contribution to inconsistent virulence and diverse clinical outcomes

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Background: *Schistosoma mansoni* was introduced from Africa to the Americas during the transatlantic slave trade and remains a major public health problem in parts of South America and the Caribbean. This study presents a comprehensive comparative analysis of three *S mansoni* strains with different geographical origins—from Liberia, Belo Horizonte and Puerto Rico. We demonstrated significant variation in virulence and host-parasite interactions.

Methods: We investigated the phenotypic characteristics of the parasite and its eggs, as well as the immunopathologic effects on laboratory mouse organ systems.

Results: Our results show significant differences in worm morphology, worm burden, egg size, and pathologic organ changes between these strains. The Puerto Rican strain showed the highest virulence, as evidenced by marked liver and spleen changes and advanced liver fibrosis indicated by increased collagen content. In contrast, the strains from Liberia and Belo Horizonte had a less pathogenic profile with less liver fibrosis. We found further variations in granuloma formation, cytokine expression and T-cell dynamics, indicating different immune responses.

Conclusion: Our study emphasizes the importance of considering intra-specific variations of *S. mansoni* for the development of targeted therapies and public health strategies. The different virulence patterns, host immune responses and organ pathologies observed in these strains provide important insights for future research and could inform region-specific interventions for schistosomiasis control.

Poster n°5

Glycoengineering of *Schistosoma mansoni* using mannosidase inhibitors

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Schistosomiasis is a neglected tropical disease caused by blood flukes of the genus *Schistosoma*, affecting over 250 million people worldwide. Understanding of the intricate parasite-host interaction is crucial for targeting this disease. Schistosomes are known to modulate the host's immune response by expressing a variety of antigens and releasing specific molecules, including glycoconjugates. Additionally, cellular and molecular processes such as protein folding and intercellular communication are dependent on glycosylation, suggesting that glycans may play pivotal roles in schistosome development.

Our research aims to develop glycoengineered living *Schistosoma mansoni* adult worms and schistosomulas and subsequently employ these to study how different glycans might contribute to the parasite's development. Glycoengineered parasites are generated in *ex vivo* and *in vitro* cultures using kifunensine and swainsonine, chemical compounds that inhibit specific α-mannosidases involved in the N-glycosylation pathway. We show that these compounds gradually altered the N-glycosylation profile from complex type glycans to hybrid and oligomannosidic N-glycan forms, resulting in a significant decrease of the immunogenic motif LacdiNAc (LDN) in kifunensine-treated adult worm tegument. No negative effects of any of the treatments on adult worm morphology or motility were observed, indicating that the basic biology of the worms in culture was not affected. In contrast, kifunensine-treated schistosomulas developed malformations after four weeks of culture, showing irregular lining and local swelling of the gut. We conclude that glycoengineered schistosomes are a promising tool to further elucidate the role of glycans during parasite development and have the potential of studying glycan-mediated effects in parasite-host interaction.

Poster n°6

Kidney involvement in schistosomiasis

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Schistosomiasis (Bilharziasis) is a Neglected Tropical Disease (NTD), which is caused by trematodes (flukes). One of the main species causing urogenital Schistosomiasis in humans is *Schistosoma haematobium*, which is highly endemic in sub-Saharan Africa.

S. haematobium has a complex life cycle. Humans are the final hosts and freshwater snails are the intermediate hosts. After a prepatent period, paired adult worms produce large amounts of eggs in the venous plexus of the bladder, which are shed from infected humans. However, some eggs trap in the tissue, leading to granulomatous formations and inflammation in urinary tract.

Here, we aim to investigate immune cells and Tubular Epithelial Cells (TECs) in urine as well as inflammatory and immune markers such as cytokines and antibodies against *S. haematobium* in blood samples. The hypothesis is: The more advanced the infection, the more immune cells, TECs and inflammatory markers are present in urine and blood.

Poster n°7

Genome-wide insights into adaptive hybridisation across the *Schistosoma haematobium* group in West and Central Africa

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Inter-species hybridisation occurs readily between certain species of schistosomes, which have the potential to change epidemiological dynamics in endemic regions. This is illustrated in areas of Cameroon where urogenital schistosomiasis, primarily due to *Schistosoma haematobium* and hybrid infections, now predominate over incumbent, intestinal schistosomiasis caused by *Schistosoma guineensis*. Though epidemiologically important, the underlying genomic architecture of introgression between these species is poorly understood. In this study, RADseq was used on archived adult worms initially identified as *Schistosoma bovis*, *S. haematobium*, *S. guineensis* and *S. guineensis x S. haematobium* hybrids from Mali, Senegal, Niger, São Tomé and Cameroon. Genome-wide evidence supports the existence of *S. guineensis* and *S. haematobium* hybrid populations across Cameroon, and no introgression is occurring within São Tomé. Additionally, all *S. haematobium* isolates from Nigeria, Mali and Cameroon indicated signatures of genomic introgression with *S. bovis*. Adaptive loci across the *S. haematobium* group showed that voltage-gated calcium ion channels could play a key role in species-specific survivability across host systems. Where admixture has occurred between *S. guineensis* and *S. haematobium*, the excess introgressive influx of tegumental and antigenic genes from *S. haematobium* has increased the adaptive response in hybrids, leading to increased hybrid population fitness and viability.

Poster n°8

A formative appraisal of Female Genital Schistosomiasis (FGS) score card results against point of-care gynaecological and molecular parasitological information within four counties of Liberia

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The West African country of Liberia has an extensive (co)burden of urogenital and intestinal 15 schistosomiasis; each being largely restricted to more inland areas. Where urogenital schistosomiasis is endemic, as both disease surveillance and case management are nascent, many women unknowingly suffer from Female Genital Schistosomiasis (FGS). Using a recently developed FGS score card, we appraised FGS score card valuations with point-of-care gynaecological and molecular parasitological information, as undertaken within typical primary care settings of four counties. A total of 400 women 100 participants from each of four endemic inland counties, underwent a cursory gynaecological examination using a speculum for visible FGS lesions, undertaken by a midwife, and provided a urine sample that was examined by centrifugation with microscopy for schistosome ova. Urine-sediments in ethanol were later analysed with molecular DNA diagnostics using a high-resolution melt (HRM) real time (rt) PCR assay. Using a combination of clinical and parasitological information, overall prevalence of FGS was <10% but of singular note, an FGS-associated co-infection with *Schistosoma mansoni* was observed. Participant interviews with the FGS score card provided an insight into at-risk lifestyle and environmental factors, for example, women who fished regularly were more likely to present with FGS whereas those who lived more than 15 km from a local river were less likely to present with FGS. In this resource poor setting of Liberia active surveillance for FGS with either clinical or parasitological methods remains challenging such that sole future use of the FGS score card is most pragmatic for primary care.

Poster n°9

Establishing *in vitro* drug sensitivity assays with *Schistosoma haematobium* field isolates obtained from local *Bulinus truncatus* snails in Lambaréné and surroundings (EVASAB project).

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Background

Urogenital schistosomiasis, caused by the parasite *Schistosoma haematobium*, is still widespread in Central Africa and poses a significant public health challenge. The life cycle of this parasite depends on freshwater snails, and human infection occurs through contact with contaminated water. Praziquantel (PZQ) is the only available drug to treat schistosomiasis. However, reduced cure rates and suspected resistance have been reported across Africa, though definitive evidence of resistance is lacking. Sustaining control efforts requires both monitoring local parasite susceptibility to PZQ and accelerating drug discovery. Maintaining the *S. haematobium* life cycle in the laboratory is critical to these efforts but is rarely established in African research institutions. This is due to the biological and technical difficulties in maintaining the vector snail *Bulinus* vector and *S. haematobium* under laboratory settings.

The EVASAB project aims to establish the *S. haematobium* life cycle at CERMEL in Gabon, focusing on the snail and early human larval stages. The long-term goal is to enable on-site in vitro drug susceptibility testing using local parasite strains.

Method

We initiated aquaculture and propagation of locally collected *Bulinus* snails. First attempts at controlled infections with *S. haematobium miracidia*, derived from eggs of an infected individual, have been carried out. In parallel, we began optimizing the transformation of cercariae, collected from wild-infected snails, into schistosomula—the early human larval stage. *In vitro* culture and initial drug susceptibility testing using reference drugs have been started. Once controlled snail infections consistently produce cercariae, transformation and drug testing will proceed using cercaria from this laboratory-established life cycle.

Results

Results of these activities, as well as further progress will be presented at the meeting.

Poster n°10

An assessment of *Schistosoma haematobium* diagnostics comparing the performance of plasma qPCR, urine filtration microscopy and UCP-LF CAA using Bayesian Latent Class Analysis in a cohort of pregnant women from Lambaréné, Gabon.

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Schistosomiasis, a neglected tropical disease caused by parasitic flatworms of the genus *Schistosoma*, is the second most impactful parasitic disease after malaria, affecting over 250 million people with significant morbidity and mortality. The WHO roadmap for NTDs by 2030 targets schistosomiasis elimination as a public health concern globally. Achieving this goal depends on developing novel, sensitive point-of-care (POC) diagnostics that improve disease mapping, treatment monitoring, and surveillance.
Current diagnostics are inadequate, especially for post-treatment surveillance and low-intensity infections. To address this gap, we compared different diagnostics using a clinical cohort of 379 pregnant women in the DFG HelmVit study in Lambaréné, Gabon. Each participant was tested using urine filtration microscopy, UCP-LF CAA, POC-CCA, and plasma qPCR on cell-free DNA. Our qPCR targets the DraI repeat (*S. haematobium*) or Sm1-7 (*S. mansoni*) and used a crude DNA extraction (Quantabio Extracta) requiring only 20µl input and minimal equipment. Though sensitivity was reduced, the qPCR still performed well as a predictor of infection, with potential for adaptation into a POC screening test. Importantly, the qPCR detected pre-patent infection, validated in *S. mansoni*-infected mice.
Given the lack of a gold standard, we applied Bayesian Latent Class Analysis (BLCA) to compare qPCR with other tests, estimate true prevalence, and assess test performance. This study underscores the need for more sensitive, specific, and scalable molecular diagnostics for schistosomiasis elimination. Further research should focus on POC molecular tools, including those for female genital schistosomiasis, praziquantel resistance detection, and xeno-surveillance.

Poster n°11

Detecting two *Schistosoma* circulating antigens – CCA and CAA – in urine and serum to improve diagnosis of human schistosomiasis.

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Schistosomiasis is caused by infection with parasitic worms and affects hundreds of millions people worldwide. The detection of schistosome circulating cathodic and anodic antigens (CCA and CAA) has proven to be highly valuable in diagnosing schistosomiasis. Combined detection of CCA and CAA was explored to further improve diagnostic accuracy. Parallel detection of CCA and CAA was performed on two banked sample sets with matching serum and urine samples from *Schistosoma mansoni* (Sm) and *S. haematobium* (Sh) infected individuals using the non-concentration based lateral flow (LF) test comprising the sensitive luminescent up-converting reporter particle (UCP) technology. Detection of both CCA and CAA increased the positivity rate for detecting both Sm and Sh infections compared to the detection of either antigen separately, demonstrating the added value of detecting both antigens in a single sample to confirm diagnosis, independent from the *Schistosoma* species. Significantly higher CCA concentrations in urine were observed in Sm infected individuals compared to Sh infected individuals, while serum CCA concentrations were similar between species. CAA concentrations were higher in serum compared to those in urine, irrespective of species. When exploring the relationship of CCA and CAA in urine, the CCA/CAA ratio in Sm infected individuals was significantly higher than in Sh infected individuals, while no differences were observed in serum. The combined and quantitative detection of CCA and CAA is indicative for identifying the infecting species, but needs further exploration.

Poster n°12

Circulating anodic antigen (CAA) detection in pregnant women during *Schistosoma haematobium* infections in Lambaréné, Gabon.

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Background
The detection of schistosome-derived antigens in urine is a highly effective diagnostic approach for controlling schistosomiasis. It offers greater sensitivity compared to parasitological methods and is more convenient as urine samples are preferred. This diagnostic approach is particularly advantageous for pregnant women and young children, as early detection of active infections can lead to prompt treatment with Praziquantel (PZQ). The freeBILy clinical trial (NCT03779347) seeks to evaluate the accuracy of the circulating anodic antigen (CAA) test for detecting *Schistosoma haematobium* (Sh) infections in pregnant women.

Methods
The accuracy of the upconverting reporter particle lateral flow (UCP-LF) CAA urine test was comprehensively evaluated in a trial, using a cross-sectional design and comparing it against other *Schistosoma* diagnostic methods, including conventional urine filtration (UF) microscopy and Schistosoma ITS2 PCR.

Results
A total of 733 pregnant women were enrolled in this study with mean age (SD) of 25.3 (6.6) years. The prevalence of schistosomiasis was respectively 18.1% (127/701), 19.1% (134/701), and 12.4% (74/595) based on UF, UCP-LF CAA test, and PCR, respectively. The Latent Class Analysis (LCA) showed a sensitivity and specificity of UCP-LF CAA of 80% and 100%, respectively, suggesting that it performs well in detecting both positive and negative cases.

Conclusion
Preliminary data show a higher prevalence of schistosomiasis based on UCP-LF CAA. Furthermore, the UCP-LF-CAA test was more suitable than the UF test to detect low infection intensity.

Keywords: *Schistosoma haematobium*, UCP-LF CAA, pregnancy, diagnostic test, praziquantel, Gabon.

Poster n°13

Performance of diagnostic tests for the detection of *Schistosoma mansoni* in Southwestern Tanzania.

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Background

In an area with moderate endemicity for soil-transmitted helminths and schistosomiasis, we used various diagnostic tests to detect *Schistosoma mansoni*.

Methodology

Samples were collected in 2019 in a village in southwestern Tanzania. A total of 1299 people aged between 14 and 65 years were visited and blood, urine and stool samples were taken. To detect *S. mansoni*, Kato-Katz microscopy (KK) of the stool and detection of circulating cathodic antigen (CCA) with urine test strips were performed. Selected samples were tested for cell-free DNA in plasma as well as egg DNA in stool.

Results

Valid results for Kato Katz and POC CCA were obtained for 1059 of the 1299 study participants. We found 34/1059 (3.2%) positive by Kato Katz, but 166/1059 (15.7%) positive by CCA POC test. In addition, The CCA test yielded 40% "indeterminate test results" with week positive bands. Among the 34 KK positive participants, the CCA test gave a negative result in 12 (35.3%) and an indeterminate or positive result in 11 (32.4%) of the samples. Cell-free PCR of plasma revealed that 34.6% of the KK positive and 34.7% of the KK negative samples tested positive for *S. mansoni* DNA. In contrast, plasma PCR found *S. mansoni* DNA in 67.5% of the positive CCA cases, in 15.1% of the indeterminates and 7.8% of the negative sample. In addition, we tested 55 stool samples. We detected *S. mansoni* DNA in 4/27 (15%) KK positive and 7/28 (25%) KK negative samples.

Conclusion

In this study area with low/moderate endemicity for *Schistosoma mansoni* infections, we found a ~5 times higher prevalence when the POC CCA was used compared to the KK microscopy. The POC CCA test had in addition weak positive test results which were difficult to interpret. However, PCR testing revealed acceptable results for POC CCA, as at least 68% of the positive results were confirmed. The KK microscopy was problematic in this study, as confirmation rate was ~33% with CCA or plasma PCR and 15% using stool PCR.

Poster n°14

Detection of *Schistosoma* eggs from potassium hydroxide (KOH) macerated placental tissue at Zomba Central Hospital, Malawi.

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Background

Schistosomiasis, also known as bilharzia, is a prevalent parasitic disease in Malawi caused by *Schistosoma haematobium* or *Schistosoma mansoni*. During pregnancy, it can affect the placenta and may contribute to poor maternal and neonatal outcomes. [1] Microscopic detection in urine samples lacks sensitivity and requires experienced and well-trained personnel. We aimed to detect *Schistosoma* eggs from placental tissue at Zomba Central Hospital (ZCH), Malawi using a previously described potassium hydroxide (KOH) based maceration technique. [2]

Methods

The placenta sample used was residual material taken from the bin of labor ward. It was sectioned into six circular pieces (about 5cm in diameter), five from the peripheral regions and one from the central region. The sections were put in individual containers filled with 0,9% saline and transported to the laboratory. Each section was further cut into 1 cm pieces and transferred into a 50 mL tube. Each tube was filled with 4% KOH to a final volume of 45 mL and incubated at 37°C for 24 hours while loosely capped. After incubation, samples were centrifuged at 2,500 rpm for 10 minutes at room temperature. The supernatant was discarded, and the remaining pellet was used to make a wet mount that was examined under microscope at 10x, 20x, and 40x objectives for the presence of *Schistosoma* eggs.

Results

Wet mount microscopic examination showed a typical background with blood cell debris. No *Schistosoma* eggs were observed in any of the slides.

Conclusion

Maceration of placental tissue offers a simple and affordable method for the detection of *Schistosoma* eggs. Even though no eggs were detected in this intent, ongoing examination may yield positive findings. This method can complement existing diagnostic strategies and may help improve detection of schistosomiasis during pregnancy.

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Poster n°15

Genomic sequencing-based hybrid characterization of *Schistosoma sp.* worms from clinical cohorts - GENOSCHIS.

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Introduction

In the backdrop of reemergence and spread of *Schistosoma* zoonotic hybrids in endemic areas, which disrupts existent diagnosis, treatment & control measures, there is an impetus for novel technologies to be able the detect and characterize hybrid infections (WHO, 2020). One way this can be achieved is by developing molecular tools to detect cell-free DNA (cf-DNA) from the parasite, circulating in the patient blood samples (Wichmann et al., 2009). And in case of hybrid infections, this can be done via sequencing and characterizing both nuclear and mt-DNA markers as shown by Cnops *et al.* 2021. For the characterization of *S. haematobium* hybrids, the targetsDra1 (Hamburger *et al.*, 2006) and 28S rDNA (Sondoval *et al.*, 2006) were chosen as nuclear, and cox1 as mt-DNA makers as well described genetic targets (Littlewood *et al.*, 1997).

Methods

174 peripheral blood (serum/plasma) samples were used in this project, a subset from the clinical study "HelmVit" (CERMEL, Gabon). We devised a workflow of qPCR/PCR assays for 3 chosen genes of interest. Of these, 28S lsr rRNA and cox1 targets were used for amplicon sequencing by Sanger and Oxford Nanopore long-read sequencing, for detection and characterization of hybrid infection from samples in the cohort.

Results

28S and cox1 amplicons were successfully obtained from one *S. haematobium*-positive sample (helmv146). Sequencing (controls vs. helmv146) amplicons with Oxford Nanopore was comparable to Sanger sequencing, in terms of median quality and length of passed reads as seen via sequence alignment. The 28S lsr rRNA (nuclear target) amplicon indicated clear alignment with *S. haematobium*. However, the result of cox1 sequencing was inconclusive in determining the hybrid nature of our sample from the mt-DNA fragment, owing to below threshold quality of reads in species specific conserved and mismatch regions.

Outcome & Discussion

Limited success in sequencing cox1 gene is likely due to constricted amount of mt-DNA fragments in cf-DNA. We can overcome the limitations in the future assays, by utilizing more target DNA rich samples such as schistosome miracidia and eggs from patient samples. Further, exploring broader genomic targets through

next generation sequencing, like Oxford Nanopore, can help identify potent genetic markers to distinguish the genetic makeup of F1 or later generation hybrid. Comprehensive genomic characterization of F1 and later-generation hybrid strains is essential for understanding recombination, inheritance patterns, etc. This can be employed via amplicon sequencing in dedicated assays, as in our case, to inform the development of novel NGS-based diagnostics as well. Targeted approaches such as amplicon sequencing offers a focused, cost effective alternative to whole-genome sequencing (WGS), enabling high-resolution analysis of specific genomic regions—particularly those associated with phenotypic traits or markers of hybrid vigor. This approach allows for deeper coverage and streamlines comparison across multiple hybrid samples, avoiding the complexity and redundancy often encountered with WGS. In addition to this, optimizing Oxford Nanopore sequencing for hybrid identification in field settings can fast-track research aims. These outlooks provide a scalable assay for characterization of hybrid genomes, supporting both basic research and translational efforts.

Poster n°16

Mitogen-Activated Protein Kinases (MAPKs) as targets for drug development against schistosomiasis.

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Protein Kinases (PKs) are well-characterized cell signalling molecules, corresponding to approximately 2% of the predicted proteome of schistosomes. Essential members include the Mitogen-Activated Protein Kinase (MAPK) subfamily, which are central in eukaryotic signal transduction required for directing cellular responses to a multitude of stimuli. Recent studies have employed RNAi to elucidate the role of several MAPKs in *Schistosoma mansoni* and the current knowledge points to a direct participation of MAPKs in the development, reproduction, and survival of this parasite. Considering the relevance of PKs in drug targeting against many human diseases, we investigated the potential use of MAPKs to work as targets for drug discovery and development against schistosomiasis. Based on *in silico* and *in vitro* studies, we identified several active compounds predicted to bind to *S. mansoni* MAPKs (SmJNK, Smp38, SmERK1, and SmERK2). *In vitro* screening assays have confirmed the effects of these compounds on parasite survival, development, and reproduction. However, demonstrating target-ligand engagement becomes a challenge in the study of parasitic proteins, which lack commercially available tools and can be difficult to express recombinantly in sufficient amounts. Therefore, we applied Cellular Thermal Shift Assay (CETSA) to enable the identification of compounds that interact with SmMAPKs by monitoring changes in protein thermal stability upon ligand binding. Since no specific antibody is available against SmMAPKs, we have used transfected Sf21 cells to express recombinant V5-tagged SmMAPKs. This method allows direct detection of ligand-target engagement on a cellular level without the need for protein purification. We have shown that predicted Type I- and Type II-kinase parasite-specific inhibitors thermally stabilize SmMAPKs similarly to some commercially available human MAPK inhibitors. CETSA's ability to provide direct evidence of target engagement within living cells makes it a powerful tool for drug discovery. In the context of drug discovery against schistosomiasis, CETSA facilitates the study of novel MAPK ligands, advancing our understanding of parasite biology and contributing to drug development for potential therapeutic use. Moreover, this approach exemplifies the integration of such techniques into parasitology research, opening new avenues for combating neglected tropical diseases.

Poster n°17

POC-CCA3: reducing batch-to-batch variation in the WHO-endorsed POC-CCA for *Schistosoma mansoni* and improving test interpretation.

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Praziquantel (PZQ) remains the first-line treatment for human schistosomiasis, which is caused by various *Schistosoma* species. Recent investigations have identified the transient receptor potential melastatin (TRPM) ion channel as the molecular target of PZQ in *S. mansoni*. Binding of PZQ to a specific ligand-binding pocket within the TRPM channel induces calcium influx, resulting in paralysis of the adult worm. However, emerging reports of reduced PZQ efficacy in *S. mansoni* have raised concerns about drug resistance. Mutations in the TRPM-PZQ binding site are potentially involved in the observed drug susceptibilities. While most current data are limited to *S. mansoni*, *S. haematobium* is an equally prevalent species, and little is known about its TRPM ion channel. Therefore, we aim to characterize the genetic variability of the TRPM-PZQ ion channel using targeted amplicon sequencing in clinical isolates of *S. haematobium* from Gabon. Furthermore, we want to evaluate if specific *S. haematobium* TRPM-PZQ variants correlate with reduced treatment efficacy of PZQ within a clinical study.

Poster n°18

POC-CCA3: reducing batch-to-batch variation in the WHO-endorsed POC-CCA for *Schistosoma mansoni* and improving test interpretation.

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Background

World Health Organization (WHO) schistosomiasis control programmes typically rely on Kato-Katz microscopy (KK) to detect *Schistosoma mansoni* eggs, although KK has limited sensitivity, especially in low-intensity infections. The WHO-endorsed point-of-care circulating cathodic antigen test (POC-CCA) is more sensitive but lacks the complete specificity of KK and has suffered significant batch-to-batch variability, compromising reliability. We evaluated an updated version, POC-CCA3, with the aim of addressing this batch-to-batch variation.

Methods

The POC-CCA3 employs recombinant monoclonal antibodies for *Schistosoma* CCA detection. School-aged children (n=870) in moderate (Tororo) and high endemicity (Mayuge) settings in Uganda were tested using KK, POC-CCA, and POC-CCA3 tests over three consecutive days. Data were analysed using descriptive statistics and Bayesian Latent Class Analysis, estimating diagnostic performance including sensitivity, specificity, receiver operating characteristic curves, and batch-specific variation and day-to-day variation.

Results

Model median prevalence estimates were 91.4% (Mayuge) and 31.2% (Tororo). A single POC-CCA3 test at G-score threshold 4 achieved estimated sensitivity and specificity, respectively, 86.3% and 92.9% in moderate and 88.1% and 95.5% in high endemicity settings. POC-CCA3 has a small increase in the probability of meeting the WHO TPP for monitoring and evaluation compared to the original POC-CCA. Overall diagnostic performance (AUC >94.2%) was higher compared to POC-CCA, with markedly lower batch-to-batch variation.

Conclusions/Next steps

The POC-CCA3 demonstrates superior performance and greater consistency compared to POC-CCA. A G-score threshold of 4 maximises performance towards WHO target product profile (TPP) requirements. However, neither test consistently meets WHO specificity requirements from a single sample, suggesting the need for continued refinement.

Poster n°19

Experiences with serum CAA in clinical diagnosis of schistosomiasis.

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Diagnosing imported schistosomiasis remains a challenge, due to the complex life cycle and the lack of a gold standard. Although several diagnostic tests are available, all have significant drawbacks. A test of cure is also urgently needed, to be able to assess efficacy of the single currently effective drug and possible new drug candidates. Studies in traveler as well as migrant cohorts have shown that assessment of circulating anodic antigen (CAA) in serum can demonstrate active infections with *Schistosoma* species. Moreover, serum CAA levels rapidly decline after treatment in the majority of patients.

Since three years, serum UCP-LF CAA testing is available for routine clinical diagnostics at the LUMC. Here, we present our experience with diagnostic interpretation and challenges in clinical practice.

Per year about 300 serum samples were tested for CAA. From a total set of 1056 tests, 525 (49,7%) were performed after positive antibody testing at LUMC and 528 as a single request, mostly from laboratories elsewhere in Europe. Of the antibody-positive initial patient samples (n=319), 114 were positive, leading to a presumed active infection percentage of 36%. For a selection of patients a (presumed) post-treatment sample was available. In a preliminary analysis of 56 patients with multiple samples, 34 subjects had a positive CAA test. Of these, 22 turned negative in the first post-treatment sample. A number of cases needed additional treatment to negativize CAA. Extended analyses are currently in progress.

In conclusion, serum CAA testing is of additional value in distinguishing active from past infections and for monitoring treatment responses, which is relevant in filling the current gaps in the clinical management of imported schistosomiasis.

Poster n°20

Molecular Isothermal Diagnostics for Schistosomiasis (MIDS) Project.

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Accurate diagnosis of schistosomiasis is crucial for effective disease surveillance and control. Mass drug administration (MDA) has significantly reduced transmission, leading to low-level infections that are often missed by standard diagnostic methods like egg microscopy. There is an urgent need for rapid, sensitive diagnostic tools that can be used in decentralized settings to accurately determine prevalence and identify infected individuals, especially for elimination efforts. Molecular diagnostics, such as PCR, detect *S. haematobium* DNA in urine with high sensitivity and specificity. This project developed and tested an isothermal Recombinase Polymerase Amplification (RPA) assay to improve point-of-care diagnosis of urogenital schistosomiasis in endemic areas.

The existing Sh-RPA assay was optimized for improved specificity, robustness, portability, and simplicity. An internal RPA control was designed to detect reaction failure and prevent false positives. Sample preparation was optimized using the SwiftDNA (Xpedite Diagnostics) method on urine samples spiked with single *S. haematobium* eggs, aiming for a simple, field-friendly protocol suitable for resource-limited settings.

The optimized Sh-Dra1-RPA assay was implemented in Zanzibar, testing 450 frozen urine samples from the Public Health Laboratories for S. haematobium DNA. The assay was robust, sensitive (detecting a single egg), and specific to *S. haematobium* group species, with DNA amplification at 42°C within 20 minutes. Results were easily visualized using a portable fluorometer or blue light. The two-step SwiftDNA extraction method required no heating and efficiently extracted DNA from single eggs, making it ideal for field use.

Implementation in Zanzibar demonstrated the assay's portability and low infrastructure needs, with 450 samples analyzed over five days (two days for preparation, three days for RPA). Prevalence was 22% by microscopy and 20% by RPA, but RPA sensitivity compared to microscopy was only 61% (93% specificity), likely due to degradation in frozen samples.

In summary, the optimized Sh-Dra-RPA platform is a simple, robust, rapid, and portable diagnostic tool with potential for supporting urogenital schistosomiasis diagnosis in resource-poor settings. Further evaluation using fresh, well-characterized urine samples from endemic areas is needed to confirm its sensitivity.

Poster n°21

RNA helicase eIF4A: a vital driver of reproduction and development in *Schistosoma mansoni*.

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Infection with *Schistosoma mansoni* causes schistosomiasis, which has been treated with a single drug – Praziquantel – for decades. The justified fear of resistance development encourages the search for new targets and drugs. One potential drug target is the eukaryotic translation initiation factor 4A (eIF4A), an RNA helicase that unwinds secondary structures in the 5' untranslated region of mRNAs. It was shown before that inhibition of eIF4A by rocaglates and pateamines has antipathogenic potential [1, 2]. To evaluate its potential as drug target, we investigated the function of schistosomal eIF4A by RNA interference (RNAi) and inhibitor treatment.

Treatment of adult *S. mansoni* with rocaglates or pateamines in vitro resulted in reduced motility and impaired worm attachment. After 7 d, the worms were incubated with EdU to analyze stem-cell effects, which revealed a reduced number of EdU+ cells in treated worms. A miracidia-hatching assay using eggs laid in vitro by treated schistosome couples showed decreased hatching efficiencies. Functional analysis of Smeif4a1 by RNAi reduced the relative transcript level by ≥ 88% in female and male worms after three weeks. After 10 d and 20 d of RNAi, egg production and worm attachment were significantly reduced, respectively. Confocal laser scanning microscopy showed disrupted testes of treated males and disorganized ovaries with reduced numbers of immature oocytes of treated females, as well as a reduction in size of both reproductive organs. EdU-staining revealed a reduction of cell proliferation in somatic and germinal stem cells. SmeIF4AI was cloned and recombinantly expressed in Escherichia coli. Preliminary data of a thermal shift assay confirmed the binding of rocaglates and pateamines to recombinant SmeIF4AI.

In conclusion, the results indicate that SmeIF4AI is involved in processes influencing worm vitality, stem-cell proliferation, embryogenesis, and the maintenance of reproductive organs (testis, ovary, vitellarium). Based on our findings we conclude that SmeIF4AI may have target potential.

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Poster n°22

Development of a rapid, field-friendly method for isolation of cell-free DNA from blood plasma and serum for diagnosis of *Schistosoma* infections.

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Having profound impact in endemic regions, parasitic infections pose a significant global health burden. Further alarming is their increasing presence in non-endemic areas due to globalization. Early and accurate diagnosis is crucial for effective control and elimination strategies, especially as many parasitic infections manifest with nonspecific clinical symptoms. Recent advances in the detection of cell-free DNA (cfDNA) - short fragments of DNA secreted by host and pathogen cells in bodily fluids such as blood and urine - have shown promise as a diagnostic biomarker for a range of pathogens.

Current cfDNA isolation methods require costly, complex procedures inaccessible in resource-limited settings. We have developed a rapid, cost-efficient, and user-friendly cfDNA isolation protocol designed specifically for field-use. The novel method utilizes magnetic particles, requires minimal equipment, and is completed in as little as 10 minutes. Unlike many commercial kits, this protocol is free of hazardous substances, environmentally friendly, and generates minimal plastic waste.

We validated the performance of our protocol using clinical specimens from patients infected with *Schistosoma mansoni* and benchmarking it against commercial kits. The work showed comparable or superior sensitivity and specificity of the new protocol. Its robustness and accessibility make our protocol a promising tool for parasite diagnostics, particularly in resource-limited regions where the burden of disease is the greatest.

By making available such a convenient non-invasive diagnostic tool, that is easy to implement at not only the point-of-care and clinical settings, but also for large-scale community screening and surveying, we are closely supporting the WHO roadmap for NTD elimination in these impacted localities. It also enables rapid case detection in nonendemic areas, offering a powerful means to address the growing challenges posed by parasitic infections in a globalized world.

Poster n°23

Approach to merge individual RAA assays into a multiplex RAA design for simultaneous detection of multiple Schistosoma species.

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Isothermal amplification methods such as LAMP and RPA/RAA are considered to be valuable tools for decentralized testing setups and field campaigns that require the use of simplified and rugged molecular diagnostic tools. The expiration of patent protection for these amplification and detection methods led to a further rise of interest in recent years. A major bottleneck of isothermal amplification methods, however, is their limited multiplexing capability. While countless single-plex isothermal assays for detection of pathogens are described in the literature, little is known how to improve the multiplexing capabilities of LAMP or RAA reagents.

Here we describe an approach to leverage the wealth of well-characterized assay designs described in the literature for a streamlined design process of duplex isothermal assays. For that, two well performing real-time RAA assays for detection of *Schistosoma mansoni* (Sman) and *Schistosoma haematobium* (Shae), respectively, were selected. After verifying the claimed performance for the individual assays, various parameters critical to assay performance were screened. Because we intend to apply the duplex Sman/Shae assay for environmental monitoring as well as clinical diagnostics, we prioritized assay sensitivity over other parameters such as assay speed.

This work proved that it is feasible to turn individually designed single-plex isothermal amplification assays into a duplex assay for simultaneous detection of more than one pathogen. Our approach allows to design a multiplex RAA assay with reduced capacities by building on the primer design work performed by other researchers, who have already screened primers and probes for optimal specificity and sensitivity.

Poster n°24

Extraction of *Schistosoma* cell-free DNA from archived blood plasma specimens for retrospective analysis.

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Cell-free DNA (cfDNA) can be detected in multiple body fluids such as blood, urine, and cerebrospinal fluid. It occurs as fragmented DNA with a typical length of up to 200 bp. Cell-free DNA has become a standard analyte for detection and monitoring of diverse purposes such as tumor staging, physical trauma situations, and transplant rejection.

In recent years, cfDNA has been gaining increasing attention in infectious disease testing. This goes back to the discovery that pathogen cfDNA is secreted into a person's bodily fluids. For detection, standard methods such as real-time PCR and NGS can be used. However, the extremely low concentration of cfDNA calls for large sample volumes and a sophisticated isolation procedure.

This work was driven by the question "Is it possible to leverage bio-banked specimens for retrospective analysis of low-concentrated, unstable biomarkers?". For that, we extracted cfDNA from 57 frozen plasma samples originating from a field study in 2019. The authors compared cfDNA levels found in blood samples of Schistosomiasis patients in Tanzania and correlated them with other clinical markers. We compared the levels of cfDNA found in paired serum/plasma samples (fresh after sampling vs archived at -25°C for 5 years) and further compared the results from the retrospective analysis with results from the two other available diagnostic methods Kato Katz egg counting and CCA antigen testing.

The study revealed a high correlation between cfDNA levels in fresh and archived samples, providing evidence that precious patient specimens can indeed be used for retrospective analysis of unstable biomarkers like cell-free DNA. This reinforces the perspective of archived specimen testing for new emerging biomarkers that had not been utilized or have even been unknown at the time of sampling. The value of such analyses lies in a deeper understanding of disease staging patterns and yet not fully understood epidemiologic behavior of diseases.

Session II - Thursday, October 9th, 1:15 PM - 2:45 PM

Category III - Clinical Disease, Co-Infections and Morbidity Management - Posters n°25 to n°36

Poster n°25

Establishing a gastrointestinal endoscopy unit for management of *Schistosoma mansoni* related hepatosplenic morbidities at Nansio District Hospital, North-western Tanzania: challenges, learning experience and achievements

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Background
In Tanzania, hepatosplenic schistosomiasis (HSS) with periportal fibrosis, portal hypertension and its related complications are a common cause of morbidity and mortality among adults. In endemic areas, the management of HSS is challenged by scarcity of human and technical resources including endoscopy. Here we report our experience in establishing a functional gastrointestinal endoscopy unit at a primary healthcare facility within the Ukerewe Schistosomiasis Control project.

Methods
An assessment of the need for an endoscopy unit at Nansio District hospital analyzed the monthly number of patients with HSS, their clinical presentation and outcome as well as the available human and technical resources for appropriate management. The resulting plan of action consisted of capacity building for nurses and medical doctors, integration of the local team in the gastroenterology team of regional and tertiary hospitals, renovation of the building, offering scholarship for residence in internal medicine, establishment of a HSS patient clinic, ultrasound service and establishment of a monthly collaborative out-reach programme.

Results
The endoscopy unit started in August 2023. To date, a total of 666 patients (66.4% male, 33.6% female) have been attended. HSS related symptoms were abdominal distension (66%), hematemesis (41%) and melena (41%). On ultrasound, 71.5% had periportal fibrosis (PPF) and 80.4% had liver image pattern C-F correlating

with the severity of PPF. Endoscopy was done in 560 of 666 patients; 52.1% had esophageal varices grade IV. Of these 84% underwent ligation. On follow-up, 90% had achieved eradication of varices.

Conclusion

The establishment of the GI endoscopy unit at the primary healthcare facility in rural Tanzania was possible through the joint efforts of different stakeholders. The partnership, mentorship and sharing of resources between the district, medical universities, regional and tertiary hospitals has made the unit operational.

Poster n°26

Plasmodium falciparum and *Schistosoma mansoni* in pregnancy in north-western Tanzania: Prevalence of co-infection, placental malaria and congenital malaria among pregnant mothers and their newborns

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Background

Plasmodium falciparum and *Schistosoma mansoni* infections pose a public health challenge in Tanzania, where co-infection is common and pregnant women are not spared. In pregnancy, co-infection of *P. falciparum* and *S. mansoni* are associated with significant morbidities ranging from malnutrition, anemia, stillbirth, low birth weight, pre-term delivery and severe hepatosplenic disease. Despite this fact, the health consequences associated with co-infection of these parasites during pregnancy and the outcome of pregnancy have received little attention. Here, we report the prevalence of placental and congenital malaria in pregnant women co-infected with *P. falciparum* malaria and *S. mansoni* infections.

Methods

A hospital-based cross-sectional study was conducted at Sengerema Designated hospital located at Sengerema district, Mwanza region. The study included pregnant women at term. From each consented participant, a single stool and urine sample was collected and examined for *S. mansoni* eggs and antigens using four Kato Katz (KK) technique and Point-of-Care Circulating Cathodic Antigen test (POC-CCA). Thin and thick blood smears prepared from peripheral, cord and placenta blood were stained with Giemsa stain and examined microscopically for presence of malaria parasites stages. The HIV serostatus and haemoglobin level were examined using rapid diagnostic test (following Tanzania algorithm) and HemoCue system.

Results

Out of the 790 pregnant women at term, 607 and 683 submitted stool and urine samples. Based on KK technique and POC-CCA rapid test, the prevalence of *S. mansoni* was 9.7% (95%CI:7.5-12.4) and 66.3% (95%CI:62.7-69.7). Based on KK, the mean egg intensity was 37.5 ± 176.4 eggs per gram of faeces, with 35.5%, 25.4% and 38.9% of participant having light, moderate and heavy infection intensities. The overall prevalence of maternal peripheral and placental *P. falciparum* malaria were 26.2% (95%CI: 23.2-29.4, 207/790) and 17.5% (138/790, 95%:14.9-20.3). Of the women with placenta infection, 72.3% (108/138) had positive peripheral blood smears for *P. falciparum* parasite. In relation to *P. falciparum* and *S. mansoni* co-infections, 25.4% and 18.3% ($\chi 2=2.5619$, P=0.11) of the primigravidae and multigravidae women with peripheral *P. falciparum* malaria were co-infected with *S. mansoni* infection. In relation to placental malaria, 20.7% of the women who had placenta malaria were co-infected with *S. mansoni*. The prevalence of congenital/cord *P. falciparum* malaria was 20.8% (164/785, 95%CI: 18.1-23.8). Of these children with *P. falciparum* infection, 52.4% were

born from mothers who were co-infected with *P. falciparum* and *S. mansoni* infections. Overall prevalence of HIV-1 and anaemia were 3.9% and 52.6% respectively.

Conclusion

P. falciparum malaria and *S. mansoni* infections are common among pregnant women in the study settings and co-infection is common. The findings call for the need to integrate interventions which addresses both infections during pregnancy.

Poster n°27

Prevalence of *Schistosoma mansoni* in pre-school aged children and caregivers' knowledge, perceptions, practices, health-seeking behaviours and acceptability of preventive mass chemotherapy against schistosomiasis targeting pre-school aged children, North-Western Tanzania: a mixed methods survey

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Objective
To assess the prevalence of *Schistosoma mansoni* in pre-school aged children and further qualitatively explore the caregiver's knowledge, perceptions, practices, health-seeking behaviours, acceptability of preventive mass chemotherapy and behaviour practices that increases the risk of acquiring schistosomiasis in this age group at Geita and Ukerewe districts, north-western Tanzania.

Design
A mixed methods descriptive cross-sectional study was conducted among pre-school aged children (PSAC) and their caregivers. A single urine sample was obtained PSAC and screened for *Schistosoma mansoni* using the point-of-care circulating cathodic antigen (POC-CCA) rapid test. Caregivers were purposively selected and involved in a descriptive cross-sectional study using Focus Group Discussion (FGD). A total of 1,063 PSAC (2-6 years) were involved in the parasitological survey and 66 (33 infected with *S. mansoni* and 33 non-infected PSCA) were involved in the qualitative study.

Results
The overall prevalence of *Schistosoma mansoni* infection was 35.8%. Knowledge about schistosomiasis transmission included both correct and incorrect modes. Water contact activities with infested lake water during bathing and playing while their caregivers and older children washed clothes and fetched water was the main route of exposure to risk environment among the PSAC. Caregivers acknowledge that PSAC were at higher risk of contracting schistosomiasis infection and the age group was prioritized for preventive mass chemotherapy. The acceptability of preventive mass chemotherapy targeting PSAC was high among caregivers.

Conclusion
Schistosoma mansoni is a public health among PSAC and caregivers demonstrated inadequate knowledge about the mode of transmission and preventive measures for schistosomiasis was noted. Caregivers acknowledged that PSAC remain at risk of schistosomiasis infections and needs to be included in the treatment programme. The availability of pediatrics praziquantel (arPZQ) offers an opportunity to include PSAC in the treatment programme.

Poster n°28

Evaluating the diagnostic performance of UCP-LF CAA for the detection of female genital schistosomiasis in comparison to colposcopy-based visual diagnosis: a cross-sectional study from rural Madagascar

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Female genital schistosomiasis (FGS) is a condition resulting from a chronic infection with *Schistosoma haematobium*. The recommended standard screening for FGS is colposcopy, visually detecting its typical signs. Laboratory methods detecting schistosome infections have the potential to detect FGS, but have not been validated yet. Using these methods in highly endemic countries, such as Madagascar, might be advantageous to overcome limitations of colposcopy. The objective of this study was to compare the diagnostic performance of colposcopy for FGS with the detection of the parasitic circulating anodic antigen (CAA).

A cross-sectional study was conducted from March to August 2021 at three primary health care centres in the Boeny region of Madagascar. Background characteristics, colposcopic images and urine samples were collected from women aged 18-49 years. Urine samples were subjected to upconverting reporter particle, lateral flow (UCP-LF) CAA analysis. Clinical diagnosis of FGS was based on an agreement of two gynecologists on FGS-specific lesions in the images. The proportions of FGS-positive results for colposcopy and schistosome infection based on UCP-LF CAA were estimated. To evaluate the performance of UCP-LF CAA in comparison to the visual diagnosis of FGS, measures of diagnostic agreement and logistic regression will be used.

From a convenience sample of 500 women, UCP-LF CAA and colposcopy results were available for 413. From this, 17.4% (n = 72) were negative in both tests, 26.4% (n = 109) tested positive with UCP-LF CAA, 20.1% (n = 83) were visually diagnosed with FGS and 36.1% (n = 149) were positive in both tests.

Preliminary results show a high prevalence of schistosome infection in alignment with previous assessments of FGS in the area. This represents an ideal setting to further assess the diagnostic performance of antigen detection methods, opening perspectives for the improvement of FGS diagnosis in highly endemic contexts, such as Madagascar.

Poster n°29

Beyond borders: unmasking female genital schistosomiasis in travellers and migrants

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Female genital schistosomiasis (FGS) is a neglected manifestation of *Schistosoma* infection with serious reproductive health consequences. Though common in endemic areas, FGS also affects travellers and migrants, yet it is frequently misdiagnosed or overlooked in non-endemic settings.

We identified 38 published cases of FGS in travellers and 33 in migrants between 1980 and 2023. In travellers, who in the majority of cases had a single exposure to infested freshwater, FGS most commonly affected the lower genital tract (vulva and cervix), with fewer cases involving the upper genital tract (Fallopian tubes, ovaries, vagina, and endometrium). Most were treated with praziquantel (40 mg/kg) in 1–3 doses, with lesion resolution in most patients within 3–6 months. In contrast, migrant women, who typically had repeated exposures to infested water before leaving endemic regions, more often presented with internal organ involvement. The upper genital tract was most commonly affected (Fallopian tubes, cervix, ovaries, and uterus), with less frequent involvement of the breasts, vulva, and vagina. These cases were often diagnosed only after years of symptoms and included severe complications such as extra-uterine pregnancy.

FGS occurs in both travellers and migrants but presents with differing patterns of morbidity, likely influenced by intensity and duration of exposure. Diagnosis in both groups was frequently delayed, typically confirmed through histopathology after surgical intervention. These delays reflect a general lack of clinical awareness and absence of standardized diagnostic pathways in non-endemic healthcare settings, highlighting the need to raise awareness among healthcare professionals in these regions.

Poster n°30

Helminth infections and anemia in pregnant women delivering at Nansio District Hospital, Ukerewe, Tanzania

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Background
Schistosoma mansoni infection is the most prevalent helminth infection in the Lake Victoria region of Tanzania. Deworming for soil transmitted helminths has been introduced into the antennal care (ANC) program in Tanzania according to WHO recommendations whereas preventive treatment for Schistosomiasis is not part of the ANC program. Our study examined the prevalence of anemia, malaria, soil transmitted helminths and schistosomiasis in pregnant women delivering at Nansio Hospital, Ukerewe, Tanzania.

Methods
During March and April 2025 women from Ukerewe island delivering at Nansio district hospital in where requested to complete a structured questionnaire and to provide a blood and stool sample for laboratory analysis. Hemoglobin was measured with the HemoCue® system. The MERISCREEN Malaria Pf/Pan Ag was used to detect malaria infection. A single fresh stool sample was examined with the Kato-Katz-Method (KK) for helminth eggs. Data on HIV-infection status and ANC were taken from the ANC file.

Results
Out of 295 women included for 125 complete data sets were available. The mean age was 27,7 years (Range 15 – 43 years). 66/125 (52,8%) were positive for *Schistosoma mansoni* (S.m.), 35 (28%) for Ascaris, 6 (4,8%) for Hookworm and 1 (0,8%) for Trichuris based on KK-technique. The mean Hb was 10,4g/dl (Range 5,5-14,4g/dl). The overall prevalence of anemia was 60,8%. 21 women had light, 35 moderate and 6 severe anemia acc. to WHO definition. For malaria the prevalence was 4/125 (3,2%). Acc. to the ANC file 106 (84,8%) of the women received deworming and 109 (87,2%) preventive treatment for malaria.

Discussion
The high prevalence of anemia in pregnancy corresponds with available data for Tanzania and is higher than in other East African countries. The high prevalence of S.m. infection in pregnant woman was comparable to the average adult population in the region, whereas the rate of STH infection was rather low. This can be interpreted as an effect of the deworming during the 2nd and 3rd trimester of pregnancy. The high rate of S.m. infections calls for integrating praziquantel treatment into the ANC program.

Poster n°31

Schistosoma japonicum infection: clinical significance of ultrasound findings

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Schistosoma (S.) japonicum infection is endemic in Southeast and East Asia. It can cause severe hepatic complications associated with portal hypertension which may lead to death by bleeding from esophageal varices. Ultrasonography (US) is used to assess hepato-splenic morbidity due to *S. japonicum*. US enables the identification of two different types of liver fibrosis characteristic for *S. japonicum* infection: interseptal fibrosis (ISF) and portal fibrosis (PF). To date, these two forms of liver fibrosis have not been sufficiently investigated with regard to their potential to cause portal hypertension. Among the 121 reports published, only 46.3% (56/121) distinguish between ISF and PF. In 55.4% (31/56) of these publications patients with only ISF, in 3.6% (2/56) patients with only PF, and in 41.1% (23/56) patients with the concomitant ISF and PF are reported. US signs of portal hypertension are reported in 40.0% (10/25) of publications reporting PF (of which 100% (2/2) of publications report PF alone and 34.8% (8/23) of publications report concurrent PF and ISF). 6.5% (2/31) of publications report that ISF alone is associated with portal hypertension. Thus, PF appears to be the main risk factor for portal hypertension. Future studies need to assess the exact nature of liver fibrosis caused by *S. japonicum* in a standardized way to clarify the individual contribution of PF and ISF to morbidity.

Poster n°32

Ultrasonographic findings in *Schistosoma mekongi* infection. A minireview

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Schistosoma (S.) mekongi is causing intestinal and hepatosplenic schistosomiasis in some South East Asian countries located along the Mekong river. Ultrasonography is the point of care method of choice for detecting and staging hepatosplenic morbidity due to schistosomiasis. We review all publications on ultrasound examinations in *S. mekongi* infected individuals. An extensive data base search revealed only five eligible publications on 1433 patients. Findings included (peri-)portal fibrosis, splenomegaly and signs of portal hypertension. Portal fibrosis was sometimes difficult to differentiate from periductal fibrosis caused by frequent co-infections with opisthorchiasis. In these cases, color Doppler was helpful in detecting intraluminar blood flow in portal but non in periductal liver fibrosis. On the other hand, interseptal liver fibrosis as seen in *S. japonicum* and gallbladder wall thickening as seen in *S. mansoni* infections were not described as typical features of *S. mekongi* infections.

Poster n°33

Burden and treatment outcomes of imported chronic schistosomiasis among long-term west African migrants in Spain

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Background
Sub-Saharan African migrants may be experiencing imported schistosomiasis, which can evolve into chronic schistosomiasis. Positive response to empiric treatment with praziquantel may indicate the presence of persistent infection.

Objectives
To determine the burden of chronic imported schistosomiasis and therapeutic response among long-term Sub-Saharan

Methods
We conducted a community screening and tested the response to praziquantel to patients with criteria of probable imported chronic schistosomiasis (past-exposure of more than 3 months, serology positive test and compatible clinical findings). Clinical and laboratory response to Praziquantel was tested at at baseline and 6 and 12 months.

Results
We recruited 522 eligible participants, 74.3% males, mean age 42.7 years (SD=11.5, range 18-76). Overall, 46.4% were from Senegal and 23.6% from Gambia. They had lived in the European Union for a median of 16 years (IQR 10-21) and 187 (35.8%) had criteria of probable imported chronic schistosomiasis. The most prevalent symptoms associated to serology positive test were chronic abdominal pain (68.8%, OR=1.79;

95%CI 1.2-2.6); eosinophilia (44.9%, OR=2.69; 95%CI 1.8-4.0) and specific symptoms associated with urinary schistosomiasis, like self-reported episodes of haematuria (37.2%; OR=2.47; 95%CI 1.6-3.8); dysuria (47.9%, OR=1.84; 95%CI=1.3-2.7) and current renal insufficiency (13.4%; OR=2.35; 95%CI=1.3-4.3). We found a significant prevalence of gender-specific genital signs and symptoms among females (mainly menstrual disorders) and males (erectile dysfunction and pelvic pain). One-hundred forty-nine eligible participants completed the post-treatment follow-up. We observed a significant decrease (P <0.001) in the number of signs and symptoms at 12 months, and 70.3% showed a total resolution of the symptoms and significant decreases in transaminase levels, eosinophilia, and abnormal glomerular filtration rates. The rates of clearance in positive enzyme-linked immunosorbent assay and immunochromatography tests were 54.7% and 24.3%.

Conclusion

The screening findings and positive response to praziquantel indicates that chronic schistosomiasis is a prevalent condition among long-staying African migrants. These results need to be confirmed in randomized clinical trials.

Poster n°34

Distinct urinary tract schistosomiasis presentation in brothers: considering the role of hybrid and non-hybrid strains

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Background

Urinary tract schistosomiasis remains a public health concern in endemic regions, with hybrid *Schistosoma* increasingly recognized due to advances in molecular diagnostics. We describe two brothers from Benin, recently migrated to Germany, both diagnosed with urinary schistosomiasis but exhibiting different clinical presentations - one infected with a hybrid strain and the other with non-hybrid *Schistosoma haematobium*.

Cases

The younger brother, a 15-year-old, presented with chronic lower abdominal pain and hematuria. Imaging revealed a pedunculated bladder mass. Urine microscopy identified numerous *Schistosoma haematobium* eggs and miracidia. Post-praziquantel therapy, the patient expelled part of the bladder mass during micturition. Histopathology confirmed a high egg burden without malignancy. Molecular analysis identified a hybrid strain of *S. haematobium* and *S. bovis*. His 17-year-old brother was asymptomatically screened and tested positive for *S. haematobium* eggs and miracidia in urine microscopy. Imaging showed no pathology and PCR analysis did not reveal hybrid *Schistosoma*.

Discussion

These cases highlight the spectrum of urinary schistosomiasis, ranging from asymptomatic infection to severe disease with bladder mass formation, even among siblings with comparable exposures and close host factors. The more severe presentation in the younger brother, associated with a hybrid *Schistosoma* strain, raises the question whether hybrid *Schistosoma* may contribute to differences in pathogenicity. Literature on hybrid-associated morbidity remains mixed, highlighting the need for more research.

Conclusion

Further studies are warranted to clarify the epidemiology, pathogenic mechanisms, and clinical impact of hybrid schistosome strains, particularly in endemic and migrant populations.

Poster n°35

Prevalence of cervical schistosomiasis of conization samples by omproved tissue maceration technique – a possible approach

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Background

Female genital schistosomiasis (FGS) represents a significant health problem for women in reproductive age living in schistosomiasis endemic areas and has gained increasing attention in the past years [1]. Approximately half (33% to 75%) of the women with urogenital schistosomiasis, caused by *S. haematobium*, are also diagnosed with FGS – a recognized and common complication [1,2]. Pathology is caused by trapped eggs, and any area of the female genitalia can be affected. This can result in infertility, precancerous conditions and contact bleeding with an increased risk of transmission of STDs including HIV [3]. The diagnosis is usually made clinically by colposcopy by identifying the pathognomonic "sandy patches" [4]. Histopathological confirmation can usually only be made by chance in surgical specimens as invasive sampling is not recommended due to the mucosal lesions it causes.

Method

Tissue maceration is a method with which human tissue can be dissolved using potassium hydroxide (KOH), while parasitic eggs are not damaged and remain detectable. This method was already described in the context of schistosomiasis in the 1960's, [5] subsequently improved in 2017 by our working group in a proof-of-concept model [6] and is recently evaluated in a non-interventional study on placental tissue in Gabon (manuscript under preparation). To the best of our knowledge, it has not yet been applied to conization biopsies. Based on experience with placental tissue, a 20-fold increased sensitivity can be assumed compared to conventional histopathology [7].

Study design

For this pilot study, 50 conization biopsies are to be examined using maceration after routine clinical interventions and after routine diagnostics have been completed at a medical center for gynecology in an endemic area for schistosomiasis. The primary objective is to answer whether schistosome eggs can be detected in conization preparations of the lower cervix using the maceration method. Secondary study objectives include the comparation of the sensitivity of maceration compared to histopathology and the prevalence of cervical schistosomiasis in patients with clinical indication for conization in areas endemic for schistosomiasis.

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Poster n°36

Effects of 24-nor-ursodeoxycholic and ursodeoxycholic acid on mitochondrial dynamics in the liver of *Schistosoma mansoni* infected mice

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Background and aims

Hepatic fibrosis and granuloma formation around tissue entrapped eggs characterize the pathology of *Schistosoma mansoni* (S.m.) infection. S.m. infection affects mitochondrial biogenesis, mitochondrial dynamics (fusion/fission), and regulates innate and adaptive immune responses. We have already shown that 24-nor-ursodeoxycholic acid (norUDCA) has anti-inflammatory and anti-fibrotic effects in S.m. induced liver injury. The mechanism behind this is not yet fully understood. We therefore aimed to investigate whether norUDCA exerts its beneficial effects on liver fibrosis in murine schistosomiasis by compensating mitochondrial dysfunction.

Methods

NMRI mice were infected with 50 S.m. cercariae and after 12 weeks received either norUDCA- or ursodeoxycholic acid (UDCA)-enriched diet (0.5% wt/wt) for 4 weeks to evaluate liver pathology, as well as analyze mitochondrial dynamic genes expression level and respiration in isolated hepatocyte mitochondria using high-resolution respirometry.

Results

NorUDCA improved mitochondrial dynamics by reduction of mitochondrial fragmentation and enhancement of mitochondrial inner and outer membrane fusion. Moreover, norUDCA but not UDCA treatment of infected animals significantly improved OXPHOS capacity and ratio of respiration in the uncoupled state, and additionally increases the electron transport system capacity and cytochrome C oxidase function.

Conclusion

Our results demonstrate protective effects of norUDCA on hepatocyte mitochondria function which in turn contributes another piece to the puzzle of the broad effects of norUDCA on S.m. associated liver pathology.

Poster n°37

The interaction of schistosomes with the maternal microbiota and effects on the offspring immune system

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Question

Schistosomes manipulate the host immune system to ensure their prolonged survival, with bystander effects on the infected host and their progeny including reduced allergic sensitivities and impaired vaccine responses. We propose that these immune alterations in the offspring stem from specific maternal signals that are modified during chronic infection. Given that 40 million women of child-bearing age are infected in Sub-Saharan Africa, it is imperative to delve deeper into these signals. One possible mechanistic angle behind these changes is the modification of the maternal microbiota, which plays a large role in shaping the offspring immune system and has been investigated during schistosome infection, but not in a fetomaternal setting.

Methods

To disentangle pre- vs postnatal effects, we carry out a cross-foster experiment in a mouse model and investigate the expression of antigen-presenting and costimulatory molecule on B cells and dendritic cells in the spleen, mesenteric lymph node and bone marrow as well as stem cell frequencies in the bone marrow. We also analyse the maternal and offspring stool microbiota from Th2 and regulatory phase of infection by 16s rRNA sequencing and complement this with metabolomic analysis of stool, serum and breastmilk.

Results

We show that the expression of antigen-presenting and costimulatory molecules is consistently increased in offspring suckled by an infected mother, compared to offspring gestated by one. We identify changes in the maternal microbiota and bile acid levels in the stool and serum due to schistosomiasis.

Outlook

We will further investigate how an altered maternal bile acid metabolism impacts the offspring immune system. We will also analyse changes in bile acids in serum samples from our human mother-child cohort (Helmvit).

Poster n°38

Schistosoma mansoni hepatosplenic markers among pediatric population in endemic foci of North-Western Tanzania: a call to integrating pediatric praziquantel distribution in community-based mass drug administration platform

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Background

Paediatric intestinal schistosomiasis caused by *Schistosoma mansoni* is prevalent across all age groups in north-western Tanzania. Despite the development of paediatric praziquantel, children aged 1–5 years are not routinely treated, putting them at risk for heavy infections and hepatosplenic morbidities. To support the urgent need for paediatric praziquantel in endemic countries, this study assessed the prevalence of ultrasound-detectable *S. mansoni* hepatosplenic markers among young children on Ukerewe Island, north-western Tanzania.

Methods

Four hundred pre-school children (2–5 years) from Bugula and Musozi villages, known *S. mansoni*-endemic areas on Ukerewe Island, were enrolled. Each child provided stool and urine samples, collected with parental assistance. Stool was examined for *S. mansoni* eggs using the Kato-Katz (KK) technique; urine was tested for *S. mansoni* antigens using Point-of-Care Circulating Cathodic Antigen (POC-CCA). All children underwent liver and spleen ultrasound (Niamey protocol).

Results

Of all participants, 51.8% were boys. Using KK, the overall *S. mansoni* prevalence was 24.7% (95% CI: 20.8–28.9), with prevalence by age: three years (23.3%), four years (20.8%), five years (37.8%). The geometric mean eggs per gram of faeces was 100.3 (95% CI: 83.5–120), significantly differing by age ($F=5.57$, $P<0.001$). Low, moderate, and heavy infection intensities were found in 51.4%, 41.3%, and 7.3% of children, respectively. POC-CCA detected an overall prevalence of 70.5% (95% CI: 66.1–74.6), increasing with age ($\chi^2=8.23$, $P<0.04$), with children aged ≥3 years showing ≥70% prevalence. Ultrasound revealed *S. mansoni*-related hepatosplenic markers in 1.8% (7/400) of children, mostly Liver Image Pattern C (71.4%) and D (28.6%).

Conclusion

Intestinal schistosomiasis poses a significant public health concern for young children on Ukerewe Island. Infections begin at an early age and can lead to hepatosplenic morbidity. These findings highlight the urgent need to deliver paediatric praziquantel through community-based mass drug administration and maternal and child health clinics.

Poster n°39

HELMSYS: The impact of helminth infections on vaccine response in humans: a systematic literature review

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Background

Immunization promises eradication of infectious diseases, but experimental evidence has shown that helminthiases can immunomodulate vaccine response hindering optimal protection.

Objectives

A systematic literature review to investigate the impact of helminth infection (RQ1) and antihelminthic treatment (RQ2) on vaccine response (immunogenicity, efficacy and effectiveness) in humans.

Methods

PubMed, Scopus, Web of Science, clinical-trial registries were searched for records from January 1970 to June 2024. Reference lists, websites were hand-searched. Two-step screening with title-abstract, full-texts; undetermined helminth-infection, natural immunity and case-studies excluded. Study setting, population, helminth-diagnostics, anti-helminthics, and vaccine outcomes extracted; means and SDs were calculated. Risk-of-bias assessed by RoB 2.0 and modified Newcastle-Ottawa Scale. A descriptive and quantitative analysis was stratified by vaccine type.

Results

41 (31 observational, 9 RCT) studies on 15 vaccines from 19 countries investigating adults, children or both, all reported immunogenicity. RQ1, infected groups: (i) tetanus: lowered IgG; (ii) BCG: raised IFN-γ; (iii) HBV: lowered IgG; (iv) polio: lowered IgG, raised cytokines; (v) HPV: lowered HPV18IgG. Non-significant trend for lowered Ab in infected groups for S. typhi, Ebola, and malaria vaccines. RQ2, infected, immunized, post-treatment groups: (i) BCG: raised IFN-γ, IL-12, lowered TGF-β; (ii) cholera: modest humoral boost (iii) Measles, influenza: transient raised Ab; (iv) meningococcal: no change. RCTs showed moderate to high; observational studies showed low to high, risk-of-bias.

Conclusion

Cumulative findings suggest inconsistent evidence of a trend for impairment of vaccine immunogenicity in infected populations with anthelminthic causing potential improvement. Clinical trial design should be optimized to ascertain if coupling antihelminthic with vaccination offers dual benefits in endemic settings.

Poster n°40

Chronic infections in Hypertensive dIsorders of Pregnancy (preeclampsia) And Colorectal CArcinoma [CHIPCA]

Establishment of a joint interdisciplinary schistosomiasis research unit - an academic expansion of an existing clinical partnership

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Background and hypothesis

Schistosomiasis, a neglected tropical disease (NTD) caused by the helminth *Schistosoma*, affects over 230 million people worldwide, primarily in sub-Saharan Africa. Female genital schistosomiasis (FGS) has been suggested as a potential risk factor for hypertensive disorders of pregnancy (HDP), but evidence remains limited.

Objectives

The study has two main objectives: (i) to assess the prevalence of schistosomiasis in all study participants; and (ii) evaluate its relationship with FGS, blood abnormalities, liver dysfunction, and postpartum outcomes. A sample repository with blood, stool, urine, vaginal swab and tissue samples from all recruited study participants is to be developed in parallel.

Methods

The study follows a two-visit design after recruitment. Visit 1: Collection of blood, urine and stool, also for biobanking, coinfection diagnostics; data on clinical manifestations and *schistosoma* exposure, colposcopy for FGS diagnosis and biobanking vaginal swab; Visit 2: delivery, post-partum and birth outcomes, maternal and cord blood, and fixed placenta for biobanking. Positive infectious diagnosis for all patients will be treated adequately; FGS prevalence will be determined through a combination of microscopy, point-of-care circulating cathodic antigen (POC-CCA) assays, and serum PCR. Associations between schistosomiasis prevalence and HDP will be analyzed using the Chi-square test for categorical variables. Multivariable regression or propensity score matching will be applied to account for confounders such as age, lifestyle, family history, other chronic diseases, and coinfections.

Implications

This study is a first milestone for capacity-building in Ghana by establishing a "joint schistosome research unit". The sample biobank will support further interdisciplinary research into integrating maternal health, non-communicable disease prevention and developmental origins of health and disease.

Poster n°41

Epidemiological profile of schistosomiasis in Moyen-Ogooué Province in 2023, Gabon, Central Africa

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Background

Schistosomiasis remains a public health issue in Gabon, where the disease has been reported for many decades. The country has adhered to the WHO recommendations for the control of schistosomiasis morbidity. However, for a tailored control program, epidemiological data are needed. The objective of the present work was to provide an updated epidemiological profile of schistosomiasis in Moyen-Ogooué, one of the nine provinces of Gabon.

Methods

We conducted an epidemiological survey from October 2022 to October 2023 in which participants aged one year and over and living in Moyen-Ogooué Province for at least six months were randomly selected and included. A standardized questionnaire was used to collect sociodemographic data and risk factor data. Urine filtration and the Kato–Katz technique were used for the detection of *Schistosoma* eggs in the urine and potentially in the stool.

Results

A total of 1017 participants were included, with a mean (SD) age of 31.7 (23.5) years and a 1.14 female-to-male sex ratio. The overall prevalence of schistosomiasis was 11% (95% CI: 9–13), with 35% of the infections classified as heavy. A greater prevalence was observed among participants aged 5–19 years (20%, 95% CI: 16–25) than among the other age groups. The prevalence was higher in Lambaréné (18%, 95% CI: 15–22) than in both rural areas: 6% (3–10) and 5% (95% CI: 3–8), respectively. Compared with participants with other daily activities, students presented a higher prevalence (18%, 95% CI: 14–22). Schistosomiasis was strongly associated with visible hematuria (OR=6.96, 95% CI: 4.59–10.58), whereas no association was found with the hemoglobin level. Participants aged 5--19 years (aOR=2.98, 95% CI: 1.40–7.39) and those with a history of taking PZQ (aOR=2.66, 95% CI: 1.54–4.51) had high odds of having schistosomiasis.

Conclusion

In 2023, schistosomiasis remains a public health concern in our community, where children aged 6 years and teenagers are the most affected.

Poster n°42

Epidemiological and molecular profiling of female genital schistosomiasis in Nigeria: an integrated protocol for future intervention strategies

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Female Genital Schistosomiasis (FGS) is a neglected manifestation of *Schistosoma haematobium* infection, primarily in sub-Saharan Africa. It contributes significantly to gynaecological morbidity—bleeding, pain, infertility—and may increase the risk of HIV and HPV infection. In Nigeria, FGS remains underdiagnosed and undocumented, despite evidence suggesting that up to 75% of infected women may develop FGS. There is a critical gap in epidemiological and molecular data linking FGS to cervical disease.

We present a protocol for a transdisciplinary research project that aims to determine the prevalence, severity, and immuno-molecular effects of FGS in three endemic Nigerian states: Cross River, Ogun, and the Federal Capital Territory. In a community-based cross-sectional study, 360 women aged ≥15 years will be examined using urine filtration, PCR diagnostics, and colposcopy. Sociodemographic, behavioral, and reproductive history will be collected to identify risk factors. In addition, cervical cytobrush samples will be analyzed using RNA-Seq to characterize host immuno-molecular responses in the cervix during FGS. Pathway analysis will reveal which inflammatory and oncogenic signatures are dysregulated. By correlating gene expression with FGS severity scores, we aim to discover severity-specific biomarkers and therapeutic targets.

This project is a collaboration between Justus Liebig University Giessen and two Nigerian institutions (University of Calabar and Federal University of Agriculture, Abeokuta), with strong emphasis on capacity building, bioinformatics training, and public health impact. The dual-purpose design supports both prevalence mapping and integration with molecular insights into disease progression. The findings are expected to inform surveillance in FGS-endemic settings.

Poster n°43

Community-based assessment of female genital schistosomiasis (FGS) in Gabon: prevalence, risk factors, and awareness

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Background

Female Genital Schistosomiasis (FGS), caused by *Schistosoma haematobium*, is a neglected tropical disease contributing to substantial reproductive morbidity, including infertility, cervical cancer, ectopic pregnancy, and increased HIV risk. Despite the high burden, FGS remains underdiagnosed and undertreated due to limited awareness, diagnostic tools, and resources. In Lambaréné, Gabon, urogenital schistosomiasis prevalence reaches 58%, with secondary infertility rates particularly high in rural areas where healthcare access is limited. However, no data exist on FGS prevalence, associated risk factors, or community awareness in this setting.

Methods

We are conducting an observational, prospective longitudinal study to assess the prevalence of FGS, its association with cervical dysplasia, and community knowledge, attitudes, and practices (KAP) regarding FGS. Sexually active women aged 15–50 years were recruited for *S. haematobium* using urine filtration. Among them, *S. haematobium*-positive women matched controls undergoes a gynaecological examination including colposcopy. Samples collection such as cervical biopsy, vaginal swab, and cervicovaginal lavage was done for FGS diagnostic. A KAP survey is administered to explore awareness of FGS symptoms, consequences, and prevention.

Results

The study will provide the first data on FGS prevalence and its relationship with cervical dysplasia in Gabon. Results of the KAP survey identifying knowledge gaps and misconceptions, and will be presented to highlight areas for targeted education and intervention.

Conclusions

Findings from this study will inform public health strategies to improve FGS diagnosis, management, and prevention. The integration of FGS screening into reproductive health services, along with enhanced community education, could reduce the burden of FGS and improve women's health outcomes in endemic areas.

Poster n°44

Incorporating acquired immunity into an individual-based model of *Schistosoma mansoni* transmission and control

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Despite extensive immunoepidemiological evidence that acquired immunity, particularly immune responses stimulated by dying worms, significantly shape schistosomiasis infection dynamics, most transmission models do not incorporate it. Instead, they rely on density-dependent fecundity to reproduce a stable endemic equilibrium and extreme age-dependent water exposure patterns to explain lower infection rates among adults. Milne *et al.* (1) recently compared deterministic models with and without immunity, finding similar performance but noting the limitation of modelling immunity only at the population level.

This study addresses this gap by incorporating acquired immunity into an individual-based modelling framework developed by Malizia *et al.* (2). The immunity mechanism is modelled following a similar approach as Milne et al., using historical individual-level data on SmTAL1-IgE responses from a highly endemic Ugandan community. Model output includes egg counts and SmTAL1-IgE measurements and is used to explore how variations in epidemiological parameters and treatment strategies influence long-term transmission dynamics.

Given that transmission models increasingly inform policy decisions, it is important that they reflect emerging evidence on acquired immunity. The few modelling studies including immunity suggest that current projections on the feasibility of achieving the WHO 2030 targets may be overly optimistic. Incorporating immunity into an individual-based model provides further insight into the prospects of reaching elimination goals and the extent to which acquired immunity influences these projections.

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Poster n°45

Novel point-of-care ultrasound protocol FASUS reveals extensive pathology in Gabonese preschool-age children with urogenital schistosomiasis

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Introduction

While school-age children (SAC) and adults have been in the focus of preventive chemotherapy against urogenital schistosomiasis (UGS) for decades, recent ultrasound data from endemic areas showed that urinary tract pathology already affects preschool-age children (PSAC). A diagnostic pilot study aimed at evaluating a novel point-of-care ultrasound (POCUS) protocol and delivering first systematic data on UGS-related pathology in Gabon.

Methods

A POCUS protocol called Focused Assessment with Sonography for Urinary Schistosomiasis (FASUS) was developed and two previously ultrasound-naïve operators were trained. Remote expert review of stored image material served as diagnostic reference. Sonographic and parasitological data were retrieved from 118 patients across age groups with hematuria, living in UGS-hotspots around Lambaréné, Gabon.

Results

Image quality was sufficient in 90% of bladder views and more than 97% of kidney views. Inter-rater agreement between operators and experts was very good ($\kappa > 0.8$) for detection of hydronephrosis and good ($\kappa > 0.6$) for bladder wall thickening [1]. Among 96 ultrasound scans of sufficient image quality in patients with microscopically confirmed *S. haematobium* infection, bladder wall thickening > 5mm was found in 9/20 (45%) PSAC, 29/51 (57%) SAC and 7/25 (28%) adults. Upper urinary tract pathology was found in 19/90 (21%) patients across age groups, up from three years of age [2].

Conclusions

FASUS is a promising point-of-care diagnostic tool for detecting urinary tract pathology in patients with symptomatic UGS. In our study setting, FASUS revealed a high rate of pathology in PSAC. These findings underpin recent WHO recommendations to urgently include this age group into mass drug administration programs.

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Poster n°46

First report of hybrid schistosomes from Gabon, Central Africa

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Introduction

Schistosomiasis is a neglected tropical disease with high prevalence across Africa, affecting over 200 million people globally. *Schistosoma* hybrids are parasites resulting from interbreeding between different Schistosoma species, particularly those involving species within the *Schistosoma haematobium* complex, and have become increasingly reported across endemic regions. These hybrids can pose new challenges due to their potential impact on transmission dynamics, host specificity, diagnostics accuracy, and the effectiveness of current control strategies; however, the epidemiologic distribution and clinical significance of these hybrids remain poorly understood.

Objective

This study aimed to analyze clinical Schistosoma DNA samples at the molecular level to identify and characterize potential hybrid genotypes from Gabon, Central Africa, using biparental genetic markers.

Method

We conducted molecular analysis of 23 urine samples from Lambaréné, Gabon, all previously confirmed positive for *Schistosoma* DNA by real-time PCR. Sanger sequencing was employed to analyze biparental markers including the COX1 mitochondrial gene (maternal inheritance) and the internal transcribed spacer (ITS) regions of nuclear ribosomal DNA (paternal inheritance). DNA sequences were assembled and refined using ContigExpress (VectorNTI 10, Thermo Fisher Scientific) and compared against reference sequences from the NCBI GenBank database for species identification and hybrid detection.

Results

Of the 23 samples examined, 10 (43.5%) showed a pure S. haematobium genotype in both COX1 and ITS regions. However, one sample (4.3%) exhibited hybrid type 1 genotypes, characterized by *S. bovis* mitochondrial profile combined with *S. haematobium* parental nuclear ITS profile (Sb + Sh pacern). Nine sample (39.1%) showed hybrid type 2 genotype with *S. haematobium* or *S. bovis* mitochondrial profile and mixed chromatogram patterns in nuclear regions (Sh or Sb + mixed pattern). Three samples were unsuitable for ITS analysis due to poor sequence quality. Phylogenetic analysis revealed that Gabonese hybrid samples clustered closely with hybrid strains previously documented in Corsica, France (GenBank accession: KT354658.1), which were thought to originate from Senegal, suggesting potential shared West/Central African evolutionary origins or similar hybridization patterns across the region.

Conclusion

This study provides the first molecular evidence confirming the presence of *Schistosoma* hybrids in Gabon. While previous reports of hybrids from Gabon were based solely on morphological observations and were never confirmed by molecular sequencing, our findings provide definitive genetic evidence, challenging

previous assumptions about the species composition in Central Africa. Morphological characteristics have proven unreliable for accurate species identification and hybrid detection in *Schistosoma* parasites due to overlapping phenotypic features and high intraspecific variation. The detection of these hybrids demonstrates the occurrence of zoonotic spillover events between human and animal schistosome species, presenting novel epidemiological challenges for schistosomiasis control and elimination programs. These findings underscore the urgent need for enhanced molecular diagnostic capabilities, updated surveillance strategies incorporating hybrid detection, and comprehensive studies to understand the clinical implications of hybrid infections on human disease progression, treatment response, and transmission dynamics. Future research should focus on determining the prevalence of these hybrids across broader geographical areas and assessing their impact on current diagnostic tools and therapeutic interventions.

Poster n°47

Anthelmintic activities of arylmethylamino steroids and dithiocarbamates

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Schistosoma haematobium is a parasitic worm with a long-standing presence in Egypt. Despite significant progress in controlling schistosomiasis, particularly *S. haematobium*, the disease continues to pose a public health challenge, especially among school-aged children. Concerns regarding potential resistance to praziquantel highlight the urgent need for alternative antischistosomal therapies. Disulfiram, known for its role in treating alcohol dependence by inhibiting aldehyde dehydrogenase (ALDH), has also shown inhibitory effects on schistosomal ALDH. Previous studies indicated its efficacy against both schistosomula and adult *S. mansoni in vitro*. Additionally, arylmethylamino steroids have demonstrated potent antiparasitic effects against chloroquine-resistant *Plasmodium falciparum* and have proven to be effective against adult *S. mansoni in vitro*.

In this study, we aimed to evaluate the activity of both compound classes against *S. haematobium* and other helminths, including *Trichinella spiralis* and *Mesostephanus sp. in vitro*. Our findings reveal that Disulfiram exhibits a significant lethal effect on adult *S. haematobium* and *Mesostephanus*, resulting in complete loss of motility and death within 48 hours, characterized by curling of worms and tegument detachment. Furthermore, Disulfiram caused a partially lethal effect on Trichinella spiralis muscular larvae, leading to coiling and a button-shaped appearance. Similarly, arylmethylamino steroids showed remarkable activity against *S. haematobium*, inducing severe deformation of adult worms, including swelling, sucker degeneration, and gut dilation. These compounds also affected *Trichinella spiralis* muscular larvae and *Mesostephanus* adults, causing loss of motility and reduced vitality, with many worms succumbing to treatment. So far, our results indicate that both Disulfiram and arylmethylamino steroids exhibit promising antiparasitic activity against various schistosome species and other helminths, underscoring their potential as candidates for novel antihelminthic treatment concepts.