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Spring Meeting

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infection, with school-aged children (SAC) disproportionately affected. The World Health Organization identified Uganda as one of the ten priority countries, highly endemic for schistosomiasis, with an estimated 4 million people infected. The national control programme focusses on mass drug administration (MDA) with praziquantel. However, MDA coverage is only ~37% of SAC and even fewer community members, and hotspots with high prevalence remain. SAC are also found to become rapidly reinfected after treatment and mean infection intensities and associated morbidity continue to be high. My interdisciplinary study aims to use ethnographic and population genetics in conjunction with standard epidemiological methods to better understand how, why and where certain children in Mayuge District become rapidly reinfected with *S. mansoni* after treatment. Observational ethnographic appraisals of rapidly reinfected and non-infected children and focus group
s with parents on water contact attitudes and practices will be undertaken. These methods will help elucidate group and/or individual behaviours that affect children's risk of reinfection and how such risks might be reduced. Concurrently, intermediate snail hosts will be collected from key water contact sites identified through the ethnographic appraisals. DNA will be extracted from *S. mansoni* cercariae shed from these snails and will be compared to DNA from *S. mansoni* miracidia found in previously collected samples from SAC and community members to understand better who is driving these reinfections. Analyses of collected data and interpretation of results will help provide recommendations for improvements to the national control programme with the aim to reduce *Schistosoma* reinfection in Uganda. I will present my study plan as well as preliminary observations from Bugoto from Nov 2017 and March 2018.

Ms Miriam Yague Capilla, *PhD Student, Instituto Parasitologia y Biomedicina Lopez-Neyra*
Poster 41 : Novel nucleotidases involved in *Trypanosoma brucei* pyrimidine homeostasis

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Nucleotide metabolism has been an area of interest for the discovery of novel targets against many diseases since a balanced pool of deoxyribonucleotides is required for correct DNA replication and repair. Particularly relevant for cell survival is the maintenance of a balanced dUTP/dTTP ratio in the pyrimidine pool as several DNA polymerases cannot distinguish between the two nucleotides and incorporate indiscriminately one or the other depending on their availability. We have previously shown that thymidine kinase (*Tb*TK) has a major role in the maintenance of the dUTP/dTTP ratio and the response to genotoxic agents in bloodstream forms of *Trypanosoma brucei*. We reported that *Tb*TK was essential for parasite viability, both *in vitro* and *in vivo* thus demonstrating that phosphorylation of deoxyuridine and/or thymidine is important for the maintenance of the dTTP pool even in the

absence of a source of extracellular pyrimidines. These observations indicated a role of the enzyme in *do novo* synthesis and pointed towards the existence of an intracellular deoxynucleoside pool available for phosphorylation. Here we have aimed at characterizing nucleotidases involved in the generation of intracellular nucleosides important for thymidylate *de novo* biosynthesis. We present data for HD domain containing nucleotidases with regard to their intracellular localization, role in cell viability, nucleotide pools and cell cycle progression and propose this class of enzymes as relevant players in nucleotide homeostasis in trypanosomes.

Dr Alena Zíková, *Group leader, Biology Centre, Institute of Parasitology*
Poster 42 : Mitochondrial metabolic remodeling during *Trypanosoma brucei* developmental differentiation

E Doleželová[3]; M Dejung[2]; B Panicucci[3]; C Janzen[1]; F Butter[2]; **A Zíková**[3];
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The *Trypanosoma brucei* mitochondrion undergoes extensive structural and metabolic remodeling during the parasite´s life cycle since the insect stage fully relies on oxidative phosphorylation (OXPHOS) to produce ATP while the mammalian bloodstream stage generates ATP by aerobic glycolysis. This complex developmental differentiation is exemplified during the flagellated protist's migration from the tsetse fly midgut to the salivary glands, a process that can now be mimicked *in vitro* by overexpressing a single RNA binding protein. Here we demonstrate that the mitochondrial membrane potential and reactive oxygen species are increased at the early transition stages. Meanwhile, respiratory complexes III and IV become reduced and the electron flow is redirected from the OXPHOS pathway to an alternative oxidase. This coincides with the increased abundance of respiratory complex II and proline degradation enzymes that may act to provide ATP by substrate phosphorylation. Molecular triggers for this metabolic rewiring are being explored.

Dr. Paul Brindley, *Professor, George Washington University*
Poster 44 : Diminished hepatobiliary disease during infection with CRISPR/Cas9-gene-edited *Opisthorchis viverrini* liver flukes