

Genomic landscape of introgression between blood flukes infecting livestock (*Schistosoma bovis*) and humans (*S. haematobium*) across Africa

Roy N Platt, Grace A Arya, Elisha Enabulele, Bonnie L. Webster, Muriel Rabone, Fiona Allan, Said Ali, Shaali Ame, Tian Bi, Miguel Brito, Tina Chisenga, Lucas Cunningham, Precious Dlamini, Fiona Fleming, Jose Figuerido, Clara Fabien, Amina Hamidou, Grace Hameja, Fatma Kabole, Toby Landeryou, Elizer N'goran, Russell Stothard, Joanne P Webster, Aidan Emery, David Rollinson, Timothy JC Anderson

Hybridization between human and animal parasites may transfer novel pathogenic traits between species, increasing virulence, host range and negatively impacting human health. Knowing when and how often these events occurs is an essential step in achieving optimal health outcomes within a One Health framework. The human parasitic blood fluke, *Schistosoma haematobium* infects millions of people across sub-Saharan Africa. *S. bovis*, a sympatric and closely related species, parasitizes livestock. Initial genetic analyses showed discordance between rDNA and mtDNA markers and indicate that these species are capable of interbreeding. Laboratory crosses between these species also suggested few reproductive barriers. To date, early generation *S. bovis* X *S. haematobium* hybrids have not been identified in studies using microsatellite, genome, or exome-wide single nucleotide variants. In the samples examined so far, it appears that hybridization between *S. bovis* and *haematobium* occurred in the relatively distant past with subsequent selection on introgressed alleles in *S. haematobium*. In particular an invadolysin gene of *S. bovis* origin has reached near fixation in West African populations of *S. haematobium* but is absent in East Africa. Here, we scored 9.6 million genome-wide, single nucleotide variants in 161 *S. bovis* and *S. haematobium* samples collected from 18 countries across the African continent. Our goals were to (1) examine hybridization and introgression events within a large-scale, biogeographic context, (2) more precisely date the admixture event(s), and (3) identify introgressed regions that may be experiencing ongoing selective pressures in different populations.