

## Opening a can of worms: Detecting zoonotic *Strongyloides* species within strongyloidiasis.

Lucas J. Cunningham<sup>1</sup>, Alexandra Juhasz<sup>1</sup>, Sam Jones<sup>1</sup>, John Archer<sup>1</sup>, William Nevin<sup>1</sup>, Jaco Verweij<sup>2</sup>, Jonathan Cracknell<sup>3</sup>, Jennifer Quayle<sup>3</sup>, J. Russell Stothard<sup>1</sup>

<sup>1</sup>Liverpool School of Tropical Medicine, Liverpool, United Kingdom

<sup>2</sup>Elisabeth-Tweesteden Hospital, Tilburg, Netherlands

<sup>3</sup>Knowsley Safari, Knowsley, United Kingdom

Since 2009, the TaqMan real-time PCR developed by Verweij et al. has been the frontline molecular diagnostic for the detection of *Strongyloides stercoralis*, yet it is actually a genus-specific assay. Taking advantage of newly designed species-specific primers and probes targeting hyper-variable regions of the ribosomal 18S gene, alongside whole-genome sequencing, we have clearly shown the presence of *Strongyloides fuelleborni* within various clinical samples. Indeed, the role of zoonotic *Strongyloides* species has been grossly underestimated, even more so as shortcomings, and failures, in serological detection come to light. Here, we present current refinements in species-specific real-time PCR assays, alongside our exploration of e-DNA typing of soils to identify sites of active transmission of *S. fuelleborni* within a captive population of baboons in a UK safari park.