

# Functional genomics approach to investigate the Giant Panda roundworm *Baylisascaris schroederi*: global proteomics for diagnostics and control.

S. C. Pye<sup>1</sup>, S. Girling<sup>2</sup>, P. M. Brophy<sup>1</sup>, I. Valentine<sup>2</sup> and R. M. Morpew<sup>1</sup>

<sup>1</sup>IBERS.

<sup>2</sup>Edinburgh Zoo

The roundworm *B. schroederi* is estimated to infect 50-100% of wild Giant Pandas. Furthermore, *B. schroederi* is also regularly found among captive individuals, causing clinical and subclinical disease, and thus presents as a threat to both captive and wild populations of Giant Pandas.

Due to the limitations of current techniques for quantitative diagnosis there is, as yet, no research utilising functional genomics approaches to aid development of novel diagnostics and vaccines. Thus, initiating functional genomics approaches in neglected parasites of protected wild and captive species is a priority to help improve our understanding of the parasite biology, allowing an insight into how the species interacts with its host, with the hope of identifying future control methods for Baylisascariasis in Giant Pandas.

Therefore, we have begun to characterise the proteome of *B. schroederi* from naturally infected Giant Pandas. Global somatic proteins from adult *B. schroederi* were subjected to both 1D GeLC approaches, for whole proteome characterisation, and 2D gel electrophoresis, followed by Western blotting with infection sera, to characterise immune recognised proteins. The application of this initial functional genomics approach will provide important data for future research into *B. schroederi* control methods via improved diagnostics and potential vaccine candidates.