

## Session 46

## Theatre 1

### **Host selection in vector-borne disease transmission: identifying wildlife hosts of tsetse flies**

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The trypanosomes which cause human African trypanosomiasis (HAT) can be carried by both livestock and wildlife, and are vectored by tsetse flies. Control of disease is particularly challenging in wildlife protected areas where trypanosomes circulate in multiple wildlife species as the relative importance of different species as reservoirs of disease is not understood. Host choice by vectors is an important factor in a host species' reservoir potential but investigations into tsetse feeding patterns have previously been limited by the techniques available, which could often only identify hosts to the level of family (eg Bovidae). New molecular techniques now provide an opportunity to identify host species. We analysed blood meal samples from over 400 tsetse flies (*Glossina swynnertoni* and *Glossina pallidipes*) collected in six different study sites in Serengeti National Park, Tanzania and sequenced a cytochrome B fragment to identify host species. In each study site host species density was quantified by transect sampling analysed using Distance software. These data were used to calculate feeding preference indices for each wildlife species. Results suggested that tsetse feed highly selectively, with over 90% of meals identified from warthog, buffalo, elephant or giraffe, despite these species having relatively low density. The highest density species were Thomson's gazelle and impala but these species were not identified in blood meals. Quantifying feeding preferences improves our understanding of the relative roles of different wildlife species as reservoirs of trypanosomes.