The impact of host-pathogen coevolution on *Trypanosoma* infection rates within wild *Glossina morsitans morsitans*.

Tsetse flies (genera *Glossina*) are the sole biological vectors of African *Trypanosoma* species, the infectious agents of African Trypanosomiasis. Vector control is a key inhibitor of disease transmission; however, long-term control measures are economically and ecologically unsustainable and therefore, alternatives must be explored. Genetic interventions influenced by host-pathogen coevolution could present one such alternative. In this presentation, we explore the genetic variation and evolution within three immune genes Attacin-A (*AttA*), Defensin (*Def*) and Toll-like receptor 2 (*TLR2*) and the consequences for symbiont and parasitic interactions within a wild *Glossina morsitans morsitans* population.

Nucleotide variation within *Def* and *AttA* was found to be similar, exhibiting eight and eleven polymorphic sites respectively, while nucleotide variation within *TLR2* was found to be considerably higher. A recent population expansion event and deviations from neutrality was also detected in all genes. Interestingly, genetic variation within *AttA* and *TLR2* was found to be maintained via purifying selection, while *Def* exhibited signs of the Red Queen arms race and balancing section. Trypanosome infection rates were unexpectedly high (69.35%), consisting of mixed species infections, although samples exhibiting Def variants under positive selection were observed to reduce infection rates within samples. Furthermore, these initial results indicate a potential correlation between *TLR2* variation and endosymbiont population variation.

The results within show that further research is required to fully understand the interactions and impacts of genetic variation on *Trypanosoma* infection rates within wild tsetse, however that an understanding of host-pathogen evolution and interactions of the could be used to inform novel genetic control methods.