EVOLUTIONARY GENOMICS OF *GLOSSINA MORSITANS* **IMMUNE-RELATED CLIP DOMAIN SERINE PROTEASES AND SERINE PROTEASE INHIBITORS**

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ABSTRACT

Several species of haematophagous tsetse flies (genus Glossina) are vectors for trypanosomes, the parasitic protozoans that cause Human African Trypanosomiasis (HAT). Although there was a reduced incidence of HAT in the mid 1960's, decreased disease surveillance has led to a resurgence of HAT in sub-Saharan Africa. Despite being efficient vectors for HAT transmission, the prevalence of G. morsitans infection by trypanosomes in the wild is surprisingly minimal. The precise mechanisms by which G. morsitans remain refractory to trypanosome infection are largely unknown although it has been demonstrated that G. morsitans mounts a strong immune response to invading pathogens. This study identifies G. morsitans immune-related CLIP domain serine proteases and their inhibitors, serine protease inhibitors (serpin) genes. It further establishes their evolutionary relationships with counterparts in Drosophila melanogaster, Anopheles gambiae, Bombyx mori, Manduca sexta and Culex quinquefasciatus. Multiple sequence alignments show conservation of most secondary structure elements for both CLIPs and serpins. Amino acid composition of the serpin reactive site loop (RSL) indicates that the G. morsitans serpins act through an inhibitory mechanism to the target serine protease. Similar to D. melanogaster and unlike A. gambiae, the transcriptome data suggest that G. morsitans does not contain gene expansions in their CLIP-domain serine protease and serpin families. The presence of alternatively spliced variants in the G. morsitans serpins transcriptome data mirrors that of the D. *melanogaster* transcriptome.

Keywords: Glossina morsitans, Drosophila melanogaster, CLIP domain serine protease, serpin.