VECTOR GENOMICS AND ARTHROPOD-BORNE DISEASES IN AFRICA

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ABSTRACT

Mosquitoes and tsetse flies are among the most important vectors that transmit malaria, dengue, encephalitis, filariasis and African trypanosomosis. Genomics and bioinformatics tools have contributed to a better understanding of the interactions between these arthropod vectors and the disease causing parasites that they transmit and provided new insights in the fight against these diseases. Recent studies have uncovered the Glossina proteolytic lectin (Gpl) that is associated with the transformation of the bloodstream trypomastigotes into the procyclic forms within the midgut of the tsetse. This is a crucial step for establishment of infection in the insect host. In this study, we identified the putative trypanosome protein (s) that act as interacting partner (s) of Gpl using the GAL4 Yeast-Two- Hybrid system. The complete ORF of the Gpl gene from *Glossina fuscipes* was used as a bait to fish for gene(s) present in a cDNA-AD fusion library constructed *in vivo* from the bloodstream forms of *Trypanosoma brucei brucei*. False positive clones were eliminated by using ADE2, HIS3, LacZ reporter genes and segregation analysis. On the other hand, the putative positive library clones were identified, sequenced and analyzed by bioinformatics. Nucleotide sequence showed 97% identity with a hypothetical *Trypanosoma brucei* gene and a 5% identity with a serine-rich protein from *Shizosaccharomyces pombe*. Interestingly, all the positive clones had undergone a deletion, a recombination that resulted as an outcome of toxicity after a strong positive protein-protein interaction. This may explain why susceptible bloodstream trypanosomes quickly transform into the procyclic forms in the tsetse midgut to escape lysis and ensure their survival within the hostile midgut environment.