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## UCT researchers assist in tsetse fly genetic code breakthrough

### Information will speed research into control of deadly trypanosomiasis

An international team, including researchers at the University of Cape Town and Yale University in the USA, has sequenced and annotated the genetic code for a representative species of the tsetse fly (*Glossina morsitans*), which carries the potentially fatal African trypanosomes to humans and animals in sub-Saharan Africa. The World Health Organisation (WHO) estimates that 30,000 people in 36 countries of sub-Saharan Africa currently suffer from human African trypanosomiasis.

Detection and treatment of trypanosomiasis (commonly known as "sleeping sickness") is expensive, difficult and dangerous. Vaccine development does not appear feasible due to the ability of trypanosomes to evade the mammalian immune system. Currently, African trypanosomiasis is controlled primarily by controlling the tsetse fly population. The information contained within the genome provides a foundational resource which will accelerate research on the tsetse's basic biology, to improve current tsetse control methods and the development of new, more effective and less expensive strategies.

The tsetse genomic sequence was produced and annotated during a 10-year collaborative effort by an international scientific team. The proteins produced from the genome of an organism are involved in every aspect of its structure and function, from the earliest stages of development to its mature form. They are basically the parts list that an organism is made from. Protein coding genes were identified and mapped to the tsetse genome by

using computer programs that “read” the sequence and compare the massive amounts of sequence data from the genome with that from other annotated organisms to predict gene structure and function.

The automated annotations were then closely examined and manually curated by a group of about 140 scientists who specialise in a wide array of topics important to understanding the biology of the tsetse fly, including: smell, taste, vision, reproduction, digestion, blood feeding, immunity, metabolism, stress response, symbiotic relationships between tsetse and its associated microbial entities, and the hormonal regulation of genes and physiological functions. The analyses performed by these research groups were used to update the automated predictions and add information to the gene predictions in the database. The process of annotation is ongoing and information will be continually added to this resource over time.

The project began in 2003 when the International Glossina Genome Initiative (IGGI) was established with seed funds from the WHO. Of the approximately 146 researchers associated with the project, at least half are from African institutions. The WHO also funded an annotation workshop at the University of the Western Cape, where a UCT researcher joined other lecturers in training African scientists in basic bioinformatics tools and annotation, and then had them annotating the Glossina expressed sequence tags (short sub-sequences of a DNA sequence). This annotation was an important contribution from the African scientists, who are all authors on this paper. The cost of the larger project, including IGGI training efforts, genome sequence at Sanger and the functional genomic studies performed in various labs building on the genome data, exceeded US\$10 million.

The UCT researchers are: Dr Heather Marco and Professor Gerd Gäde of the Department of Biological Sciences at UCT; and Associate Professor Nicola Mulder, the head of the Computational Biology Group in the Institute for Infectious Disease and Molecular Medicine at UCT. All three are co-authors of the *Science* paper on the tsetse fly genome. Dr Marco, an alumnus of UCT’s Science and Health Science Faculties, is a relatively young staff member at the senior lecturer level and is the major scientist in the annotation group for neuropeptide genes and their receptor genes. Dr Marco and Professor Gäde (A-rated scientist and retired Chair of Zoology at UCT) plan to pursue research to unravel some of the genetic peculiarities of the tsetse fly which uses the amino acid proline to generate energy to power its flight muscles (most other flies use carbohydrates). If they can find

ways to block this energy metabolism, it may be a way to combat the distribution range of the tsetse fly.

### **Evolutionary biology resource**

Beyond disease control, the genome is an important resource for evolutionary biology. Tsetse flies are unique from most other insects in multiple aspects of their biology. An example of this is the tsetse's evolution of lactation – a defining aspect of mammalian biology. The independent evolution of this physiology in the tsetse allows the comparison of the commonalities and differences between the two systems. Surprisingly, analyses of proteins in tsetse milk reveal significant similarities to those found within mammalian milk. The tsetse also develops its young in the uterus and gives live birth, while most other insects lay eggs.

Insights gained from such comparisons will increase understanding of how such dramatic changes develop at the genetic level in related organisms.

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***Issued by: UCT Communication and Marketing Department***

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