

TSETSE FLY GENOME BREAKTHROUGH: THE FAO AND IAEA CRACK THE CODE



A pregnant female of the tsetse species *Glossina morsitans*.

(Photo: Geoffrey M. Attardo, Research Scientist, Yale School of Public Health, Yale University, USA)

With the breakthrough in sequencing the genome of the tsetse fly species *Glossina morsitans* in April 2014, another milestone has been achieved in helping to solve a problem that has had horrendous ramifications for Africa.

Tsetse flies, large biting flies, which populate most of mid-continental Africa between the Sahara and the Kalahari deserts, are vectors for single-cell parasites known as trypanosomes. This specific parasite causes trypanosomiasis, or sleeping sickness, in humans. Konstantinos Bourtzis, a Molecular Biologist with the Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, explained the potential gravity of the tsetse bite for human health, for which a vaccine is not available and for which costs of medical treatment are very high. He mentioned that, currently, approximately 70 million people face the risk of sleeping sickness while over 50 000 people are estimated to be infected. Sleeping sickness attacks the central nervous system, changes the biological 'time clock', and causes changes in personality including confusion, slurred speech, seizures and difficulty in walking and talking.

Livestock on the other hand can be hit by nagana, a wasting disease that is transmitted when the tsetse flies bite animals to feed on their blood. Nagana is the root cause of a debilitating chronic condition that reduces fertility, weight gain, meat and milk production, and makes livestock too weak to be used for ploughing or transport, which in turn affects crop production. It results in the yearly death of around 3 million animals, with over 50 million animals facing the risk of infection. For African farmers, the tsetse flies are a nightmare; they also impact food security and socio-economic progress in sub-Saharan Africa.

Finding a solution to the havoc created by tsetse flies to livestock has been a major challenge for the combined scientific efforts of the IAEA and the Food and Agriculture Organization of the United Nations (FAO), as well as for the World Health Organization (WHO), which has focused on combating human sleeping sickness.

Joint research over the past decades to block the spread of severe infection from tsetse flies resulted in the introduction by the FAO and IAEA of the environmentally friendly sterile

insect technique (SIT), a biologically-based method for the management of key insect pests of agricultural, medical and veterinary importance. A form of insect birth control, the SIT involves releasing mass-bred male flies that have been sterilized by low doses of radiation into infested areas, where they mate with wild females. These do not produce offspring and, as a result, the technique can suppress and, if applied systematically on an area-wide basis, eventually eradicate populations of wild flies.

The newly acquired knowledge of the tsetse fly genome provides a wealth of information for the improvement of the entire SIT package and can help unravel interactions between tsetse flies, symbionts and trypanosomes. The decoding of the genome was detailed in a press release issued by the IAEA on 24 April 2014 entitled *Tsetse Fly Genome Breakthrough Brings Hope for African Farmers*.

The successful unravelling of the tsetse fly genetic code has been part of an international collaboration that involved the FAO/IAEA Insect Pest Control Laboratory and the support of over 140 scientists worldwide. This scientific

breakthrough will enable a better understanding of the biological and genetic potential of the tsetse flies including their nutrition, reproduction, immunity and vectorial capacity, explained Bourtzis.

Bourtzis further elucidated that this discovery will enable scientists to enhance the SIT by integrating it with new and complementary methods in an area-wide approach to control the devastating impact from tsetse flies on animals and humans, and that the purpose of developing solutions is not to eliminate a tsetse species but to eradicate local populations of tsetse flies.

Tsetse flies were successfully eradicated in 1997 from the Tanzanian island of Zanzibar using the SIT. Ethiopia and Senegal are making significant progress in infested areas with the same method. The FAO and IAEA are helping 14 countries control tsetse populations through applying area-wide integrated pest management approaches.

Aabha Dixit, IAEA Office of Public Information and Communication

FACT BOX — TSETSE FLIES

Tsetse flies are known to have established sophisticated symbiotic associations with three different symbiotic bacteria. All tsetse fly species examined to date harbour an obligate symbiont of the genus *Wigglesworthia*, which has a long-lasting symbiotic association with tsetse flies providing them important nutrients, such as vitamins, which are not available in human and animal blood.

Tsetse flies have also established a symbiotic association with another bacterium, namely *Sodalis*. Recent experimental work suggests that both tsetse fly midgut-associated symbionts (*Sodalis* and *Wigglesworthia*) can affect trypanosome development and thus can be exploited in order to prevent the establishment and transmission of these parasites.

Tsetse's third symbiont is the alphaproteobacterium, *Wolbachia*. This

bacterium is the most successful symbiont on Earth since it infects more than 40% of all insect species. *Wolbachia* is known to manipulate the reproductive properties of its hosts, most commonly causing cytoplasmic incompatibility, a kind of male sterility. Recently in mosquitoes, it has been shown that this symbiont prevents the establishment and transmission of major human pathogens that cause such diseases as dengue, chikungunya and malaria.

Whether *Wolbachia* can also prevent the establishment and transmission of African trypanosomes in tsetse flies, thus blocking the spread of sleeping sickness and nagana, is currently under investigation. Interestingly, the deciphering of the genome of *Glossina morsitans* also unraveled the presence of hundreds of *Wolbachia* genes in the tsetse fly genome. The potential function of these genes, if any, is as yet unknown.