

# Modelling flies, people and livestock in the struggle against sleeping sickness



**Advanced mathematical modelling techniques were combined with research methods involving local people to create a new model that can be used to test disease interventions and warn of future outbreak threats.**

The disease human African trypanosomiasis (commonly known as sleeping sickness) occurs in distinct areas in sub-Saharan Africa. The Luangwa Valley in Eastern Zambia was first identified as one such area in 1908 and since then sporadic outbreaks have occurred which have profoundly influenced development in the Valley.

The acute, eastern and

southern form of the disease is invariably fatal if untreated. Unless individuals are treated within weeks of becoming infected, treatment is only possible using toxic drugs, which in themselves cause the death of one in 20 patients.

In addition, especially in its early stages, the disease's symptoms are similar to those of more common illnesses and many cases are misdiagnosed

due to poor facilities and medical staff with insufficient training.

The sleeping sickness disease system is complex. Many wild animals and all domestic ones are capable of carrying the parasite that causes the disease, in other words of being the 'reservoir' for the infection. People suffer from the 'spillover' of infection from these animals, with the disease-causing parasite transmitted through the bite of a tsetse fly (*Glossina* species). In between sporadic epidemics, human cases are rare which makes the disease system difficult to study and, in particular, to model.

The risk of being bitten by an infected tsetse fly is not distributed evenly across the Valley, with areas closer to undisturbed wildlife habitats supporting higher density of flies. In addition, the behaviour of individuals varies according to their livelihoods and position in the household. This in turn influences their movement patterns and therefore their risk of infection.

Researchers in the Dynamic Drivers of Disease in Africa Consortium developed a



A child walks by a cattle enclosure Image: Neil Anderson

mathematical model to represent this complex disease system that incorporated human, livestock and tsetse populations alongside important behavioural, ecological and physical characteristics.

The researchers conducted a household and livestock census so actual populations were known. They carried out a tsetse survey to evaluate the distribution of the fly and land cover and physical features, including waterholes, rivers and roads, were mapped and used to define human and animal movement patterns. A detailed questionnaire provided quantifiable data about human movements, and published literature and local informed opinion were also used to develop the model.

Researchers worked with local people, leading participatory mapping and focus groups and carrying out transect walks to understand human behaviour and movement patterns. At the same time, this enhanced engagement with local communities.

In this way, the research team found out about people's routines for collecting water and firewood, washing clothes by streams, grazing livestock, checking beehives and other

regular activities – and all this information provided insights into which parts of daily routines and livelihood activities are most risky, and which people are most at risk from disease, for example by gender, age group or livelihood.

Through this detailed research work an agent-based model (a method for simulating disease transmission in a complex system with separately acting 'agents') was created. The agents included people, livestock and tsetse. The resulting model predicted one or two human infections in a six-month period – an accurate representation of the real situation in the study area.

### **Disease prevention**

A valuable feature of this model is its practical application. It can be used to study the impact of changes in human or livestock populations on disease transmission and this in turn can be used to guide disease prevention strategies. In particular, the model can be used to test the conditions in which livestock can become the primary disease reservoir if wildlife populations decline further than they already have. As such, the model will help guide policy formulation at

the national level and provide guidance through veterinary officers on managing animal health to local communities. The model will also inform development policies so that risk to local people can be minimised and environmental sustainability enhanced.

Researchers shared an early iteration of the model with key policymakers in Zambia during a Consortium workshop in 2016. They also held feedback sessions with the communities involved with the research in which the results of the livestock and human trypanosomiasis surveys were discussed. Despite there currently being few reported cases, local people are aware of sleeping sickness and its seriousness.

As part of the interdisciplinary work in the Consortium, the impact of future scenarios was examined by scientific experts and compared with local communities. These future scenarios can now also be further tested using the model, including studying the potential effects of land-cover change and climate change on disease transmission – so providing an early warning of disease risks for local communities.



Cattle can host the trypanosomiasis pathogen Image: Neil Anderson

*This is one of a series of impact case stories produced by the Dynamic Drivers of Disease in Africa Consortium, an ESPA-funded research programme designed to deliver much-needed, cutting-edge science on the relationships between ecosystems, zoonoses, health and wellbeing with the objective of moving people out of poverty and promoting social justice. Find more info at [www.driversofdisease.org](http://www.driversofdisease.org).*

