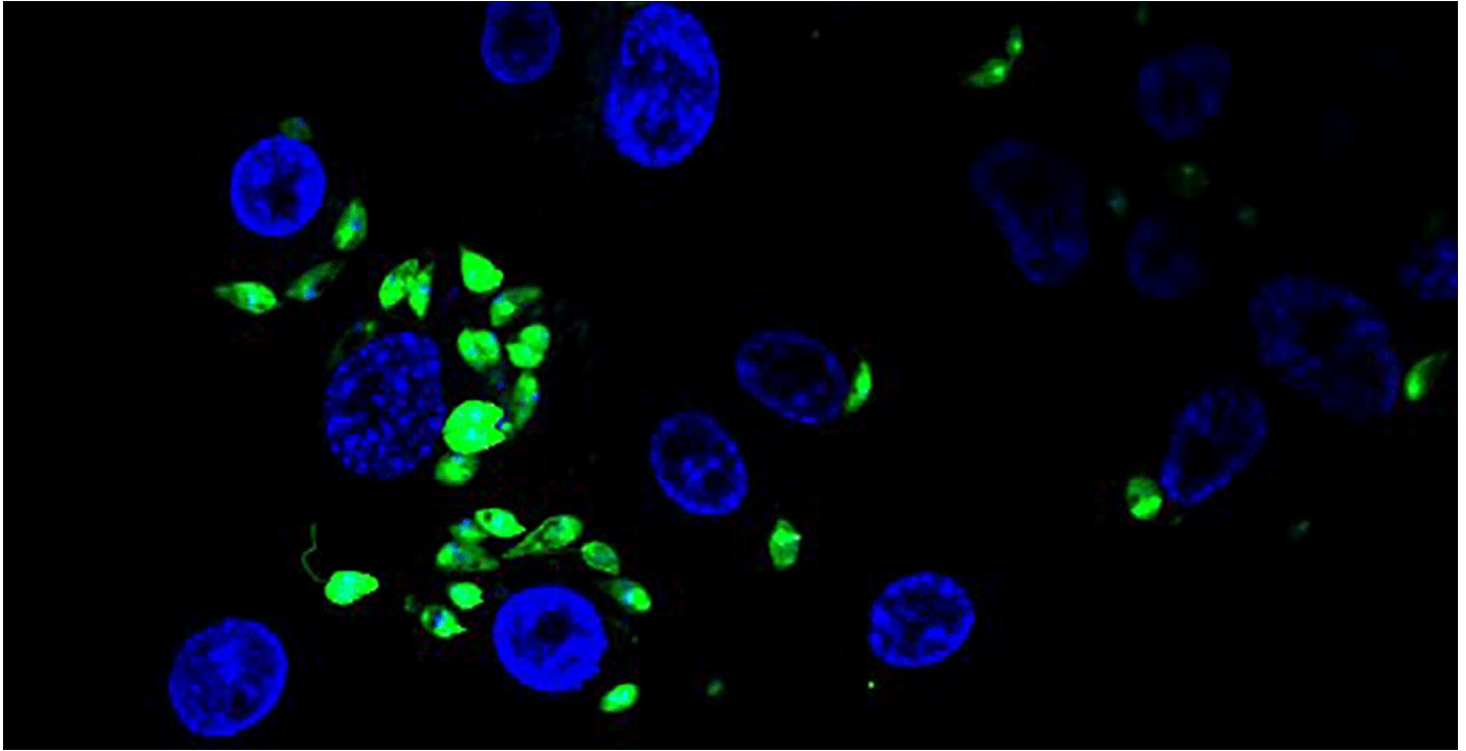


Unique Antwerp data set uncovers the mystery of neglected disease

Series of ITM studies paints a clearer picture on parasite causing neglected tropical disease leishmaniasis.

23-11-17



Dit is de omschrijving

Leishmaniasis is a parasitic disease that still affects two million people each year in nearly one hundred countries, resulting in approximately 50,000 deaths. As a result of climate change and interference in nature, the disease now occurs in humans in Southern Europe again, whilst it was never eradicated in dogs in Europe.

The *Leishmania* parasite is a smart creature that adapts to humans and the few available medicines that are used to combat this parasite. How the parasite developed resistance was a mystery until recently. The Institute of Tropical Medicine Antwerp (ITM) in Belgium is about to change that, based on clinical samples from the Indian sub-continent. In five years time, experts of ITM and Sanger Institute in the UK developed a unique dataset with genome analyses of patient samples from among others India and Nepal.

The data set enabled ITM professor Jean-Claude Dujardin and his team to uncover the mystery of the *Leishmania* parasite slowly but steadily. First, the investigators mapped the [evolutionary history of the parasite on the Indian sub-continent since 1850](#), with their results proving a perfect match to the historical sources left by British doctors in India about the first epidemics of leishmaniasis.

Recently, the investigators demonstrated how [the parasite goes into a state of hibernation](#), making it invisible to medication and the immune system.

In a next study, the researchers from Antwerp discovered that [Leishmania plays with their amount of chromosomes to adapt to its environment](#), which leads to disease in humans (Down syndrome for example).

Scientists from the Pasteur Institute in Paris and the Center for Genomic Regulation (CGR) in Barcelona join in a fourth episode of the investigation. Together with ITM they performed further analyses on the data set. These analyses revealed that [populations of Leishmania are made of genetically different cells forming a kind of mosaics](#). Each of these individual cells would have different adaptive capacities. Such genome variations are also common in many types of cancer. The new results were published in the journal Nature Ecology & Evolution this month.

Professor Jean Claude Dujardin, Head of ITM's Department of Biomedical Sciences: "By further uncovering the mystery of the *Leishmania* parasite, we are getting ever closer to finding solutions to this neglected tropical disease, which does not receive enough attention and resources."

"A fantastic aspect of modern science is that all data from genome analyses are made public, which results in new collaborations, such as the one between ITM, the Pasteur Institute and the CGR. The new study also confirms that ITM has a valuable asset in the form of a unique collection of parasite samples from developing countries together with their associated genomic information."

Link

- [Haplotype selection as an adaptive mechanism in the protozoan pathogen *Leishmania donovani*](#), Nature Ecology & Evolution

