

# A study to maintain food security in Uganda

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The study is based on a research program carried out from start to finish by EPFL. Credit: LASIG / EPFL

By identifying the genes involved in resisting Africa's most widespread cattle disease, researchers at EPFL have developed a map of Uganda showing cattle farmers where the riskiest areas are.

"We hope that our research will have an impact, because it addresses some major issues regarding food security in Africa over the medium and long term," says Stéphane Joost, who works in EPFL's Laboratory of Geographic Information Systems (LASIG) and is the corresponding author of a study recently published in scientific review *Frontiers in Genetics*.

Theileriosis is a tick-borne [cattle](#) disease. The parasite involved kills thousands of cattle each year in central and eastern Africa. According to the Food and Agriculture Organization (FAO) of the United Nations, the disease causes financial losses estimated at 170 million dollars per year in the region. Those losses lead to food insecurity for many families and are partly responsible for rural depopulation.

## **Novel method**

The study, in which LASIG post-doctoral researcher Elia Vajana was first author, produced a map showing the areas of Uganda where this deadly disease is most prevalent. The map is the result of a novel method compiling epidemiological data collected from 823 indigenous cattle along with their location. Using an environmental genomics approach – which combines the probability of being bitten by a tick, the risk of infection by the parasite and the genetic characteristics of cattle populations – the researchers were able to identify the genes potentially involved in resisting theileriosis.

The method developed by the team aims to help local veterinarians – who took part in the study as well – to see where the riskiest areas are. Farmers' associations will also be able to make better choices about which breeds to raise, depending on their region. For the researchers, the study furthermore shows the importance of preventing indigenous breeds from crossing with other breeds, particularly European ones. Zebu breeds that migrated from India to Africa around 4,000 years ago are

resistant to the disease vector, whereas imported breeds die just a few months after infection.

## Why cross-breeding is a mistake

"Our study shows that the cross-breeding carried out in Africa in the last few years – pushed by European corporations with the promise of higher yields in terms of milk and meat – is a mistake based on a short-term approach. Diluting indigenous breeds reduces the cattle's resistance to this disease," says Vajana. In particular, the study documents the role played by two genes in the disease resistance process. As a result, the study could be a first step towards implementing breeding programs that exploit this [disease](#) resistance process.

The publication is based on a research program carried out from start to finish by EPFL as part of NextGen, a European research project that began in 2010 (FP7). According to Joost: "The study involved large amounts of environmental data produced by meteorological stations and satellites, and large amounts of genetic and health data collected on the ground as part of the NextGen project. Extensive IT resources were also used to develop the statistical models and produce the results. This field of geocomputational molecular ecology combines some of the unique environmental engineering skills that we have developed here at EPFL."

**More information:** Elia Vajana et al. Combining Landscape Genomics and Ecological Modelling to Investigate Local Adaptation of Indigenous Ugandan Cattle to East Coast Fever, *Frontiers in Genetics* (2018). [DOI: 10.3389/fgene.2018.00385](https://doi.org/10.3389/fgene.2018.00385)

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