2019 Thomas C. Alber Science & Engineering for Global Health Fellow

Sarah Guth, UC Berkeley PhD Candidate in Integrative Biology, Boots Lab

Sarah is a PhD candidate in Mike Boots lab at UC Berkeley. Her work focuses on the exchanges of pathogens between wildlife and human populations, with an emphasis on the drivers of spillover. She applies a combination of epidemiological models, geospatial analyses, genomics, and field-based approaches to understand questions regarding the evolutionary and spatial dynamics of emerging and re-emerging zoonoses. She graduated from Middlebury College with a B.A. in Conservation Biology, and spent two years working for the Planetary Health Alliance. As an Alber Science & Engineering Fellow, she will use genomic surveillance and phylodynamic inference to begin mapping transmission routes of zoonotic viruses in Madagascar.

Fellowship Proposal

Canine rabies is a highly unique zoonosis; the virus is both 100% lethal and preventable. This single-stranded negative RNA virus results in roughly 60,000 human deaths annually. The vast majority of these cases occur in the developing world where there is limited access to vaccines and post-exposure prophylaxis (PEP). In Madagascar, the risk of contracting rabies is particularly high. The virus maintains endemic transmission in the domestic dog population, yet a lack of resources has prevented sufficient rabies control. However, rabies surveillance in Madagascar currently relives exclusively on passive civilian reporting and does not exist outside of the District of Antanararivo – home to the capital city and the only authorized national laboratory for rabies diagnostic testing. Given such limited surveillance, rabies underreporting in Madagascar is likely substantial.

Achieving the WHO goal to eradicated canine rabies by 2030 will require identifying and vaccinating source populations, which is currently not feasible in Madagascar. Underreporting prevents identifying source populations, and the country lacks the healthcare infrastructure and financial resources needed to implement widespread surveillance and vaccination. Targeted genomic surveillance has the potential to be an effective solution. A fast-evolving RNA virus, rabies accumulates genetic variation on the same timescale as epidemiological processes. Researchers can use viral sequences to characterize the population structure of a circulation rabies virus, and by applying phylodynamic inference, subsequently map transmission routes within a host population.

Madagascar currently lacks the capacity for genomic surveillance. However, with recent advances in sequencing technology, genomic research is now feasible in settings with minimal infrastructure. The MinION (Oxford Nanopore Technologies) is a novel, pocket-sized, light weight nanopore-based sequencing platform with low startup costs, capacity for long-read outputs, and easy data transfer. MinION genomic surveillance has been used successfully in the control of both the recent Zika and Ebola epidemics. This project

seeks to implement real-time genomic surveillance of canine rabies in the District of Antananarivo, Madagascar using MinION sequencing. The goal of this project is to build capacity for effective rabies surveillance in Madagascar and using phylodynamic inference, develop an understanding of rabies transmission dynamics.