

Outbreak of cutaneous leishmaniasis due to *Leishmania tropica* amongst militia members in a non-endemic district under conflict in the lowlands of Somali Region, Eastern Ethiopia

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Cutaneous leishmaniasis (CL) in Ethiopia is typically caused by *Leishmania aethiopica* and occurs in temperate, high-altitude regions. Following the recent onset of conflict, an outbreak of CL emerged among over a thousand militia members at an unusually low altitude (500 meters) in the Somali Region—an area not previously known for CL transmission, raising significant public health concerns. We conducted a rapid outbreak assessment at the affected site, collecting clinical and entomological data. A total of 1,050 patients were recruited; all male militia members who had been displaced into the area within the year preceding their symptoms. Targeted sequencing identified *L. tropica* as the causative species, challenging the prevailing assumption that *L. aethiopica* is the sole agent of CL in Ethiopia. Nearly all cases (99.1%) presented with more than three lesions, and 77.0% had over ten. *Phlebotomus orientalis* and *P. sergenti*—vectors for visceral leishmaniasis (VL) and CL in North Africa, respectively—were detected in the area, along with hyraxes, the animal reservoirs of *L. tropica* and *L. aethiopica* in Kenya and Ethiopia. However, these observations are based on limited sampling. Further in-depth research is needed to investigate the eco-epidemiology of this outbreak and assess patients' treatment responses. Findings will inform control strategies, guide clinical management, and help prevent further spread of this emerging CL form, including the potential for hybridization with *Leishmania* strains responsible for VL in the region.

Adugna Abera earned his BSc in Medical Laboratory Technology from the College of Health Sciences at Addis Ababa University in 2005. He completed an MSc in Medical Microbiology at the same university in 2009 and is currently pursuing a PhD in Microbial Sciences and Genetics there. His research focuses on emerging NTD diseases, with a focus on molecular epidemiology, drug resistance, diagnostics, and metagenomics.



His research experience began as an assistant researcher at AHRI in March 2010, investigating the use of *Leishmania* antigens for diagnosis and vaccine development. His responsibilities included cell isolation, parasite culturing, and molecular techniques. In 2016, he became a researcher at EPHI, where he managed malaria and NTD projects and received training in molecular biology and bioinformatics. He has authored over 55 articles as first and co-author, mainly focusing on malaria and leishmania, along with other infectious pathogens.

During the COVID-19 pandemic, he played a key role in establishing a dedicated testing laboratory. Together with his colleagues, he secures grants from NIH and EDCTP-3. He collaborates with various national and international institutions, such as the Ministry of Health, CDC-Africa, CDC-Atlanta, and ITM, on research areas including malaria, AMR, NTDs, acute febrile illnesses, genomics, and bioinformatics.