We identified visceral leishmaniasis caused by *Leishmania donovani* in a previously unknown focus in northern Somalia. Clinical and epidemiologic characteristics of 118 cases during 2013–2019 in Bosaso, the region’s commercial capital, have raised suspicion of visceral leishmaniasis endemicity status there.

**Visceral Leishmaniasis, Northern Somalia, 2013–2019**

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stibogluconate (20 mg/kg) combined with paromomycin (20 mg/kg), both intramuscularly. However, because of the low availability of paromomycin, sodium stibogluconate monotherapy was administered when paromomycin was unavailable. Outcome records were available for 103 (87%) patients, 85 (85%) of whom were clinically cured. Eighteen (17%) patients died. As part of routine data collection, the patients’ origins were documented: all patients came from Sanaag and Bari regions in northern Somalia and had no history of traveling outside this area.

For 3 patients, we attempted to identify Leishmania species by extracting DNA from microscopy slides and sequencing partial fragments of the PCR-amplified HSP70 gene (6). In 2 patients, L. donovani was identified (European Nucleotide Archive study PRJEB34786, accession nos. LR723650 and LR723651 [Appendix, section 1]).

Suspected VL patients whose illnesses fit the case definition first underwent rapid diagnostic testing to exclude malaria (5). During 2013–2019, only 2 were found positive for malaria, which was confirmed by microscopy. Both also had confirmed VL and subsequently received antimalarial and antileishmanial therapy. In accordance with national guidelines (5), patients also were tested for HIV; no VL patient was positive. Screening for other underlying conditions was undertaken when feasible; for example, with chest radiograph. One VL case-patient with concomitant pulmonary tuberculosis was referred to the tuberculosis center after finishing antileishmanial treatment.

We describe a previously unreported focus of VL in northern Somalia. The age distribution of the case-patients indicates that VL seems to be endemic in this region; it is unlikely that all cases were imported or present as an “outbreak” such as that described in Huddur (Bakool region) in 2001 (7). From the perspectives of families of the patients and the local health workers, the disease has been known in this area for years. Despite ongoing war and unrest in southern Somalia and the prevalence of displacement in the country, it appears implausible that the VL patients in Bosaso came from there. The nearest known focus is across the Gulf of Aden, in southern Yemen (8,9), where Somali diaspora is present. Because sea travel with small wooden boats is common across the gulf and has been for centuries, this focus might play a role in the cases described here and merits further exploration. Surveillance for VL should be strengthened in northern Somalia, and access to adequate diagnosis and treatment must be provided to reduce transmission, illness, and death. Support and collaboration across stakeholders, including WHO and national health actors, must be continued to tackle the disease in a comprehensive manner. Further investigation (e.g., a cross-sectional survey) might be considered to define the infection rate in this newly identified focus and determine its level of endemicity.

About the Author
Dr. Aalto is a surgeon in the surgical department of Bosaso General Hospital. His primary research interests include malaria, leishmaniasis, and the control of their vectors.

References

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Appendix

1. Short Summary on Methods of HSP70 Identification and Molecular Typing

We identified *L. donovani* in 2 samples coming from different patients:

- BGH 201812 03
- BGH 201812 23

As described elsewhere (1), two partial *Leishmania* HSP70 coding sequences were amplified in both samples with the following HSP70 primers:

- **Fragment N:** HSP70-F25 5’ GGACGCCGGCAGCAGTCT 3’
- HSP70-R617 5’ CGAAGAAGTGCCGATACGAGGGA 3’

- **Fragment T:** HSP70–6F 5’ GTGCACGACGTTGCTGGTGTGCTGTCG 3’
- HSP70-R1310 5’ CCTGGGTGTTGTTTCAGCCACTC 3’

The PCR fragments were sequenced from both sides. As the fragments overlap, one sequence contig was constructed for each of both samples, and the sequences were found identical.

Sequences were deposited at European Nucleotide Archive (ENA)

Study accession number in the European Nucleotide Archive is PRJEB34786

https://www.ebi.ac.uk/ena/data/view/PRJEB34786

Accession numbers of both sequences are:

- LR723650: MHOM/SO/2018/BGH201812_03
- LR723651: MHOM/SO/2018/BGH201812_23
The sequences were used to construct the dendrogram (Appendix Figure), as described elsewhere (1). The two Somali samples (red square) cluster clearly with *L. donovani* strains.

2. In Vitro Culture Methods.

*Leishmania* culture was performed in vials of tryptone yeast extract agar with 5% human blood at 25°C until positive or for 30 days.

Reference