

Letter to the Editor

Schistosoma bovis Infecting Humans in Nigeria

Dear Editor,

We read the article entitled “*Human Schistosomiasis due to Schistosoma bovis in Nigeria*” by Enudi et al., published in *The American Journal of Tropical Medicine and Hygiene*.¹

In the article, an *S. bovis* cytochrome c oxidase subunit 1 (COX1) gene profile was identified in a pool of eggs from a human sample. It was suggested that *S. bovis* could infect human beings. Unfortunately, the authors did not include a nuclear marker in their genetic analysis. The authors also used a pool of *S. haematobium* eggs for DNA extraction. Ideally, a single egg is more appropriate to avoid genotyping a mixed *Schistosoma* species infection.

The inference that *S. bovis* was the causative agent of human schistosomiasis was based on an incomplete dataset. *Schistosoma bovis* COX1 profiles have previously been identified in samples from Nigeria^{2,3} and other parts of Africa alongside an *S. haematobium* internal transcribed spacer (ITS) profile representing mitonuclear discordance, resulting from either ancient or extant hybridization between *S. bovis* and *S. haematobium*.⁴ It is also important to highlight that two mitotypes, *S. bovis* and *S. haematobium*, can sometimes be recorded in *S. haematobium* populations, particularly in West Africa.^{2,5,6}

Although the COX1 and ITS markers are traditionally used to genotype *Schistosoma* species, there are suggestions that the markers are inadequate, and scientists genotyping based on the two markers alone should interpret their results with caution.^{2,6} Therefore, the title and conclusion of the article are potentially misleading without the nuclear marker profile for the sample reported.

OLUWAREMILEKUN G. AJAKAYE
Department of Animal and Environmental Biology
Adekunle Ajasin University
Akungba Akoko
Ondo State, Nigeria

Laboratory of Molecular Parasitology and Genomics of
Neglected Tropical Diseases
Adekunle Ajasin University
Akungba-Akoko
Ondo State, Nigeria
E-mail: remilekunf@gmail.com

ELISHA E. ENABULELE
Laboratory of Integrative Parasitology and Pathogen Genomics
Texas, USA
E-mail: enabuleleegie@gmail.com

Published online January 7, 2025.

This is an open-access article distributed under the terms of the Creative Commons Attribution (CC-BY) License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

REFERENCES

1. Enudi AO, Nmorsi OPG, Egwunyenga AO, 2024. Human Schistosomiasis due to *Schistosoma bovis* in Nigeria. *Am J Trop Med Hyg* 111: 1230–1236.
2. Ajakaye OG, Enabulele EE, Balogun JB, Oyeyemi OT, Grigg ME, 2024. Extant interspecific hybridization among trematodes within the *Schistosoma haematobium* species complex in Nigeria. *PLoS Negl Trop Dis* 18: e0011472.
3. Onyekwere AM, Rey O, Allienne JF, Nwanchor MC, Alo M, Uwa C, Boissier J, 2022. Population genetic structure and hybridization of *Schistosoma haematobium* in Nigeria. *Pathogens* 11: 425.
4. Rey O, Webster BL, Huysse T, Rollinson D, Van den Broeck F, Kincaid-Smith J, Onyekwere A, Boissier J, 2021. Population genetics of African *Schistosoma* species. *Infect Genet Evol* 89: 104727.
5. Agniwo P, et al., 2023. Genetic profiles of *Schistosoma haematobium* parasites from Malian transmission hotspot areas. *Parasit Vectors* 16: 263.
6. Platt RN 2nd, et al., 2024. Genomic data reveal a north-south split and introgression history of blood fluke (*Schistosoma haematobium*) populations from across Africa. bioRxiv [Unreviewed Preprint]. doi: 10.1101/2024.08.06.606828.