

# Investigating the genetic diversity of *Schistosoma bovis* and its hybrids across Africa



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## Background

Hybridisation between species within the *Schistosoma* genus is an emerging public health concern. Particularly the hybridisation between *Schistosoma bovis*, a veterinary parasite, and *S. haematobium*, a human parasite, which has been found to be widespread raises questions related to potential zoonoses and animal reservoir hosts, both of which could impact disease control. It is imperative to investigate if these hybridisation events are a recent phenomenon or an ancient event resulting in fixed introgression. Further studies are required to understand these inter-species interactions, where, how and if they occur, together with the consequences related to human and animal health, and schistosome genetics.

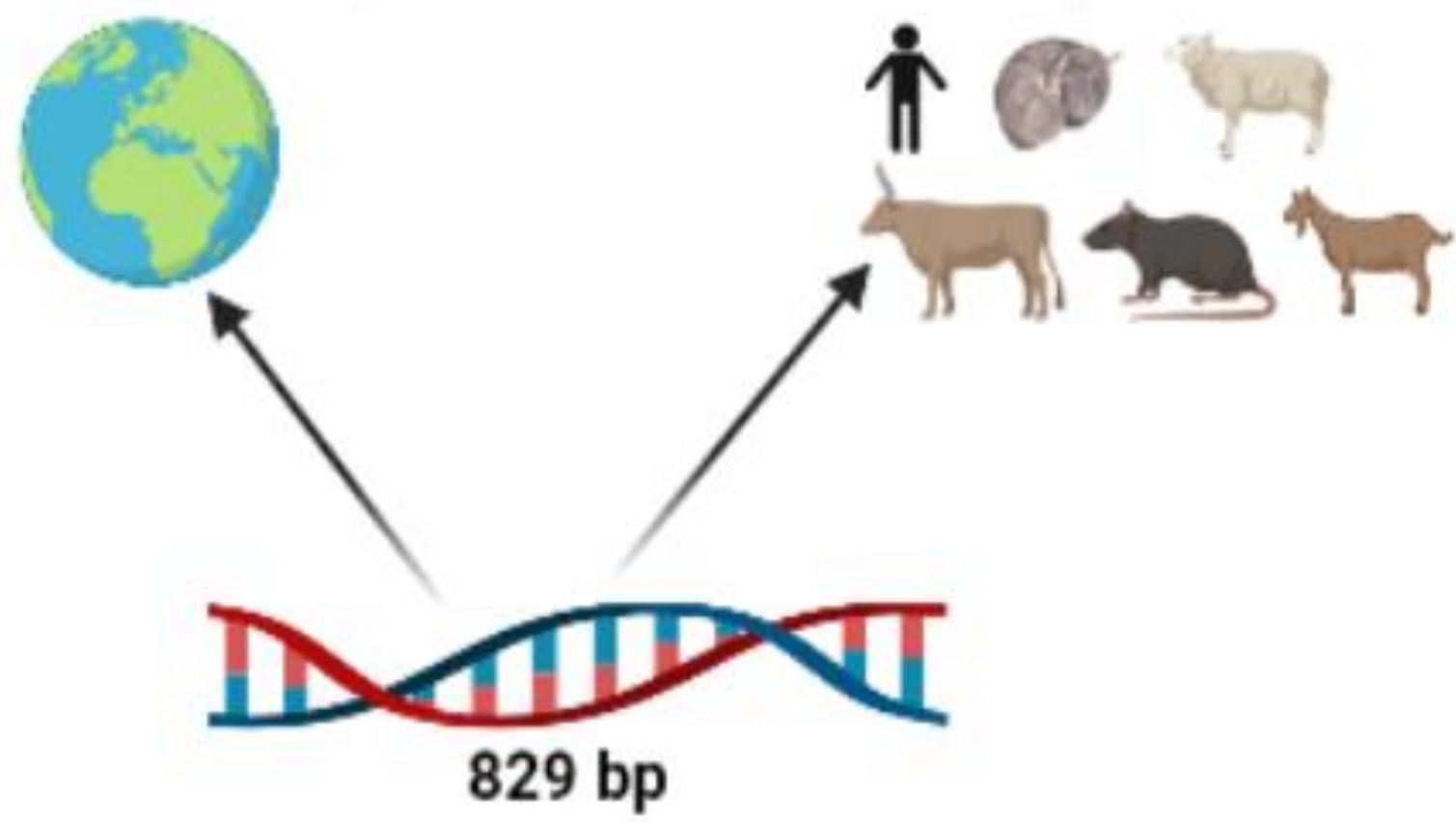
## Aims of study

- To investigate the geographical and host structuring of *S. bovis* and *S. haematobium-bovis* hybrids across Africa
- To determine the genetic diversity of *S. bovis* across Africa

## Methods

Broad geographical range (Europe, Central, East and West African countries)

Different hosts (humans, cows, goats, sheep, rodents and snails)



*S. bovis* & *S. haematobium-bovis* hybrid *cox1* sequences (published or generated from samples from the Schistosomiasis Collection at the Natural History Museum (SCAN)).



Multiple sequence alignment



TCS haplotype network analysis performed using Population Analysis with Reticulate Trees (PopART)

## Results

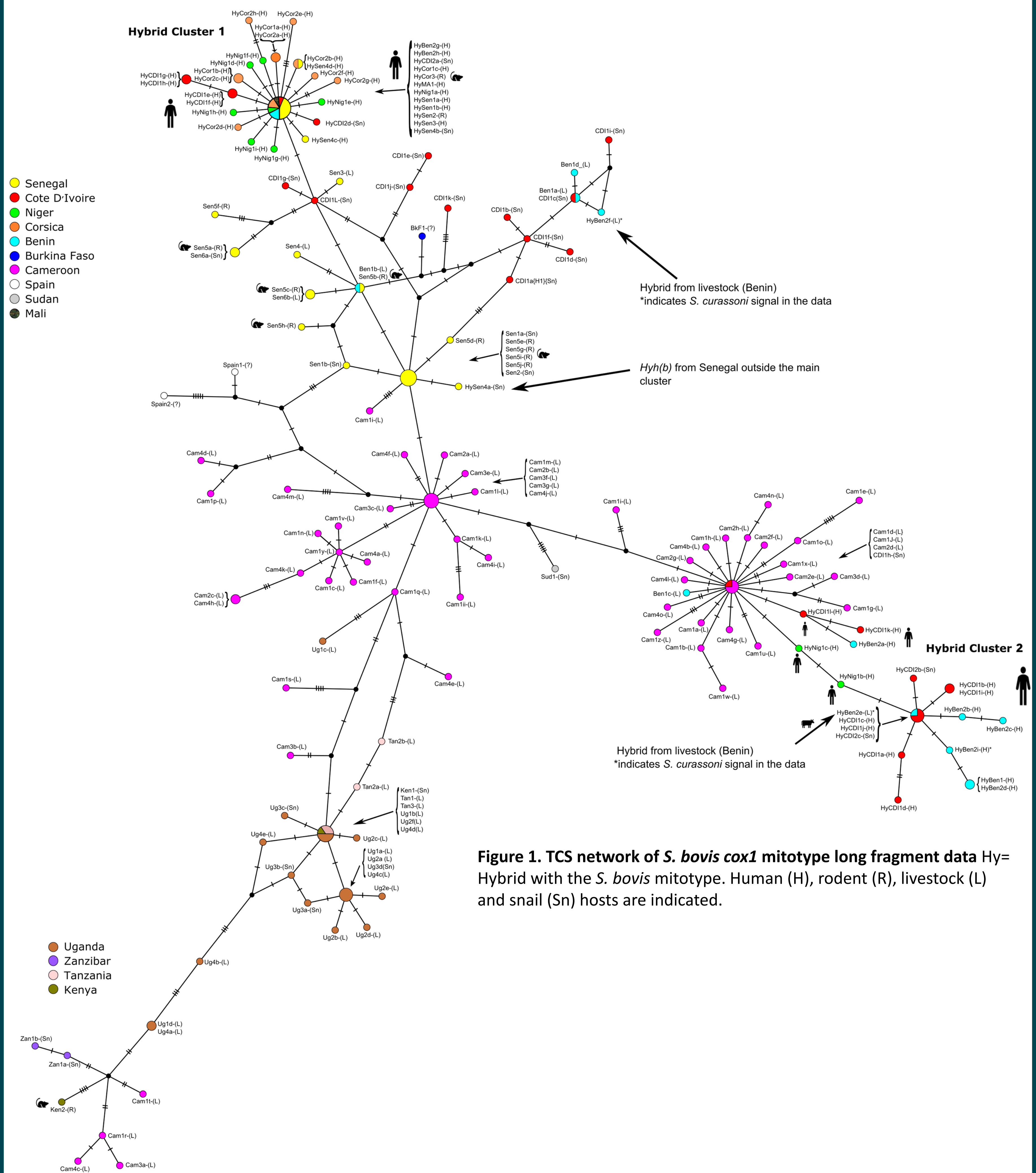


Figure 1. TCS network of *S. bovis* *cox1* mitotype long fragment data Hy= Hybrid with the *S. bovis* mitotype. Human (H), rodent (R), livestock (L) and snail (Sn) hosts are indicated.

## Discussion

- The extremely low genetic diversity and cluster within the *S. haematobium-bovis* hybrids suggests genetic selection/ or bottlenecking may occur during hybridisation.
- There was little apparent mixing between hybrid and *S. bovis* populations, suggesting the hybrid genetic signatures we see in our human hosts may not be the result of active inter-population interactions, as highlighted within recent genomic analysis.
- S. bovis* appears to be a diverse species with a level of structuring across different geographical zones.
- S. bovis* populations from different hosts are clearly mixing and there also appears to be cross over between adjacent geographical regions, probably supported by livestock movement.
- Further studies are warranted to elucidate the risk factors associated with these hybrid populations, especially the possibility of zoonotic transmission.

## Key findings

- The dataset included 119 published and 59 new *cox1* *S. bovis* mitotypes, from *S. bovis* or *S. haematobium-bovis* hybrids.
- The hybrids were almost entirely from humans and *B. truncatus* snails, indicating stringent restricted host use.
- Although *cox1* data were available from three rare hybrid samples from non-human hosts in Senegal and Benin (rodent and livestock).
- The *cox1* dataset formed a complex haplotype network for *S. bovis* but, apart from two haplotypes, all data from samples identified as *S. haematobium-bovis* hybrids formed two distinct genetic clusters.
- These clusters showed little diversity with the majority being identical mitotypes from different hosts and countries.
- The clusters did not form part of the *S. bovis* network, which showed geographical structuring.

## References

- Methodology figure created with Biorender.com.
- Djuikwo-Teukeng, F., Kouam Simo, A., Allienne, J., Rey, O., Njanyou Ngappagna, A., Tchuem-Tchuenté, L. and Boissier, J., 2019. Population genetic structure of *Schistosoma bovis* in Cameroon. *Parasites & Vectors*, 12(1).
- Leger, E. and Webster, J., 2016. Hybridizations within the Genus *Schistosoma*: implications for evolution, epidemiology and control. *Parasitology*, 144(1), pp.65-80.
- Platt, R., McDew-White, M., Le Clec'h, W., Chevalier, F., Allan, F., Emery, A., Garba, A., Hamidou, A., Ame, S., Webster, J., Rollinson, D., Webster, B. and Anderson, T., 2019. Ancient Hybridization and Adaptive Introgression of an Invasiveness Gene in Schistosome Parasites. *Molecular Biology and Evolution*, 36(10), pp.2127-2142.
- Rey, O., Toulza, E., Chaparro, C., Allienne, J., Kincaid-Smith, J., Mathieu-Begné, E., Allan, F., Rollinson, D., Webster, B. and Boissier, J., 2021. Diverging patterns of introgression from *Schistosoma bovis* across *S. haematobium* African lineages. *PLoS Pathogens*, 17(2), p.e1009313.
- Webster, B., Diaw, O., Seye, M., Webster, J. and Rollinson, D., 2013. Introgressive hybridization of *Schistosoma haematobium* Group Species in Senegal: Species Barrier Break Down between Ruminant and Human Schistosomes. *PLoS Neglected Tropical Diseases*, 7(4), p.e2110.