High levels of genomic differentiation between Nigerian *Schistosoma haematobium* and *S. bovis* indicates strong barriers to gene flow

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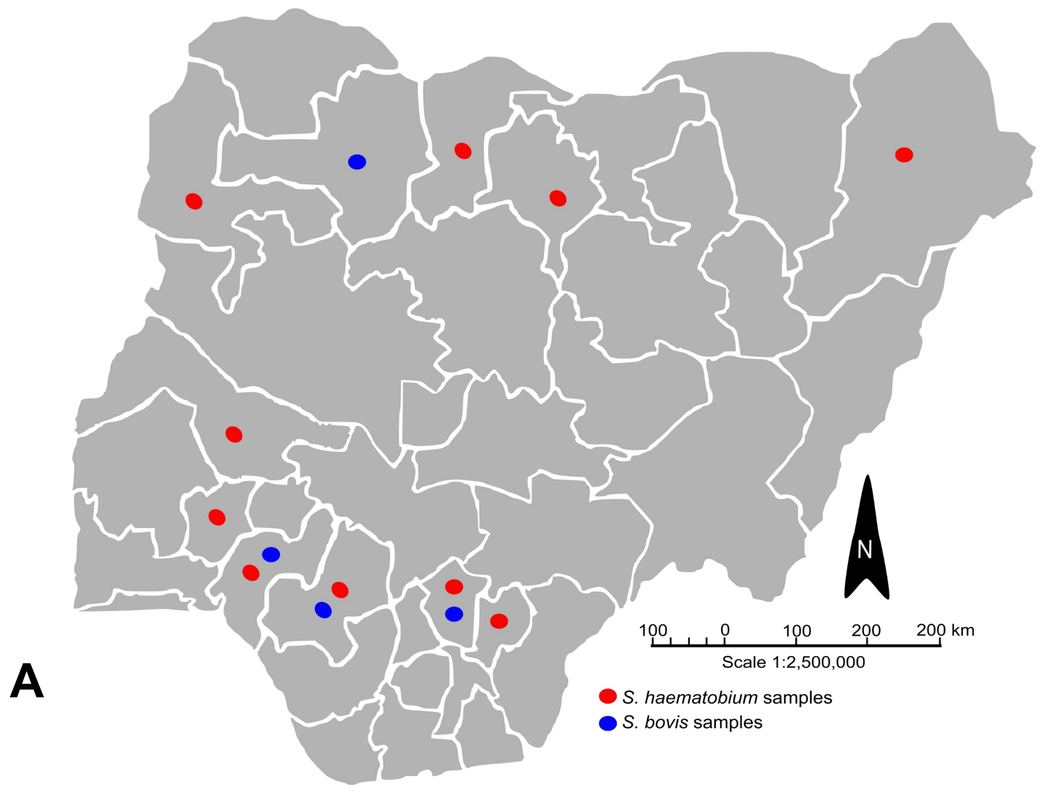
Background

Schistosoma species are parasitic blood flukes responsible for schistosomiasis disease in humans and animals. *Schistosoma haematobium* and *S. bovis* are sympatric species which cause human urogenital and livestock schistosomiasis respectively. Earlier molecular investigation on *Schistosoma* species based on few gene markers provided evidence for mito-nuclear discordance suggesting hybridization between *S. haematobium* and *S. bovis*. However, recent studies based on exome and genomic data have presented evidences for past hybridization events with subsequent introgression of *S. bovis* alleles into *S. haematobium*. To understand the evolutionary relationship between *S. haematobium* and *S. bovis*, we for the first time generated population genomics data for both species which were collected from humans and cattle in several states in Nigeria.

Methods

Whole genome amplification and sequencing of *S. haematobium* miracidia hatched from eggs collected from human urine and adult *S. bovis* from cattle were used to generated the genomic data for bioinformatics analysis.



Figures 1 (A) Sampling locations for *S. haematobium* and *S. bovis* in Nigeria. (B) PCA of unlinked, common SNVs (MAF>0.05) identified three groups corresponding to two population os *S. haematobium* and *S. bovis*. (C) Supervised and unsupervised admixture analyses show only a small *S. bovis* component associated with *S. haematobium* from Nigeria.

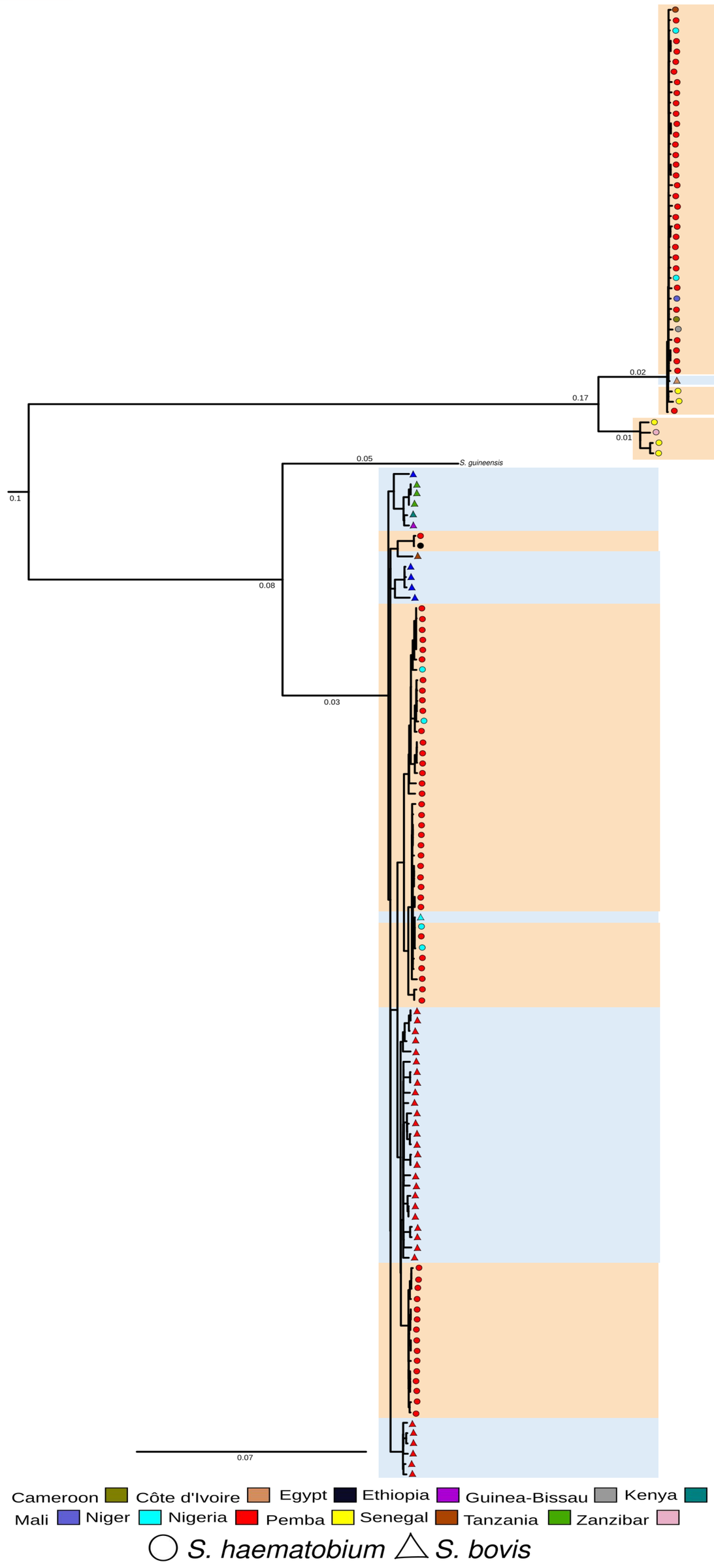


Figure 4. Maximum likelihood phylogram from circularized mitochondrial genomes rooted on *S. margrebowiei* and included *S. matthei, S. intercalatum*, and *S. guineensis.* The samples from Nigeria are in red circles and triangles. Other samples are from schistosomiasis collection at the Natural History Museum (SCAN). Highlight colors: Light brown, *S. haematobium* and light blue, *S. bovis.*

Major Conclusions:

1. Our results are consistent with hybridization between both species being ancient: *S. bovis*-like mtDNA was found in *S. haematobium* or *S. bovis* fall into distinct clusters. If hybridization was common we would expect mtDNA trees to be intermingled.
2. Other analytic approaches demonstrate that the nuclear genomes of these species are well differentiated, suggesting strong barriers to gene flow.
3. Our data suggests introgression between both species is unidirectional (*S. bovis* -> *S. haematobium*).
4. We conclude that the chimeric *S. haematobium* genomes found in the samples from Nigeria resulted from rare hybridization, followed by adaptive introgression of *S. bovis* genes, and that gene exchange between these species occurs on an evolutionary rather than an epidemiological timescale.

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