

# Barcoding and infection dynamics of intermediate snail hosts of human and livestock schistosome flukes

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## Abstract/background

The epidemiology of schistosomiasis in Senegal is very dynamic. While *Schistosoma mansoni* was the dominant parasite at the onset of the epidemic, the urinary species, *S. haematobium*, was mostly absent. Nowadays this pattern is almost completely reversed. In addition, molecular analyses revealed children to be infected with hybrids between *S. haematobium* and *S. bovis*, the latter being a livestock parasite. This species uses *Bulinus truncatus* to complete its life cycle, while *S. haematobium* mainly uses *B. globosus*. If the hybrid is able to use the same host as *S. bovis*, it could explain the rise in urinary schistosomiasis because *B. truncatus* is very abundant across the Senegal River Basin (SRB).

## Questions

- Which are the dominant snail species in the SRB?
- What is their role in schistosome transmission?
- Which host is responsible for the transmission of the hybrid schistosomes?

## Material and Methods

- Snails were collected along the SRB in 2012-2014 (Fig1 and 2)
- A 600bp fragment of cytochrome oxidase 1 (*cox1*) was sequenced and used to identify to species level and construct a phylogeographic network (Fig. 2).
- Each snail was tested for schistosome infection using a PCR targeting a nuclear repeat (DRA PCR; Amarir et al., 2014) and one targeting *cox1* mtDNA (RD-PCR; Van Den Broeck et al, 2011).

## Results 1

- Out of the 243 successfully barcoded *Bulinus* snail specimens, 171 were assigned to *B. truncatus* (70%) and 72 to *B. globosus* (30%)
- *B. globosus* only occurred in the Lower Valley of the SRB (Fig 1)
- 56% of *B. globosus* and 44% of *B. truncatus* snails were infected with schistosome DNA based on either or both PCRs
- *B. truncatus* was only infected with *S. bovis*, except in the Middle Valley, where this species is also infected with *S. haematobium* and in one case with the hybrid (note that this population is highly divergent from the other populations (see Fig 2))
- *B. globosus* was infected with *S. haematobium* and the hybrid parasite; never with *S. bovis*

## Results 2

- The haplotype distribution network of *B. truncatus* (Fig 2) shows that there is no clear population structure in the Lower Valley
- Unique haplotypes can only be found in the population from the Middle Valley (Fig 2)
- These haplotypes are very divergent from the remainder haplotypes (not shown)

Fig 2: Population genetic structure of *B. truncatus* based on *cox1* (590bp)

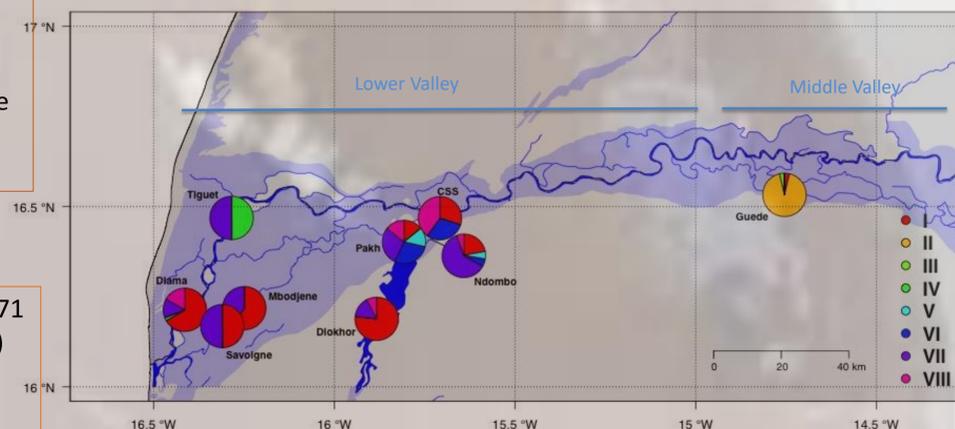


Fig 3: Morphological plasticity within *B. globosus* warranting a barcoding approach

## Conclusions

- *B. globosus* is the main intermediate host of the hybrid schistosome species.
- Its restricted distribution could explain the restricted distribution found for the hybrids in a previous study (Boon et al., in review)
- The higher infection intensity – as compared to *B. truncatus* – could compensate for its lower abundance
- *B. truncatus* is the most abundant and widespread snail species
- There are two divergent *B. truncatus* strains in the SRB, with the population in the Middle Valley being highly differentiated from the Lower valley
- This population can act as a host for human schistosome species (namely *S. haematobium*), and should therefore be monitored for spreading to the Lower Valley

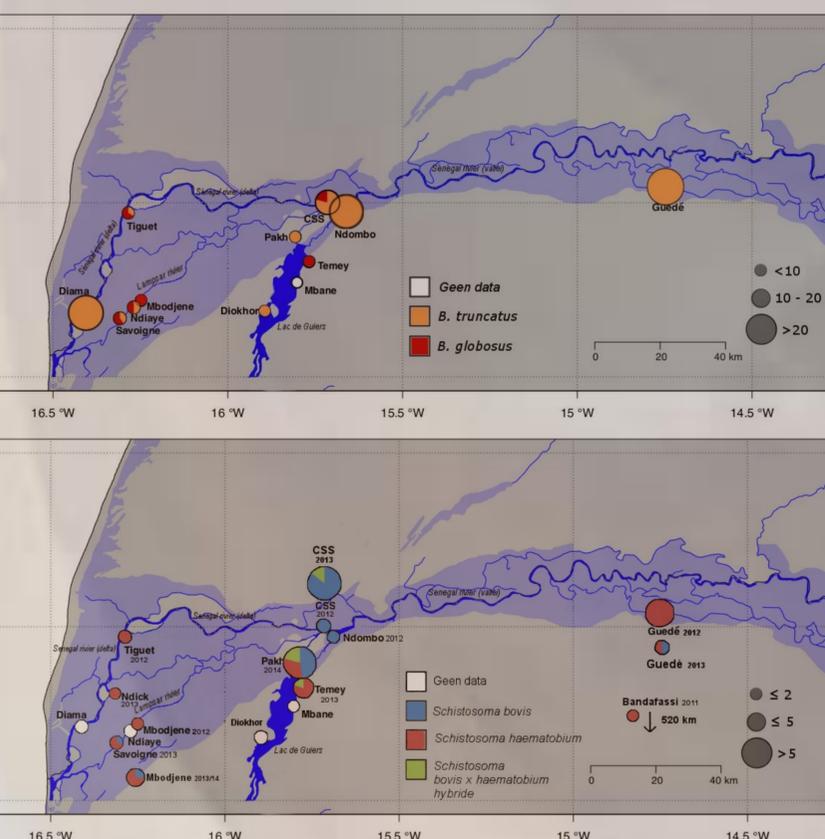


Fig. 1: Distribution of *B. truncatus* and *B. globosus* based on *cox1* identification (above); distribution of hybrids and pure schistosome species along the Senegal River Basin (below; from Boon et al., in review).

## References:

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