

Abstract

First molecular identification of *Bulinus africanus* in Lake Malawi with discussions on its transmission potential for human schistosomes

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The freshwater snail genus *Bulinus* plays a vital role in transmitting parasites of the *Schistosoma haematobium* group. Three species within the *S. haematobium* group cause urogenital schistosomiasis while five others typically infect wild and domestic ruminants. Using DNA-based identification methods, a hybrid schistosome between *S. haematobium* and *S. mattheei* has been recently detected in school children along the Lake Malawi shoreline in Mangochi District. This finding raised the need for contemporary reevaluation of local interactions between schistosomes and snails, with particular focus on snail species within the *Bulinus africanus* group. In 2017, 2018 and 2019, malacological surveys sampled several freshwater sites in Mangochi District. Collected snails (n= 250) were first characterised using shell morphology before closer inspection of the cytochrome oxidase subunit 1 gene (*cox1*), with DNA barcoding of the 'Folmer' region and a rapid PCR-RFLP typing assay with double digestion with *HaeIII* and *SacI* restriction enzymes. DNA *cox1* sequence analysis, with phylogenetic tree construction, suggested the presence of at least three taxa in Lake Malawi, *B. globosus* alongside first reports of *B. africanus* and *B. angolensis* which could be differentiated by PCR-RFLP methods. The latter species is morphologically unusual for it is typically placed with the *B. truncatus/tropicus* complex. Further to *B. nyassanus* which plays a key role in the transmission of *S. haematobium* within the lake, the distribution of *B. globosus* was only present in small water bodies around its margins whereas *B. africanus* and *B. angolensis* were found within it. This study provides new insight into the recent changes in the epidemiology of urogenital schistosomiasis as likely driven by a new diversity of *B. africanus* group snails within the lake. Inspection of additional DNA loci is needed to further characterise *B. angolensis*, comparing this population more broadly.