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Nonhuman mammalian reservoirs of human schistosomiasis in western Africa: prevalence, risks, and implications for elimination

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ADMINISTRATIVE INFORMATION

Support - ZJE.

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Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 7 July 2025 and was last updated on 7 July 2025.

INTRODUCTION

Review question / Objective To investigate the role of nonhuman mammalian as resersoirs of human schistosomiasis in West Africa.

Background Schistosomiasis, a neglected tropical disease (NTD) of profound public health significance, remains a leading cause of morbidity in sub-Saharan Africa (SSA), particularly in West Africa, where more than 90% of the global burden resides[1-5]. In 2019, schistosomiasis accounted for 1.6 million disability-adjusted life years (DALYs), with a moderate prevalence (10–49%) across most West African nations[3, 6, 7]. While primarily transmitted through freshwater snails, the persistence of the disease is increasingly linked to zoonotic spillover from nonhuman mammalian (NHM) reservoirs—a critical yet underaddressed challenge for elimination efforts[8-10]].

Human schistosomiasis in SSA is driven by Schistosoma haematobium (urogenital) and S. mansoni (intestinal), with sporadic cases of S. intercalatum and S. guineensis [4]. Chronic infection leads to fibrosis, anaemia, and organ damage, with S. haematobium implicated in bladder cancer and S. mansoni in hepatic complications[11-14]. High-risk groups—children, farmers, and women with water-dependent livelihoods—face disproportionate exposure due to socioeconomic and ecological factors [13, 15].

Current strategies, anchored in the mass drug administration (MDA) of praziquantel to school-aged children, fall short of the WHO's 2030 goals for elimination (≤1% high-intensity infections) and transmission interruption[16-18]. The WHO's "One Health" framework underscores the need to integrate human, animal, and environmental interventions, yet control programs rarely account for NHM reservoirs or emerging hybrid strains (e.g., S. haematobium × S. bovis), which complicate transmission dynamics[19-22].

Shared water sources amplify interactions between humans, livestock (e.g., Bos taurus), and wildlife (e.g., rodents), facilitating schistosome spillover and hybridization [21, 23-25]. Schistosoma mansoni is the major source of human intestinal

schistosomiasis and has been found to infect nonhuman primates (chimpanzees and baboons) in Kenya, Ethiopia, and Uganda[26, 27]. Evidence from livestock in Senegal, Benin, and Ghana and from wild rodents in Senegal, Ethiopia, and Kenya confirms NHMs as reservoirs for S. mansoni and S. haematobium, with the prevalence reaching 50% in hotspots[28]. Hybridization between human- and animal-infective species (e.g., S. haematobium × S. bovis) may increase parasite adaptability, undermining diagnostics and treatment[22, 29]. However, surveillance systems and policies remain anthropocentric, neglecting NHM infections in burden estimates [21, 26].

Rationale Western Africa, comprising 16 mainland countries and UK overseas territories, is Africa's second most populous region (~445 million people) [30] and bears the highest schistosomiasis burden in sub-Saharan Africa, with 85.4 million people requiring preventive chemotherapy [19]. Schistosoma mansoni and S. haematobium are endemic across the region [39], whereas zoonotic S. haematobium × S. bovis hybrids—reported in Mali, Senegal, Niger, and Benin—complicate transmission dynamics and control efforts [31, 32]. This high-transmission setting, combined with frequent human–animal–water contact, creates ideal conditions for persistent zoonotic transmission.

METHODS

Strategy of data synthesis A systematic literature search was conducted from March 25 to April 30, 2025, across PubMed, Scopus, Embase, and Web of Science to identify studies on HISs (S. mansoni, S. haematobium, S. haematobium × S. bovis, S. guineensis, and S. intercalatum) in NHMs in western Africa. The key search terms included the following: (1) pathogen-specific terms ("human schistosom"*, "Schistosoma mansoni", "Schistosoma haematobium", “Schistosoma intercalatum”, “Schistosoma guineensis”, "intestinal bilharz*", "urogenital schistosom*", and "urogenital bilharz*"; (2) transmission-related terms (*infection, prevalence, and epidemiology); and (3) geographic terms (West Africa*, western African countries, Côte d'Ivoire, Mali, Niger, Nigeria, Guinea, Senegal, Gambia, Sierra Leone, Benin, Liberia, Togo, Ghana, Guinea-Bissau, Cabo Verde, Cape Verde, and Mauritania), combined with Boolean operators (AND/OR). French translations of search terms were used to capture regional literature. To ensure comprehensiveness, we manually searched African Journal Online (AJOL) and screened the reference lists of the included articles.

Eligibility criteria No restrictions were applied to publication dates, but only English/French studies were included.

Source of evidence screening and selection The identified studies were imported into EndNote 21 for deduplication, followed by a two-stage screening process. First, titles/abstracts were screened for reports of HISs (S. mansoni, S. haematobium, S. haematobium × S. bovis, S. guineensis, or S. intercalatum) in NHMs within western Africa. Eligible studies progressed to full-text review if they met the following three criteria: (1) documented natural (nonexperimental) infections; (2) used validated diagnostic methods (parasitological, necropsy, immunological, or molecular techniques); and (3) provided species-specific data. The reasons for exclusion were systematically recorded; no restrictions were applied to sample sizes to maximize evidence capture. Interrater reliability was assessed during screening, with discrepancies resolved by consensus.

Data management Key data, including authorship, publication year, study location (country), design (cross-sectional/longitudinal), host species, sample size, diagnostic methods (e.g., parasitological, molecular), and infection outcomes (e.g., positive cases), were systematically extracted from the eligible studies. Studies encompassing multiple hosts (NHMs, humans, or snails) were noted. The data were organized in Microsoft Excel 2021 and analysed to determine (1) temporal/geographic publication trends (GraphPad Prism 10), (2) NHM infection incidence (with 95% CIs), and (3) species-specific positivity rates. The spatial distribution of HIS-infected NHMs was visualized via QGIS 3.38.3 to identify high-risk zones.

Reporting results / Analysis of the evidence The results will be reported in terms of characteristics of the included studies along with sampling strategies, biological sampling and diagnostic approaches, and epidemiological patterns of transmission of zoonotic schistosomiasis.

Presentation of the results Results will be presented in the form of tables and figures.

Language restriction Only evidence published in English and French was included.

Country(ies) involved China.

Keywords Schistosomiasis elimination, zoonotic transmission, nonhuman mammalian reservoirs, hybrid schistosomes, West Africa, integrated disease control.

Dissemination plans Our review will be disseminated through publication in a peer reviewed journal and presentation at international conferences.

Contributions of each author

Author 1 - Benjamin Sanogo - Author 1 contributed in conceiving the review. Author 1 conducted the literature search, analyzed and synthesized information, and drafted the manuscript.
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Author 2 - Isaac Echoru - Author 2 conducted the literature search, analyzed and synthsized information and revised the manuscript.
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Author 10 - Susan Christina Welburn - Author 10 conceived the review, contributed to the medthology and approved the final version of the manuscript. Author 10 also managed and coordinated the contributions of other authors.
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Other relevant information The review is initiated in China and researchers involved in writing the review come from China, Mali, and the United Kingdom.

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