

## Original Article

### SLEEPING SICKNESS IN LIBERIA – A HISTORICAL REVIEW

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#### ABSTRACT

Sleeping sickness or Human African Trypanosomiasis (HAT) caused by *Trypanosoma brucei gambiense* is a vector-borne protozoan disease occurring in central and western Africa. HAT caused devastating epidemics during the last century. Due to sustained efforts of surveillance and control measures the disease incidence dropped dramatically during recent years. HAT is now targeted for elimination for the year 2020. The epidemiological significance of ancient HAT foci not being surveyed or the non-provision of data recording for long periods, due to war riots and civil unrest like in Liberia is not clear. Its assessment, however, is essential for the implementation of future control strategies. The review compiles the history of HAT of Liberia with results of known but partly unpublished details of active and passive surveillance of ancient foci (Lofa and Bong Counties). Forty-three HAT cases mainly of Bong County are listed for the years 1967 to 1989; no cases were diagnosed in the ancient Kissi focus. An experimentally proven antelope-*Glossina palpalis gambiense*-antelope cycle of *T. b. gambiense* emphasizes the epidemiological role of animal reservoir hosts in the Liberian rainforest with implication for the resurgence of the disease.

**Keywords:** Sleeping sickness; Liberia; history; wild animals; reservoir hosts

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## INTRODUCTION

Human African Trypanosomiasis (HAT) is a vector-borne protozoan disease caused by the species *Trypanosoma brucei* transmitted by the bites of tsetse flies (*Glossina* spp.) which have acquired their infection from human beings or animals harbouring human pathogenic trypanosomes. HAT occurs in 36 sub-Saharan African countries. People most exposed to tsetse flies and therefore the disease live in rural areas and depend on agriculture, fishing, animal husbandry or hunting (WHO, 2017). The disease occurs in two forms, the chronic Gambian form caused by *T. b. gambiense* found in Central and West Africa, and the acute form of the zoonotic disease caused by *T. b. rhodesiense* found in eastern and southern Africa. Generally, both forms of the disease are fatal if untreated although for Gambian HAT healthy parasite carriers and self-cure were described (Jamonneau et al., 2012). The disease caused devastating epidemics during the last century (Büscher et al., 2017). Due to sustained efforts of surveillance and control measures launched in 2007 and put in place 2011 (WHO, 2012), the disease incidence dropped dramatically to 2804 new reported cases in 2015 (Büscher et al., 2017), of which 2733 were caused by *T. b. gambiense*. HAT is now targeted for elimination for the year 2020 (fewer than 2000 cases per year) and for the elimination of transmission for 2030 (Franco et al., 2017). For Gambian HAT, 55 million people are still estimated to be at risk of infection (period 2010 – 2014), with 1.2 million at very high risk and high risk (most of them in the Democratic Republic of Congo followed by the Central African Republic), and 9 million at moderate risk living in areas where Gambian HAT is considered being still a public health problem. In West Africa, only Guinea, Ivory Coast and Nigeria are still reporting significant levels of the disease (Franco et al., 2017). For countries with long-lasting civil wars in the past, civil unrest or outbreaks of Ebola virus disease like Guinea, Sierra Leone and Liberia, the reported cases (if at all) and the actual incidence might differ considerably (Büscher et al., 2017). From Liberia with its known ancient Gambian HAT foci

(Hutchinson, 1962; Hutchinson et al., 1964) no cases and no surveillance activities have been reported to WHO since decades (Courtin et al., 2008; Franco et al., 2017).

In the context of reduced incidence of Gambian HAT in sub-Saharan Africa and the efforts towards the targeted elimination of the disease it has been strongly advised to re-consider the epidemiological relevance of old classical foci not being surveyed for long periods which might be still active or the source for the resurgence of the disease (Büscher et al., 2017). To meet this recommendation this paper aims at contributing knowledge on the occurrence and distribution of sleeping sickness cases in the West African rainforest region by reviewing the trypanosomiasis history of Liberia, by filling the gap of information on unpublished HAT cases diagnosed during the pre-civil-war period 1981 to 1989 (Annual Reports of the Liberia Research Unit (LRU) of the Tropical Institute Hamburg, Bong Mine, Liberia, unpublished, in: BNI Archive, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany) and by looking at the post-civil-war period.

## LOOKING BACK TO THE BEGINNING

Sleeping sickness in Liberia became noticeable early in the 20th century. The Vai tribe in the western part of the country had a local name („konje kira“) for the disease which may be translated as „ball sickness“ or „gland sickness“ (Johnston, 1906). However, it was not before 1926 when the first authentic record of human trypanosomiasis was made by the Harvard Expedition in five patients in a cluster of villages (Nyalai, Betala, Paiata and Bakratown) near the St. Paul River, northwest of Suakoko, Bong County (former Central Province) when trypanosomes were detected in gland punctures (Strong, 1930).

Before 1930, sedentary life prevailed among tribes of the interior, few people ever leaving the confines of the clan or tribe. At that time, trypanosomiasis might have been restricted to a few endemic areas such as those discovered by the Harvard Expedition







### THE ANIMAL RESERVOIR OF *T. B. GAMBIENSE*

*T. b. gambiense* group 1 (Gibson, 2001) have been found in various domestic (pigs, sheep, dogs goats) and wild animals (mammals and reptiles) in West and Central Africa; relevant investigations were summarized and discussed most recently as to their epidemiological significance for HAT (Franco et al., 2017; Büscher et al., 2017). Non-human hosts have been assumed as one of the principal factors associated with the persistence of Gambian HAT in endemic areas in spite of chemotherapeutic campaigns. Using the concept of a next generation matrix (NGM) to understand the transmission dynamics of the disease, Funk et al. (2013) found indications for an independent transmission cycle in wild animals and assumed that reintroduction of HAT would usually occur shortly after elimination of the infection from human populations. The proof of maintenance of *T. b. gambiense* in separate transmission cycles in wild animals would have important implications for elimination strategies (Franco et al., 2017). In this context, we recall experimental studies carried out with autochthonous antelopes in Liberia. It was shown that human-derived *T. b. gambiense* multiplied and persisted in antelopes with low and intermittent parasitaemias over long periods without showing any clinical symptoms in the experimental animals (Mehlitz, 1986): Black-backed duikers (*Cephalophus dorsalis*) were infected cyclically through *G. p. gambiensis* with the *T. b. gambiense* stock TH Gamey Dolo/A, group 1 according to Gibson (2001), isolated in Gbao, Bong County, and analysed by combined use of restriction endonuclease digestion, gel electrophoresis and molecular hybridization (Paindovaine et al., 1986). Parasites were detected for up to 718 days *post expositionem* (daily examination with the m-AECT) with low parasitaemias hardly exceeding 50 trypanosomes/ml blood with aparasitaemic intervals of more than 200 days. Further, it was shown that *T. b. gambiense* was transmissible through *G. p. gambiensis* in the antelope-fly-antelope cycle and that the characteristics of human infectivity of group 1 *gambiense* remained stable after cyclical re-isolation under

experimental conditions for several years (Mehlitz, 1986). Further, infections rates of 3.6 % with *T. brucei* spp. in wild ungulates (n = 140) were observed in the endemic HAT rainforest region of Bong County (*Cephalophus dorsalis*, *Cephalophus niger*, *Philantomba maxwellii*, *Tragelaphus scriptus*) diagnosed parasitologically (m-AECT) (Mehlitz, 1984). Studies on the bio-ecology of the vector (*G. palpalis* s.l.) of HAT in Bong County showed that 31 % of flies feed on humans, 30 % on reptiles and 24 % on wild ungulates, 15 % on others (domestic ruminants, dogs, birds, pigs) (Kaminsky, 1987; Mehlitz, 1990). These transmission experiments, the field studies on infections rates in antelopes and the host preference of the vector of HAT described strongly point to the existence of separate transmission cycles *G. palpalis* s.l. - wild animals - *G. palpalis* s.l. of *T. b. gambiense* and highlight the significance of animal reservoir hosts responsible at least to a certain degree for the maintenance of HAT in persistent foci or the resurgence of the disease.

### CONCLUSIONS

Liberia has not been listed in the maps (atlas) for the distribution of population at risk of the HAT for decades where any level of risk has been identified until 2014 (Franco et al., 2017). This brief review is intended to draw attention to ancient HAT foci in the West African rainforest areas where no surveillance could be carried due to war riots, outbreaks of fatal epidemics like Ebola virus infection or another priority setting of national health stakeholders during recent decades. Recalling and summarizing HAT case findings for the period 1967-1977 (passive case detection) and for the pre-civil-war period 1981- 1989 (active case detection) give evidence that Gambian HAT was endemic in Bong County of Liberia and has survived over decades in restricted areas of the country. Only a surveillance uptake of humans and animals (domestic and wild) can clarify whether HAT is still present in this focus. The absence of HAT in the old Kissi focus (Lofa County), however, might be the results of demographic and landscape changes over time. The most important trajectories

of land use have been associated with loss of forest cover: 15 % of the 1975 forest cover compared to 2013 have been lost. The most significant losses occurred in the Upper Guinean rainforest (Lofa County with the Kissi chiefdoms) which has been replaced by degraded forest, thickets savannah and slash-and-burning agriculture. The concerns of desertification due to high levels of deforestation are obvious (USGS, 2015). Climatic changes, particularly the decrease in rainfall to 1300 mm in the forest-savannah boundary region in the north of the country associated with increased human density, intensification of land use particularly upland and swamp rice farming along with the decline of pig farming, change of tsetse habitat not favorable for *G. palpalis*, the decrease of wild animals, as well as the possible changes of the vector competence or human-vector contact, might have contributed to the disappearance of the disease in this region (Courtin et al., 2008). The observations and results for Liberia - so far missing and not discussed in most recent publications on the occurrence and distribution of HAT in West Africa - might foster the discussions on the changes of the repartition of Gambian HAT (Courtin et al., 2008). The experimentally proofed transmission cycle antelope-*G.p.gambiensis*-antelope with human-derived *T. b. gambiense* supports the epidemiological significance of animal reservoir hosts of the HAT in West and Central Africa being potential sources for the resurgence of the disease.

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