Opinion

Do Cryptic Reservoirs Threaten Gambiense-Sleeping Sickness Elimination?

Informal Expert Group on Gambiense HAT Reservoirs


Trypanosoma brucei gambiense causes human African trypanosomiasis (HAT). Between 1990 and 2015, almost 440,000 cases were reported. Large-scale screening of populations at risk, drug donations, and efforts by national and international stakeholders have brought the epidemic under control with <2200 cases in 2016. The World Health Organization (WHO) has set the goals of gambiense-HAT elimination as a public health problem for 2020, and of interruption of transmission to humans for 2030. Latent human infections and possible animal reservoirs may challenge these goals. It remains largely unknown whether, and to what extent, they have an impact on gambiense-HAT transmission. We argue that a better understanding of the contribution of human and putative animal reservoirs to gambiense-HAT epidemiology is mandatory to inform elimination strategies.

Can Cryptic Reservoirs in Humans and Animals Compromise the Sustainable Elimination of gambiense-HAT?

HAT is caused by two closely related parasites that are transmitted by tsetse flies. Trypanosoma brucei gambiense is responsible for the Western and Central African form of the disease and Trypanosoma brucei rhodesiense occurs in Eastern and Southern Africa – both forms of the disease are usually fatal if untreated [1]. Between 1990 and 2016, a total of 437,971 cases of gambiense-HAT were reported, with a peak of 37,385 cases in 1998. Thanks to large-scale deployment of a serological screening test (CATT/T. b. gambiense) (see Glossary), drug donations, and intense efforts by national and international stakeholders, this epidemic has been brought under control, with fewer than 2200 cases reported in 2016. This represents a marked reduction in human suffering caused by the disease. Inspired by this progress, the WHO has set elimination of gambiense-HAT as a target for the near future; elimination as a public health problem by 2020 and the interruption of transmission to humans by 2030.

The rationale to shift from HAT control to elimination is based on several arguments, such as the epidemiological vulnerability of gambiense-HAT as a presumed anthroponotic infection,
historic examples of elimination in several West African foci, the availability of new medicines and diagnostics, the political will of endemic countries, and the commitment of national control programs [2]. Furthermore, a drug donation agreement between pharmaceutical companies and WHO has made treatment freely available to endemic countries.

gambiense-HAT control classically relies on three pillars: vector control, case finding, and treatment. HAT is a vector-borne disease, and the reduction of human–fly contact below a critical threshold would lead to zero transmission. Although vector control is critical to achieve the elimination/eradication goals, in practice, it will be hard to sustain control of all tsetse fly populations in all endemic areas. Vector control being only part of the solution, gambiense-HAT control will continue to rely on a great extent on surveillance, diagnosis, and treatment, both for reducing transmission and for monitoring progress towards these goals.

The introduction of individual rapid diagnostic tests (RDTs) for gambiense-HAT may increase serological screening coverage as they can be performed in remote dispensaries devoid of technical facilities. Thus, they facilitate the integration of passive screening in the health system and play a role in a sustainable surveillance system. However, RDTs also have limitations – like CATT/T. b. gambiense, they only detect antibodies, and their specificity is not 100% [3]. As a consequence, given the adverse effects and logistic constraints of current treatment, individuals who test positive in an RDT or in CATT must undergo microscopic examination of blood or lymph node fluid to confirm the presence of the parasite, followed by a lumbar puncture for stage determination, as different drugs are required to treat early- and late-stage disease [2]. In recent years, the highly toxic melarsoprol regimen, used to treat late-stage disease, has been replaced by a safer, though still rather complex, treatment requiring parenteral administration and hospitalisation. An oral treatment might become available in late 2018, and a single-dose treatment is entering phase III clinical trials [4].

Whereas HAT elimination by 2020, as a public health problem, seems within reach, the sustained global elimination of HAT appears more challenging. Indeed, as long as the knowledge gaps surrounding the reservoir of T. b. gambiense in interepidemic periods are not filled, the concept of eradication of gambiense-HAT cannot be considered.

We present the current research evidence about potential human and animal T. b. gambiense reservoirs and discuss their importance in the light of the gambiense-HAT elimination goals.

**Human Reservoir**

Mathematical models show that the sustained transmission of HAT can be explained if a fraction of the HAT cases is systematically missed by the screening operations [5]. Unfortunately, this is the case in many settings as a number of T. b. gambiense infections remain undiagnosed for several reasons [6]. First, not all infected people are reached by screening activities. Second, current diagnostic techniques do not pick up all T. b. gambiense infections due to lack of sensitivity of serological screening tests, of molecular techniques, or of the parasitological confirmation tests [7]. These undiagnosed, yet infected, people will act as a human reservoir of the parasite and might sustain transmission, forming a maintenance population [8]. Still another potential category of human reservoir may consist of latent infections, also called ‘healthy carriers’, who do not always progress to clinical disease, though the relative contribution of these individuals to parasite transmission still needs to be documented (Box 1). These latently infected people may carry trypanosomes for years or even decades, as was first described half a century ago in West Africa, and later in patients refusing treatment in Côte d’Ivoire [9,10]. More recently, a HAT case with a latent infection of at least 29
years was documented [11]. Whether latently infected persons transmit the parasite sexually [12], and whether sexual and congenital transmission plays a significant role in the epidemiology of gambiense-HAT [13], remains hypothetical. In Guinea, asymptomatic or latent infections were found to have consistently high titres in CATT/T. b. gambiense and to be positive in the immune trypanalysis test, although no parasites could be detected in blood or lymph node fluid during a 2-year follow-up period [14]. This observation is in line with the fact that trypanosomes can survive in the extracellular spaces of diverse organs such as the heart, the central nervous system, and the skin [15–17]. Experimental infections in animals confirmed that parasites may be undetectable in the blood but hidden in different organs and tissues [18–21], including the skin, from where they can be ingested by tsetse flies [22,23]. It was only recently that researchers began to investigate the underlying host–parasite interaction mechanisms responsible for those latent infections. Microsatellite profiles and genomic sequencing of parasites from latent infections and from clinical HAT patients are indistinguishable, suggesting that the latent infection phenotype is determined primarily by the host rather than by the parasite [24]. Studies on host genetic polymorphism show that tumor necrosis factor-α-308 A, HLA-G-UTR-2, APOL1 N264K, and APOL1 G2 are associated with increased risk of infection or with disease progression, while IL10 -592 A, IL6 -4339, APOL1 G1, and other polymorphisms in HPR and APOL1 are associated with decreased risk of infection or with latent infection [25–30].

Other studies have found associations between the innate and the adaptive immune response and infection outcome, for example, self-cure and high levels of interleukin-8 (IL-8); latent infection and high levels of IL-6 or specific interferon-γ-producing T cells; disease progression and high levels of IL-10, TNF-α, and sHLA-G [31–33]. In view of the global elimination of HAT, it is of the utmost importance to clarify the extent to which these human reservoirs contribute to the transmission of the parasite and hence to gambiense-HAT persistence and potential resurgence.

Animal Reservoir

Compared to latent infections in humans, our current knowledge of T. b. gambiense infections in animals is very limited and fragmented. The presence of T. b. gambiense in animals has been demonstrated in several studies (Figure 1) [34,35]. Several authors have suggested that animals can act as a reservoir for gambiense-HAT [36–45]. In rhodesiense-HAT, sustained parasite transmission cycles exist in both livestock and wildlife, from which the parasite can spill over to humans [46]. For T. b. gambiense, despite early data generated on its infectivity and transmissibility in animals, the epidemiological significance of any animal reservoir is not well understood and may depend on the specific ecosystem of the HAT focus. Even if the parasite can be transmitted to and from animals, factors such as the proportion of blood-feeding on that species by tsetse will determine the epidemiological significance of the species to act as a maintenance population or part of a maintenance community. T. b. gambiense can infect a variety of domestic animals and wildlife, as shown in Table 1. Following infection, most of these animals remain asymptomatic and generally show low to very low parasitaemia. For instance, in pigs infected with a T. b. gambiense strain isolated from a human patient, only xenodiagnosis and blood culture succeeded in revealing an infection but conventional microscopy failed to detect parasites [47–51]. Moreover, experimental studies have shown that human-derived T. b. gambiense strains that were cyclically transmitted by tsetse flies between animals for more than a year remained transmissible to humans [48].

Studying natural T. b. gambiense infections in animals is challenging. Major drawbacks are the usually low parasitaemia and the necessity to distinguish T. b. gambiense from other trypanosome species such as T. brucei brucei, T. congolesense, T. vivax, T. suis, and T. simiae. In particular, T. b. gambiense is morphologically identical to the nonhuman infective T. b. brucei.
Among the molecular tests, only those targeting the single-copy TgsGP gene are gambienespecific, thus limiting their analytical sensitivity to >100 trypanosomes per ml of blood [52,53]. Biochemical assays, such as isoenzyme profiling, are only applicable on parasite strains that have been isolated and adapted to laboratory rodents or to in vitro cultures [54–56], and phenotypic assays such as the blood incubation infectivity test are only readily applicable on isolated strains and are not fully gambienespecific [57]. Tests that detect antibodies against gambienespecific antigens, such as the variant surface glycoproteins (VSGs) LiTat 1.3 and LiTat 1.5, may be more useful in revealing T. b. gambienese infections in animals. However, the immune trypanolysis test (TL), which is considered 100% specific in humans, still has to be validated in different species of animals. Ancillary information on the T. b. gambienese animal reservoir can be drawn from analysing T. b. gambienese infection in taestae, in combination with its feeding behaviour, to assess the vectorial transmission of the parasite from the animal reservoir to humans [58]. In summary, there is a need to further improve our tools and increase our understanding regarding the importance of an animal reservoir in gambienes-HAT.
epidemiology. If further evidence indicates that an animal reservoir may threaten *gambiense*-HAT elimination, synergy with the control of animal African trypanosomiasis should be considered [59].

**Filling the Knowledge Gaps**

The presence of multiple reservoirs is a critical obstacle to the sustained elimination of any infectious agent [60]. For example, when the Guinea worm eradication programme was rolled out, the possibility of an animal reservoir was initially overlooked, but the recent finding of Guinea worm infections in dogs led to the hypothesis that dogs could have acted as a reservoir that caused the reappearance of human cases in Chad [61]. The existence of a human reservoir, in the form of post-kala-azar dermal leishmaniasis, and possibly also latent infections, is a challenge for the sustained elimination of visceral leishmaniasis (VL) from the Indian subcontinent [62].

The importance of investigating how HAT can re-emerge in so-called silent foci is clearly illustrated by the fact that a 9-year-old child was diagnosed with *gambiense*-HAT in Ghana in 2013, 10 years after the last detected case [63]. Also, the finding of a *gambiense*-specific PCR-positive squirrel in Equatorial Guinea on Luba island in 2014, where the last human HAT case was reported in 1995, is worrying [43]. Therefore, in the context of *gambiense*-HAT elimination, a key question is whether human and/or animal reservoirs are capable of maintaining
### Table 1. Animals Successfully Infected with T. b. gambiense Strains Isolated from Human Patients

<table>
<thead>
<tr>
<th>Animal species</th>
<th>Origin of trypanosome strain</th>
<th>Infectiveness to tsetse</th>
<th>Minimum observed duration of infection</th>
<th>Refs</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Domestic animals</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cat</td>
<td>Senegambia and Congo Free State</td>
<td>Not tested</td>
<td>12 days</td>
<td>[73]</td>
</tr>
<tr>
<td>Cattle</td>
<td>Nigeria</td>
<td>Yes</td>
<td>50 days</td>
<td>[66,74]</td>
</tr>
<tr>
<td>Chicken</td>
<td>Unknown</td>
<td>Not tested</td>
<td>75 days</td>
<td>[75]</td>
</tr>
<tr>
<td>Dog</td>
<td>Senegambia and Congo Free State, Nigeria, Belgian Congo</td>
<td>Yes</td>
<td>109 days</td>
<td>[36,48,73]</td>
</tr>
<tr>
<td>Donkey</td>
<td>Senegambia</td>
<td>Not tested</td>
<td>14 days</td>
<td>[73]</td>
</tr>
<tr>
<td>Goat</td>
<td>Senegambia, Nigeria, Belgian Congo</td>
<td>Yes</td>
<td>13 months</td>
<td>[48,73,74]</td>
</tr>
<tr>
<td>Horse</td>
<td>Senegambia</td>
<td>Not tested</td>
<td>5 months</td>
<td>[73]</td>
</tr>
<tr>
<td>Pig</td>
<td>Côte d’Ivoire, Congo Beige, Nigeria</td>
<td>Yes</td>
<td>18 months</td>
<td>[47,51,76]</td>
</tr>
<tr>
<td>Sheep</td>
<td>Côte d’Ivoire</td>
<td>Not tested</td>
<td></td>
<td>[77]</td>
</tr>
<tr>
<td><strong>Primates</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Agile mangabey (Cercopithecus galenatus agilis)</td>
<td>Belgian Congo</td>
<td>Yes</td>
<td></td>
<td>[48]</td>
</tr>
<tr>
<td>Green monkey (Cercopithecus callithrix, C. aethiops tantalus)</td>
<td>Congo Free State, Nigeria</td>
<td>Yes</td>
<td>3 months</td>
<td>[36,73]</td>
</tr>
<tr>
<td>Wolf’s mona monkey (Cercopithecus wolf)</td>
<td>Congo Beige</td>
<td>Yes</td>
<td>15 days</td>
<td>[47]</td>
</tr>
<tr>
<td>Patas monkey (Erythrocebus patas patas)</td>
<td>Nigeria</td>
<td>Yes</td>
<td>3 months</td>
<td>[36,78]</td>
</tr>
<tr>
<td>Rhesus macaque (Macacus rhesus)</td>
<td>Senegambia and Congo Free State</td>
<td>Not tested</td>
<td>1 month</td>
<td>[73]</td>
</tr>
<tr>
<td>Chimpanzee (Pan satyrus, Pan troglodytes verus)</td>
<td>Senegambia, Nigeria</td>
<td>Not tested</td>
<td>17 months</td>
<td>[73,78,79]</td>
</tr>
<tr>
<td>Dwarf galago (Galagoëdes demidovi)</td>
<td>République populaire du Congo</td>
<td>Not tested</td>
<td>28 days</td>
<td>[80]</td>
</tr>
<tr>
<td><strong>Ungulates</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bay duiker (Cephalotus dorsalis)</td>
<td>Belgian Congo</td>
<td>Yes</td>
<td>24 months</td>
<td>[48]</td>
</tr>
<tr>
<td>Waterbuck (Kobus ellipsiprymnus)</td>
<td>Uganda</td>
<td>Not tested</td>
<td></td>
<td>[50]</td>
</tr>
<tr>
<td>Reedbuck (Redunca redunca)</td>
<td>Uganda</td>
<td>Yes</td>
<td>15 months</td>
<td>[50]</td>
</tr>
<tr>
<td>Bushbuck (Tragelaphus spekei)</td>
<td>Uganda</td>
<td>Yes</td>
<td>22 months</td>
<td>[50]</td>
</tr>
<tr>
<td><strong>Rodents</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gambian pouched rat (Cricetomys gambianus)</td>
<td>République populaire du Congo</td>
<td>Yes</td>
<td>154 days</td>
<td>[37,80,81]</td>
</tr>
<tr>
<td>Thicket rat (Thamomys rutlans), Jackson’s praomys (Praomys jacksoni), African marsh rat (Dasymys incommutus), Striped grass mouse (Lemniscomus)</td>
<td>République populaire du Congo</td>
<td>Not tested</td>
<td>131 days</td>
<td>[80]</td>
</tr>
</tbody>
</table>

ASSURED criteria: Affordable, Sensitive, Specific, User-friendly, Rapid and robust, Equipment-free and Deliverable to end-users; RDTs for gambiense-HAT detect antibodies against predominant gambiense-specific antigens.

**Reservoir**: A host where the pathogen can maintain itself and from where it can be transmitted to another host; a reservoir host is essential to sustain infection.

**Self-cure**: Infection that is cleared by the host without treatment.

**Specificity**: The specificity of a diagnostic test is the probability that the test result is negative when the test person is not infected. It is usually expressed as a percentage and is calculated by dividing the number of test negatives by the number of true negatives x 100.

**Stage determination**: HAT develops from an early stage, with parasites in the peripheral tissues, towards a late stage, with parasite invasion into the central nervous system. Treatment is different for both stages, thus requiring stage determination before drug administration. Determination of the stage is achieved by examination of the cerebrospinal fluid for the presence of trypanosomes and the number of white blood cells.

**Stochastic mathematical model**: Stochastic models include chance events so that two simulations with the same parameter values and initial conditions may lead to different outcomes. Chance events become more important at very low prevalences such as in pre-elimination or re-emergent settings.

**Variant surface glycoprotein (VSG)**: In the vertebrate host, the cell surface of trypanosomes is covered with a layer of identical VSGs of one particular variant antigen type (VAT), that protects the trypanosomes against innate immune defence mechanisms of the host; VATs are highly immunogenic, but periodic switches of the VAT of the VSG (antigenic variation) enable the trypanosome to escape the host humoral immune response; during the course of the infection, the host blood contains antibodies against a wide spectrum of different VATs.

**Xenodiagnosis**: Diagnostic method based on detection of the parasite in...
transmission and causing a resurgence of the disease in different geographical areas and epidemiological settings (see Outstanding Questions).

As with the mathematical modelling of other neglected tropical diseases [64], models on HAT epidemiology may help to improve our epidemiological knowledge and inform elimination strategies. Models can explore if, and how, animal and human reservoirs could sustain endemity in HAT foci [65]. However, model predictions heavily depend on the availability of accurate information for their construction, parameterisation, and fitting. To date, a few models have attempted to infer the contribution of reservoirs in *gambienne*-HAT transmission maintenance by fitting to human epidemiological data. Funk et al. [66] suggested that animals were necessary for persistent transmission in Bipindi focus in Cameroon. Studies of existing *gambienne*-HAT models in a few foci (i.e., D. R. Congo, Guinea, and Chad) suggest that some type of additional infection reservoir is needed to match the observed dynamics of reported HAT cases [5,67,68]. This could arise from another human reservoir (including undiagnosed and latent infections), an animal reservoir, and/or heterogeneities in human risk exposure and surveillance coverage. A different modelling exercise considered the implications on transmission and control of whether animals function as reservoirs or as zooprophylaxis but did not address which was more likely [69].

Due to the current lack of knowledge surrounding latently infected people (including their frequency, disease progression, their relative infectivity to tsetse, and the duration of this infectious stage) modelling latent infections in humans is challenging, and these uncertainties will impact the models’ predictions. In particular, latent infections have only been explicitly incorporated in one *gambienne*-HAT model, and the potential role of these individuals in maintaining transmission or hindering elimination has yet to be fully analysed [70]. Arguably, long-duration infections, which eventually progress to late-stage disease, are captured by the stage 1 exponential distributions used in many modelling frameworks, but modifications could better represent self-cure and nondetection of latent infections in active screening. Many recent modelling studies have concluded that existing vector-control methods have the ability to quickly reduce transmission to and from tsetse to all hosts, and may be critical for elimination in regions where reservoirs exist [67–72].

New data and investigations into latent human infections and animal infections will help shape the way in which future models are developed and parameterised by factoring in improved biological evidence. Some critical gaps in our knowledge, which influence modelling choices, are shown in Figure 2 (Key Figure). As well as refining formulation and parameterisation of the existing deterministic models, it is also clear that a new generation of models is needed.

Table 1. (continued)

<table>
<thead>
<tr>
<th>Animal species</th>
<th>Origin of trypanosome strain*</th>
<th>Infectiveness to tsetse</th>
<th>Minimum observed duration of infection</th>
<th>Refs</th>
</tr>
</thead>
<tbody>
<tr>
<td>striatus, Rusty-nosed rat</td>
<td>(Canomys hypoanthus), African</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>brush-tailed porcupine (Atherurus</td>
<td>Striatus)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>africanus</td>
<td></td>
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</tbody>
</table>

*For reasons of traceability, we use the name of countries and the scientific name of animals as mentioned in the original publication: Senegambia = Senegal and The Gambia; Belgian Congo, Congo Free State and Congo Belge = Democratic Republic of the Congo; République populaire du Congo = Republic of the Congo.
**Figure 2.** Solid lines represent progression between disease states, and dashed lines represent transmission of the parasites to and from the tsetse vector. Red boxes denote people or animals that may be infective to tsetse, with the darker shades denoting possible greater infectiveness. The figure highlights key unknown elements in disease progression and transmission including: (1) the probability of an infection leading to latent or stage 1 disease in humans – if, and how frequently; (2) self-cure of infected humans or (3) animals arises; (4) the duration of latent infection in humans, or (5) any infections in animals; and (6) the relative probability of transmission to tsetse from different types of infections (accounting for host feeding preferences).
**Stochastic models** are better suited to capture the chance events that determine the role of cryptic reservoirs and their implications for elimination. In conclusion, improved mathematical models on HAT epidemiology, combined with additional field and experimental data, are needed to help understand the respective roles of these reservoirs.

**Concluding Remarks**

We believe that attaining the elimination (zero transmission) target of *gambiense*-HAT by 2030 is feasible but, as observed for other neglected tropical diseases, latent infections — whether human or animal — may constitute cryptic parasite reservoirs and thus add another challenge to sustained elimination. To inform evidence-based elimination strategies, a better understanding of the contribution of these putative human and animal reservoirs on the epidemiology of *gambiense*-HAT is required, more in particular on (i) the frequency and duration of latent human infections and infections in animals, (ii) the infectiveness of latent human infections and animal reservoirs to tsetse flies, (iii) the ability of latent human infections or animal reservoirs to sustain transmission in interepidemic periods, and (iv) the possible existence of an animal transmission cycle in the absence of human transmission and its ability to seed a new transmission cycle in humans. To investigate these issues, we urgently need to improve our toolbox for the identification of latent and self-cured infections, including prognostic and diagnostic markers. Also, more accurate and preferably high-throughput tests to detect and monitor *T. b. gambiense* infections in animals should be developed, along with improved mathematical models for exploration of epidemiological hypotheses.

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**Resources**


**Supplemental Information**

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