Combatting African Animal Trypanosomiasis (AAT) in livestock: The potential role of trypanotolerance

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Abstract

African Animal Trypanosomiasis (AAT) is endemic in at least 37 of the 54 countries in Africa. It is estimated to cause direct and indirect losses to the livestock production industry in excess of US$ 4.5 billion per annum. A century of intervention has yielded limited success, owing largely to the extraordinary complexity of the host-parasite interaction. Trypanotolerance, which refers to the inherent ability of some African livestock breeds, notably Djallonke sheep, Ndama cattle and West African Dwarf goats, to withstand a Trypanosomiasis challenge and still remain productive without recourse to chemotherapy, is

an economically sustainable option for combatting this disease. Yet trypanotolerance has not been adequately exploited in the fight against AAT. In this paper, we describe new insights into the genetic basis of trypanotolerance and discuss the potential of exploring this phenomenon as an integral part of the solution for AAT, particularly, in the context of African animal production systems.

Keywords: Trypanotolerance, African Livestock, Breeds, Trypanosomiasis, Tsetse fly

1. Introduction

African Trypanosomiasis is a chronic debilitating disease caused by extracellular flagellate trypanosome protozoans (*Trypanosoma* species) and is spread mainly by the infected Tsetse fly vector (Diptera: Glossinidae) (Bruce, 1915; Brun et al., 2010; Hill et al., 2005; Mony and Matthews, 2015). The disease affects a wide range of mammalian species including humans (Jha et al., 2015; Matovu et al., 2001; Mwai et al., 2015; Seck et al., 2010). The three main trypanosome species endemic to Africa are *Trypanosoma vivax* (Dutonella) and *Trypanosoma congolense* (Nanomonas) that mainly infect livestock, and *Trypanosoma brucei* (Trypanozoon) which affects both humans and animals (Bezie, 2014; Kato et al., 2015; Nakayima et al., 2012). *T. brucei* has three sub-species of which two, *T. b. gambiense*, and *T. b. rhodesiense* mainly infect humans, whereas the third, *T. b. brucei* infects only domestic and wild animals (Munday et al., 2015; Sima et al., 2011; Welburn et al., 2001; Welburn et al., 2009). The distribution of the trypanosome vector, Tsetse fly (*Glossina* spp.), correlates closely with the trypanosome parasites throughout the 10 million km^2 prevalence region, thereby facilitating the entrenchment of the disease (Hill et al., 2005). Trypanosome parasites usually invade the animal's lymphatic vessels, the blood circulation, and eventually the brain causing a wide range of pathologies, most commonly severe anaemia, weight loss, foetal abortion, and cachexia. It can result in the death of the host if left untreated (Matovu et al., 2001; Sima et al., 2011; Stijlemans et al., 2015). Other symptoms reported for African Trypanosomiasis include infertility, sleeping disorders, psychiatric disorders, paralysis, neuroendocrine dysfunctions and coma (Courtin et al., 2008; Steverding, 2008).

Although acknowledged as a neglected tropical disease for several decades, African Animal Trypanosomiasis (AAT) remains endemic in 37 of the 54 countries in Africa, affecting and an

area of approximately 10 million square kilometers of arable land, and reduces the efficiency of productivity of over 150 million cattle and 260 million sheep and goats (Baker, 1995; Jahnke et al., 1988; Leigh et al., 2015; Nyimba et al., 2015). AAT is a very significant economic and animal health issue for this sub Saharan region (Habila et al., 2012; Namangala, 2012; Shaw, 2009). Furthermore, the disease has an extended impact on crop agriculture, human settlement and welfare, because 7 million square kilometers of the region's land is rendered unsuitable for mixed crop-livestock ecosystems (Nigatu et al., 2015; Peregrine, 1994). AAT is estimated to cause annual losses of more than US$ 4.5 billion dollars through direct and indirect agricultural production costs (Dagnachew and Bezie, 2015; Leigh et al., 2015; Sanni et al., 2013). It is not surprising, that the 21 countries where Trypanosomiasis is endemic are included in the world's 25 poorest countries (Shaw, 2009), and 32 were considered highly indebted (IAEA, 2002).

Over several decades, the existence and use of just a few therapeutic drugs for AAT; that have limited efficacy against the parasites, but which are highly toxic to the host, has fueled the emergence of widespread drug resistance across the region (Delespaux and de Koning, 2007; Delespaux et al., 2008; Matovu et al., 2001). The continued lack of a vaccine for the disease has also lead to an over-reliance on limited number of drugs (Tsegaye et al., 2015). Ongoing efforts directed to controlling the Tsetse fly vector across the sub Saharan Africa region have largely been ineffectual (Goossens et al., 1999; Hendrickx et al., 2004; Holmes, 1997; Torr and Vale, 2015). These factors, coupled with the persistent political instability and armed conflicts in the region (particularly during the post-colonial independence era) have ensured that AAT has persisted across the region (Brun et al., 2010; Geerts et al., 2001).

Certain African livestock breeds such as Djallonke sheep and Taurine cattle, which entered Africa from the near east around 5000 BC and 7000 BC respectively, have evolved tolerance to Trypanosomiasis, probably as a result of natural selection (Dolan, 1987; Gautier et al., 2009; ILRI, 2009; Muigai and Hanotte, 2013; Murray et al., 1984; Mwai et al., 2015; Naessens, 2006). This innate ability of these livestock breeds to survive and remain productive under trypanosome challenge without resorting to the use of trypanocidal drugs, is referred to as trypanotolerance. Trypanotolerance has been described as an economical and sustainable option for combating AAT (Geerts et al., 2009; Goossens et al., 1997; Murray et al., 1982; Namangala, 2012). If implemented as a control strategy, trypanotolerance could have a major positive effect on long term food security for the region (Osaer et al., 1994). In this review, we detail the key challenges remaining after a century of intervention against AAT, and the new insights on the genetics and mechanisms of trypanotolerance. Finally, we discuss the potential benefit of harnessing livestock trypanotolerance in the context of sub Saharan African livestock systems.

2. A Century of Intervention against AAT

The history of intervention programs against African trypanosomiasis involves the contributions of parasitologists, zoologists, entomologists, veterinarians and clinicians. However, with regards to AAT the landmark events are the findings of Bruce and Evans in the last decade of the 19th century (Cox, 2004). Between 1891 and 1898, Evans identified *T. evansi* in equine spp. and Bruce identified *T. brucei* in cattle (Cox, 2004). In 1909 Bruce also identified the Tsetse fly as the vector that transmitted trypanosome parasites. These important findings marked the start of attempts to combat AAT using a variety of measures,

and the next 100 years was spent trying to eradicate this disease, to no avail (Steverding, 2008). Throughout the 20th century, there have been several attempts to control Trypanosomiasis by attempting to control the transmitting Tsetse fly vector. These control methods included; the sterile insect technique, the destruction of fly habitat, the use of Tsetse traps, the use of insecticide treated livestock, and coordinated mass spraying of insecticide (Doyle et al., 1984; Hendrickx et al., 2004; Hill et al., 2005; Holmes, 1997; Torr and Vale, 2015). These interventions have yielded limited positive outcomes against Trypanosomiasis, but have often been associated with attendant negative environmental consequences including insecticide pollution of water bodies and deforestation (Goossens et al., 1999; Hendrickx et al., 2004; Holmes, 1997; Torr and Vale, 2015). Other attempts at curbing Trypanosomiasis through targeting the parasite via anti-trypanosome drugs have not yielded the desired results because of the rapid development of resistance to these trypanocides (Alsford et al., 2013; Kaufmann et al., 1992). In 2008, 17 sub Saharan countries reported veterinary trypanocide drug resistance problems, and by early 2015 this number had risen to 21 countries (Delespaux et al., 2008; Tsegaye et al., 2015). This resistance was expedited in part by the reliance on predominantly three drugs for treating AAT over 50 years (Delespaux et al., 2008; Geerts et al., 2001; Munday et al., 2015; Peregrine and Mamman, 1993). Facilitating the development of resistance and cross resistance of trypanosomes to these drugs is the fact that these drugs have similar chemical compositions (Peregrine, 1994). Furthermore, these few AAT drugs have high host toxicity, and limited efficacy (Matovu et al., 2001; Peregrine and Mamman, 1993; Steverding, 2015). Other factors contributing towards drug resistance include the high degree of re-infection rates among treated livestock, and significant levels of misuse of trypanocide by farmers as a consequence of the deregulation and privatization of veterinary services (Geerts et al.,

2001). In 2008, a report indicated that, out of an estimated 35 million doses of veterinary trypanocide drugs administered, diminazene aceturate, isomethamidium chloride and ethidium bromide accounted for 33%, 40% and 26% respectively (Delespaux et al., 2008). Peregrine and Mamman (1993) reviewed the causes and mechanisms for parasite resistance development for each of the drugs used against AAT. Drug resistance continues to interfere with effective therapeutic management of AAT, and is reported to be responsible for many widespread outbreaks of Trypanosomiasis, in different parts of the region, that did not respond to standard chemotherapeutic regimens (Holmes, 1997; Mamoudou et al., 2008).

The hope of developing an effective vaccine based on the surface glycoprotein antigens of trypanosomes remains elusive due to the complexity of the parasite's antigenic repertoire (Hill et al., 2005; McCulloch et al., 1997). Horn (2014), Manna et al. (2014) and Taylor and Rudenko (2006) have provided comprehensive reviews on the mechanisms of trypanosome antigenic variation. Although significant understanding of the structure and mechanism of this antigenic variation of trypanosome parasites has occurred over the past 40 years, to date no vaccine is available (Manna et al., 2014; McCulloch and Field, 2015; Mony and Matthews, 2015). These factors are the main reasons why most research efforts aimed at developing a vaccine for trypanosomiasis have since shifted from variable surface (VSG) antigen towards the identification of other, invariant, structural components of the parasite (Alsford et al., 2013; Taylor, 1998; Tsegaye et al., 2015).

Towards the late 1990s, the recognition of the systematic failure of existing Trypanosomiasis control methods led African scientists to set up a regionally coordinated initiative to tackle the disease (Maudlin, 2006). In 2000, the Pan-Africa Tsetse and Trypanosomiasis Eradication Campaign (PATTEC), was endorsed at the 37th African Union

summit in Togo (Kabayo, 2002). Central to that new initiative was a “Money Map” of the region that shows the anticipated benefit of eradication of trypanosomiasis in US$ per Km^2 over 20 years to illustrate the magnitude of economic loss caused by the disease (Shaw, 2009). PATTEC received support from multinational agencies including the World Health Organisation, the Food and Agriculture Organisation and the International Atomic Energy Agency. Unprecedented support in the fight against Trypanosomiasis also came from a long list of non-governmental organisations and pharmaceutical companies including the Bill and Melinda Gates Foundation, Bayer, Bristol-Mayers Squibb, and Aventis Pharma (WHO, 2002). PATTEC, although stipulating a holistic and integrated approach to combatting trypanosomiasis, was criticized for overly focusing on Tsetse fly eradication at the expense of other methods such as the use of trypanotolerant breeds (IAEA, 2002). Furthermore, the tsetse fly control module used in the program was criticized as unsuitable and unrealistic for application in the 10 million square kilometer affected area of sub Saharan Africa, although it was used successfully in the isolated and small region of Zanzibar (IAEA, 2002; Kabayo, 2002). The reality is, that despite all these varieties of control measures targeted at AAT, the disease persists, and is not likely to be completely eradicated soon (Dolan, 1987; Magez and Radwanska, 2014; Nakayima et al., 2012). Therefore, exploiting additional measures including natural trypanotolerance of livestock is imperative, particularly for the vast majority of resource poor smallholder livestock keepers in the region for whom the existing chemotherapy and vector control programs are neither accessible nor affordable.

3. Genetic Basis for Trypanotolerance

Trypanotolerance, which is the characteristic ability inherent in certain breeds of livestock to withstand trypanosomiasis, was first reported as early as 1904 and 1913 in West and East Africa respectively (Dolan, 1987; Murray et al., 1982). A growing number of studies have corroborated the use of trypanotolerance as the most economically sustainable option for tackling AAT (Mattioli et al., 2000; Murray et al., 1982; Naessens, 2006). Despite this endorsement, the extent, the mechanisms and the effects of trypanotolerance has remained largely unexplored as a control measure for the disease (Dolan, 1987; Kosgey and Okeyo, 2007). Research findings from both experimental and natural livestock populations have confirmed that trypanotolerance is heritable in breeds such as Ndama cattle (Hanotte et al., 2003; Murray and Black, 1985; Naessens et al., 2002; Namangala, 2012; Trail et al., 1991), Muturu and Baoule cattle (Naessens et al., 2002), Djallonke sheep and the west African dwarf goat (Geerts et al., 2009; Osaer et al., 1994). For example, in a natural Trypanosomiasis challenge study on an Ndama cattle population in Gabon, a high heritability of 0.64 was estimated for the ability to control anaemia as measured by the average packed red blood cell volume, a characteristic feature of trypanotolerance (Trail et al., 1991). Different crosses of trypanotolerant and trypanosusceptible breeds in both cattle and sheep have produced phenotypes with varying intermediate degrees of tolerance to the disease, indicating a complex and varied genetic control mechanism (Goossens et al., 1997; Goossens et al., 1998; Goossens et al., 1999; Murray and Trail, 1984). Examples of this are the crosses that were produced from trypanotolerant Djallonke and trypanosusceptible Sahelian sheep (Goossens et al., 1999), and from trypanotolerant Ndama and trypanosusceptible Boran cattle (Hill et al., 2005). Beyond trypanotolerance, the wild Cape buffalo (*Syncerus caffer*) is the only ruminant species in the region that is known to have an absolute resistance to infection from all species of trypanosomes (Namangala, 2012).

However, the Cape buffalo with an estimated population of only one million, is also a reservoir for the spread of many other important livestock diseases in the region such as bovine tuberculosis, brucellosis, anthrax and foot and mouth disease (Michel and Bengis, 2012).

Subsequent genomic investigation using microsatellites (Dayo et al., 2009; Hanotte et al., 2003), and single nucleotide polymorphisms (Gautier et al., 2009) identified quantitative trait loci (QTL) regions for trypanotolerance in Ndama cattle. These findings provided novel molecular genetic insights into trypanotolerance, but the QTL regions detected were too large for downstream applications such as genomic selection for trypanotolerance in the breed. A follow-up investigation within the identified genomic regions using a denser panel of microsatellites identified a polymorphic allele in one of the four previously identified candidate regions which was strongly associated with anaemia control (Dayo et al., 2012).

So far no trypanotolerance study has focused on a next generation whole genome sequencing approach for the detection of putative loci for trypanotolerance. The identification of trypanotolerance loci will pave the way for the widespread application of genomic selection (Hayes and Goddard, 2010). Recently, it has been shown that whole genome sequencing of pools of individuals provides a higher resolving power for identification of candidate regions or genes of adaptive selection signatures than the use of microsatellites (Bergland et al., 2014; Kofler et al., 2015). For example a re-sequenced pooled whole genome of samples of 50 to 100 *Drosophila melanogaster* precisely revealed seasonally associated polymorphisms in the flies (Bergland et al., 2014). Since trypanosomes have co-evolved with the trypanotolerant breeds over several millennia (Murray and Black, 1985; Mwai et al., 2015), it is expected that signatures of selection for

resistance will exist in their genomes. Consequently, a whole genome sequencing approach may be a suitable way to identify trypanotolerance QTLs.

4. Mechanism of trypanosome infection and trypanotolerance

The hallmark of trypanosomiasis pathology is the remarkable ability of trypanosome parasites to elucidate responses from virtually every component of the host innate and acquired immune response system (Magez and Radwanska, 2014; Mansfield et al., 2014; Naessens et al., 2002). Trypanosomes are extracellular parasites with more than 1,000 different VSG genes and pseudogenes, of which only one is transcribed at any one time. These numerous VSG genes and pseudogenes allow a trypanosome to produce successive waves of up to 10^7 different VSG antigens sequentially, and this provides a mechanism that allows sub populations of the parasite to evade the humoral adaptive immunity of the host (Cnops et al., 2015; Donelson, 2003; Manna et al., 2014; Mansfield et al., 2014; Taylor and Rudenko, 2006). This classical immune escape mechanism makes a trypanosome infection difficult to stop once established (Donelson, 2003; Taylor and Rudenko, 2006). Matthews et al. (2015) provided a comprehensive review on the within-host dynamics that facilitate trypanosome infection including a novel quorum sensing mechanism. Earlier reports have suggested that adaptive immunity in the form of VSG-specific B- and T- lymphocytes was mainly responsible for trypanotolerance in resistant breeds (Taylor, 1998). However, more recent evidence points at the host's innate immunity in the form of activated macrophages as key to trypanotolerance (Liu et al., 2015; Mansfield et al., 2014). Recently it has been shown that the adaptive immune response to trypanosome infection is short-lived and is effective only against a sub-population of the possible VSG types (Cnops et al., 2015; Magez and Radwanska, 2014). The report also indicates that no effective immunological memory is

developed in the host during trypanosome infection, and hence the successive waves of infection destroy the host's B cell compartment, leading to the failure of adaptive immunity (Magez and Radwanska, 2014). The failure of the host adaptive immunity is identified haematologically by dramatically increased levels of parasitaemia and anaemia, which is progressively followed by several of the pathological symptoms previously mentioned in this review and potentially the death of the host, if left untreated (Goossens et al., 1998).

However, trypanotolerant breeds exhibit a capacity to control this characteristic anaemia and parasitaemia that accompany the trypanosome infection (Goossens et al., 1998; Murray et al., 1982; Murray et al., 1984). This capacity to control anaemia is crucial for trypanotolerance, and permits the host to remain productive under disease challenge (Naessens, 2006; Naessens et al., 2002; Trail et al., 1990; Trail et al., 1991). Generally, trypanotolerant livestock thrive better with low to medium intensity challenge than with high intensity parasite challenge (Holmes, 1997). In parts of west and central Africa, where the trypanosome challenge is very high, Diminazene chemotherapy has been used to help trypanotolerant breeds maintain desirable levels of production (Peregrine and Mamman, 1993). The high levels of the disease challenge in these parts of Africa excludes the farming of trypanosusceptible breeds, given the huge cost of trypanocides that would be required (Peregrine and Mamman, 1993).

Similar to resistance to other parasitic infections of ruminants, trypanotolerance has also been found to be enhanced in hosts with a high plane of nutrition and *vice versa* (Coop and Kyriazakis, 1999; Coop and Kyriazakis, 2001; Cunningham-Rundles et al., 2005; Van Houtert and Sykes, 1996). Conversely, the presence of inter-current parasitic infection in the host reduces trypanotolerance, as does physiological stress factors such as gestation (Coop and Kyriazakis, 1999; Murray et al., 1982; Murray et al., 1984). The deleterious effect of mixed

infections of trypanosome and other parasites, particularly gastrointestinal helminths, in trypanotolerant breeds have been very well documented (Goossens et al., 1997; Goossens et al., 1999; Kaufmann et al., 1992; Okaiyeto et al., 2010). In Djallonke sheep, mixed infection is generally characterised haematologically by a fall in packed cell volume, high levels of eosinophils, immunosuppression, weight loss and mortality, if left untreated (Goossens et al., 1999; Okaiyeto et al., 2010). A similar observation was also made in Ndama cattle (Kaufmann et al., 1992). In an experimental infection of Djallonke sheep, more severe acute symptoms were observed when infection with trypanosomes was followed by concurrent *Haemonchus* infection. Conversely a more chronic form of the disease was observed when the sequence of infection was reversed (Goossens et al., 1997; Kaufmann et al., 1992). This observation suggests that trypanosome infection has an immunosuppressive effect on the Djallonke sheep, and renders it more susceptible to subsequent infection by *Haemonchus*. In another study, abrogation of immunity to *Heligosomoides polygyrus* in previously immunized mice was attributed to the immunosuppressive effect of a concurrent trypanosomes infection (Fakae et al., 1997).

Recent studies suggest that the associated immunosuppression is due to the extensive apoptosis of the splenic B cell compartment of the host during trypanosome infection (Cnops et al., 2015; Magez and Radwanska, 2014; Radwanska et al., 2008)**.** The mixed infection phenomenon presents an obstacle to exploring trypanotolerance in most livestock production systems in sub Saharan Africa (Alvarez et al., 2012). However, trypanotolerant livestock are often resistant to other important livestock diseases such as helminthiasis, anaplasmosis, babesiosis and heartwater (Murray et al., 1982; Murray et al., 1984; Tano et al., 2003). Attempts to achieve genetic introgression of trypanotolerance through indiscriminate crossbreeding with trypanosusceptible breeds is common in livestock

production systems in many parts of sub Saharan Africa, but leads to the diluting of the trait (Alvarez et al., 2012; Bradley et al., 1994; Geerts et al., 2009; Kosgey and Okeyo, 2007). Morris (2007) reports that a considerable number of trypanotolerant Ndama and western African short horn cattle have already been introduced into 19 countries within the central African region in response to the disease challenge. A recent microsatellite and SNP marker analysis within trypanosomiasis candidate regions of trypanotolerant and trypanosusceptible cattle confirmed significant levels of admixture of the two breeds (Smetko et al., 2015). Most of these indigenous African livestock breeds are now endangered due to indiscriminate crossbreeding and breed replacement, and there is a high risk of their adaptive traits being lost forever (Mwai et al., 2015). This excessive genetic introgression will pose a major challenge for the sustainable use of the trypanotolerant trait for the control AAT if deliberate programmes for the preservation and development of trypanotolerant breeds are not put in place.

5. Trypanotolerance in the context of Africa livestock production

The existing AAT control and eradication programs have not, and might never, reach the level of effective implementation required to rid the region of this complex disease. The main livestock systems in sub Saharan African are small holder pastoral, agro pastoral, mixed crop–livestock and peri-urban livestock systems (Kosgey and Okeyo, 2007; Tano et al., 2003; Zougmoré et al., 2015). These systems are characterised by low input, low technology, and with a considerable level of subsistence production (Jahnke and Jahnke, 1982). Over the last century, the sheer complexity and diversity of socio-politico-cultural elements of the different countries within the sub Saharan African region have constrained the effective

coordination of many anti-trypanosomiasis programs between member states, and also with regional and international partners (Black et al., 1985; Ford, 2007; Smith et al., 2015). The persistence of civil conflicts and wars within the sub Saharan African region has been directly linked to the re-emergence of the disease in many affected countries (Ford, 2007). For example; the trypanosomiasis epidemic outbreak of Uganda in the late 1970's resulted from political turbulence, and the outbreak in Angola that started in 1975 during the post-independence civil war period. The presence of large populations of wildlife reservoirs of Trypanosome parasite in some parts of the region has also worked against the total eradication of the disease (Murray et al., 1982). There is a general lack of capacity for local, mostly smallholder, livestock farmers to diagnose or treat such a complex disease (Geerts et al., 2001; Murray et al., 1984). The appropriate use of trypanotolerant breeds would mitigate the high annual losses incurred by the vast majority of these smallholder livestock farmers (Tano et al., 2003). Mitigating losses is particularly important because the improvement of smallholder agricultural productivity in Africa is fundamental to overcoming the problem of poverty in the region (Babikir et al., 2015).

Breeding livestock for disease resistance is a widely accepted concept in developed countries (Piedrafita et al., 2010; Raadsma and Fullard, 2006), and has been extensively studied in breeds such as the Scottish Blackface sheep (Bishop et al., 2002; Stear et al., 1997). There are ongoing extensive and equally successful breeding programs for disease resistance in Australian Brahman cattle (Frisch et al., 2000), and in sheep in Australia and New Zealand (Van der Werf, 2007). For example, AUD$ 8 billion in extra earnings was realized within 30 years of the exploitation of the parasite resistance genes of Brahman cattle via a landmark cross breeding program within the Northern Australian beef industry (Frisch et al., 2000; Morris, 2007). Most research and application has involved parasitic

diseases, but Bishop and MacKenzie (2003) provide a comprehensive model framework for the utilization of disease resistance for the control of bacterial and viral infections in livestock.

However, in the context of sub Saharan Africa livestock production systems, measures would need to be put in place to preserve the genetic purity of known trypanotolerant breeds, and to protect those breeds from excessive genetic introgression by trypanosusceptible breeds (Geerts et al., 2009). To this end, a molecular characterisation of all trypanotolerant livestock breeds for the purpose of reliable identification, will also expedite future genetic improvement programs for trypanotolerant breeds. This effort can take the form of establishment and coordination of regionally or nationally supported satellite open nucleus breeding stations for pure trypanotolerant breeds across sub Saharan African region to sustain this intervention.

6. Conclusion

After a century of intervention against AAT, the disease persists, as does its staggering impact on the livelihoods of the population in sub Saharan Africa. A diverse range of interconnected factors has contributed to the entrenchment of the disease. Given the current perspective, imminent eradication of this disease does not seem a possibility. Although, advancement in scientific technologies has been accompanied by a greater understanding of the mechanisms of the disease over this period, the existing control measures remain largely inadequate. We are of the view that an improved outcome in the battle against AAT will require a more holistic approach that is dynamic and context-specific to the different livestock production systems across sub Saharan Africa. Therefore,

management of the disease including the development of structured programs for the use of trypanotolerant breeds will be a more realistic and achievable objective. The exploitation of naturally trypanotolerant breeds of livestock will not only add an economically sustainable option to the mix of interventions, but is also compatible with livestock production systems in the region.

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Conflict of Interest

The authors declare that there is no conflict of interest

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