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The Bovine Major Histocompatibility Complex and Its Role in Tick and Tick-borne Disease Resistance in Indigenous Cattle Breeds in Sub-Saharan Africa: A Review

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Abstract

Ticks present a major challenge in livestock production, given the increased demand for animal protein worldwide. In addition to being vectors of numerous diseases in livestock, ticks cause blood loss, worry and damage hides. Anaplasmosis, Theileriosis, Babesiosis and cowdriosis are amongst the critical tick-borne diseases causing havoc across the world in the livestock industry. Global economic losses caused by these ectoparasites amount to billions of dollars annually. Although there are different methods of tick control, they all have shortcomings which frustrate the efforts of farmers in controlling ticks and tick-borne diseases. This has motivated researchers to search for sustainable alternative methods of tick control which include the genetic selection of naturally resistant breeds. The Major Histocompatibility complex (MHC) also known as the Bovine Leukocyte Antigen (BoLA) in cattle has been associated with tick-borne disease resistance in some cattle breeds. Different breeds have different levels of resistance to ticks and tick-borne diseases. The *Bos indicus* breeds and their crosses are known to be more resistant to ticks and tick-borne diseases than the *Bos Taurus*. Given the downsides of acaricides, vaccines and other tick-control methods, the use of tick and tick-borne disease-resistant cattle breeds is a promising choice for tick and tick-borne disease control. This review summarizes the role of the MHC in resistance to ticks and tick-borne diseases in indigenous cattle breeds of Sub-Saharan Africa.

Keywords: BoLA, *Bos indicus*, sub-Saharan Africa, tick-borne disease resistance, tick resistance.

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Introduction

Rainfed agriculture produces the majority of the food consumed in sub-Saharan Africa (SSA) and it is the backbone of rural economy and food security for the majority of the rural population in SSA (Abrams, 2018). However, rainfall variability, ectoparasites and diseases remain major obstacles in agricultural production, resulting in major losses in especially livestock production. Ticks and tick-borne diseases are responsible for major losses by impacting animal production directly (feeding on their hosts causing blood loss and weight loss) or indirectly by acting as vectors of pathogenic diseases (Sahara et al., 2019). Global losses (which include costs associated with diseases caused by *Rhipicephalus microplus* and control of this tick) are estimated to be between USD 13.9-18.7 billion per year (Hurtado & Giraldo-Ríos, 2018). Different tick control methods include; vaccinations, chemical control, biological control and traditional control methods. Each control method has its advantages and disadvantages. Chemical control is the primary method used to combat tick infestations. However, the costs of acaricides are considerable, and most importantly, there is a rising concern for the development of chemical resistance in some ticks. Furthermore, there is increasing concern regarding the accumulation of chemical residues in organs and the environment and consequent adverse effects on food quality, with risks for human health (Sparagano & Giangaspero, 2011). Owing to the drawbacks of acaricides, alternative methods such as the utilization of host resistance to ticks could reduce the use of acaricides.

The origin of ancient and modern cattle in Africa is still a matter of debate among researchers. Mitochondrial and Y-chromosome DNA evidence suggests independent domestications of indicine or humped cattle in South Asia and taurine or straight-backed cattle in Southwest Asia (Loftus et al., 1994). It is hypothesized that taurine cattle were the first to arrive in Africa around 7000 BP from Southwest Asia (Brass, 2013) and spread to southern Africa around 2000 BP (Smith, 2000). Since their arrival in Africa, extensive crossbreeding occurred between taurine and indicine cattle resulting in Sanga cattle (Hanotte et al., 2002). Today, there are three groups of modern cattle in Africa; taurine, indicine (Zebu) and taurine-indicine (Sanga). The distributions of *Bos indicus*, *Bos taurus* and their crossbreeds in sub-Saharan Africa is shown in Figure 1.

Efforts to characterize indigenous cattle breeds in SSA at a molecular level are underway with the primary focus on improving productivity and increasing disease resistance (Madilindi et al., 2020). Genetic variability for bovine tick resistance in cattle breeds in SSA has been studied (Yessinou et al., 2018; Mapholi et al., 2017; Wambura et al., 1998), showing potential for the improvement of this trait. It is widely accepted that *B. indicus* breeds are more resistant to ticks than *B. taurus* breeds. This is due to their long history of being reared in tick and Tick-borne diseases (TBDs) endemic areas and have hence evolved mechanisms that enable them to co-exist with specific pathogens making them a valuable source of genetic material (Mapholi et al., 2017).

The major histocompatibility complex (MHC) has been identified as one of the candidate genes coding for tick and TBDs resistance in bovines, and over several decades, numerous studies on genomic analysis of the bovine MHC have confirmed the association with tick and TBD resistance (Haikukutu et al., 2017; Duangjinda et al., 2013; Porto-Neto et al., 2011; Untalan et al., 2007; Martinez et al., 2006; Acosta-Rodríguez et al., 2005; Stear et al., 1984). These studies and many more were driven by the need to develop improved methods of ectoparasite and TBD control and have primarily focused on identifying associations of MHC genes with TBDs or ectoparasites. This has yielded information that is of value in breeding practices with a primary focus on breeding for parasite and TBD resistance and also on the design of novel vaccines.

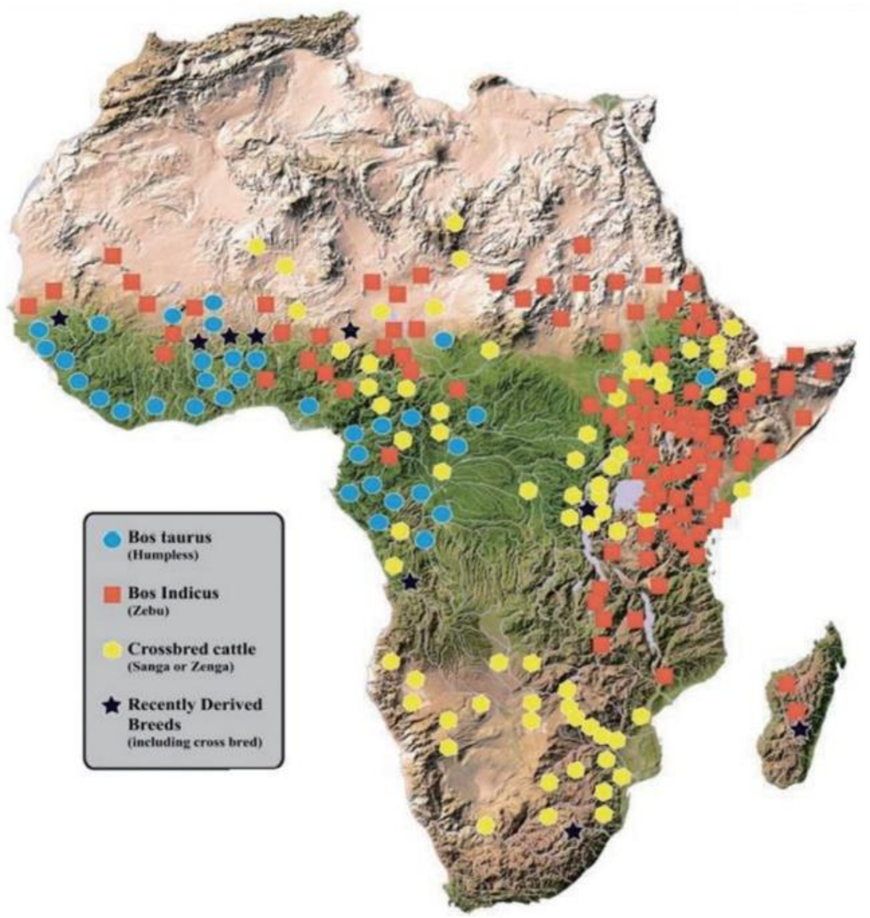

Figure 1: Distributions of indigenous cattle in sub-Saharan Africa (Adapted from Mwai et al., 2015).

The use of natural ticks and TBD resistant animals show a promising solution in efforts to increase productivity and mitigate ticks and TBDs in SSA. Interestingly, resistance and susceptibility to infections other than TBDs are also associated with the MHC (Derakhshani et al., 2018; Gutiérrez et al., 2017; Lei et al., 2012). Found in most vertebrates, the MHC plays a central role in the function of the immune system, and this is mainly due to the polymorphic nature of the genes encoding the MHC. Genes within the major histocompatibility complex encode many proteins involved in antigen processing and presentation. Most MHC studies to date have been carried out on *B. taurus* breeds, with limited analysis of African *B. indicus* cattle breeds.

The bovine major histocompatibility complex (BoLA)

The MHC of cattle also known as the Bovine Leukocyte Antigen (BoLA) is located on the short arm of chromosome 23 with an estimated size of about 4000 Kb containing 154 genes (Elsik et al., 2009). This vital component of the immune system plays a significant role in eliminating or neutralizing pathogens by binding to peptide fragments derived from pathogens and displaying them on the cell surface for recognition by the appropriate T cells (Janeway et al., 2001). The existence of BoLA was established over 35 years ago (Spooner et al., 1979), and since then, the MHC has been a significant focus of most disease association studies. The MHC is well known for its polygenic and polymorphic nature enhancing the repertoire of epitopes that an individual can recognize, hence virtually elimination of pathogens. Similar to humans and mice, three different groups of MHC molecules exist in bovines; Class 1, class II and class III. These classes differ in their structure and function are therefore found on different cells. While class I molecules are found on all nucleated cells, class II molecules are expressed on antigen-presenting cells (APCs), such as B lymphocytes, dendritic cells and macrophages. Class I molecules present peptides to $CD8^+$ T-lymphocytes, consequently killing virus-infected and neoplastic cells, whereas class II molecules have a function of presenting peptides derived from extracellular pathogens to $CD4^+$ T cells (Abbas et al., 2007). It is essential to understand that several evolutionary events have contributed to MHC diversity resulting in duplications/deletions of some loci (Ellis & Ballingall, 1999). A comprehensive review of the major histocompatibility complex in bovines was documented by Behl et al., (2012) concluding that high polymorphism of MHC genes could be useful in marker-assisted selection.

The BoLA consists of two functional gene components, namely: the DR and DQ molecules. Both molecules present processed pathogen antigens to $CD4^+$ T lymphocyte cells. Because the DRA chain is monomorphic, the DRB chain is the primary source of diversity in DR molecules (Norimine & Brown, 2005). BoLA-DQA also exhibits polymorphism but is not as well documented as the BoLA-DRB. The BoLA-DRB3 is known to be the only functional DRB gene and is the most polymorphic locus in MHC class II genes. The genetic linkage map of the BoLA is shown in Figure 2.

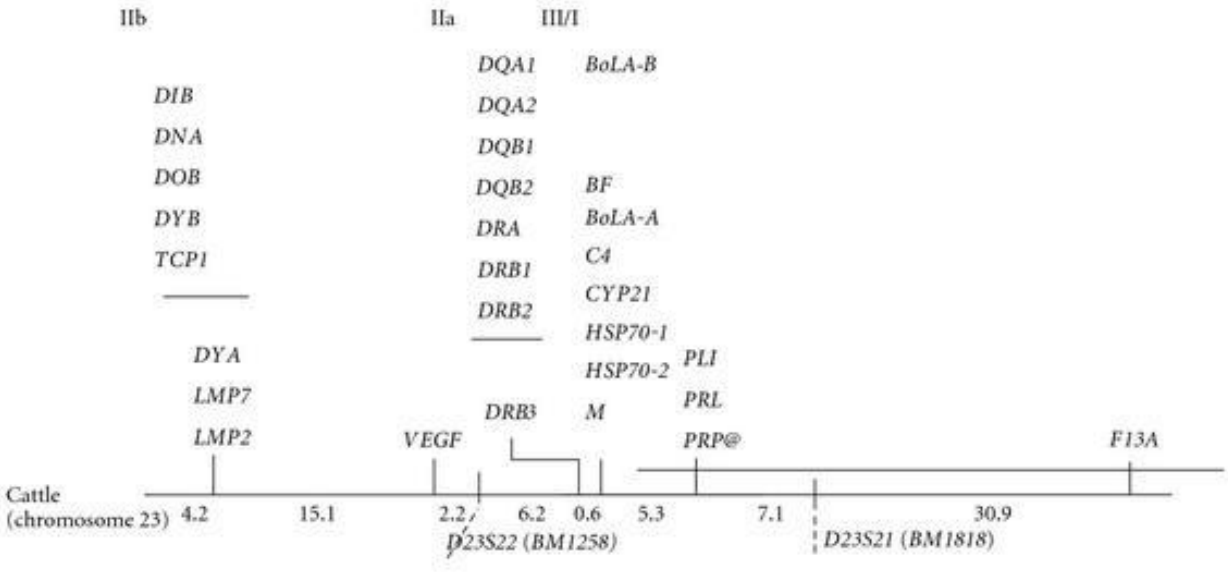

Figure 2: Genetic Linkage map of the central histocompatibility complex region in cattle (Adapted from Amills et al., 1998).

Genetic diversity of the BoLA and its role in ticks and tick-borne disease resistance in sub-Saharan African *Bos indicus* cattle and their crossbreeds

The genetic diversity of the BoLA has been well studied, more so in *B. taurus* than in *B. indicus* breeds, leaving the molecular diversity of local indigenous breeds in SSA untapped. Molecular markers are useful tools used in investigating and quantifying genetic diversity. Application of molecular markers in bovine genetics research includes markers in milk quality and production (He et al., 2006; Grisart et al., 2002), disease resistance (Coussens & Nobbis, 2002), thermo-tolerance in cattle (Hansen, 2004) and meat tenderness (Casas et al., 2006). Molecular markers can also be used efficiently in breeding and management decisions in order to increase productivity. Various molecular markers exist such as restriction fragment length polymorphisms (RFLPs), microsatellites and single nucleotide polymorphisms (SNPs) markers. These markers differ in many ways, including costs, technical requirements, the amount of genetic variation detected and reproducibility.

Livestock diversity of the *B. indicus* is threatened as these breeds become replaced by the more productive *B. taurus* breeds or through indiscriminate crossbreeding. Breed characterization allows for the evaluation of genetic variability using different genetic markers (Singh, 2014). Molecular markers can allow prediction of breeding values for traits such as parasite and disease resistance that had previously been difficult to measure and hence were not included in the selection criterion (Beckmann & Soller, 1987).

The *BoLA-DRB3* is the most polymorphic bovine MHC gene, and by 2017, at least 136 different alleles were reported (Maccari et al., 2017). Most MHC studies on *BoLA-DRB3* diversity have been carried out on *B. taurus* breeds and *B. indicus* breeds from Asia and South America, with very few studies on African *B. indicus* cattle breeds. Peters et al. (2018), assessed the level of genetic diversity of BoLA DRB 3.2 in four African cattle breeds; N'Dama, Sokoto Gudali, White Fulani and Muturu and reported higher haplotype frequency in these breeds compared with Asian cattle breeds. Estimated diversity indices suggested that N'Dama cattle exhibited relatively highest diversity at the *DRB3.2* locus with ten haplotypes. The high haplotype frequency observed in African cattle was attributed to the numerous parasites and disease challenges predominant in the continent. Haikukutu et al., (2017) analyzed the genetic diversity of four BoLA microsatellite loci in Namibian Sanga, Namibian Afrikaner, South African Nguni and South African Bonsmara (crossbreed) and Hereford (*B. taurus*). The study revealed high BoLA diversity in *B. indicus* breeds (Namibian Sanga, Namibian Afrikaner, South African Nguni) and the Nguni crosses (South African Bonsmara) compared to the *B. taurus* breed (Hereford). The number of alleles ranged from 5.5 alleles in Namibian Afrikaner to 7.7 alleles in South African Nguni and Bonsmara cattle. Unbiased heterozygosity values ranged from 0.66 (Namibian Afrikaner) to 0.76 (South African Bonsmara). The level of genetic diversity could not be correlated with tick counts due to tick control programs followed by the breeders. Results from the BoLA genetic diversity and structure analysis of Sudanese *B. indicus* cattle breeds (Baggara, Butana, Kenana) revealed 53 alleles, including 7 new alleles (Salim et al., 2020). Genetic diversity at the *BoLA-DRB3* locus was investigated in N' Dama (*B. taurus*) and African Zebu (*B. indicus*) cattle revealing extensive genetic diversity of 18 alleles (Mikko & Andersson, 1995).

The diversity *of BoLA-DQ* genes and their role in disease resistance is not well documented as the *BoLA-DRB3*. *The BoLA-DQA* gene exhibit some level of polymorphism, although not as high as the *BoLA-DRB3*. Ballingall et al. (1997) analysed the genetic diversity of *BoLA-DQA* loci in Kenyan Boran, Ethiopian Arsi (*B. indicus*), and Guinean N'Dama (*B. taurus*) cattle and identified 13 *DQA*1 alleles, 5 DQA2 alleles and 7 DQA3 alleles. The author concluded that the differences in *DQ* and *DRB3* diversity are open to speculation; however, the diversity observed in African cattle populations can be attributed to their domestication and subsequent inter-mixing. In another study on African cattle (Boan and N'dama), 12 *DQA*1 alleles were reported (Gelhaus et al., 1995). These markers are therefore important in selecting breeds that are resistant to ticks and can tolerate TBDs and can optimally adapt to harsh conditions and endemic tick areas of SSA (Medugorac et al., 2009).

Genetic diversity of the BoLA and its role in tick and tick-borne diseases resistance in Asian and South American *Bos indicus* cattle and their crosses

Extensive research on BoLA diversity has been done on Asian and American Zebu cattle populations. The first study showing MHC genes association with tick infestation was done in Mexico in Zebu crossbreeds. However, the pioneering work of Francis & Ashton (1967) paved the way for all studies on markers for tick resistance. Acosta-Rodríguez et al. (2005), analysed the *BoLA-DRB 3.2* association with *Boophilus microplus* tick infestation in Zebu crossbreeds. The author reported a positive association between alleles *DRB3-184, BM1815-152, DRBP1-130* and tick infestation. In another study, Zebu cattle and their crosses were found to exhibit a high tolerance to TBDs (*Anaplasma marginale*, *Babesia bigemina*, *Babesia bovis*) and alleles associated with resistance and susceptibility to these TBDs were also identified (Duangjinda et al., 2013). In South America, *BoLA-DRB3* diversity analysis in Zebu cattle breeds (Nellore, Brahman, and Gir) revealed high levels of polymorphism with a number of alleles ranging from 19 in Gir to 33 in Nellore-Brahman (Takeshima et al., 2018). Moreover, these Zebu breeds had a gene diversity score higher than 0.86, a nucleotide diversity score higher than 0.06. Thirty-seven BoLA-DRB3.2 alleles were detected in Indian *B. indicus* (Malnad Gidda, Hallikar, Ongole) using PCR-RFLP (Das et al., 2012). Moreover, 18 *BoLA-DRB3* new alleles were characterized using PCR-RFLP typing method in Zebu Brahman cattle in Martinique, revealing the uniqueness of this breed (Maillard et al., 1999). A study that involved a Brahman–Angus cross cow demonstrated that *BoLA-DQ* molecules derived from inter-haplotype and intra-haplotype pairing of A and B chains are functional in presenting *Anaplasma marginale* and *Babesia bovis* peptides (Norimine & Brown, 2005). This suggests that the *BoLA-DQ* genes also play essential roles in TBD resistance. These markers are, therefore crucial in selecting breeds that are resistant to ticks and can tolerate TBDs and can optimally adapt to harsh conditions and endemic tick areas of SSA (Medugorac, et al., 2009). Even though these studies were not done in Africa, they have paved the way for researchers in Africa to research on the association of MHC class II genes with tick resistance.

Tick and Tick-borne diseases resistance in *Bos indicus* and their crossbreeds

Bos indicus (Zebu or humped cattle) makes up the majority of cattle in Africa and are mainly found in the northern as well as eastern parts of Africa (Kim et al., 2017). The Sanga cattle (taurine-indicine hybrids) are predominantly found in the central and southern part of Africa. The majority of indigenous African cattle are still managed under traditional semi-extensive systems in communal areas and are subjected to intense environmental pressures (heat, drought) and diverse disease challenges (Musisi & Lawrence, 1995). There is a consistent agreement that *B. indicus* cattle exhibit higher resistance to ticks than *B. taurus* breeds (Constantinoiu et al., 2010; Piper et al., 2009). Utech et al. (1978), defined tick resistance as the ability of cattle to limit the number of ticks that survive to maturity. It has long been suggested that cattle resistance to ticks is hereditary (Hull, 1912). Subsequently, numerous studies have reported the heritability of tick resistance in different cattle breeds (Ayres et al., 2013; Porto Neto et al., 2011; Budeli et al., 2009).

A cohort study done in Tanzania assessed natural tick infestation on Zebu cattle in Tanzania based on geographical locations, animals were dipped once every two to three weeks to control the tick challenge. Results revealed that more animals ($P < 0.05$) were infested with ticks in Tarime district (96.1 %) than in Serengeti (61.7 %) suggesting that Serengeti Zebu herds exhibited high resistance to ticks than Tarime Zebu herds (Laisser et al., 2016). The Nguni breed of South Africa is one of the most researched Sanga breeds. Numerous studies reported significantly high resistance of Nguni to ticks compared to other South African cattle breeds (Marufu et al., 2011; Rechav & Kostrzewski, 1991; Spickett et al., 1989). Mapholi et al. (2016), used SNP markers to assess host resistance of South African Nguni to ticks and however, obtained a low heritability estimate ranging from 0.02 ± 0.00 to 0.17 ± 0.04. Tick resistance in Afrikaner and Drakensberger breeds of Sanga cattle in South Africa has also been reported by Fourie et al. (2013) and attributed to coat score and hide the thickness. Magona et al. (2011), demonstrated differences in tick resistance of Ugandan Nkedi Zebu cattle to *R. decoloratus*, *A. variagatum*, *R. appendiculatus* suggesting that cattle can possess species-specific resistance to ticks.

Given that *B. taurus* breeds are more susceptible to ticks, genetic management for ticks in exotic breeds is mainly attained by crossbreeding *B. indicus* with *B. taurus* breeds thus introgressing tick resistance genes into improved breeds (Taberlet et al., 2008). The Bonsmara breed (Afrikaner-exotic crossbreed) has been reported to possess high levels of tick resistance in several studies (Nyangiwe et al., 2011; Budeli et al., 2009; Spickett et al., 1989). The crosses between Horro (Zebu) and Jersey cattle in Ethiopia have also been reported to exhibit a high degree of tick resistance (Irvin et al., 1996). In another study, acquired immunity against *Theileiria parva* was demonstrated in two Tanzanian indigenous cattle breeds (Tarime and Sukuma cattle) in the Lake zone (Laisser et al., 2016). In Kenya, Zebu cattle from an East Coast Fever (ECF) endemic area were reported to have a better ability to control the course of the ECF disease and recover in a shorter period than Friesian (*B. taurus*) cattle (Ndungu et al., 2005). In Zambia, over 200 000 cattle have been exposed to Babesiosis and Anaplasmosis (Makala et al., 2003). However, not all animals developed overt disease the Sanga cattle due to enzootic stability suggesting high resistance of indigenous breeds to TBDs. This indicates that there are differences in susceptibility to ticks and TBDs between breeds. Most cattle in Africa live in a state of enzootic stability concerning TBDs, where the majority of the population is infected and immune, and little or no clinical disease occurs. Existence of enzootic stability in a cattle population to TBDs, thus limits the worst of the impact of TBDs (Musisi et al., 1995). High natural resistance implies that there may be a genetic basis to host resistance to ticks and TBDs which if characterized, could be used in selecting for resistant breeds.

African indigenous cattle breeds are adapted to their local environments that are generally unsuitable for exotic cattle breeds. Such environments are characterized by high temperatures, frequent droughts and vector-borne diseases. Despite their adaptations, indigenous African cattle are perceived as inferior to exotic cattle because of their low meat and milk production potentials compared to exotic cattle (Mapiye et al., 2007). However, these assumptions do not factor in the fact that these cattle are reared in low-input environments, whereas exotic cattle are reared in high-input environments. There have been some reports of indigenous cattle with good dairy and beef characteristics (Kugonza et al., 2011; Musa et al., 2005; Schoeman, 1989) such as high calving rate (89,6%) within the Sanga (Nguni) cattle in South Africa and Namibia (Schoeman, 1989). In efforts to reach a balance between ticks and TBDs resistance and improved productivity, Nguni cattle development projects were initiated in communal areas of South Africa (Mapiye et al., 2007). These projects were introduced to solve production constraints faced by Nguni cattle farmers. Nguni cattle have the potential and ability to produce high-quality beef that is comparable to exotic breeds (Musenwa et al., 2008). Mapiye et al. (2007), stressed that the development and research programmes aimed at reintroducing the Nguni breed in the rural areas should take a holistic and participatory approach in agro-processing and value-addition of their products.

Crossbreeding *B. indicus* with *B. taurus* for beef production provides the necessary improvement in productivity or potential but is accompanied by lowered resistance to ticks (Musisi et al., 1995). Several studies (Nyangiwe et al., 2011; Budeli et al., 2009; Scholtz et al., 2005; Spickett et al., 1989) have been conducted to determine the level of tick resistance of the Bonsmara breed. Results have shown that this breed possesses some resistance to ticks although not as high as the Nguni breed but neither as low as the Hereford breed (Musisi et al., 1995). This suggests that tick resistance decrease in *B. indicu*s crosses. Marufu et al. (2011), attributed the low resistance of the Bonsmara to the coat thickness. Crossbred cattle do not only exhibit resistance to ticks but also TBDs. In Uganda, Ankole cattle were investigated for TBD resistance and were found to possess moderate resistance with optical density (OD) values for antibodies against *T. parva* (1.030–1.302); *A. marginale* (0.442–0.603) and *B. bigemina* infections (0.863–2.154) coupled with a moderate production potential (Magona et al., 2011). The Horro (Zebu) × Jersey crosses in Ethiopia have also been reported to exhibit a high degree of tick resistance (Irvin et al., 1996).

Ticks and Tick-borne diseases of economic importance in sub-Saharan Africa

Ticks are considered to be the most important ectoparasite of livestock in tropical and sub-tropical regions (Rajput et al., 2006). Approximately 900 species of ticks are recognized globally, of which about 700 species are hard ticks, and 200 species are soft ticks (Madder et al., 2013). The most notable ones belong to the *Rhipicephalus*, *Hyalomma* and *Amblyomma* genera; these are responsible for causing significant economic losses in SSA (Walker et al., 2003). Ticks of veterinary importance in SSA are as shown in Table 1. Tick-borne diseases (TBDs) are one of the most important causes of livestock losses in SSA. Approximately 70% of global beef cattle production and significant dairy production occurs in regions that have the highest prevalence of ticks (Porto-Neto et al., 2011). There is substantial literature on the adverse effects of ticks on productivity in beef (Jonsson, 2006; Frisch & O‟Neill, 1998) and dairy production (Perera et al., 2014; Jonsson et al., 1998; Madalena et al., 1990). The most notable cattle TBDs in SSA include; Anaplasmosis, Babesiosis, Theileriosis and Heartwater (Madder et al., 2013).

Ticks transmit Tick-borne pathogens to cattle in various ways. Transovarial transmission involves the transmission of pathogens from the parent to the offspring via the ovaries (da Cruz et al., 2015). *Babesia bovis* and *Babesia bigemina* are transmitted in this manner by *Rhipicephalus (Boophilus)* species (Madder et al., 2013). Transstadial transmission occurs when parasites acquired by ticks at one life stage (nymph) are transmitted in the next life stage (adult). *Dermacentor ticks transmit Anaplasma specie*s via trans-stadial means (Kocan et al., 2015). Other routes of transmission include co-feeding (uninfected ticks feeding with infected ones) and intra-stadial (within the same tick life stage, by males) transmission. Pathogens can also be transmitted when infected blood is transferred to susceptible animals via contaminated fomites or mouthparts of biting flies (Kocan et al., 2004).

Table 1. Ticks of veterinary importance in sub-Saharan Africa

Tick species	Description	Pathogens transmitted	Life cycle
Rhipicephalus (*Boophilus*)	Bluish tick short mouthparts faint/absent anal groove eyes small/absent	*Babesia bigemina,* *Babesia bovis,* *Anaplasma marginale*	One and Two- host ticks
Rhipicephalus appendiculatus	Uniformly brown scutum short mouthparts reddish-brown legs	*Theileria parva* *Anaplasma bovis* *Theileria taurotragi*	Three-host tick
Rhipicephalus evertsi evertsi	Dark brown scutum short mouthparts medium-sized beady-eyed ticks with reddish-orange legs	*Anaplasma marginale* *Borrelia theileri*	One-host tick
Hyalomma truncatum	Dark-brown scutum long mouthparts banded legs, eyes present	Toxins	Three-host tick
Amblyomma variegatum	Brightly ornamented ticks beady eyes long mouthparts	*Ehrlichia ruminantium* *Ehrlichia bovis*	Three-host tick
Rhipicephalus decoloratus	Yellowish conscutum Short mouthparts Eyes present Pale yellow, slender legs	*Babesia bigemina* *Anaplasma marginale* *Borrelia theileri*	One-host tick
Amblyomma hebraeum	Brightly ornamented scutum flat eyes long mouthparts	*Ehrlichia ruminantum* *Theileria mutans* *Theileria velifera*	Three-host tick

Sources: Horak & Fourie (1991), Walker (1991) and Coetzer et al., (1994).

Conclusions

The BoLA is an essential candidate gene in ticks and TBD resistance as it codes for the two essential molecules (DRB3 and DQA) that present antigens to CD4$^+$ T cells. Both the DRB3 and DQA have previously been reported to be associated with tick resistance (Duangdjinda et al., 2013; Miyasaka et al., 2011; Untalan et al., 2007) in Japan, USA and Thailand, respectively. These genes can be used as markers for selecting tick and TBD resistant breeds in SSA. Numerous studies have proven that *B. indicus* is more resistant to ticks and TBDs than the *B. taurus,* which makes them an ideal choice for marker-assisted selection. As emphasized by Shyma et al. (2015), the selection is most efficient in improving productivity if a multi-trait index is developed incorporating breeding values for both production and resistance traits. Crossbreeding *B. indicus* with *B. taurus* increases productivity and also ensures that the tick resistance trait is transmitted to the offspring, thus reducing the susceptibility of a population in a given enzootic area.

Good management practises, regulating cattle movements, and minimal use of acaricide should also be encouraged to attain livestock production goals.

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Disclosure of conflict of interest

The authors declare no conflict of interest.

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