



Review Article

Towards a genomics approach to tick (Acari: Ixodidae) control in cattle: A review



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ABSTRACT

Ticks and tick-borne disease (TBD) are major challenges to cattle production in the tropics and subtropics. Economic losses associated with ticks amount to billions of dollars annually. Although efforts to eradicate ticks and TBD using chemical control strategies have been implemented in many developing countries for decades, these acaricides are costly, and cattle susceptibility to ticks remains unchanged. Traditional breeding methods, where the farmer selected animals using records to improve the host genetic resistance to ticks (HGRT), are less than fully effective and time consuming. The HGRT has been reported in literature. To date, solutions to fight ticks and TBD are still unclear. Development of single-nucleotide polymorphism (SNP) technologies has created an opportunity to estimate breeding values of animals from DNA samples. The use of SNP technology for genomic selection allows information retrieval from the genotype even before the gene is expressed; thus potentially giving farmers the ability to make selection decisions on HGRT at an earlier age. This review discusses factors that affect HGRT, breeding selection, immunology, and genomic approaches and their application to improve HGRT in order to enhance livestock production.

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Introduction

There is greater demand for animal protein worldwide, especially with the increasing affluence in the emerging markets of Brazil, Russia, India, China, and South Africa. This has led to increased consumption of beef and dairy products and necessitated an expansion of global cattle production. Ticks are a major challenge to increased cattle production affecting an estimated 1.4 billion cattle worldwide (FAO, 2011). On a global basis, ticks are one of the most important vectors of disease pathogens in livestock and companion animals (Ghosh et al., 2006). Tick-borne diseases (TBD) result in huge economic losses in both dairy and beef production systems, especially in tropical and subtropical areas (Rajput et al., 2006). Direct effects of tick infestation on cattle include the sucking of blood which causes anaemia and damage to the skin or hide, with downstream effects resulting in reductions in fertility, body weight, and milk production, and in toxicoses, paralysis, and mortality (Turton, 2001; Jongejan and Uilenberg, 2004; Kaufman et al., 2006).

Conventional tick control is based on application of acaricides. The use of these acaricides has increased the incidence of acaricide-resistant ticks and exacerbated the occurrence of environmental and food contamination (Parizi et al., 2009). Together, these problems generate a rising economic and social demand for alternative approaches to reduce tick infestation and thereby enhance the contribution of cattle to the world economy. Natural immunity, developed by cattle in environments where ticks are endemic, shows promise for genetic tick control strategies which will reduce expenditure on acaricides and other chemical control methods (Frisch, 1999; FAO, 2004). Tick control strategies targeted at the host's immunity require that immunity can be assessed using an appropriate and accurate method.

Mapping of the bovine genome has opened new avenues for determining the genetic basis for host genetic resistance to ticks (HGRT), using technologies such as single-nucleotide polymorphisms (SNPs) and copy number variants, and thus enabling their control in cattle (Piper et al., 2008). The current review discusses the distribution of common tick species, their economic impact on cattle production, and their control. Host resistance to ticks, breed variability in susceptibility to tick infestation, classic breeding and selection approaches to reducing susceptibility or increasing tolerance to ticks, as well as genomic tools to improve resistance are also discussed.

Geographical distribution of common ixodid ticks in Africa

Tick species distribution in Africa

There are approximately 879 known tick species worldwide. These species are grouped into 3 families: Argasidae or soft bodied

ticks (186 species), Ixodidae or hard bodied ticks (692 species), and Nuttalliellidae (1 species) (Navas et al., 2009). The present review focuses on ixodid ticks, as they have devastating impacts on cattle. In Africa, there are over 650 tick species belonging to 7 genera. Of the 7 genera of hard-bodied ticks that affect livestock in Africa, 3 are of economic importance in cattle (Table 1). These are: *Rhipicephalus* (including the new subgenus *Boophilus*), *Amblyomma*, and *Hyalomma* (Sonenshine, 1991; Walker et al., 2003; Jongejan and Uilenberg, 2004).

Factors affecting tick distribution

Broad-scale factors that limit the ranges of tick species have not been definitively established. Given that most tick distributions are not limited by those of their host species, it can be inferred that a primary factor preventing expansion of tick species ranges is a direct effect of climate (Cumming, 2002). Olwoch et al. (2009) suggested that if global warming leads to temperature increases, the incidence of ticks will further increase in regions where ticks are endemic. This could have serious implications for seasonal variation in tick infestation, TBD incidence, and TBD control strategies. In South Africa, for example, increased environmental temperature is thought to have caused displacement of the indigenous African species *Rhipicephalus decoloratus* by the Asiatic intruder *Rhipicephalus microplus* (Tønnesen et al., 2004; Nyangiwe et al., 2013). Except for extremely cold and dry areas, *R. microplus* has extended its range and is now present in all warm and humid areas of the country. The bont tick (*Amblyomma hebraeum*) was reported to occur only in the warm, moist coastal areas of South Africa (Coetzer et al., 1994). However, it has recently been reported that *A. hebraeum*'s distribution is expanding to the inland semiarid areas of South Africa (Nyangiwe et al., 2011). The expansion in distribution of the bont tick in South Africa may be associated with more intense periods of drought especially in the inland highlands areas as hypothesised by Estrada-Peña et al. (2008) for the bont tick in Zimbabwe.

The distribution and abundance of ticks are also impacted by factors other than climate such as presence of alternative hosts,

Table 1
Common tick species in Africa, their life cycle, and pathogens transmitted by them.

Tick species	Life cycle	Pathogens transmitted
<i>Amblyomma hebraeum</i>	Three-host	<i>Ehrlichia ruminantium</i>
<i>Rhipicephalus decoloratus</i>	One-host	<i>Babesia bigemina</i>
<i>Rhipicephalus microplus</i>	One-host	<i>Anaplasma marginale</i>
		<i>Babesia bovis</i>
		<i>Babesia bigemina</i>
		<i>Anaplasma marginale</i>
<i>Rhipicephalus appendiculatus</i>	Three-host	<i>Theileria parva</i>
<i>Rhipicephalus evertsi evertsi</i>	Two- or three-host	<i>Anaplasma marginale</i>

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