Novel Theileria genotypes from wildlife in a *Theileria parva*-endemic area in Kenya

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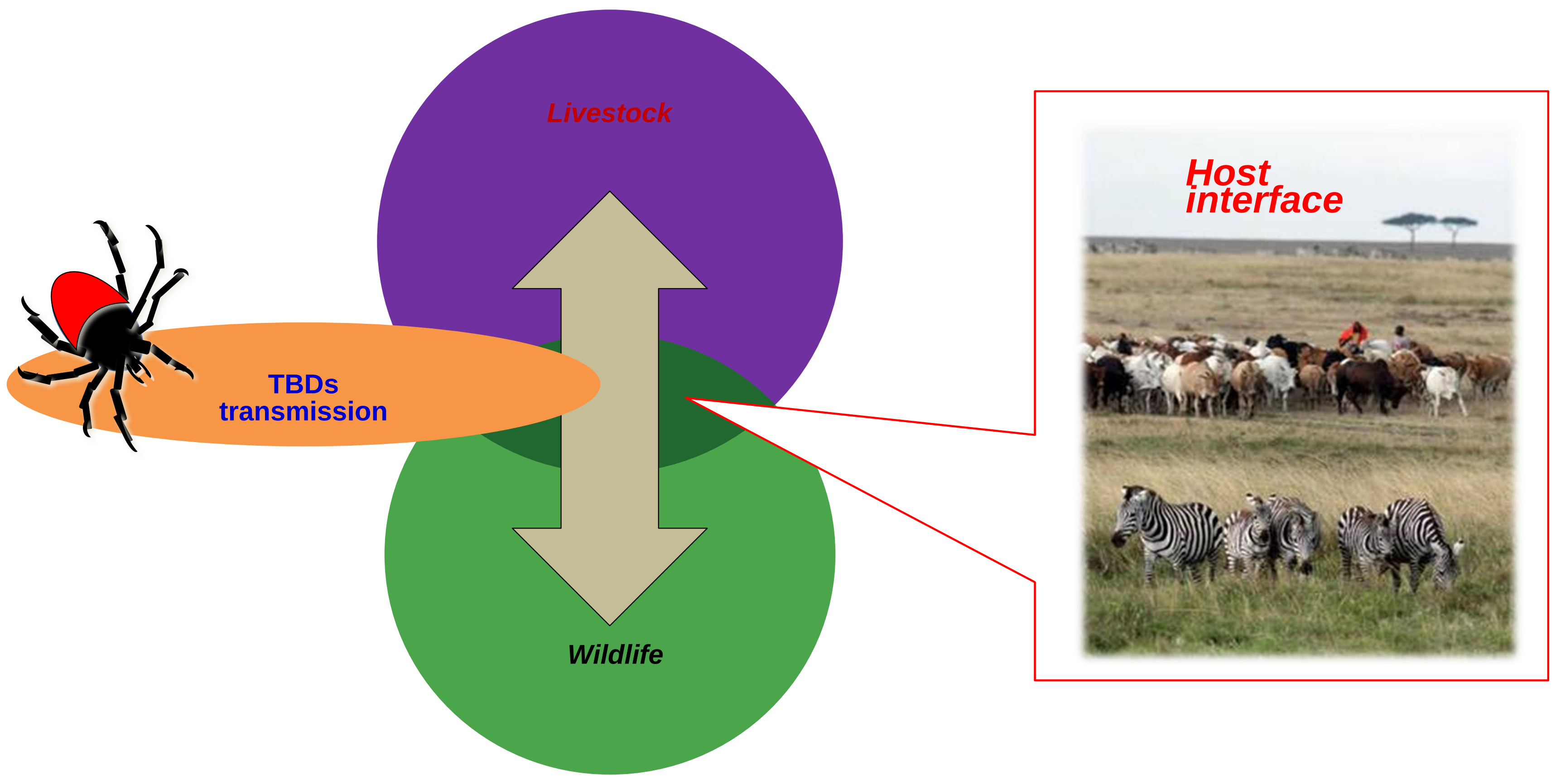
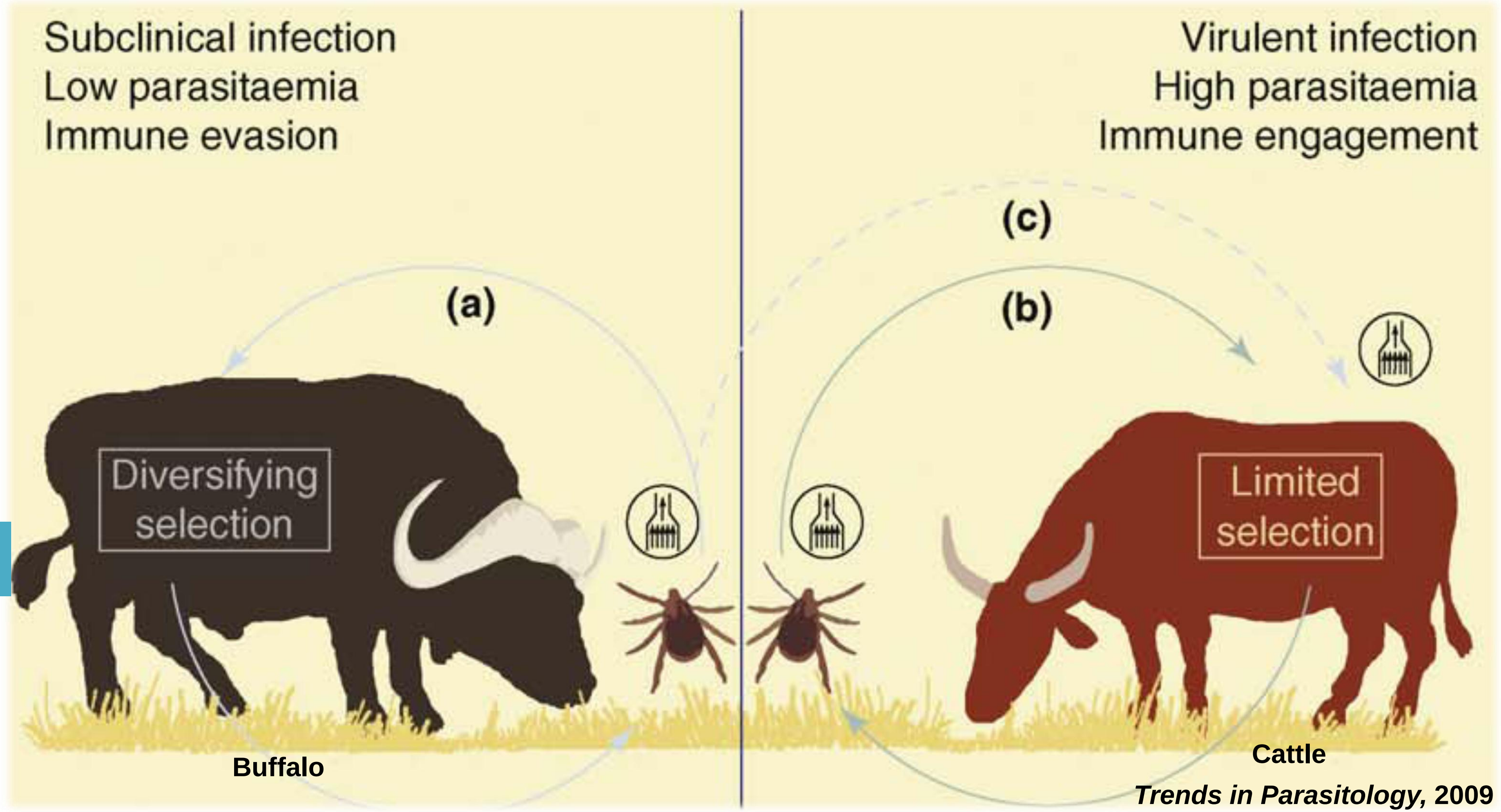
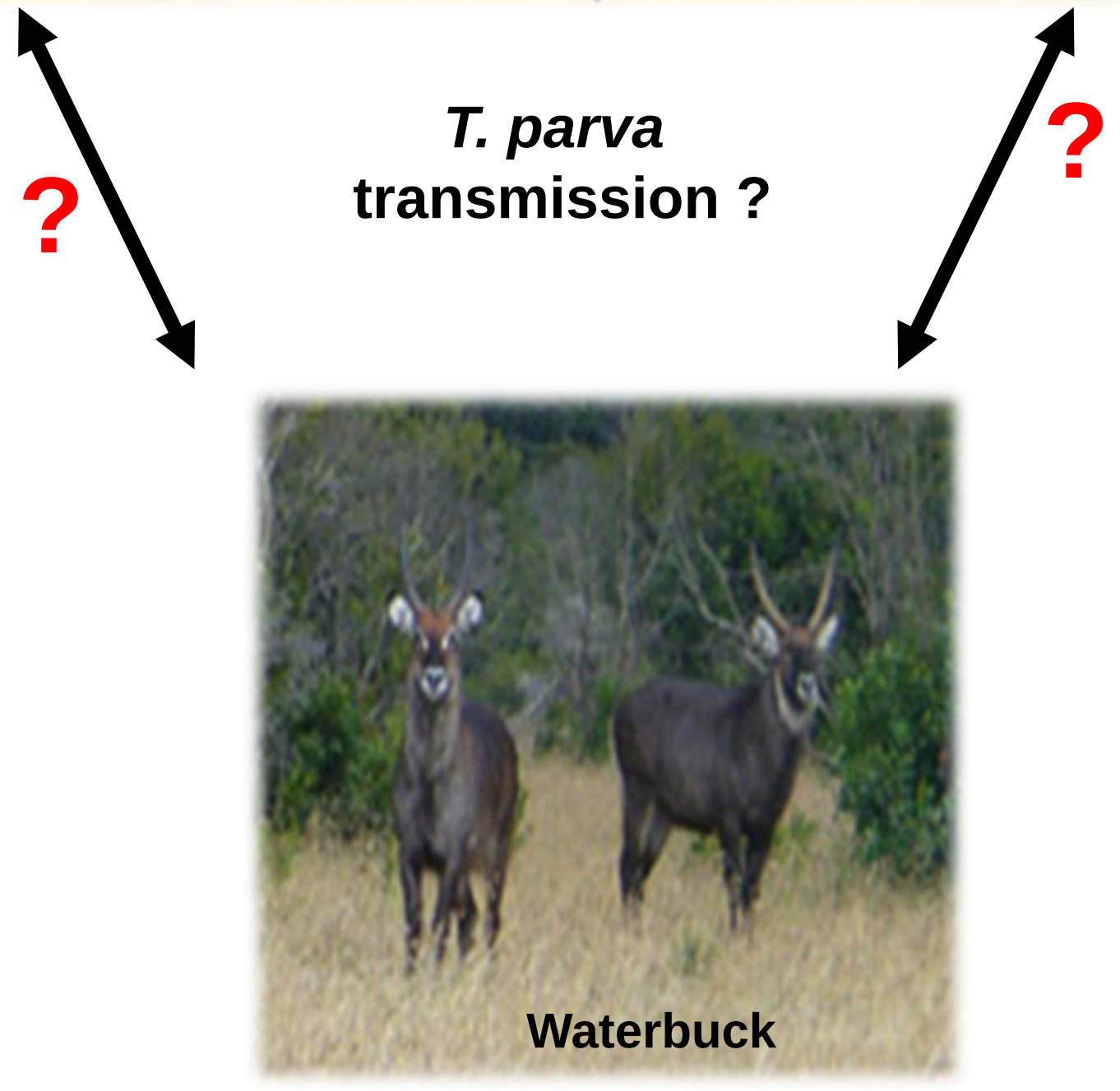
Background



In Africa, the primary cause of theileriosis in cattle is the sporozoan parasite *Theileria parva* that occurs naturally in the Cape buffalo (*Syncerus caffer*). Waterbuck are infested by large numbers of *Rhipicephalus appendiculatus*, the tick vector for *T. parva,* and previous *in vitro* data suggests that the species may be a source of *T. parva* transmission to cattle. However, there is no evidence that *T. parva* is transmissible to the waterbuck under field conditions.



***Trends in Parasitology*, 2009**



Materials and Methods

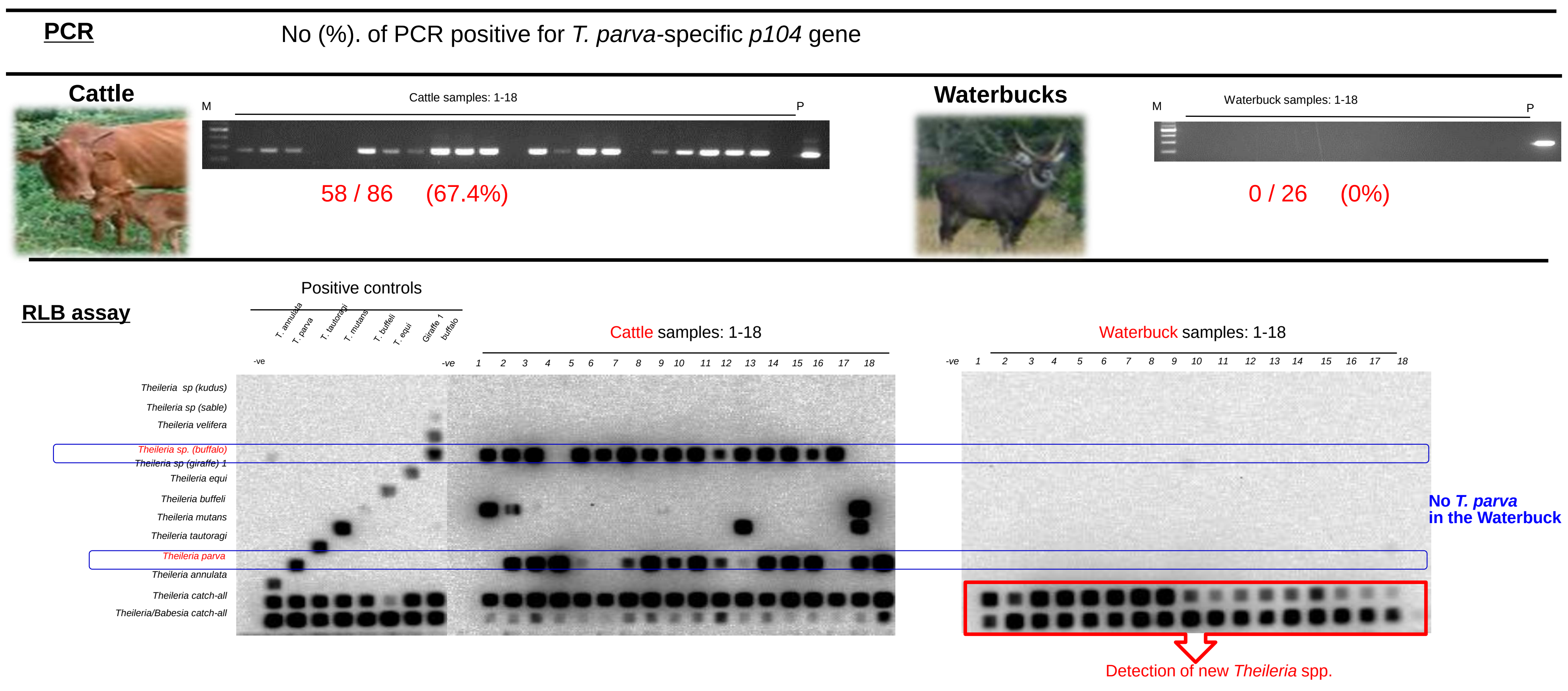
- **Sampling sites:**
  Marula area (a *T. parva-endemic* area in Kenya)
- **Blood samples:**

Cattle (*n*=86)

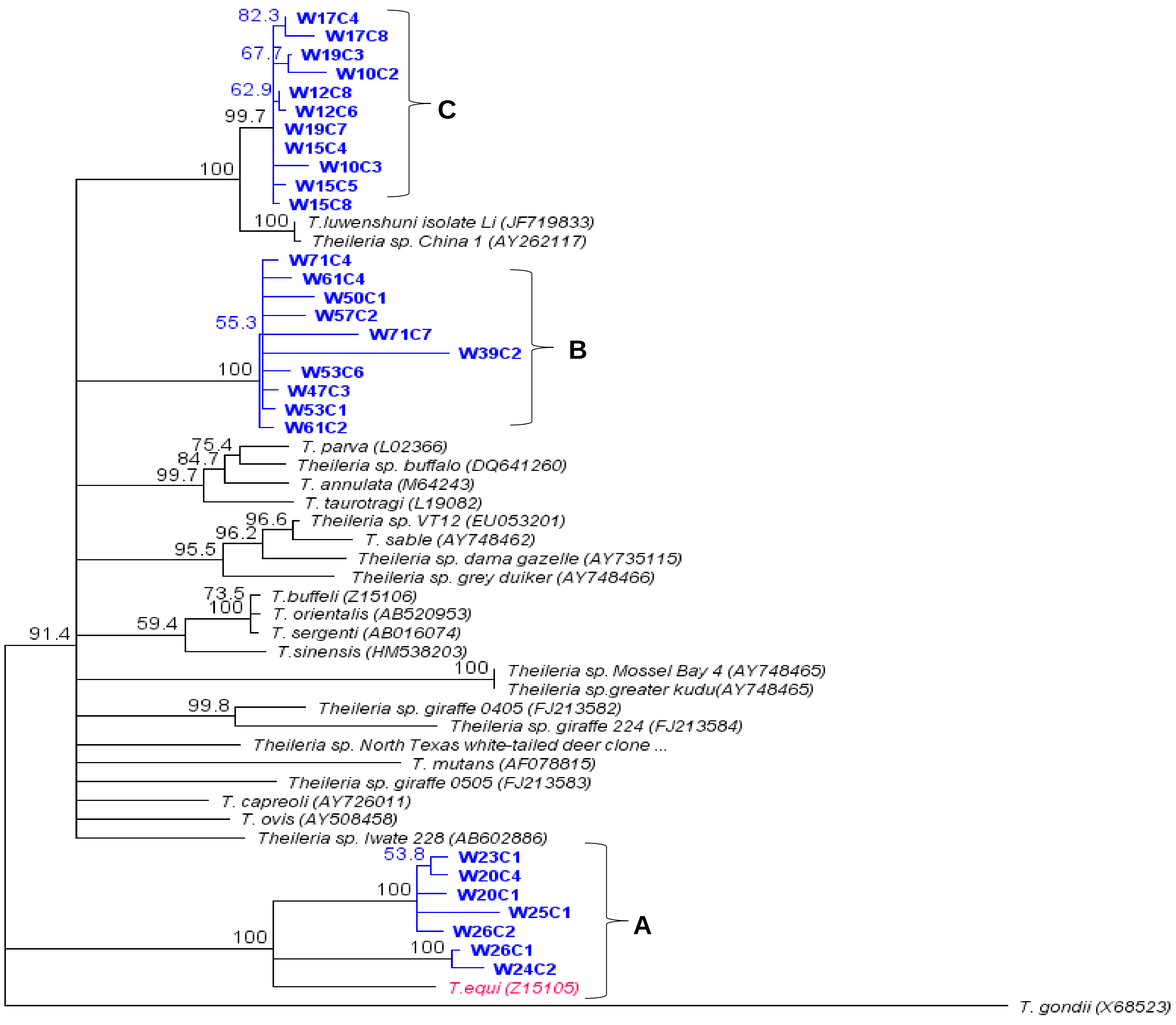
Waterbucks (*n*=26)

- **Detection of parasites:**
  1) A nested PCR assay targeting a highly conserved region of *T. parva* single copy gene <u>p104</u>
  2) **R**everse **L**ine **B**lot (using oligo probes for all *Theileria* species so far described in livestock and wildlife in Kenya)
- **Genetic analysis**
  Cloning and sequencing of the <u>18S rRNA</u> and ITS gene markers

Results



- ***T. parva* and *Theileria* sp (buffalo) detected in the cattle but not waterbuck samples.**
- **Phylogenetic analysis of the 18S rRNA and ITS sequences within the RLB-positive waterbuck samples revealed the occurrence of three *Theileria* genotypes of unknown identity:**
- **Group A clustered with *Theileria equi*, a pathogenic *Theileria* species infective to domestic equids. Group B parasites clustered closely with *Theileria luwenshuni* while Group C was closely related to *Theileria ovis* that is infective to sheep.**



Conclusion and significance of the findings

The results from this investigation provided no evidence that waterbuck plays a role in the transmission of *T. parva*. However, the finding of novel *Theileria* types, genetically related to pathogenic species occurring in both equids and small ruminants is an unexpected result and worthy of further investigation. The finding of a *T. equi*-like parasite in a non-equid host species is of interest since recent data suggests that *T. equi* occupies an intermediate phylogenetic position with respect to *Theileria* and *Babesia* (Kappmeyer et al., 2012).

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