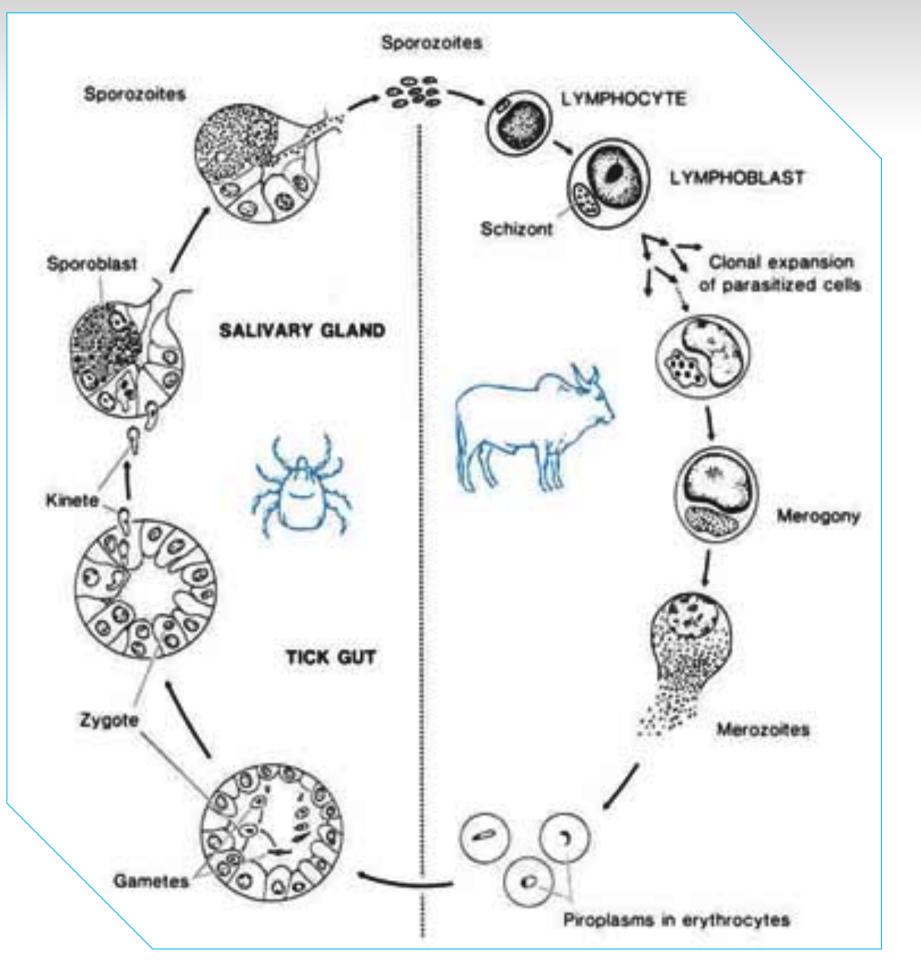
# Relative fitness contribution of BoLA alleles in *T.parva* immune cattle: Interface with parasite genetic diversity

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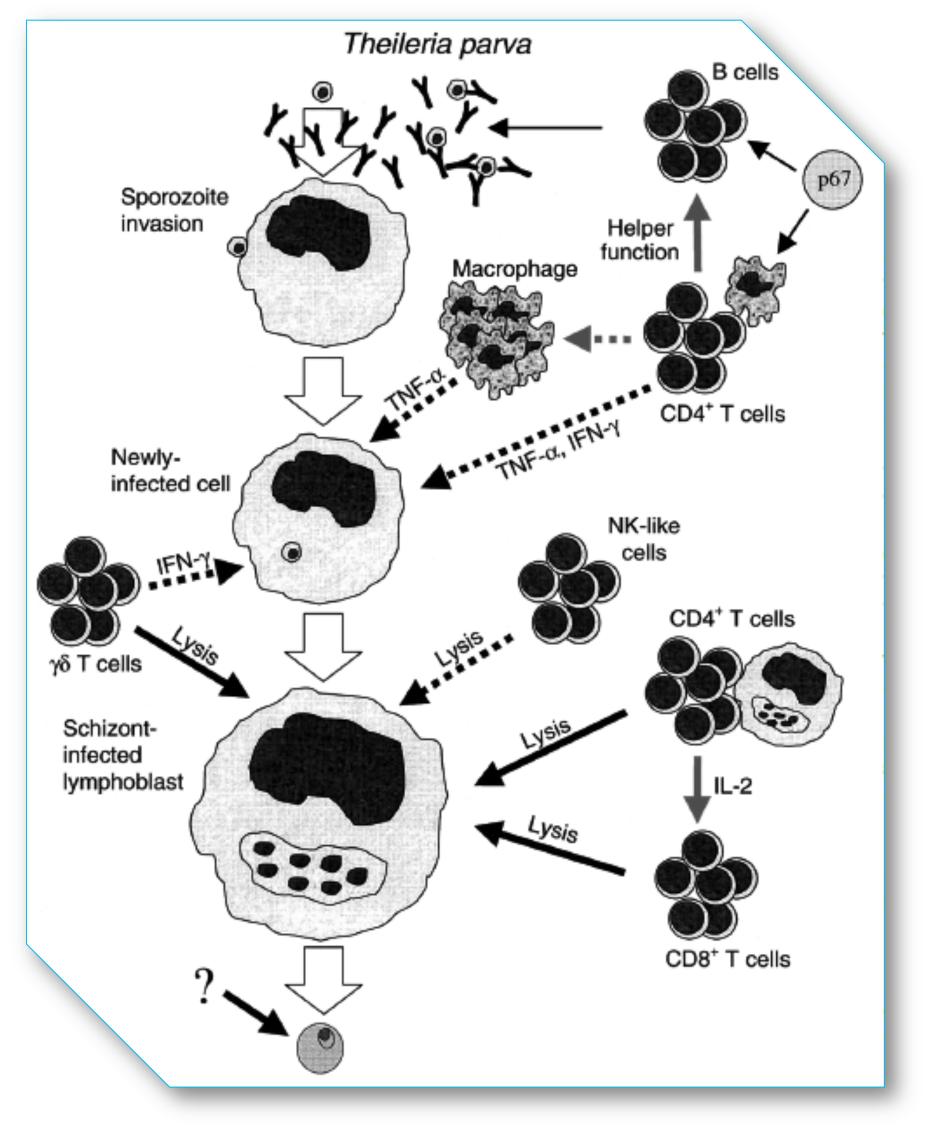
#### Introduction

East Coast Fever is a tick-borne parasitic leukosis of cattle caused by Theileria parva and transmitted by Rhipicephalus appendiculatus ticks. ECF is endemic in eastern, central and southern Africa with substantial economic impact

### **Objectives**

Establish if allelic diversity at the extensively polymorphic and principal expressed MHC class II DRB3 locus plays a role in determining variation in protection against T. parva challenge with the polymorphic 67 KDa major sporozoite p67 antigen

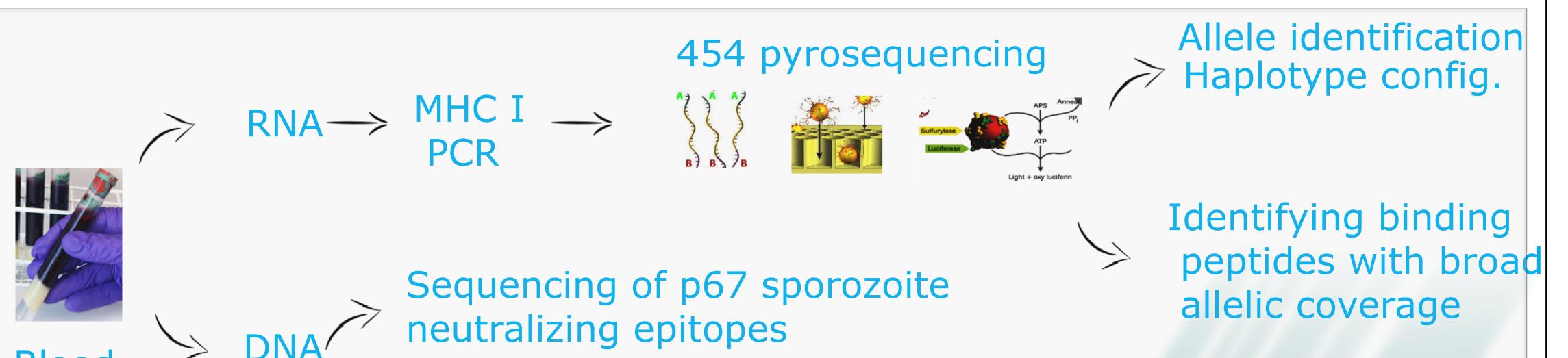
### T. parva life cycle



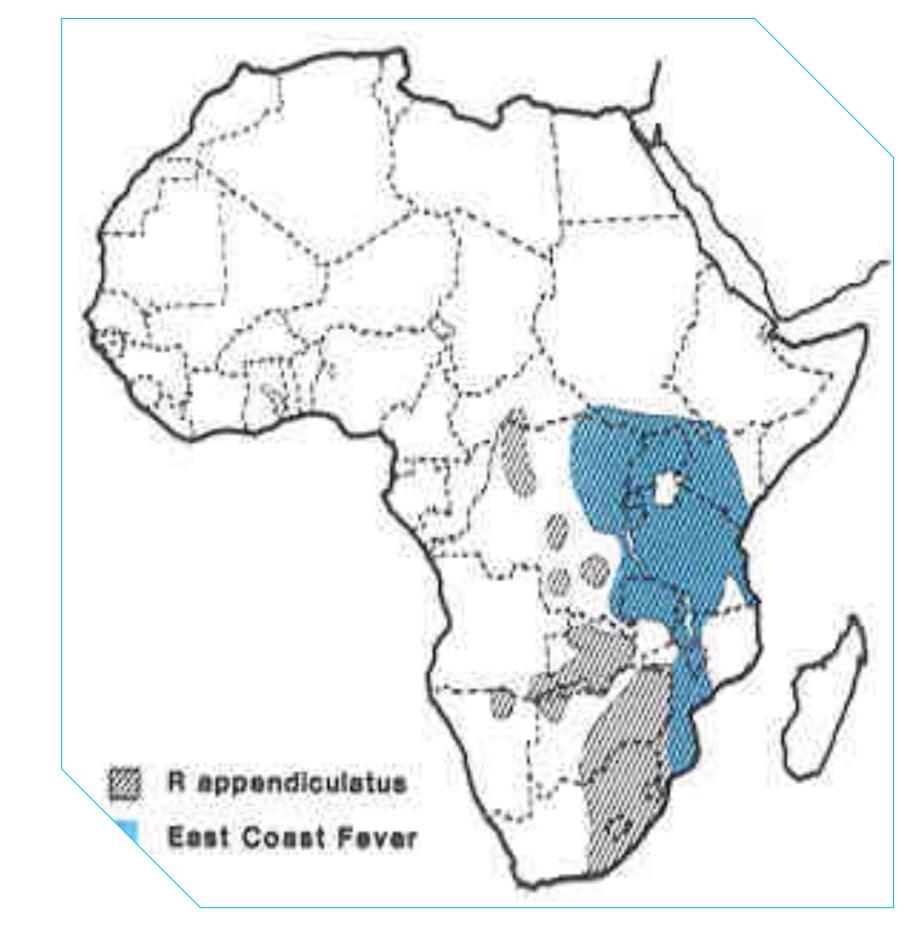
Identify and quantitate both known and novel BoLA class I allelic variants in cattle populations of different genetic compositions by simultaneous ultra deep amplicon pyrosequencing

Establish the hierarchy of dominance in the capacity of individual MHC class I specificities as restricting elements for T parva specific CTLs and predict the binding specificities of the expressed BoLA class I alleles

# Methods



# *T. parva* immunity



#### > DNA'

Sequencing of the extensively polymorphic and principal expressed MHC class II DRB3

# Results

Blood

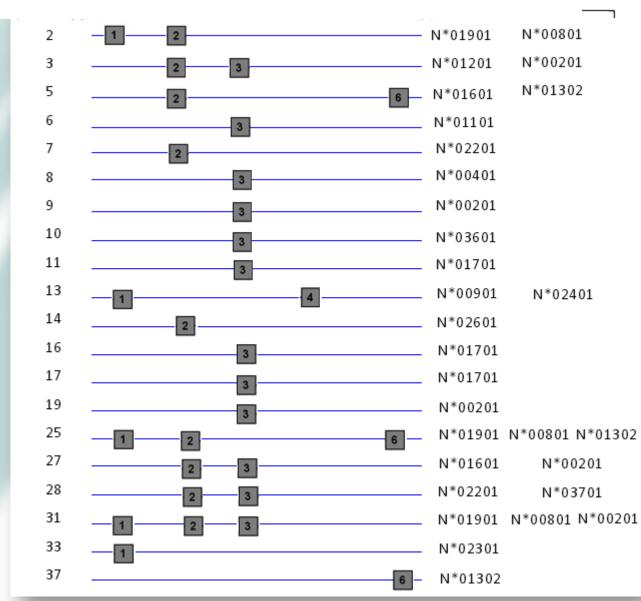
Characterization of the bovine MHC class I locus: variable haplotype composition, interlocus recombination and novel alleles

Genes 1, 2 and 3 are equally polymorphic, under selection pressure and presumed to be functional. They can be used to predict a subset of peptides mediating cellular immunity, and providing broad allelic coverage

Additional MHC I sequences detected that cannot be assigned to any of the 6 putative classical class I I genes

## p67/MHC class II DRB3 genotyping

p67 allele 1 (129 bp deletion in the central region), and allele 2 (no deletion) identified in addition to novel alleles that have not been previously detected in East



### T. Parva distribution

# Conclusion

ala 19GRQIRFPEQEKNEDSTLSTDISP-TIPTPVSEEIITPTLQ	TQTKEEVPPASSSDSEQEDSEENGGDGLKNGRTDGKNGDAG STDSVTRPVPS-PGAPGIIIRELGNRAMETDIVQFLGRFKPKPRTYEGDTTNV
	TQTKEEVPPASSSDSEQEDSEENGGDGLKNGRTDGKNGDAG STDSVTRPVPS-PGAPGIIIRELGNRAMETDIVQFLGRFKPKPRTYEGDRTNV
	TQTKEEVPPASSSDSEQEDSEENGGGGLKNGRTDGKNGDAG STDSVTRPVPS-PGAPGIIIRELGNRAMETDIVQFLGRFKPEPRTYEGDRTNV
Marula_08 DNVKQQQDTKGNKSDSEQEKNEDSTLSTDISP-TIPTPVSEEIITPTLQ	TQTKEEVPPASSSDSEQEDSEENGGDGLKNGRTDGKNGDAG STDSVTRPVPS-PGAPGIIIRELGNRAMETDIVQFLGRFKPEPRTYEGDRTNV
Marula_10 DNVKQQQDTKGNKSDSEEE-NEDSTVSTDVSP-TIPTPVSEEIITPTLQ	ACTREEVPPASSSDSEQEDSEENGDNVLKNGRTDGKNGDAG PTDSLTRPVPS-PGAPGIIIRELGKKDKGYC
Marula_28 DNVKQQQDTKGNKSDSEEE-NEDSTVSTDVSP-TIPTPVSEEIITPTLQ	ACTKEEVPPASSSDSEQEDSEENGDNVLKNGRTDGKNGDAG PTDSLTRPVPS-PGAPGIIIRELGNRTMETDIVQFLGRFKPEPRTYEGDRTNV
Marula_07 DNVKQQQDTKGNKSDSEEE-NEDSTVSTDVSP-TIPTPVSEEIITPTLQ	ACTKEEVPPASSSDSEQEDSEENGDNVLKNGRTDGKNGDAG PTDSLTRPVPS-PGAPGIIVRELGNRTMETDIVQFLGRFKPEPRTYEGDRTNV
Marula_26 DNVKQQQDTKGNKSDSEEE-NEDSTVSTDVSPNHFLLQFSEEIITPTLQ	AQTKEEVPPASSSDSEQEDSEENGDNVLKNGRTDGKNGDAG PTDSLTRPVPS-PGAPGIIIRELGNRTMETDIVQFLGRFKPEPRTYEGDRTNV
Marula_11RTCKATARYKGNKSDSEEE-NEDSTVSTDVSP-TIPTPVSEEIITPTLQ	AQTKEEVPPASSSDSEQEDSEENGDNVLKNGRTDGKNGDAG PTDSLTRPVPS-PGAPGIIVRELGNRTMETDIVQFLGRFKPEPRTYEGDRTNV
Marula_12 SNSKILRETNQISEEE-NEDSTVSTDVSP-TIPTPVSEEIITPTLQ	AQTKEEVPPASSSDSEQEDSEENGDNVLKNGRTDGKNGDAG PTDSLTRPVPS-PGAPGIIIRELGNRAMETDIVQFLGRFKPEPRTYEGDRTNV
Marula_18LLLAQQILREQIRFQNKKKMETKIAPLVQISLRPFLLQYQKKLSHQLFK	hkrkkkfllqtsqikfrqtv3dseeedgdsslgtdernlkktlppgktstgettldqdlk viepkiglpgst3ApvptrppgSStdtrpAS5gp3ApGgpgLSSR5-GgtRStD
Marula 31 APQDIRETIQYPNKKESEVAP	TQTREEVPPADLSDQVPSNGSDSEEEDGDSSLGTDERNLKKTLPPGKTSTGETTSDQDLK VIEPKIGLPGSTSAPVPTRPPGSSTDTRPASSGPSAPGGPGSSSRS-GGTRSTD
Marula_04 -wFLQTTIPVQDNVKHSKILRETNQISEQEKNEDSTLSTDISP-TIPTPVSEEIITPTLQ	TQTREEVPPADLSDQVPSNGSDSEEEDGDSSLGTDERNLKKTLPPGKTSTGETTSDQDLK VIEPKIGLPGSTSAPVPTRPPGSSTDTRPASSGPSAPGGPGSSSR5-GGTRSTD
Marula 17GNKTDSEEENEDSTVSTDVSP-TIPTPVSEEIITPTLQ	AQTREEVPPADLSDQVPSNGSDSEEEDNKSTSSKDEKELKKTLQPGKTSTGETTSGQDLN VIEPKIGLPGSTSAPVPTRPPGSSTDTRPASSGPSAPGGPGSSSRS-GGTRSTD
Marula 25GKQTDSEEENEDSTVSTDVSP-TIPTPVSEEIITPTLQ	AQTREEVPPADLSDQVPSNGSDSEEEDNKSTSSKDEKELKKTLQPGKTSTGETTSGQDLN VIEPKIGLPGSTSAPVPTRPPGSSTDTRPASSGPSAPGGPGSSSRS-GGTRSTD
	AQTKEEVPPADLSDQVPSNGSDSEEEDNKSTSSKDEKELKKTLQPGKTSTGETTSGQDLN VIEPKIGLPGSTSAPVPTRPPGSSTDTRPASSGPSAPGGPGSSSRS-GGTRSTD
	AQTKEEVPPADLSDQVPSNGSDSEEEDNKSTSSKDEKELKKTLQPGKTSTGETTSGQDLN VIEPKIGLPGPPSAPVPS-PGAPGIIVRESGNRAMETDIVQFLGRFKPEPRAYEGERTNV
	AQTKEEVPPADLSDQVPSNGSDSEEEDNKSTSSKDEKELKKTLQPGKTSTGETTSGQDLN VIEPKIGLPGPPSAPVPS-PGAPGIIVRESGNRAMETDIVQFLGRFKPEPRAYEGERTNV AOTKEEVPPADLSDOVPSNGSDSEEEDGDSSLGTDERNLKKTLPPGKTSTGETTSDODLK VIEPKIGLPGSTSAPVPTRPPGSSTDTRPASSGPSAPGGPGSSSR5-GGTR5"
_ DIGDIN CONCERNED DEDEGIDARY DIFFERENCE THE	AQTKEEVPPADLSDQVP3NGSDSEEEDGDSSLGTDERNLKKTLPPGKTSTGETTSDQDLK VIEPKIGLPGSTSAPVPTRPPGSSTDTRPASSGPSAPGGPGSSSR5-GGTR5

A truly global analysis of immune responses to T. parva by simultaneous genotyping the multiple co-amplifying MHC class I loci, high throughput computational epitope searches, assessing the allelic diversity at the extensively polymorphic and principal expressed MHC class II DRB3 locus and the sporozoite neutralizing p67 antigen will support the rational development of vaccines based on subunit components of the parasite .





Follow-Up Conference "German-African Cooperation Projects in Infectology" Bonn, 28 – 30 June 2012

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