Potential Figures and Tables

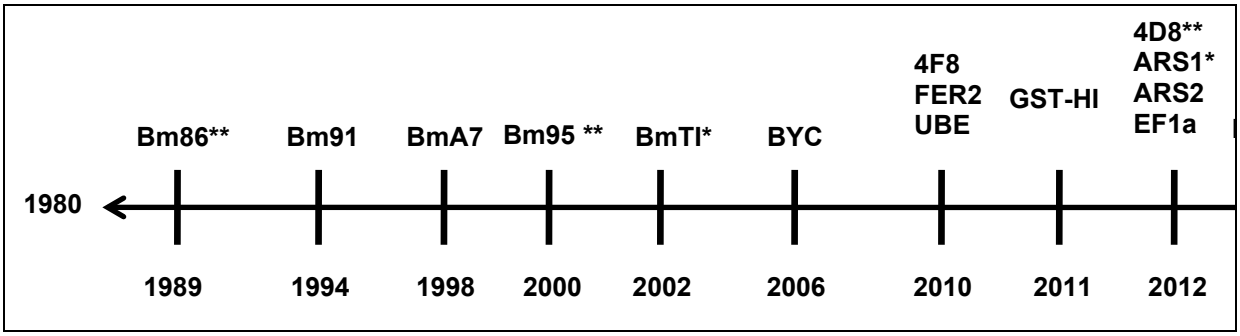

Figure 1. Timeline of cattle vaccination trials using available tick antigens for the cattle tick, *R. microplus*. Indicated are the current antigens and the first year when they were applied in cattle trials to assess protection against *R. microplus* infestations. Also indicated are antigens that showed a vaccine efficiency of >70% (*) and >80% (**), respectively. Not indicated are combinations of antigens that were also applied in trials.

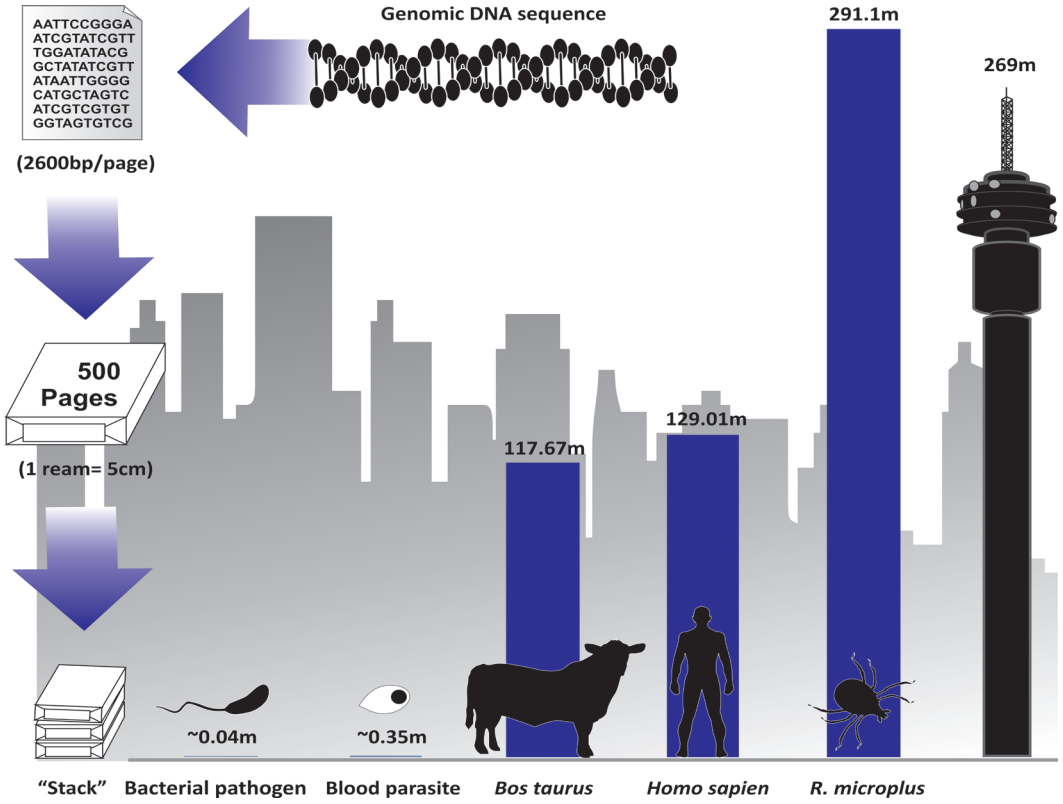

Figure 2. Comparisons of pathogen and host genome sizes to the parasite vector *R. microplus*. Indicated are the relative heights A4 ream (consisting of 500 pages) stacks if an organisms full genome sequence was typed on an A4 page with standard margins (New Times Roman, 12pt, all capitals). The genome "stack" of the cattle tick *R. microplus* is compared to that of its cattle host (*Bos taurus*) and the human (*Homo sapien*) genome. Also indicated are the relative sizes of bacterial pathogens such as *Anaplasma marginale* (causing Gallsickness) and *Ehrlichia ruminantium* (causing Heartwater), as well as blood parasites such as *Theileria parva* (causing East Coast fever/Corridor disease) and *Babesia bovis* (causing Redwater). The Hillbrow Tower in Johannesburg is considered the tallest structure in Africa at 269m

(http://en.wikipedia.org/wiki/Hillbrow_Tower) and has been added to this comparison for perspective. It is however eclipsed by the "stack" of the cattle tick genome in terms of height.

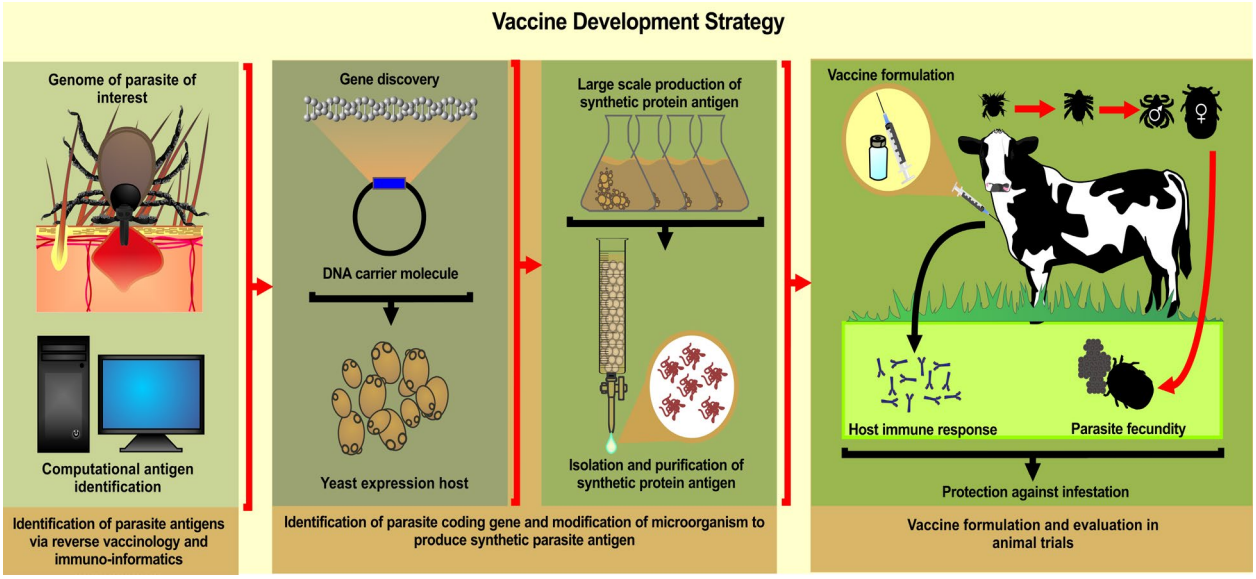

Figure 3. Vaccine development strategy. Utilizing genetic data available of the parasite of interest a set of potential parasite antigens can be identified using computational methods. Combining this data with other selection criteria such as biological relevance and molecular characteristics, a final set of genes are selected. These genes of interest are then are produced synthetically and used to modify a host microorganism (i.e. yeast) and produce the encoded protein synthetically in large-scale fermentation. The final synthetic parasite antigen is then purified and formulated into an injectable cocktail containing and adjuvant. The final step in vaccine development is evaluation of protection afforded against parasite infestation by the selected candidates in animal vaccination studies. These studies involve assessment of both host immunological responses, as well as the ability of the parasite to complete its life cycle and produce viable offspring.

Table 1. Pathogenic agents, possible reservoir hosts and vectors of zoonotic tick-borne diseases in Africa. Indicated are some of the most prominent tick-borne zoonotic diseases, their pathogens, vectors, reservoir hosts and distribution in Africa (adapted from Cutler et al., 2010; Gray et al., 2010; Esemu et al., 2011; Keshtkar-Jahromi et al., 2011 and Bitam, 2012).

Disease	Pathogen	Possible tick vectors (if any specific species were identified)[a]	Possible animal reservoirs[b]	Main distribution
Tick-borne rikettsiosis or African tick-bite fever	*Rickettsia africae*	*Amblyomma compressum; Amblyomma hebraeum; Amblyomma lepidum; Amblyomma variegatum; Hyalomma dromedarii; Hyalomma impeltatum; Rhipicephalus annulatus; Rhipicephalus decoloratus; Rhipicephalus evertsi evertsi; Rhipicephalus geigyi; Rhipicephalus sanguineus*	Ruminants such as cattle	Sub-Saharan Africa
Tick-borne borreliosis or tick-borne relapsing fever	*Borrelia spp.*	*Ornithodoros sp.*	Domestic poultry and suids, other mammals or rodents	Sub-Saharan Africa
Human monocytic ehrlichiosis	*Ehrlichia chaffeensis*	*Rhipicephalus sanguineus*	Wild and domestic dogs, domestic ruminants and rodents	Sub-Saharan and North Africa
Crimean-Congo hemorrhagic fever	*Nairovirus*	*Hyalomma marginatum rufipes; Hyalomma truncatum*	Wild and domestic animals such as cattle, sheep, goats and poultry.	Sub-Saharan Africa
Human babesiosis	*Babesia spp.*	Unknown	Ruminants such as cattle and rodents	South Africa, Egypt
Rift Valley fever	*Rift Valley fever virus (RVFV)*	*Amblyomma variegatum; Rhipicephalus appediculatus*	Domestic ruminants such as cattle, sheep and goats, as well as camels	Sub-Saharan and North Africa

[a.] Additional vectors might be present that have not been indicated

[b.] Some reservoir animals are assumed based on North American and European known reservoir animals.

Table 2. Pathogenic agents and vectors of tick-borne diseases affecting cattle in Africa. Indicated are some of the most prominent tick-borne diseases, the pathogens, vectors and distribution that affect cattle in Africa (adapted from Walker *et al.*, 2003; Jongejan and Uilenberg, 2004 and Marcelino *et al.*, 2012).

Disease	Pathogen	Principal tick vector(s)	Main distribution
Tropical theileriosis	*Theileria annulata*	*Hyalomma anatolicum anatolicum; Hyalomma detritum*	Northern Africa and Sudan
East Coast fever/ Corridor disease	*Theileria parva*	*Rhipicephalus appendiculatus; Rhipicephalus zambeziensis*	Eastern, central and southern Africa
Tropical bovine babesiosis, Redwater	*Babesia bovis*	*Rhipicephalus microplus; Rhipicephalus annulatus; Rhipicephalus geigyi; Rhipicephalus bursa*	Most tropical and subtropical regions, including Sub-Saharan Africa
Tropical bovine babesiosis, Redwater	*Babesia bigemina*	*Rhipicephalus microplus; Rhipicephalus decoloratus; Rhipicephalus annulatus; Rhipicephalus bursa; Rhipicephalus evertsi evertsi*	Most tropical and subtropical regions, including Sub-Saharan Africa
Malignant anaplasmosis, Gallsickness	*Anaplasma marginale*	*Rhipicephalus microplus; Rhipicephalus decoloratus; Rhipicephalus annulatus; Rhipicephalus bursa; Rhipicephalus evertsi evertsi; Rhipicephalus simus*	Tropical and subtropical regions, including Sub-Saharan Africa and Mediterranean

Heartwater	*Ehrlichia ruminantium*	*Amblyomma astrion; Amblyomma gemma; Amblyomma hebraeum; Amblyomma lepidum; Amblyomma marmoreum; Amblyomma pomposum; Amblyomma tholloni; Amblyomma variegatum*	Sub-Saharan Africa and Madagascar
Dermatophilosis or cutaneous streptothrichosis	*Dermatophilus congolensis*	*Amblyomma variegatum*	West Africa