Lack of evidence for safe vaccination with the Muguga cocktail in Sudan

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Dear Editor,

Referring to the article of Kivaria *et al*. (2012), 'Epidemiological perspectives of ticks and tick-borne diseases in South Sudan: Cross-sectional survey results', in your journal, we wish to comment on the statement made by the authors that the Muguga cocktail can be used for the immunisation of cattle in South Sudan.

This statement is mainly based on the molecular analysis of a genomic locus p104 of *Theileria parva*, which is known to have only two alleles in all cattle populations analysed so far. The Muguga cocktail is a multicomponent vaccine containing three dominant genotypes (Muguga - Kiambu and Serengeti transformed), covering the two-p104 cattle alleles. The unknown allele is probably an atypical amplification result, as the analysis was only based on Restricted Fragment Length Profiles. It is impossible to verify this, as no full amplicon lengths or sequence data are given.

The main concern is that characterisation using one single low-polymorphic locus is meaningless when making a statement about the possible use of a live vaccine. Even extended multi-locus characterisation data would only be able to assist in the isolation of dominant genotypes in an area surveyed for vaccine deployment. These isolates should then be used in cross-immunity tests in order to be sure that the vaccine will protect against circulating strains in that area. A potential danger is the fact that the vaccine stock(s) could cause a new epidemic if cross-protection from local strains is absent.

A second concern is that the epidemiological situation in South Sudan might be such that the diversity in the parasite population is low, as transmission intensity is low. This implicates that using a cocktail in such a situation would be very unwise if not based on cross-immunity data. But here again, it is difficult to collect meaningful data from the manuscript. The mean tick number per calf seems to be no more than five *Rhipicephalus appendiculatus*, indicating a low-grade challenge consistent with what is already known from the area. All other data seem to confirm an epidemic or unstable endemic situation.

There also seem to be differences between the various Sudanese States. The authors claim that the area has an overall *T. parva* prevalence of 27%. However, Table 5 clearly shows that the seroprevalence varies between 50% (Central Equatoria) and 6% (Lakes).

There is definitely a problem with advocating vaccination with a live vaccine in order to reduce mortality in the epidemic (6% – 27% seroconversion) or endemic unstable (50%) States. The choice to vaccinate in such areas using live vaccines (creating a carrier status as in *T. parva*) is a very difficult decision to make.

Furthermore, the approach in an epidemic or endemically unstable situation is completely different. Economics (cost of vaccines versus treatment versus vector control), frequency and seasonality of outbreaks, and mortality would be important parameters to consider further in the decision. In addition, there is no information available from South Sudan to come to a sound decision in this respect.

To conclude, we certainly do not agree with the conclusions put forward in this article, and the data presented here do not at all support the conclusions in the article.