

GENETIC DIVERSITY OF EHRLICHIA RUMINANTIUM IN MOZAMBIQUE

Laure Bournez^{1,2}, Nidia Cangi^{1,3,4}, Jonathan Gordon^{1,2}, Rosalie Aprelon^{1,2}, Valérie Pinarello^{1,2}, Thierry Lefrançois^{1,2}, Luís Neves^{3,5} & Nathalie Vachieri^{1,2}

1. CIRAD, UMR ASTRE, F-97170 Petit-Bourg, Guadeloupe, France
2. INRA, UMR ASTRE, F-34398 Montpellier, France
3. Centro de Biotecnologia-UEM, Eduardo Mondlane University, Av. de Moçambique, km 1.5, C.P. 257 Maputo, Mozambique.
4. Université des Antilles, F-97157 Pointe-à-Pitre, Guadeloupe, France
5. Department of Veterinary Tropical Diseases, University of Pretoria, Faculty of Veterinary Science P/Bag X04, Onderstepoort 0110, South Africa.

The tick species, *Amblyomma hebraeum* and *A. variegatum*, are the main vectors of Heartwater, a tropical infectious bacterial disease of ruminants caused by *Ehrlichia ruminantium*. In Mozambique, these tick species have a parapatric distribution, with *A. variegatum* present in the central and northern regions and *A. hebraeum* in the South. A narrow overlap area between the distributions of the two species occurs around parallel 22° south. In order to determine the prevalence of *E. ruminantium* in *A. hebraeum* and *A. variegatum* and to determine the genetic diversity and structure of isolates from different localities, adult ticks feeding on cattle and wild ruminants were sampled across the south and center of Mozambique as well as in the adjacent Kruger National Park (KNP), South Africa. The prevalence of *E. ruminantium* in *Amblyomma* ticks in relation to the tick species and gender, locality and tick abundance was analyzed. Afterwards, Mozambican *Ehrlichia* isolates were typed using Multi Locus Sequence Typing and the distribution of groups clustering genotypes were analysed. In total, 722 and 388 of *A. hebraeum* and *A. variegatum* ticks were collected from 31 localities and screened for *E. ruminantium*, using *pCS20* nested PCR and *Sol1*^{TqM} qPCR. The prevalence of *E. ruminantium* in ticks feeding on cattle varied from 0% to 26.7%, with no infected ticks determined in 7 localities. In ticks feeding on wild ruminants, the prevalence was 8.2 % in the KNP and 6.2% in hunting concessions of the Sofala province. After accounting for the effects of tick gender and sampling sites, no significant difference in prevalence was found between tick species. Most MLST genotypes from Mozambique clustered into subgroup 2C and 2E, which were present in similar proportions in 5 of the 19 localities. Interestingly, MLST genotypes from group G1 and G2D were exclusively found in areas of *A. variegatum* distribution, while

subgroup G2C was only detected in *A. hebraeum* areas. Moreover, genotypes from subgroup G2E were found in both *A. hebraeum* and *A. variegatum* areas. These results contribute to a better understanding of spatial distribution of *E. ruminantium* and will aid in improvement of heartwater monitoring and control strategies in Mozambique.