One Health
9th Tick and Tick-borne Pathogen Conference & 1st Asia Pacific Rickettsia Conference

Cairns, Queensland, Australia

27 August - 1 September 2017

POSTER PRESENTATIONS

(Abstract number order)
Ehrlichia ruminantium prevalence in ticks and its genetic diversity in Mozambique

POSTER SESSION 2

Nidia Cangi¹,², Laure Bournez¹,³, Jonathan Gordon¹,³, Rosalie Aprelon¹,³, Valérie Pinarello¹,³, Thierry Lefrançois¹,³, Luis Neves²,⁴, Nathalie Vachiery¹,³

¹CIRAD UMR ASTRE, F-97170 Petit-Bourg, France, ²Centro de Biotecnologia-UEM, Eduardo Mondlane University, Maputo, Mozambique, ³INRA UMR ASTRE, F-34398 Montpellier, France, ⁴Department of Veterinary Tropical Diseases, University of Pretoria, Faculty of Veterinary Science, Onderstepoort, South Africa

In order to determine the prevalence of E. ruminantium in A. hebraeum and variegatum and the E. ruminantium isolate structure in Mozambique, cattle and wildlife 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 relation to the tick species and locality was analyzed. Mozambican Ehrlichia isolates were typed using MLST 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™ qPCR. E. ruminantium tick prevalence in cattle varied from 0% to 26.7%, with no infected ticks determined in 7 localities. In wildlife, the prevalence was 8.2% in the KNP and 6.2% in hunting concessions of the Sofala province. However, no significant difference in prevalence was found between sampling sites and 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.