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**POSTER PRESENTATIONS**

**(Abstract number order)**

***Ehrlichia ruminantium* prevalence in ticks and its genetic diversity in Mozambique**

POSTER SESSION 2

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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*<sup>TqM</sup> 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.