



WAAVP

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Sifting and Winnowing the Evidence in Veterinary Parasitology



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Abstract Book

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E. ewingii nor *A. phagocytophilum* by both PCR assays. The cumulative incidence of *E. canis* infection was 38.46%. Sequencing analysis of the nested PCR products revealed 100% and 98.1% identity of *E. canis* and *R. parkeri*, respectively. We found a dog co-infected with *E. canis* and *R. parkeri*. It is concluded that high prevalence and incidence of *E. canis* in the dog population of Yucatan were detected and age (>3 years old) was the only factor associated with *E. canis* infection in dogs. This study presents the first report of a *R. parkeri* active infection in a domestic dog in the state of Yucatan, Mexico, presented as a co-infection with *E. canis*.

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PS02.63 Transcriptome Analysis of *Haemonchus Contortus* Infecting Goats from Breeds with Differing Resistance Levels

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Haemonchus contortus is the main small ruminant gastrointestinal parasite in tropical areas. Different host breeds present variable levels of overall resistance against these parasites. Moxotó goat breed is locally adapted to the Brazilian semi-arid and it is known for its resistance against these nematodes. Nevertheless, resistant animals still carry gastrointestinal nematodes but in lower numbers than the susceptible counterparts. In this study, parasite-free goats from two breeds (20 Moxotó and 5 Saanen) known to differ in resistance against nematodes (Moxotó > Saanen) were experimentally infected every two weeks with the same *H. contortus* population for

six months. At the end of this period the animals were euthanized, adult *H. contortus* were collected, counted and stored for RNA extraction. Adult parasite counts were consistently lower on Moxotó goats with the exception of 4 animals that had counts similar to Saanen goats. Total RNA was extracted from pools of 20 adult male *H. contortus* from the three most resistant ($\bar{x}=243\pm70$ parasites) and susceptible Moxotó goats ($\bar{x}=1,981\pm445$ parasites) and from three Saanen goats ($\bar{x}=2,511\pm549$ parasites). RNASeq was done on these samples with 718 million paired reads generated (160 bases long) by Illumina sequencing. The paired-end reads were splice-aligned to the *H. contortus* assembled genome (PRJEB506) using HISAT2 and assembled in 32,460 genes by StringTie. Using Ballgown, 220 genes were determined to be differentially expressed among the treatments and were blasted in order to determine their identities. These results are currently under analysis and we expect to shed some light on the mechanisms related to parasite survival in hosts of different resistance levels.

PS02.64 Cytokine Expression in Calves Experimentally Infected with Two *Theileria Parva* Stocks

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Cytokines play a vital role in the immunity and immunopathogenesis of parasitic diseases. However, most of the studies on the role of cytokines in infection by the tick-transmitted protozoan parasite *Theileria parva*, were performed in in vitro cell lines. Furthermore, there are no comparative studies for different stocks of *T. parva* even though cattle theileriosis caused by *T. parva* manifests in different disease syndromes (East Coast fever and Corridor disease), depending on whether the parasite strain is cattle-derived or buffalo-derived. Hence, an in vivo study was performed to investigate the expression