

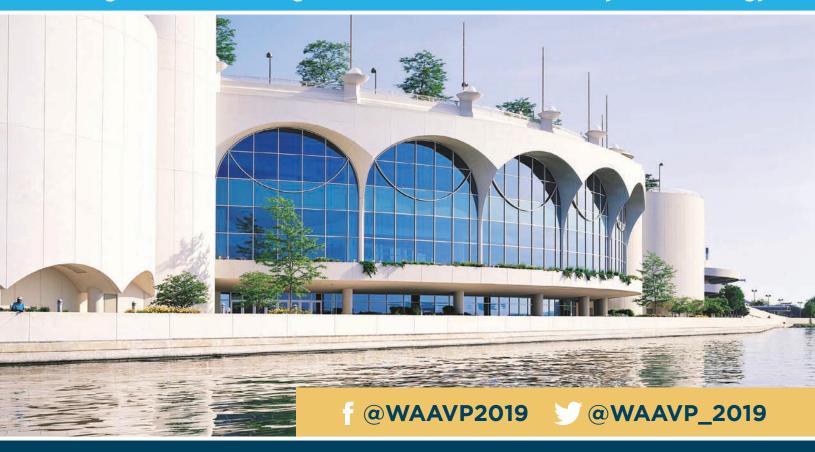
## WAAUP

27<sup>th</sup> Conference of the World Association for the Advancement of Veterinary Parasitology

**JULY 7 - 11, 2019 | MADISON, WI, USA** 

Dedicated to the legacy of Professor Arlie C. Todd

## Sifting and Winnowing the Evidence in Veterinary Parasitology



## Abstract Book

Joint meeting with the 64<sup>th</sup> American Association of Veterinary Parasitologists Annual Meeting & the 63<sup>rd</sup> Annual Livestock Insect Workers Conference

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**OA18** Leishmania

Resistance I

in the Punjab province of Pakistan. First, we examined the dihydrofolate reductase locus in 38 P. vivax isolates to look for evidence of positive selection pressure in human patients. The S58R (AGA)/S117N (AAC) double mutation was most common, being detected in 10/38 isolates. Single mutation S117N (AAC), I173L (CTT) and S58R (AGA) SNPs were detected in 8/38, 2/38 and 1/38 isolates, respectively. The F57L/I (TTA/ATA) and T61M (ATG) SNPs were not detected in any isolates examined. Although both soft and hard selective sweeps have occurred with striking differences between isolates, there was a predominance of hard sweeps. A single resistance haplotype was present at high frequency in 9/14 isolates, providing a strong evidence for single emergence of resistance by the single mutation, characteristics of hard selective sweeps. In contrast, 5/14 isolates carried multiple resistance haplotypes at high frequencies, providing an evidence of the emergence of resistance by recurrent mutations, characteristics of soft selective sweeps. Our phylogenetic relationship analysis suggests that S58R (AGA)/S117N (AAC) and S117N (AAC) mutations arose multiple times from a single origin and spread to multiple different cities in the Punjab province through gene flow. Interestingly, the I173L (CTT) mutation was present on a single haplotype, suggesting that it arises rarely and has not spread between cities. Our work shows the need for responsible use of existing and new antimicrobial drugs and their combinations, control the movement of infected patients and mosquito control strategies.

PSO1.78 Transcriptomic Analysis of ABC-Transporters (P-GP, MRP and HAF) in Haemonchus Contortus Isolates With Different Susceptibility to IVM

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Inadequate and intensive use of anthelmintic compounds has led to the emergence of high

levels of parasite resistance in nematodes of sheep. Changes in drug target sites and the up-regulation of detoxification systems seem to be implicated in this phenomenon. Several studies have shown that ATP-binding-cassette (ABC) transporters such as P-glycoprotein (P-gp) play an important role in multidrug resistance in many organisms, including several nematode species. The goals of the current work were: 1) to compare the gene expression of several cellular transporters in both a susceptible (S-IVM) and a highly ivermectin (IVM)-resistant Haemonchus contortus isolate (HR-IVM); 2) to assess the effect of IVM on ABC transporters expression patterns in the HR-IVM isolate under in vivo conditions. To this end, the transcriptional levels of ABC transporters in adult HR-IVM H. contortus recovered from IVM-treated lambs (2 mg/kg) at 12 and 24 hours post-treatment, were compared to those obtained from the S-IVM and HR-IVM specimens collected from untreated lambs. The phylogenetic tree with the transporter sequences of the reference nematode Caenorabditis elegans and H. contortus allowed us to found the putative orthologous genes P-gp 1, 2, 3, 9.1, 10, 11, 13, 16 and 17; MRP 3, 4, 7 and 8; and Haf 2, 3, 4, 6 and 9. Next generation sequencing analysis showed that both H. contortus isolates express 6 of the 9 P-gps, 3 of the 5 multidrug resistant proteins (MRPs) and 4 of the 5 Half (HAF) transporter genes. Some of these ABC transporter genes are differentially expressed in the S and HR isolates. IVM treatment induced slight changes in the mRNA levels of MRP-4 and P-gp transporters, but the biological significance of the observed changes may not be enough to explain the high level of IVM resistance displayed by the isolate under study in the current trial.

PS01.79 Sheep, Strongyles and Sequencing: Investigating Ivermectin Resistance in UK Field Populations

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