treatment indicates that both avermectins removed adult but not immature populations present at time of treatment. Pooled fecals collected one month after treatment revealed Cooperia, Ostertagia and Haemonchus were the predominant genera in the avermectin groups. Insufficient larvae were present in the Safe-Guard group to conduct a differential count. During the previous five years Ivomec or Dectomax pour-on had routinely been given to calves at weaning. This treatment history and the reduced efficacy measured on day 14 post-treatment indicate the possibility that selection occurred on this farm for avermectin resistant nematodes. Cattle anthelmintics should be evaluated periodically using fecal egg counts at and 14 days after deworming; when animal performance is questionable this method (FECRT) can determine if anthelmintic resistance is involved.

45

Validation of genomic regions influencing nematode resistance in a *Bos taurus* X *Bos indicus* cross population.

MAGDA V. BENAVIDES, FLAVIO A. M ECHEVARRIA, TAD S. SONSTEGARD, CURTIS P. VAN TASSELL, L.C. GASBARRE*. BOVINE FUNCTIONAL GENOMICS LABORATORY, USDA, ARS, BELTSVIILE, MD.

A study was performed using 230 Brazilian Brangus cattle (5/8 Aberdeen Angus + 3/8 Nelore) which were exposed to natural challenge of gastrointestinal (GI) parasites. Animals at 12, 18, and 24 months of age were kept under extensive grazing conditions on naturally contaminated pastures during the spring and summer at the Embrapa Southern Brazilian Sheep & Cattle Research Centre in Bage, RS, Brazil (31.3oS 54.1oW). The predominant parasite genera were *Haemonchus*, *Ostertagia*, *Trichostrongylus* and *Cooperia* spp in the younger animals, while in the adult cattle *Haemonchus*, *Ostertagia* and *Oesophagostomun* were most prevalent. DNA from these animals was used to generate microsatellite marker genotypes for association analyses between egg counts (EPG) and genomic regions on six bovine chromosomes previously identified . These regions were selected because previous work at the USDA, ARS in Beltsville, MD had shown to contain quantitative trait loci (QTL) associated with nematode resistance. Marker genotypes for 12 microsatellite loci were amplified by multiplexing and analyzed by fragment analysis using a ABI 3730 Sequencer. Statistical analyses were performed on a set of 91 progeny from four sires. The results showed that the average logEPG (logEPG+25) was significantly different for the BM8124 microsatellite marker ($P=0.045$) on BTA6. Year of birth, birth season and sex were significant fixed effects ($P<0.001$) for this trait. This result confirmed at least one of the parasite resistance QTL detected in earlier studies in the herd at Bage. The genetic composition of these cattle (i.e. a *Bos taurus* X *Bos indicus* cross) combined with the different parasite transmission conditions in southern Brazil makes this chromosomal region attractive for further study into the basis of genetic resistance in cattle.