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Goat transcriptomics and gastrointestinal parasite resistance - Monteiro J.P.<sup>1\*</sup>, Zaros LG.<sup>2</sup>, Sider L.H.<sup>1</sup>, Teixeira M.<sup>1</sup>, Coutinho L.L.<sup>3</sup>, Vieira L.S.<sup>1</sup>

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Goat farming is an important socio-economic activity worldwide. Infections by antihelmintic resistant nematodes, such as Haemonchus contortus, is one of the major challenges currently facing this livestock sector. However, host resistance against nematode parasites varies widely among different individuals and breeds. Reports show that Saanen and Anglonubian goats are generally considered susceptible and resistant breeds, respectively. Third generation crossbred individuals (Saanen x Anglo-nubians) were used in a transcriptomic approach for the identification of genes and SNPs associated with resistance against gastrointestinal nematodes. Animals were treated with anthelmintics, kept on contaminated grasslands and characterized using weekly fecal egg counts (FEC). Once the mean FEC for the entire group reached 800, the ten most resistant and susceptible animals were identified and treated one more time. Both resistant and susceptible animals were subject to a second natural challenge and abomasal tissue samples were collected from euthanatized animals. High quality RNA samples were obtained and are being subject to RNA-Seq using a HiScan SQ (Illumina). The data is currently being prepared for assembly and analysis using Bioinformatics tools such as Trinity, Velvet-Oases and the BLAST algorithm. This work will result in differentially expressed genes and SNPs associated with both conditions and will contribute to the understanding of the host response to nematode infection. Results may also be used as markers for animal breeding programs.

Key-words: goats, gastrointestinal parasites, transcriptome

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