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Many studies have demonstrated that the genome of the parasitic nematode, Haemonchus contortus, undergoes large scale genome rearrangements as a consequence of the parasite's obligatory requirement for large volumes of host blood. During gonotoxic treatment of the juvenile host, a large proportion of the parasites arrest development and eventually undergo apoptosis, apparently releasing transcriptionally competent parasites. In order to facilitate the identification of genes expressed during the development of H. contortus, the nematodes were treated with the monoamine oxidase inhibitor, isometamidium chloride (ISM) to induce apoptosis. The ISM-induced transcriptome was generated using the SOLiD platform and reads were mapped to the H. contortus genome. The combined transcriptome and proteome data sets were analyzed by sequence similarity searches, a gene ontology (GO) classification of the encoded proteins, and a comparative analysis of the H. contortus and Caenorhabditis elegans genomes. Approximately 1.6 million expressed sequence tags (ESTs) were generated from the ISM-induced H. contortus. The combined transcriptome and proteome data sets were found to encompass 990 unique transcripts, 831 proteins, and 73,842 unique peptides. Protein-protein interactions (PPIs) were identified in the predicted interactome that were mapped to predicted PPI networks in other nematodes (such as C. elegans) and genes encoding for potential drug targets were identified. The H. contortus genome provides an excellent starting point for

functional studies of genes involved in the regulation of parasite development during host infection. PMID:22940960 5ec8ef588b

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