

The abstract from the paper is included below:

The human and canine parasitic nematode *Strongyloides stercoralis* utilizes an XX/XO sex determination system, with parasitic females reproducing by mitotic parthenogenesis and free-living males and females reproducing sexually. However, the genes controlling *S. stercoralis* sex determination and male development are unknown. We observed precocious development of rhabditiform males in permissive hosts treated with corticosteroids, suggesting that steroid hormones can regulate male development. To examine differences in transcript abundance between free-living adult males and other developmental stages, we utilized RNA-Seq. We found two clusters of *S. stercoralis*-specific genes encoding predicted transmembrane proteins that are only expressed in free-living males. We additionally identified homologs of several genes important for sex determination in *Caenorhabditis* species, including *mab-3*, *tra-1*, *fem-2*, and *sex-1*, which may have similar functions. However, we identified three paralogs of *gld-1*; *Ss-qki-1* transcripts were highly abundant in adult males, while *Ss-qki-2* and *Ss-qki-3* transcripts were highly abundant in adult females. We also identified paralogs of pumilio domain-containing proteins with sex-specific transcripts. Intriguingly, *her-1* appears to have been lost in several parasite lineages, and we were unable to identify homologs of *tra-2* outside of *Caenorhabditis* species. Together, our data suggest that different mechanisms control male development in *S. stercoralis* and *Caenorhabditis* species.

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