Deciphering gonad-transcriptomes in *Schistosoma mansoni* provides novel and exploitable insights for basic and applied research

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As one of the exceptional biological features of schistosomes, the adult female achieves sexual maturation only if it is constantly paired with the male. Although the male is sexually mature before pairing, it is assumed that the male-female interaction of schistosomes is a bidirectional process. However, not much is known about the complexity of pairing-dependent gene expression, especially with respect to the gonads. Based on a recently established isolation approach for complete reproductive organs, we performed comparative transcriptomics with RNA of ovaries and testes from both paired and unpaired adult *S. mansoni*. By RNA-seq we identified transcripts of >7,000 genes in the gonads of both sexes. Although transcript levels of the majority of these genes (>4,000) were pairing-unaffected in both gonads, transcripts of 243 (testes) and 3,600 (ovaries) genes occurred pairing-dependently. Among these, 309 and 42 differentially transcribed genes showed ovary-specific and testis-specific transcriptional activity, respectively.

Detailed bioinformatics analyses provided new insight into the role of the *S. mansoni* kinome, which consists of 357 kinases. Of these 268 protein kinases (pks) and 83 non-protein kinases (non-pks) are transcribed in adult *S. mansoni*. Remarkably, many of the adult-stage pk and non-pk genes exhibited a pairing-dependent and gonad-preferential transcript occurrence. This highlights the importance of kinases in the reproductive development of this parasite. In schistosomes GPCRs represent the largest receptor family comprising 115 receptors in *S. mansoni*. Of these 60% are transcribed in adults, covering all classes of the phylogenetic analyses. Furthermore, we obtained new insights into the potential roles of GPCRs in the male-female interaction, including participation in both gonad-specific functions, and in gonad-unrelated, pairing-dependent processes. Finally, a first GPCR-selective *in silico* comparison to *Fasciola* genome data revealed a high congruence between both GPCR*omes*.

Importantly, kinases and GPCRs represent interesting molecules as they are potentially druggable targets. New targets are urgently needed in the face of drug resistance and an alarmingly limited repertoire of available drugs to fight schistosomes and other parasitic worms. Therefore, the work reported here has relevance for both basic and applied parasitology research.