The potential role of transposable elements in the development of Schistosoma mansoni

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Abstract

With the completion of a high quality genome for the human parasite Schistosoma mansoni, we have performed a thorough identification and annotation of transposable elements (TEs) within this non-model species. By manually curating the data, a library of 81 TE families was produced where we not only discovered novel families, but also redefined previously existing ones. As observed, we did not find any new class II elements apart from the three that were already described. The most recent expansion is observed in LINE and PLE elements, while LTR elements had an earlier expansion which has now decreased.
A structural analysis showed a concordant distribution among the different chromosomes, except for the sex specific part of the sexual chromosomes, with an accumulation in subtelomeric regions. Interestingly, we found TEs are as frequently present in intergenic regions as in gene bodies, where they are preferentially inserted in introns showing an increasing frequency towards the end of the gene.

Analysing expression of TEs along the life cycle, we observe different patterns that characterize each stage, including all Penelope elements being strongly expressed in the miracidia stage. We are currently investigating if the expression correlates with gene expression that correlates with the metabolic processes specific for each stage.
We also looked at differential expression in paired and unpaired adults. In males, we observe different families being expressed, but these changes remain moderate. When looking at paired versus unpaired females, we observe a drastic increase in expression of the majority of the TE families. This is significant as females undergo sexual maturation when paired and might indicate a possible role in the processes controlling sexual maturation in Schistosoma.

Keywords: Transposable element, expression, development, parasite

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