

Abstract

Some species of parasites, including helminths, can inhibit carcinogenesis in their hosts. The antitumoral effect has been discovered in the tapeworms *Taenia crassiceps* and *Echinococcus granulosus*, which genes associated with cancer regression have been identified. The effect of melanoma suppression has also been observed in tapeworm *Mesocestoides corti* by the Laboratory of Helminthology, Department of Parasitology, Faculty of Science, Charles University, however the mechanism-of-action, remains unknown. For the upcoming research it was essential to have the complex molecular data such as transcriptome of the developmental stages of *M. corti*. This work is focused on the transcriptomic profiling of the tapeworm *M. corti* and the differential gene expression in two different strains of murine hosts (inbred and outbred) using the RNA-Seq. The main goal was to identify upregulated transcripts in the tapeworms from the murine hosts that could have a potential effect on cancer regression. Differential gene expression analysis was performed, and the results showed that tapeworms in murine hosts (regardless of strain) had more upregulated transcripts than tapeworms cultured *in vitro*. Analysis of highly upregulated transcripts in the tapeworms that were grown in the murine hosts identified several transcripts that have been previously described as potential tumor suppressors. Some of these proteins/genes include: KATNA1, PTPRJ, ZC3H14 and CD148. On the other hand, in *in vitro* cultured tapeworms, the most upregulated pathways are related to cellular, environmental, and genetic processes. Studying of the anticancer effect of tapeworms and understanding the molecular mechanisms could significantly help in further research of the cancer treatment.

Keywords: transcriptome, differential gene expression, cancer, bioinformatics analysis, tapeworm, *Mesocestoides corti*