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Insight into the *Hymenolepis diminuta* lifecycle and its adaptation to parasitism by comparative proteomic analysis of larval and adult stages.

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Cestodiasis are common parasitic diseases of animals and humans. As cestodes have complex life-cycles their larvae and adults produce proteins allowing them to establish the invasion (cysticercoids), and survive in the hostile environment of the host (adults). *Hymenolepis diminuta* is the most commonly used model organism in experimental cestodology. The aim of the present study was to perform comparative proteomic analysis of two consecutive developmental stages of *H. diminuta* (cysticercoid, adult) and find out which proteins are stage specific and which are exclusive. This should reveal the mystery of the evolutionary success of tapeworms. Somatic proteins of *H. diminuta* were isolated from six-week cysticercoids and adult tapeworms, obtained respectively from the beetle *Tribolium castaneum* and experimentally infected rats. LC-MS/MS identified proteins were classified according to molecular function, cellular components and biological processes. Our study showed a number of differences in the protein profiles of cysticercoids and adults. We identified 284 cysticercoid and 232 adult proteins, among them 149 were specific for the cysticercoid and 97 were present exclusively in the adult. Both developmental stages share 135 proteins. Proteins were divided according to their scientific significance into three groups: antigens, vaccine candidates and drug targets. Twenty-four of the common proteins are known as antigens, 14 represent vaccine candidates and 15 are drug targets. The results have new implications for understanding the biology of invasion, and cestode adaptations to a parasitic way of life. Moreover, these data may help to improve effectiveness of treatment, prevention and molecular diagnostics.

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