Proteomic analysis of *Hymenolepis diminuta* (Cestoda) cysticercoid larvae – an insight into the biology of invasion

Anna Sulima¹, Justyna Bień², Daniel Młocicki^{1,2}

¹Department of General Biology and Parasitology, Medical University of Warsaw, Warsaw, Poland ²W. Stefański Institute of Parasitology, Polish Academy of Sciences, Warsaw, Poland

Corresponding Author: Anna Sulima; e-mail: anna.sulima@wum.edu.pl

Hymenolepis diminuta may parasitize both animals (e.g. rats) and humans, and so is an important model in experimental parasitology. Despite *H. diminuta* being one of the best described parasites, many aspects of its biology, such as adaptations to parasitism and mechanisms involved in invasion, remain unknown. The aim of this study was to identify the key cysticercoid proteins in the process of invasion by using modern gelbased proteomic tools and mass spectrometry.

Cysticercoids were isolated from *Tribolium castaneum*. SDS-PAGE was used to separate and identify cysticercoid proteins. Two-dimensional gel electrophoresis (2DE) immunoblotting was used to verify which spots contained proteins reacting with antibodies from the sera of infected rats. LC-MS/MS analysis enabled identification of the cysticercoid proteins, including those with antigenic properties. The identified proteins were categorized according to their functions with the use of the UniProtKB database.

LC-MS/MS allowed 284 cysticercoid proteins to be identified, among which 149 are considered to be stage specific. These proteins were classified according to molecular function, cellular components and biological processes. They are predominantly associated with catalytic activity, metabolic and single organism processes. Gene ontology analyses revealed that they are associated with cells, organelles and macromolecular complexes. Additionally, cysticercoid proteins were subdivided according to their scientific significance into three groups: antigens, and vaccine and drug candidates. Antigenic proteins were associated with response to stress (HSP) and catalytic processes (MDH, GST, SOD), while some represent structural proteins (actin, myosin). Potential drug targets include 14-3-3P, CBP, PyK and HSP90, whereas vaccine candidates include calpain, filamin and SOD.

Our results are essential for understanding the molecular foundations of the function of parasites within the host. As many of the identified proteins have antigenic properties and are engaged in host-parasite interactions, the present study provides an important insight into the biology of invasion and sheds more light on the adaptations of cestodes to parasitism. In addition, our data provides the knowledge necessary for experiments on new treatments, diagnostics and parasitic immunomodulation.

Funded by the National Science Centre Poland (grant number: 2012/05/B/NZ6/00769).