ABSTRACT

Anisakis simplex is a parasitic nematode that causes anisakiasis in humans. Consumption of fish containing live *A. simplex* larvae may pose a health risk because of their ability to penetrate the gastrointestinal mucosa, as may foods contaminated with parasite allergens, which can cause severe allergic reactions in humans. The increasing popularity of eating raw fish and the rapid increase in the population of this nematode, as well as the expansion of its range, are leading to an increase in the number of cases of anisakiasis. So far, the biology of this parasite does not seem to be fully understood. Therefore, it seems useful to thoroughly study the proteome of this nematode, as it has not been fully characterized so far, which may shed light on the molecular mechanisms of the parasite's growth and development, as well as host-parasite interactions.

The main objective of this study was to identify and characterize the proteome of the parasitic nematode *A. simplex* at global and tissue levels. As a result of the first experiment, the global proteomes of the two developmental stages, L3 and L4, of the *A. simplex* nematode were described. The most accurate and comprehensive proteome of this species was identified and characterized for the first time using ultra high-performance liquid chromatography coupled with high resolution tandem mass spectrometry (LC-MS/MS) and isobaric tandem mass tagging (TMT) of peptides for relative quantification of proteins. The second experiment sought to identify nematode proteins in the tissues responsible for host contact, i.e., intestine and cuticle. By using a similar proteomic workflow and complex analysis of proteomic data, comprehensive sets of proteins characteristic of the nematode tissues studied were identified.

The results on the global proteome and the tissue proteome of *A. simplex* may serve as a basis for the development of new drugs against anisakiasis and, in the future, alleviate the symptoms of this disease or eliminate it in humans.

Moreover, using quantitative TMT-based proteomics, the presented methodology can serve as a universal tool for the analysis of global proteome dynamics in the stages and tissues of parasitic nematodes.