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P0208 Application of proteomic methods (MALDI-TOF MS) for studying of protein profiles of *Ascaris lumbricoides* and *Ascaris suum*

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Background: Proteomic studies (identification of the pathogen based on the analysis of its protein spectrum) are a relatively new direction in the laboratory diagnosis of infectious diseases. Taking into account the experience of foreign scientists, we used the MALDI-TOFF MS method to study the protein profiles of one of the most common parasitic human disease - ascariasis. The purpose was to study the potential of proteomic analysis methods using the example of MALDI-TOFF MS for the taxonomic differentiation of ascariasis pathogens.

Materials/methods: The material for the study is based on the head ends of the five young, immature *A. lumbricoides*, and five *A. suum*, isolated from the intestines of human and pigs. To carry out MALDI-TOF MS analysis, the helminths were washed in a 0.9% NaCl solution with the addition of 100 units / ml of phenoxymethylpenicillin (penicillin V) and 100 µg / ml of streptomycin during 24 hours. Sample preparation of the material was carried out according to the unique author's method. Mass profiles of homogenized protein were obtained using Microflex LT MALDI-TOF MS (Bruker Daltonics) with Flex Control software (Bruker Daltonics), visualized using Flex analysis 3.3 software (Bruker Daltonics).

Results: Mass spectrometry analysis of ascaridate protein extracts showed spectra with high-intensity peaks in the 2-20kD range. The distribution of patterns and intensities of spectral (mass-passing) peaks with a similar mass was similar in all samples of the same type of ascaridate, which was proved by identical profiles when the mass spectrometry peak was superimposed on each other. However, when using Flex analysis, it is noted that the spectra profiles obtained from the ascaris *A.suum* and *A.lumbricoides* proteins differ in 5 out of 8 major peaks, which makes it possible to differentiate one type from another according to the protein profile.

Conclusions: The obtained results show the possibility of species differentiation of nematodes using the method of mass spectrometry. It can serve as an effective taxonomic tool in parasitological studies. Creating a library of mass spectrometric profiles of nematodes based on the MALDI Sepsityper Kit 50 will allow application of this method along with the "gold standard".