Abstract

Anisakis simplex is a parasitic nematode of marine mammals. Accidental consumption of *A. simplex* L3 larvae in raw or undercooked fish meat can cause gastrointestinal problems. The disease caused by these parasites is called anisakiasis, and more than 20 000 cases of this disease are diagnosed worldwide each year.

A. simplex larvae develop in anaerobic environments where carbohydrates serve as the primary source of energy. The direct effect of exogenous glucose on the L3 and L4 developmental stages of *A. simplex* has not yet been clarified. Further investigation of these issues may be crucial for understanding the biology of the parasite and identifying the mechanisms that enable its survival in the host organism.

The aim of the study was to identify differences and similarities in the transcriptome profile between the L3 and L4 stages of *A. simplex* in the presence of glucose at the whole-organism level and to determine the expression of genes related to saccharide transport in L3 and L4 larvae of *A. simplex* in response to the presence of glucose in the environment. Second-generation RNA-seq sequencing methods were used to profile the transcriptome of the whole organism, and nLC-MS/MS proteomic analysis was also performed. This is the first comprehensive multi-omic analysis investigating the effect of glucose on *A. simplex* in two developmental stages: L3 and L4. To characterize carbohydrate transport, an in silico protein analysis was performed, enabling the identification of genes regulated by glucose, followed by the examination of their expression in *A. simplex*.

The results of the study emphasise that in *A. simplex* the developmental stage has a greater impact on transcriptomic profiles than the effect of glucose alone. The differences observed between these stages, both in the global transcriptome profile obtained by second-generation sequencing methods and in the expression of glucose transporters, confirm different feeding strategies.