

It remains a mystery how a large number of soil species with potentially identical food niches can coexist. One hypothesis explaining this phenomenon (which somewhat contradicts the ecological theory of competition) assumes that there are undiscovered differences in resource utilization among species. Indeed, the trophic status of many groups of soil invertebrates remains uncertain or conceptual, as traditionally used research methods, such as direct observation of feeding behavior, gut content analysis, enzyme activity assays in whole body homogenates, cultivation on various nutrient sources, and food choice tests, typically provide only limited information about the feeding which is a complex process.

One of the challenges to be addressed in trophic ecology research is that, for many groups of mesofaunal animals, the significant contribution of the microbial enzymatic apparatus needs to be ruled out, as it may mask the animal's endogenous digestive capabilities. Furthermore, the situation could be even more complicated by the presence of previously unidentified cryptic complex species in many groups of invertebrates, as individual lineages (separate species) may differ from each other in specific ecological and physiological properties.

Potworms (Enchytraeidae) are a widely distributed family of small, mainly terrestrial, earthworm-like annelids (Annelida, Clitellata). They are engaged in many important soil processes, such as humification, soil structure formation, microbial activity stimulation, and 'microbes' dispersion. Although potworms play an important role in many ecosystems, their position in the soil food web is ambiguous. Similar to earthworms, it is generally believed that microorganisms (bacteria and fungi) play an essential role in potworm feeding, being an important source of enzymes, including cellulases. However, to date, none of the Enchytraeidae family members have been the subject of molecular studies to reveal their endogenous digestive capabilities.

The aim of this doctoral dissertation was to determine the trophic position of the white potworm (*Enchytraeus albidus*) based on information about its digestive capabilities obtained through both classical (e.g., RNA isolation, RT-PCR, and cloning) and modern molecular biology techniques (RNA-Seq). The obtained data were subjected to extensive bioinformatic analyses. The main part of the project involved the identification of transcripts of genes engaged in the production of digestive enzymes and the generation of a transcriptome for the PL-A strain (homogeneous in terms of mtDNA) of *E. albidus*. The obtained data were used to determine the trophic position of the studied species in the soil food web.

As a result of the conducted research, it was found that among a whole range of glycosidases, *E. albidus* exhibits endogenous expression of genes encoding cellulases from the GH9 family, as well as the expression of genes involved in the digestion of microorganisms, including a specialized, digestive i-type lysozyme (GH22i), which additionally contains SH3b domain (presumably involved in binding and recognizing peptidoglycan). Therefore, *Enchytraeus albidus* exhibits intermediate traits between primary decomposers (sapromacrophytophages) and secondary decomposers (sapro-microphytophages) and can thus be described as an intermediate-type decomposer.