

## **Microbiome composition of the model spider *Parasteatoda tepidariorum* (Theridiidae, Araneae) in relation to biological and environmental conditions**

Spiders are the objects of scientific interests for many reasons, most often due to the unusual properties of spider silk and the possibility of using it as a biomaterial. Also many studies deal with antibacterial proteins that are part of the secretion of venom glands and hemolymph of spiders. These proteins are considered a potential replacement for classic antibiotics, for which many strains of bacteria have gained resistance. What is more, the complexity of ontogenetic development, the diversity of mating and hunting strategies make spiders a group of invertebrates that is very attractive in terms of behavior. Many research teams also emphasize the importance of spiders in the ecosystem by reducing the amount of insects, including crop pests.

Spider *Parasteatoda tepidariorum* (Theridiidae, Araneae) selected for research is a cosmopolitan, synanthropic species that is considered as a model organism for evolution and developmental tests of the Araneae order. *P. tepidariorum* has got a sequenced genome, but there is no data on the microbiome of this invertebrate. As is known, microbiota plays a very important role in processes related to development, reproduction, maintenance of homeostasis and adaptation to environmental changes in host organisms. Investigating changes in the composition of microorganisms in spiders under the influence of biological and environmental factors would fill the gap in knowledge about the biology of these invertebrates.

Due to the growing use of metagenomics and the lack of data on the *P. tepidariorum* microbiome, comprehensive and innovative research on changes in the composition of microbiota in the studied spider during particular stages of ontogenetic development, between the sexes and between the internal and external surfaces are planned. In order to check the impact of environmental conditions on the composition of microorganisms in the tested spider, experimental groups were designed with a division into a: a) breeding strain, maintained under constant, controlled conditions (25°C, humidity 50-60%, photoperiod 16D: 8N) for 5 years at the Faculty of Biology and Protection Environment of the University of Silesia and b) wild spiders from the natural environment near human settlements. In addition, *P. tepidariorum*, among laboratory-breed strain, there were additionally separated experimental groups differing in the way of feeding: a) standard feeding spiders - *Drosophila hydei* fruit fly and *Calliphora* sp. fly larvae; b) experimentally fed spiders - exclusively *D. hydei*; c) spiders fed with *D. hydei* and *Calliphora* sp. larvae, deprived of food for 14 days; d) spiders fed experimentally only with *D. hydei*, then deprived for food for 14 days. In order to complete the image of changes in the microbiome composition under the influence of the diet, it is also planned to sequence the bacterial genome in the insects being the food of *P. tepidariorum*, which will allow to check whether there is a transfer of microorganisms from the prey to the spider.

Planned research are innovative and multithreaded, providing the basis for analysis of the impact of biological (stages of ontogenesis, sex) and environmental factors (temperature, humidity, diet) on the microbiome composition of the model spider *Parasteatoda tepidariorum*.