

Mutualistic symbioses, defined as close, long-term interactions between distinct organisms where both partners benefit, are widespread in nature. Among the many known examples of symbiosis, the relationship between insects and microorganisms is of particular interest. Insects are the most numerous and diverse class of animals that inhabit almost all environments on Earth. They owe their huge evolutionary success to the symbiosis with microorganisms, which allowed them to adapt to various environmental conditions, exploit previously unavailable food, and master new ecological niches. Symbiosis with microorganisms plays a crucial role in the biology of sap-feeding hemipterans, as their diet is deficient in essential nutrients. These insects host specialized intracellular symbionts that produce and supply them with essential amino acids and vitamins.

The proposed project focuses on symbionts of Auchenorrhyncha - an ecologically and economically important group of Hemiptera, which includes cicadas and other hoppers. The symbiosis between auchenorrhynchans and microorganisms began about 300 mln years ago when the common ancestor of this group of hemipterans was infected and colonized by two different bacteria. Mutual benefits resulting from this interaction resulted in its maintenance and consolidation in the next generations. As a result of symbiont replacement, the significant diversification of symbiotic systems in different evolutionary lineages of Auchenorrhyncha took place during the evolution of insects. Thanks to advances in DNA sequencing techniques, it is possible to reconstruct the evolution of symbiosis in Auchenorrhyncha. However, it requires extensive analyses of the symbiotic systems of huge numbers of insects from different regions of the world. In addition, the observed diversity of symbionts raises many questions about the sources and causes of this variability.

The proposed project aims to investigate factors affecting the composition of insect microbiome i.e., geographic isolation and host-insect food preferences. We plan to comprehensively characterize the heritable microbiome of auchenorrhynchans from 3 Baltic islands: Gotland, Oland, and Bornholm, and continental Europe (Poland, Germany, Estonia, and Sweden). Insects collected from various habitats (e.g. meadow, raised bogs) will be classified into the appropriate trophic group (monophage, oligophage, polyphage) and then characterized using next-generation sequencing techniques and microscopic analyses. The planned research allows understanding the microbiome composition of examined auchenorrhynchan species and detailed characteristics of symbionts, including the role of symbionts in the host-insect biology, their localization in the insect's body, and mode of inheritance.

The results obtained will contribute to a better understanding of the evolution of symbiosis in Auchenorrhyncha and will allow us to address many questions about the causes of variability of insect microbiome, e.g. Do the food preferences of host-insect determine the number of symbionts? Do the separated geographical insect populations differ in heritable microbiome composition? And whether and how newly arrived microorganisms affect the functioning of ancestral symbionts. Since many Auchenorrhyncha species are plant pests and vectors of plant viruses, the results of this project could be used in the planning of biological protection of natural resources.