

Many aspects of insect biology are determined by microorganisms, primarily bacteria and fungi, that live in their tissues. These microbes have repeatedly established non-pathogenic, stable associations with insects (symbioses), often forming multi-species communities inhabiting tissues of the same host (microbiomes). Because of the symbioses' importance to the biology of insects relevant to ecosystem function and the human economy, they are highly relevant to fundamental biological research, but also applied sciences including agriculture and medicine. During the last twenty years, thanks to the rapid advances in DNA sequencing technologies, the understanding of the diversity and evolution of the insect symbionts has improved dramatically. In particular, focused research on model organisms such the honeybee and the pea aphid has enabled the description of many aspects of the symbiont biology. However, outside of these model systems, information regarding the diversity of insect symbioses remains fragmented.

The goal of the proposed project is a broad, comprehensive survey of the microbial symbioses in a massive insect collection. We will do this in close collaboration with Insect Biome Atlas (IBA), a project that samples flying insects throughout Sweden during all of 2019. IBA will provide us with their data regarding species distribution in time and space, as well as with the access to the collected insect specimens. We will use them for the microbiome characterization using modern, high-throughput next-generation sequencing. First, to understand the effects of the host taxonomy and biology on symbioses, we will screen microbiomes in several thousand insect species collected across Sweden during a single week. Then, to describe the seasonal changes, geographic variation, and the effects of environmental factors on microbiome composition, we will select insect species broadly distributed among IBA-sampled sites and collection dates, and for each of these species characterize the microbiomes in large numbers of specimens. The final stage of the project is going to be the reconstruction of the patterns and mechanisms of the symbiont transmission among insect species. We will achieve this through sequencing the metagenomes of a subset of specimens, and the comparison of the phylogenetic trees for the symbionts and the hosts.

The proposed project will expand the knowledge about the diversity of symbiotic microbes in thousands of insect species. It will enable the description of the factors that shape the microbiome composition, provide information on how the microbiomes change in space and time, and how they influence hosts. Our broad conclusions, but also the sequence data and the extensive DNA sample collection generated during the study, will make a valuable resource to the international research community in many biological fields. Combined with the data regarding the insect biodiversity in Sweden, our data will help describe the full range of factors that shape insect communities. Finally, the project will enable and support the development of laboratory protocols, computational tools, and broad expertise in high-throughput next-generation sequencing, one of the most rapidly developing and impactful methods of modern biology.