


Project number	2021/43/B/NZ9/00991
Project title	Population genetics of saproxylic beetle assemblages in protected and managed forests
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Implementing entities	Institute of Systematics and Evoliton of Animals PAS, Institute of Animal Production, Forest Research Institute, University of Wrocław
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Project description	 <p>Maintaining biodiversity is one of the most important problems of our time, due in part to habitat loss and climatic changes. Forests are particularly affected by human activities because they are used for timber production. At the same time, wood is a microhabitat that is home for numerous organisms called saproxylics. Bacteria, fungi and invertebrates are responsible for decomposing wood and releasing micronutrients to the soil, completing the chemical cycle in forests. Many of the saproxylic organisms depend on dead wood, while others utilize wood of living trees. The availability, quality and quantity of deadwood in many forests is severely limited due to the requirements of timber production in forest management.. This forces many species to live only in some remnants of natural forests (mostly in protected areas). For many rare wood-dwelling species, this may be the last opportunity for this type of study. Other saproxylic organisms benefit from forest management and some of them might even be detrimental to forestry, especially during outbreaks. For proper protection of rare and threatened taxa, and for effective management of eruptive species (called 'pests'), it is necessary to understand what determines the viability and structure of their populations. Thanks to the development of modern DNA sequencing and genotyping techniques, it is now possible to study genetic polymorphism in detail to understand the factors and microevolutionary processes that shape population structure. The addition of environmental features to genetic data (via landscape genetics) makes it possible to find answers to the question of which features of the environment (e.g. availability and connectivity of old-growth forests, quantity and quality of deadwood, etc.) determine the genetic polymorphism of saproxylic beetle populations.</p> <p>In this project we propose to use saproxylic beetle species, both relicts of primeval forests and common taxa (including those with eruptive populations), with different species-specific traits (such as phylogenetic and trophic relationships, habitat and food specialization) to find answers to the following questions.</p> <p>First, we will wonder how genetic polymorphism of saproxylic beetles varies in forests with different habitat quality and microhabitat quantity. Second, we want to know how the duration of protection preserves the high genetic variability of saproxylic beetle's populations. Thanks to the third question, we will find out how the spatial distribution of suitable patches determines the dynamics of meta-populations of saproxylic beetles. Next, we will test how distance to refuges in old-growth forests reduces genetic polymorphism of saproxylic beetles. Finally, we are planning to examine how population genetics of saproxylic beetles are influenced by traits such as specialization, abundance, and phylogeny.</p> <p>We plan to collect selected saproxylic beetle species from multiple sites in old-growth, protected and managed forests. Sampling will focus on Polish forests, as there are still primeval forests in this country known to be hot-spots for relict for deadwood beetle species. The sampled beetles will be genotyped using next-generation sequencing technology and modern bioinformatics, which will allow the description of molecular polymorphism. Next, we will combine the genetic data with information on the environmental conditions of the sampled sites and species-specific traits. The results of the proposed project will be of broad interest and relevance to the fields of landscape genetics, molecular ecology, or biological conservation, as well as to field-specific areas such as entomology and forestry. Information on environmental factors and species traits influencing genetic polymorphism of saproxylic beetle populations will likely stimulate scientists to new research ideas. The extensive collection of tissue and DNA samples and the sequence data generated by the project will serve as a valuable resource to the international research community in the fields of biology and forestry. Many saproxylic organisms are experiencing a major biodiversity crisis, while others are causing important problems in forestry. To address these scientific problems, we will also make our results available to nature conservation services and organizations, as well as forest management services. We expect that this project will enable appropriate protection of threatened taxa and effective management of outbreak species.</p>

## Articles:

Amer N.A., Krovi R.S., Wierzbicka A., Plewa R., Kadej M., Jaworski T., Smolis A., Oleksa A., Szmatoła T., Oczkowicz M., Kajtoch Ł. (preprint) Geography and forest naturalness as drivers of genetic diversity in saproxylic beetles. biorxiv <https://www.biorxiv.org/lookup/doi/10.1101/2025.11.29.691121>

Krovi R.S., Amer N.R., Oczkowicz M., Kajtoch Ł. 2025. Meta-analysis of spatial genetic patterns among European saproxylic beetles. *Biodiversity and Conservation*. 34: 1–27  
<https://doi.org/10.1007/s10531-024-02940-8>

Kolasa M., Krovi R.S., Plewa R., Jaworski T., Kadej M., Smolis A., Gutowski J.M., Sućko K., Ruta R., Olbrycht T., Saluk S., Oczkowicz M., Kajtoch Ł. 2025. Host trees partially explain the complex bacterial communities of two threatened saproxylic beetles. *Insect Molecular Biology*. 34: 311–321  
<https://doi.org/10.1111/imb.12973>