Project Title: How characteristics of the hosts and forest environments shape the microbiomes of saproxylic beetles

Project Goal: This project aims to fundamentally understand the intricate relationships between two ecologically significant saproxylic beetle species, *Cucujus cinnaberinus* (a rare keystone species for close-to-nature forests with substantial amount of deadwood) and *Ips typographus* (a widespread species, considered a serious timber pest, and their associated microbial communities. By investigating these interactions, we seek to gain insights relevant to both biodiversity conservation and sustainable forest management.

Description of Research: This research employs an innovative integrated approach, analyzing both the genetic makeup of individual beetles and the composition of their bacterial and fungal microbiomes. I will use existing host genetic data (ddRADseq) and generate new microbiome data through amplicon sequencing of 16S rRNA and ITS regions. This paired analysis will allow us to directly link host genetic variation with microbiome diversity and composition, overcoming limitations of studies that examine these aspects separately. I will compare these relationships in *C. cinnaberinus* and *I. typographus*, a two species that both belong to saproxylic organisms, but being on two opposite sites (rare vs common; forest quality specialist vs generalist; tree host generalist vs specialist), collected across close-to-nature and commercial forests to understand how forest management impacts both the hosts (beetles) and their microbiomes. Although there are some previous studies on the microbiome of these species, none of them considered the environment as a factor, nor did they simultaneously confront host genetics with a diversity of bacteria or fungi.

Reasons for Attempting the Research: *Cucujus cinnaberinus* is a crucial indicator species, and understanding its ecological requirements, potentially mediated by its microbiome, is essential for effective conservation strategies aimed at preserving valuable close-to-nature forest ecosystems. Conversely, *Ips typographus* causes substantial economic damage in planted forests, and identifying microbial factors influencing its outbreaks could lead to novel and environmentally sound pest management strategies. The choice of these two taxa is a tradeoff between expectations towards this type of research and the possibilities of the Preludium grant competition. Studying these two ecologically contrasting species within different environmental contexts will provide a comprehensive understanding of host-microbe interactions in forest ecosystems. The availability of existing host genetic data provides a unique opportunity to efficiently conduct this integrated analysis.

Substantial Results Expected: I expected that this research would yield novel insights into the microbial underpinnings of habitat specialization, ecological resilience, or pestiferous behavior in these keystone beetle species. I anticipate identifying specific microbial signatures associated with the restricted distribution of *C. cinnaberinus* and potential drivers of *I. typographus* outbreaks. The unique paired genetic and microbiome dataset generated will be a valuable resource for the scientific community, leading to impactful publications in leading peer-reviewed journals. Furthermore, the findings have the potential to inform conservation guidelines for old-growth forests and contribute to the development of sustainable forest management practices. The presented approach could be extended in the future to other taxa, depending on available resources or collaborations. While amplicon sequencing will provide valuable information, future metagenomic analysis could further elucidate the functional roles of the identified microbial communities.