

Institute of Environmental Sciences

**Topic:** Population genomics of outbreaks - neutral evolution in spruce bark beetle

**Name of supervisor:** prof. Wiesław Babik / dr Krystyna Nadachowska-Brzyska  
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**Background information:**

A major goal in evolutionary biology is to understand which processes shape the genetic diversity of natural populations. Classic population genetic theory provides a solid mathematical framework to study genetic variation and predicts the efficacy of selection relative to drift under equilibrium conditions. However, natural populations often experience large size fluctuations that make prediction less straightforward. For example, epidemic outbreaks of many pests are characterised by sudden changes in population size, spanning orders of magnitude. Such outbreaks are known from ecological studies of closely monitored species of economic importance. However, little is known about the genetic consequences of outbreaks. An ideal system to examine such consequences is the spruce bark beetle (*Ips typographus*). Spruce bark beetle is the most destructive pest of Norway spruce forests because under specific conditions (e.g. following storms) populations may outbreak, causing mass mortalities of spruce stands.

**The main question to be addressed in the project:**

The primary purpose of this project is to test how extreme fluctuations in population size of outbreaking species affect the dynamics of neutral genetic variation.

**Information on the methods/description of work:**

The student will compare populations of spruce bark beetle that have experienced frequent, recent outbreaks and populations that did not experience outbreaks in the recent past. The PhD student will be working with extensive, whole-genome resequencing data obtained from several populations and >500 individuals. By combining the existing knowledge on biology and ecology of the species with newly generated, large-scale genomic data, the student will address questions about the relationship between genome-wide variation and fluctuating effective population size. Specifically, the PhD student will

analyse patterns of variation along the genome as well as infer beetle's demographic history using coalescent-based simulations.

**Additional information (e.g. Special requirements from the student) :**

The position is within the recently awarded project *Population genomics of outbreaks* (PI dr Nadachowska-Brzyska). The student will closely collaborate with other members of the team that are focusing on theoretical investigations and adaptive variation. The candidate should have a strong interest in Evolution, Population Genetics and/or Genomics as well as experience with, or a keen interest in learning, Bioinformatics and Computational Biology. Strong English language, communication, and organisational skills are essential.

**Place/name of potential foreign collaborator:**

prof. Fredrik Schlyter (SLU, Sweden), Prof. Paal Krokene (NIBIO, Norway)

**References (3):**

Mayer, F. et al. Comparative multilocus phylogeography of two Palaearctic spruce bark beetles:

Influence of contrasting ecological strategies on genetic variation. *Mol. Ecol.* 24, 1292–1310 (2015).

Pélissié, B. et al. Rapid evolution in insect pests: the importance of space and time in population

genomics studies. *Curr. Opin. Insect Sci.* 1–9 (2018).

Kausrud K, Økland B, Skarpaas O, Grégoire JC, Erbilgin N, Stenseth NC. 2012. Population dynamics in

changing environments: The case of an eruptive forest pest species. *Biol. Rev.* 87:34–51.