

Animals from different locations differ in terms of their genetic variants. This spatial differences are mainly shaped by two processes: demography (i.e. population growth, migrations, etc), and selection. It is still not clear what is the relative role of each of those processes.

To answer this question, in the proposed project we will study bank voles *Myodes glareolus*, small rodent inhabiting woodlands in European lowlands, and their parasites, the nematode *Heligmosomum mixtum*.

Previous studies have shown that genetic variance of voles is shaped by their migration from glacial refugia after the last glaciation. However, these studies used only one locus in the genome. Although some studies suggested that rodents originating from different refugia may differ in physiological traits, it is not clear how much genes are affected. In the proposed project we will answer this question by studying genome-wide variance, not single genes as previously.

Moreover, recent work have shown that immunity genes generally do not follow the pattern described above. This poses a question about the mechanisms of local adaptations that we plan to answer by analysing variance in genomes of the frequent nematode parasite infecting voles, the nematode *H. mixtum*. Parasites are the major selective force affecting host fitness, and thanks to their geographic variation, they are an excellent study system for investigating the impact of local selection on host genetic variation.