

Abstract

In recent years, due to the development of molecular methods, a great level of cryptic diversity across multiple taxa was discovered. One of these groups are freshwater amphipods. Amphipods due to lower dispersal and recolonization abilities present a suitable model system for studying potential ecological interactions among genetically distant lineages during their secondary contact. In this thesis, I studied the cryptic species complex *Gammarus fossarum* in a contact zone of several genetically divergent lineages known from the previous research in the Vsetin region. I focused on two main questions: Firstly, whether there are preferences among individuals from different lineages for sexual partners from the same lineage rather than from the different one (i.e., I test for the potential existence of prezygotic reproduction barrier between the lineages). I tested this hypothesis by collecting pairs from natural contact zone and also (in a limited extent) by an aquarium experiment. Secondly, I tested whether these lineages differ in mesohabitat (pool versus riffle) distribution in syntopy, which may indicate competition among lineages and potential diversification of their ecological niches. Animals from nine localities (with expected contact of two lineages per locality) were examined. In more than half of the cases, I also detected a third lineage at the respective locality. At all localities one lineage was dominant (more than 64 % of identified individuals). In natural conditions, only one precopulatory pair out of 102 examined ones was formed by a male and a female from different lineages. This confirms the existence of an efficient prezygotic reproduction barrier among these lineages. However, in the pairing experiment, I observed the formation of pairs between individuals from different lineages (in the treatment with access to potential partners of both own and different lineage, as well as in the no-choice treatment with access only to a partner from another lineage). Results from the field support previous molecular evidence indicating that there is no recent gene flow between the lineages, which we can consider as reproductively isolated species. I did not detect differences in distribution of lineages between different mesohabitat (pool vs. riffle). However, the total amount of samples analyzed per season, locality and habitat was relatively low and for a better examination of this topic is necessary to increase the number of analyzed samples in the future. The absence of differences on this relatively rough ecological scale does not exclude other possible ecological differences among studied lineages, which may affect their coexistence.