

Abstract

Amphipods are an important component of temperate permanent freshwater macrozoobenthos. They have poor dispersal abilities, lack dormant stages, and their phylogeographies often reflect old historical processes. The genus *Gammarus* itself includes more than 200 described species spread in the Palearctic region. Many of the taxa previously described are, in fact, diversified species complexes, which is case of our most common *Gammarus* (*G. fossarum*). We have studied their diversity on the transect across the Bohemian Massif and the Western Carpathians, which form a significant biogeographical boundary for a number of other organisms. We tested whether the border between these areas is reflected in the phylogeography of *G. fossarum* as a representative of permanent aquatic fauna. Analysis of two mitochondrial markers revealed the presence of eight divergent *G. fossarum* lineages, which also differed in the nuclear genome. All eight lineages were found in the Western Carpathians, while the Czech Massif is inhabited only by two. The microendemic areas of some lineages and the occurrence of two apparently basal lineages of this complex, which were not found in southern regions, support the hypothesis that these amphipods survived Pleistocene glacial cycles even in West Carpathian refuges. We assume that warm mineral springs, which are common in the Carpathians, could play a key role in ensuring a stable environment even in cold and dry periods. In the Vsetín region, I studied the local contact of four lineages. The position of a locality along the stream, which is related to width or depth and flow intensity, as well as the position of the stream itself in the landscape, could be important explanatory factors affecting the distribution of the lineages at small scale. In individual catchments, up to three lineages were found, often in syntopy, and their distribution frequently differed between the upper and lower parts of the streams. Consistent results from mitochondrial (16S) and nuclear (28S) markers support the hypothesis that studied lineages do not hybridize even in syntopy. At this local scale, we used for determination of individuals not only sequencing but also amplification of 16S gene fragments using lineage-specific primers. This method will be used in future research focusing on the ecological interactions between divergent lineages.

Key words: *Gammarus fossarum*, species komplex, cryptic diversity, Bohemian Massif, Western Carpathians, lineage-specific primers