DESCRIPTION FOR THE GENERAL PUBLIC

Snails belonging to the superfamily Truncatelloidea, having a global distribution, are mainly residents of springs and ground waters, including caves. One of the centres of their distribution, in other words the areas of their greatest biodiversity, are the Balkans, especially in their north-western part. The Balkans were repeatedly a refugium, protecting the fauna in Europe during the glaciations. At the same time, the decrease in the level of the Mediterranean Sea, about 100 m and even more, resulted in invasion of many species from areas of Asia, and even Africa. As a result of these events, the Balkan fauna is extremely rich. On the other hand, the springs, to say nothing on caves, are small in size, specific habitats, isolated from each other. This potentially raises still more biodiversity. From about 350 obligatory subterranean aquatic gastropods known worldwide (97% of them represent Truncatelloidea), 148 species representing 41 genera and six families, inhabit NW Balkans. Similarly high biodiversity could be found only in Indochina.

Isolation of such populations, although intuitively quite obvious, need not necessarily be a fact. The studies done so far usually detected some levels of gene flow – which means migration – between localities. The biology of these snails is so poorly understood that we cannot exclude any, unclear to us but quite effective migration paths - probably passive (most probably transportation by birds) – between the local populations. Moreover, there are extensive data confirming that endemism – thus degree of isolation – of the cave fauna is much higher for terrestrial than for aquatic animals. The interstitial habitats – underground waters filling unconsolidated sediments bordering and underlying streams and rivers. Those parts of the interstitial habitat are neither rare nor discontinuous, forming corridors, making thus possible migration between caves. However, this has not been proved so far, and this is one of the aims of our research. In transects, the interstitial snails would be collected between the caves and springs, and comparison of the genetic structure between the samples – for a few fragments of DNA – should confirm or not functioning of those corridors – does migration really take part thrue those habitats.

At the same time we will determine how to shape the genetic variation within a population - this will allow a better understanding of the formation of this type of population. Genetic structure of the populations of the animals inhabiting caves is poorly understood, it has been studied so far for not many animal species, in it in only a few species of snails. Meanwhile, the caves are – in contrast to the springs – long-lasting (at least in the thousands of years), more or less isolated habitats of small size and specific conditions stable throughout a year. So they are inhabited by a specific fauna. We do not know whether the caves are a sort of museums, which shelter species, which later have not survived on the surface, or whether they are rather laboratories, where fast evolutionary processes are taking place. Such processes - especially speciation – in such small populations may run much faster than in populations with larger number of specimens (thus higher evolutionarily effective population size). Specific conditions probably cause a sharp selection. On the other hand, minimal (if any present) income of immigrants, as well as the simplicity of biocenoses ensuring the reduction of competition, must shape the genetic structure of these populations. However, these are only presumptions, and our research will allow to test these hypotheses, as well as to decide whether there is more museum or laboratory.

The competing “climate-relict” and “adaptive-shift” hypotheses have been proposed to explain the origins of cave organisms. According to the “climate-relict” model, preadapted ancestors colonized caves when the surface climate was altered by glaciation or aridification, and gradually adapted to the cave environment. Climatic oscillations caused local extinctions of the surface populations, leaving each relict population to evolve allopatrically in a separate cave system. The “adaptive-shift” model supposes that preadapted ancestral species actively colonized caves to exploit novel resources and diverged under a gene flow scenario. Divergent selection between surface and subterranean habitats gradually overcame the homogenizing process of gene flow and eventually led to parapatric speciation. Our data should solve the question: which of the above models holds for those snails?