

Members of the family Endomychidae are known as handsome fungus beetles. There are known about 1800 species of this family around the globe. Many of them have attractive colour patterns, with contrasting marking on the elytra, usually in red and black, that serve as an advertisement of their possible toxicity to potential predators and remind us of ladybirds (family Coccinellidae). Handsome fungus beetles have been traditionally considered as close relatives of this group of well known, ubiquitous beetles. Instead of roaming around plants and feeding on small arthropods like ladybirds, the handsome fungus beetles feed on a wide variety of types of fungi, from molds growing on grains to puffballs or hard bracket fungi growing on dead logs. One of the few exceptions to the fungivorous habits are species of the Oriental genus *Saula* that predate on small arthropods just like their ladybird relatives, suggesting fascinating scenarios about the evolution of these beetles. It has been hypothesized that the predatory habits of insects like the highly diverse and successful ladybirds evolved from ancestors who used to feed on fungi. For this reason, understanding the way that the handsome fungus beetles have evolved is crucial for shedding a light into the processes that have shaped the way they look, what they eat and how they relate to each other.

In order to understand the evolution of living organisms, it is necessary to take a look at the present as well as the past of the organisms. Nowadays, evolutionary biologists heavily rely on reconstructing the kinship of taxa by analysing their genetic sequences, expecting to find the “true” signal of their ancestry. Sometimes the reconstructions that scientist can draw based on the information contained in their genome confirm centuries of observations done by naturalists and comparative morphologists, but many others are contradictory to the morphology studies. However, we should not relegate to a secondary plane the information about the physical traits of living and extinct organisms, as the body of the organisms being in a direct interaction with their environment, carry millions of years of evolutionary and ecological information to decipher.

The handsome fungus beetles are illustrative example where different ideas about phylogenetic relationships have been proposed. The analysis of morphological characters suggested the handsome fungus beetles formed by twelve subfamilies share a common ancestor. However, when the sequences of a handful of genes were analysed the results pointed out to the Endomychidae being an assembly of groups with different origins where three of the former subfamilies excluded and were raised to family status. Why do the genes tell us a different history from what we can derive by comparing their morphological traits?

In order to overcome this conundrum we propose to combine the information derived from the genetic sequences and the morphology of, not only living species, but also extinct species of different ages. There are nearly 20 species of Endomychidae known from deposits of the upper Cretaceous of Myanmar or the Eocene epoch in the Baltic amber. Specimens embedded in amber give us the unique opportunity to take a deep and intimate look at a moment frozen in time. Through careful examination of the morphology of these organisms we can compare them to contemporary groups and place them within the framework of an evolutionary tree. For this reason we will use modern techniques of micro-computed tomography (micro-CT) in order to reconstruct three-dimensional models of the fossils organisms. Additionally we will use micro-CT to investigate the nature of their morphological modifications like pores in the exoskeleton that probably help in the dispersal of spores of their host fungi or internal glands associated to their defensive strategies like reflex bleeding of toxin-full hemolymph. Also, by knowing the temporal succession of their evolutionary events we will be able to provide a biogeographical explanation about the present distribution of the family around the globe.

Our research will utilise large-scale molecular and morphological data to provide the first robust phylogeny and a fossil-calibrated time-tree for the family Endomychidae. Main goals of the project include: to test existing competing hypotheses regarding phylogenetic relationships; construct a fossil calibrated time-tree for Endomychidae; reconstruct the historical biogeography of the family; reconstruct the dietary preferences of the members of handsome fungus beetles; track the evolution and systematic significance of morphological features associated with fungivorous habits.