

The main goal of the project is to reconstruct the phylogeny of a highly speciose group of hermaphroditic land snails (the door-snails, family Clausiliidae, subfamily Phaedusinae) indicating shifts in their reproductive mode in their evolutionary history.

Phaedusinae comprises ca. 600 species inhabiting Eastern and South-eastern Asia (eastern Phaedusinae), as well as old and less diverse taxa from Pontic region (western Phaedusinae). The connectivity of their range was probably interrupted in Miocene due to the increasing aridity of Central Asia. The origin of monsoonal climate, emergence of volcanic arcs and temporary land connection between islands on the Sunda Shelf and the Asian mainland during the Pleistocene glacial maxima might enhance their further spreading and diversification. The extant Phaedusinae are forest and rock dwellers. Their range covers a variety of climatic conditions from tropical rainforest (Borneo) to temperate (Hokkaido) climates. Due to anthropogenic pressure on natural habitats (land conversion, logging, mining, etc.), their diversity in SE Asia is under threat and unknown number of species have already disappeared.

The current taxonomy of Phaedusinae is based on conchological characters alone and requires a revision based on molecular phylogeny and detailed anatomical studies of the reproductive tract. Among Phaedusinae two reproductive modes (oviparity and viviparity) occur but the knowledge of life histories is limited to only 2% of species. Consequently, it is impossible to ascertain when the viviparity appeared in the group or if it facilitated diversification.

We are going to assess the molecular diversity within Phaedusinae with a set of nuclear and mitochondrial markers (Cytochrome Oxidase subunit I, 28S rRNA, Internal Transcribed spacer 1 and 2, Histone H3, Histone H4). Multimarker phylogeny will be reconstructed and Bayesian chronogram calibrated based on fossils. To determine when and how often the alternative reproductive strategies have evolved, we will perform Bayesian Ancestral State Reconstruction and model the dynamics of speciation and extinction on the phylogenetic tree. Reproduction mode of species, representing different genera, will be ascertained during observations in lab culture, dissections and supplementary analysis of shells in museum collections with μ -CT. This technic allows to confirm a viviparous reproduction mode and to indicate the number and size of brooded embryos. Anatomical and histological analysis of genitalia in Phaedusinae will be conducted to reveal adaptations towards alternative reproduction modes and to reconstruct the evolution of male and female reproductive organs in different phylogenetic lineages. Additionally, the type of embryo nourishment will be identified. We will also reconstruct climatic niche models of viviparous taxa by examining the distribution of the species ranges and available climatic data relevant to snail reproductive activity.

Land species richness and phylogenetic diversity is still only fragmentarily documented in SE Asia. The study will surely fill a large gap in biodiversity assessment of the most threatened diversity hotspots of the world. Without such knowledge, it is hard to imagine an effective campaign preventing or at least minimising the loss of biodiversity, which is one of the top priorities of global agendas for nature conservation.