Announcement

Master Thesis

"Evolution of host associations in the weevil subfamily Ceutorhynchinae (Curculionidae, Coleoptera) – a phylogenomic approach"

Background

Coevolutionary interactions with plants is a fundamental mechanism for insect radiation. Understanding of differential host use as the trigger to accelerate herbivore radiation requires a robust hypothesis on the phylogenetic relationships and divergence times of the target insect group. The proposed project focuses on the weevil subfamily Ceutorhynchinae (Curculionidae, Coleoptera) as a model to explore the macroevolutionary mechanisms that potentially generate and maintain herbivore diversity. Ceutorhynch weevils are of special interest, as the host associations of many representatives constitute a considerable impact on agriculture and horticulture. Among known hosts are plants protected by potent allelochemicals like hemp (*Cannabis*), garlic (*Allium*), wolfsbane (*Aconitum*), poppy (*Papaver*), joint-pine (*Ephedra*), and crucifers (*Brassica*).

Goals

Reconstruction of the relationships, divergence times and the biogeographic history of Ceutorhynchinae. Inference of abiotic (climate) and biotic (host associations) factors shaping the diversification of Ceutorhynchinae.

Tasks

Compilation of a phylogenomic data set (laboratory work including DNA extraction and Illumina library preparation). Phylogenetic tree reconstruction and subsequent analyses of ecological trait evolution. Due to intensive computational analyses of large datasets, experiences with UNIX/Linux, command line or R is helpful.

Schedule

Work may begin March 2022 or soon thereafter and is scheduled for one year. Publication of results is intended. The project is ideally suited as MSc thesis work in the curricula Zoology or Ecology & Ecosystems at the University of Vienna.

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