

A large-scale phylogeny and evolution of immature stages in megadiverse family Muscidae (Diptera)

Insects representing more than half of living species reached astonishing evolutionary success and an amazing variety of natural histories. Studying evolutionary histories within certain insect lineages will allow to understand how the majority of organisms diversity on Earth evolved. The evolution of phenotypic traits depends on many factors. In consequence two opposite patterns of rates of morphological diversification may occur, i.e., rapid phenotypic changes or long-term phenotypic stasis in evolutionary lineages. On the other hand, particular habitats may elicit evolution of overall similar morphological traits. To overcome the issue of constraints in trait's ability to change, organisms may adapt to new local environments by means of introduction of phenotypic innovations.

Diptera represents one, out of four, insects super radiations. Dipteran taxon Cyclorrhapha, which includes almost half of 150 000 named dipteran species, achieved great evolutionary success for example due to modifications in larval morphology. In this project, using megadiverse cyclorrhaphan family Muscidae, app. 5 200 species, as a model group we will investigate whether adaptations to various feeding strategies within certain lineages of living organisms may lead to certain structural changes. However, a vital first step for exploration of evolutionary issues by means of the phylogenies is robustly resolved taxonomic relationships. Since taxonomic relationships within Muscidae remains questionable, in this project we will use various next generation sequencing (NGS) approaches, a way allowing to resolve puzzling phylogenetic relationships, to reconstruct a large-scale phylogeny of Muscidae. We will study and describe details of preimaginal stages morphology of all evolutionary lineages within Muscidae. For the first time we will identify traits of immature stages morphology conserved across Muscidae clades and will use them as a corroboration of certain nodes in phylogenetic tree to build a new robust classification system. This study will provide new, highly desirable, insights into the phylogenetic relationships within a family Muscidae, a group of insects of high agricultural, medical and veterinary importance to humans. Taking the advantage of phylogenetic comparative methods, we will investigate whether certain modifications of immature stages morphology in various Muscidae lineages are correlated with feeding strategies such that feeding strategies in Muscidae reflect certain modifications in larval morphology. Subsequently we will perform a stochastic mapping to infer the ancestral feeding strategy and ancestral traits of larval morphology of Muscidae to explore their evolutionary histories and investigate mechanisms involved in adaptations to local environments. This will allow us to explore evolutionary mechanisms involved in adaptations to local environments.