

The goal of this study is to solve some of the key problems of the evolutionary history of the Andean faunas based on data on the phylogeny and distribution patterns of butterflies of the subtribe Pronophilina.

The Andes were selected as the study area, in particular, because they are the region of the globe where the highest number of species of plants and terrestrial animals are found. Their enormous biotic diversity is related to their magnitude, as they are the largest mountainous system of the World, spreading across the entire tropical and subtropical zone, into subantarctic areas, and to their ecological diversity, expressed by the presence of nearly all terrestrial habitats along altitudinal and latitudinal gradients. Hence, the great importance of the Andes in uncovering the origins and evolution of montane faunas, not only on a continental but also on a global scale, and as a study area in multidisciplinary research, in particular in the field of ecology and biogeography. The understanding of how Andean faunas evolve through time and space is, therefore, of general interest. Our knowledge about these patterns is still, despite several works published in the recent years, very superficial.

One of the best tools in recognizing these patterns is a comprehensive information about the phylogenies of selected groups of organisms. Such a group has to fulfill several conditions, the most important of which is its high diversity expressed, in this case, in the large number of species and genera. The group of butterflies selected for this study, the subtribe Pronophilina, is the most species-rich not only in the Andes but also in all the tropical mountains of the Earth. It comprises more than 650 species belonging to approximately 45-50 genera. Their vast majority are strictly tropical Andean species, however several of them occur also in Central America, the Guyana highlands, along the Atlantic coast of Brazil and in the Argentinian pampa. Many of the species are highly endemic, in some cases restricted to single mountainous massifs, and frequently restricted to narrow bands of altitude.

The phylogeny Pronophilina butterflies is very poorly understood. Even though some data on several genera were published, this is such a diverse group, that the relationships between the genera, as well as with other groups of butterflies are only superficially researched. Importantly, phylogenetic studies were done exclusively based on a limited number of, generally, 3-5 molecular markers. That is why the methodology to be applied here is novel, as it involves the sequencing of several hundred markers per each species. Moreover, it allows to obtain DNA material from old specimens preserved in museums for many years. From this perspective, it is of utmost importance that the overwhelming majority of species of Pronophilina, over 600, are available now in the scientific collection of the Jagiellonian University in Kraków, which has the largest holdings of this group of butterflies in the World. In order to achieve a full image of the phylogeny of the study group it is, however, necessary to collect the remaining species during field work in the Andes. Material deposited in this collection will be used not only for comprehensive morphological and molecular studies but also constitute a valuable source of data on geographical ranges and altitudinal distributions of species. These data, coupled with phylogenetical trees, will allow the reconstruction of evolutionary pathways of the studied group on a geographical scale, in other words the carrying out of the phylogeographical analysis.