

Biodiversity is one of the most important topic of scientific research today. Subsequent studies indicate the importance of biodiversity for nature conservation, proper functioning of ecosystems and importance to human health as well. However our knowledge of this part of life is still very poor. There is estimated that only c. 25% of living organisms are described so far, and also that 30 species (many of them undescribed) disappear from the Earth every day. For this reason, taxonomists have the urgency to describe and allow to know the unknown Earth's biodiversity. Unfortunately, taxonomy is basic science and not popular for students nowadays, and because of it requires many years of work on a particular group of organisms to develop a good specialist, many taxonomists die with his knowledge and experience, not leaving them to the next generation. Consequently, expected to the crisis in taxonomy, resulting in lack of opportunities to explore and describe the living world.

Basic way to expand our knowledge concerning biodiversity are various works concerning well defined species as revisions and floras. Orchidaceae as the biggest family of the flowering plant is without doubt one of the most significant element of vegetation in many regions, especially tropics. Knowledge about selected groups of orchids could be very important source of data for biodiversity studies.

The main aim of the scientific project is to prepare a comprehensive taxonomic revision of the genera *Aa* and *Myrosmodes* (Orchidaceae). The work will be equipped by keys for determination of all species treated, now not available anywhere. In effect many of the herbarium material also collected recently are determined doubtfully or only at the generic level. Description of every species will contain detailed information about morphology of vegetative and generative structures, with discussion on diagnostic characters, data about ecology and distribution, including maps with indication by points an occurrence of species (data mainly from herbarium specimens) and detailed drawings of habits and flower parts of every species. Secondly, reconstruction of phylogeny of *Aa* and *Myrosmodes* will be conducted. Both genera are closely related and previous molecular studies show that together form monophyletic clade, but *Aa* is probably paraphyletic without *Myrosmodes*. One of the aim of presented project is to resolved relationships between these two genera. Additionally, molecular clock analysis will be used for estimation of time of diversification these two taxa and its representatives. Last but not least, species potential distribution modelling will be conducted for as many species as it possible. Representatives of *Aa* and *Myrosmodes* occur on páramo, which distribution range was highly variable since Last Glacial Maximum (LGM) until today. These changes could promote diversification in both genera, since evolutionary process on páramo are comparable to those on the archipelagos of islands.