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Overestimation of molecular and modelling methods and underestimation of traditional taxonomy leads to real problems in assessing and handling of the world's biodiversity

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Abstract

Since the 1992 Rio Convention on Biological Diversity, the earth's biodiversity is a matter of constant public interest, but the community of scientists who describe and delimit species in mega-diverse animal groups, i.e. the bulk of global biodiversity, faces ever-increasing impediments. The problems are rooted in poor understanding of specificity of taxonomy, and overestimation of quantitative approaches and modern technology. A high proportion of the animal species still remains to be discovered and studied, so a more balanced approach to the situation is needed.

Key words: Biodiversity, taxonomy, trends, impediments, perspectives

Climbing a steep trail above Morgins, in the Swiss Alps, 12 year-old Thomas noticed an odd creature balancing on a branch. The animal was about two cm long, black with numerous light spots on its back, and with the head extended by a trunk reminiscent of that of an elephant. Unfortunately, neither his parents, nor later his teacher, were able to satisfy Thomas' eager curiosity to discover what kind of animal he had encountered. Not so long ago, any teacher would have known it is a beetle, and any teacher with at least a slight interest in nature would probably have recognized a weevil. Today, this kind of knowledge is disappearing even among biologists, whose ability to recognize forms of life may be reduced to that of Thomas; a paradox, given that there are numerous environmental organisations and societies active all around the world. This comes at a time when the effects of humans on the environment are reaching a tipping point, so we need more than ever reliable information about the world's biodiversity.

This issue reoccurred to me during the course of working on a Catalogue of Palaearctic Coleoptera (Löbl & Smetana 2003, 2004, 2006, 2007, 2008, 2010, 2011, 2013). The aim of that work was to give readers an overview of a the Palaearctic beetle fauna, particularly because the beetles are the most species-rich order of all organisms that inhabit our planet (Ślipiński *et al*. 2011) and comprises about a quarter of all recognized multi-cellular species. The area considered is also the most extensive biogeographical region: it covers Europe, Africa north of the Sahara, the Arabian Peninsula, and Asia except for its tropical areas south of the Himalayan Range and China. The work began in 1999 and was completed in collaboration with 202 experts in May, 2013, giving basic taxonomic and distributional information on 18,468 genera, subgenera and their synonyms, and 170,778 species, subspecies and their synonyms. This work pointed also to problems taxonomists encounter, and to the necessity of discussing trends that currently impede efforts to assess species-richness in mega-diverse animal groups.

From well before Linnaeus' landmark work was published (Linnaeus 1758), naturalists have continuously tried to document the diversity of living forms. The task has become even more urgent recently, due to extinctions caused by relentless human pressure on the environment (Collins *et al*. 1991). All organisms are subjected to that pressure, but the small ones are infinitely more species-rich, and have a major ecological impact on ecosystem functioning (Kim 1993). Information about the diversity of organisms is summarized in catalogues that are required for the unambiguous nomenclature used in both biology and conservation, with valuable historical perspectives. It may appear strange that in spite of all the efforts made since the mid-18th century, there is still a lack of adequate catalogues for large groups of organisms. Many of the scientists who contributed to the Palaearctic beetle catalogue dealt with inherent ambiguities in the field. These are partly rooted in the notion of species: unlike individuals, species are hypotheses, based on observed

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enable identification of 95% of sampled specimens once half of the Bavarian species are barcoded. Molecular data are useful in many fields, as in the study of diet by examination of gut contents (Klimaszewski *et al*. 2013), identification of larvae (Sewell 2006) and cryptic species (e.g., Burns *et al*. 2008), and analyses of phylogeny (e.g., Short & Fikáček 2013) needed for understanding evolution of organisms. A closer examination of the situation reveals, however, that barcoding focusing on local and well known faunas, such as the Bavarian, provides to a large extent just an additional tool for identification of species that are common, widely distributed, and often may be readily distinguished by traditional means not requesting complex and expensive technology, many recognized even with the naked eye. Similar projects launched in European countries, such as Austria, Germany, the Netherlands, and Switzerland, are necessarily largely redundant. While traditional identification tools and associated data usually provide a large amount of information on morphological characters, biology, habitat preferences, host association, and distribution of the identified species and other taxa, the barcodes provide a restricted array of information. The images of the voucher specimens exhibited on the web sites are often uninformative, and the maps that are supposed to show the respective species distribution are often grossly incomplete. In addition, the traditional approach is rather holistic and leads quite often to array of new discoveries, while the use of barcodes provides at best only species names, unless also flagging potential cryptic species and used in conjunction with the traditional approach. A more important issue is the fact that barcodes may be species-specific in some animals but are not discriminatory in others (Meier *et al*. 2006), and the method is far from being universally accepted (Lipscomb *et al.* 2003, Taylor & Harris 2012, Will & Rubinoff 2004, Yeates *et al*. 2011). Meanwhile, resources are shifted towards the use of barcoding in a number of institutions, including universities and museums. This reduces the pool of expertise available to identify samples of poorly known species, and enhances the on-going dark age of modernity in studies of diversity of a large part of the world fauna.

Underestimating and/or misunderstanding traditional taxonomy leads to a vicious circle in which needs and the development of substitutes are increasing, and the supports redirected to the substitutes impede the efforts to meet the needs. As only sound taxonomy underpins robust data about the diversity of existing life forms, a change in this logic is required. What is needed is some understanding and good will of decision-makers who distribute public resources. Practical and efficient first steps would be an evaluation of biodiversity based on the research undertaken by taxonomists rather than knowledge based on new modelling and rough and unverifiable estimates, and a shift in priorities from meta-analyses and faunal barcoding to true and comprehensive studies of species and their diversity.

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