

Opinion paper

No Name, No Game

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“The most efficient solution to speeding taxonomic production, ultimately, is to train and hire more taxonomists.” (Deans *et al.* 2012: 81)

In an interesting contribution Joppa *et al.* (2011) revisit some aspects of the taxonomic impediment (Evenhuis 2007; <http://www.cbd.int/gti/>) and come to the conclusion that, contrary to the generally accepted idea, both the rates of species description and the number of taxonomists have increased exponentially since the 1950's. Joppa *et al.* (2011) also note a marked decline in the number of species described per taxonomist which they attribute to the difficulty of finding new species in an ever declining ‘missing species pool’. Therefore, their results might be interpreted that today's taxonomic workforce is sufficient to describe the remaining (shallow) ‘pool of missing species’. In this contribution, we question if this is indeed the case and propose a solution for speeding up taxonomic descriptions.

We feel that Joppa *et al.* (2011) are overly enthusiastic, probably because their test cases represent a selection of the better-studied taxa (flowering plants, *Conus* snails, spiders, amphibians, birds and mammals). Contradicting the findings of Joppa *et al.* (2011) and using a much broader taxon sampling, which includes many poorly studied groups, Costello *et al.* (2011) observe that species description has roughly remained constant since the second World War, at least for terrestrial species. These results are congruent with other counts of species descriptions (Bacher 2012; Chapman 2009; May 2011; Zhang 2010; <http://species.asu.edu/SOS>). So it seems that the increasing rate of species description as reported by Joppa *et al.* (2011) is taxon specific rather than general.

In stark contrast to the constant rate of species description is the rate with which species are discovered by using DNA sequence data. Exhaustive bio-inventory initiatives to map diversity of poorly explored areas around the world (e.g. <http://laplaneterevisitee.org/>; <http://mooreabiocode.org>) in combination with large-scale barcoding efforts (Hajibabei *et al.* 2007; Valentini *et al.*, 2009) result in an explosion of species/sequences in repositories such as Genbank and Bold Systems that are not linked to known species. This growing number of what have been called ‘dark taxa’ by Page (<http://iphylo.blogspot.com/2011/04/dark-taxa-genbank-in-post-taxonomic.html>), makes one question the use of proper taxonomic names at all. Indeed, it can be argued that a lot of biology does not *per se* require formally described taxon names. However, the value of scientific names exceeds the field of biology *sensu stricto* and matters

for society as a whole. For instance, the international legislation that controls the trade of endangered species (CITES) uses species names as currency, just as the Convention on Migratory Species and the Convention on Biological Diversity and its associated Access and Benefit Sharing Protocol.

The widening gap between discovered and described biodiversity and the difficulties of linking this new diversity to existing names could very well represent the true Achilles' heel of the taxonomic system. Descriptive taxonomy is slow, despite cybertaxonomy and biodiversity informatics. 250 years of modern taxonomy makes that we now recognize nearly 2 million species (Chapman 2009), but in many groups a multitude of synonyms exists for every accepted name. Godfray (2002) clearly exaggerated when he compared the past to a dead weight choking every serious attempt of a modern revision. But, it is certainly true that linking clades, discovered through modern day molecular phylogenies, to often long forgotten names and their type material, consumes a too disproportionate amount of time for taxonomists. Such is unacceptable and therefore curators of natural history collections have started to firmly embrace and invest in the possibilities of the internet to make their collections available and searchable digitally. Taxonomists have also started to explore new ways in making available their research findings faster and more transparently for their peers. Examples of good practice include the EU-funded EDIT Platform for Cybertaxonomy (<http://wp5.e-taxonomy.eu/>) and Scratchpads (<http://scratchpads.eu/>) projects and the US NSF funded morphbank (<http://www.morphbank.net/>) and morphobank (<http://www.morphobank.org/>) projects. Some (Deans *et al.* 2012) dwell on roughly the same ideas and propose to go even further by establishing a database ('Phenobank') that stores standardized, machine-readable semantic descriptions of specimens, not taxa. It remains to be tested if such approach would outcompete classical descriptions of taxa, not specimens, especially if these are framed into an integrative taxonomic approach (Padial *et al.* 2010).

Another underestimated part of the problem is that most taxonomists *sensu* Joppa *et al.*, that is 'those individuals who describe new species' can only devote a fraction of their time on the description of new species. Apart from the multitude of tasks that refrains many from inventorying and describing biodiversity, taxonomists also face a hypothesis driven scientific system that is ruled by Impact Factors or other metrics. This reality seduces many taxonomists to publish an ecological, evolutionary or biogeographic story rather than descriptive taxonomic papers.

So given that species names matter, and that we need to close the gap between discovery and description of diversity, what to do? The answer, just as 'anecdotally' hinted by Joppa *et al.* (2011), might be to increasingly involve those developing countries that have pro-actively chosen to document their biodiversity. This could be done by installing operational hubs in these countries, where local taxonomists as well as specialized technical staff are trained. Development Cooperation agencies from all over the world might be interested in providing financial aid to such initiatives, given of course, that they can be convinced that 'no name means no game'. The Belgian Development Cooperation has, through its taxonomic capacity building program (<http://www.taxonomy.be>), realized this already several years ago.

The *European Journal of Taxonomy* (*EJT*) which publishes descriptive taxonomy, (including re-descriptions of taxa) regional or global checklists as well as taxonomic revisions and monographs, might serve as the ideal forum to release the obtained results, as long as the quality of the descriptions is rigorously assured through thorough peer review and firm editorial policy. If *EJT* accepts this challenge, it will become instrumental in speeding up the delivery of taxonomic names. By doing so, *EJT* will drive the implementation of legally binding international treaties in the field of biodiversity conservation and sustainable management.

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