



Biodiversity, taxonomy and metagenomics

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To cite this article: Ettore Olmo & Ferdinando Boero (2017) Biodiversity, taxonomy and metagenomics, *The European Zoological Journal*, 84:1, 141-141, DOI: [10.1080/11250003.2016.1262634](https://doi.org/10.1080/11250003.2016.1262634)

To link to this article: <https://doi.org/10.1080/11250003.2016.1262634>



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Published online: 28 Feb 2017.



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EDITORIAL

Biodiversity, taxonomy and metagenomics

GenBank (Benson et al. 2013) is a database that contains genetic sequences of species. Godfray (2007) proposed that metagenomics can replace taxonomy in identifying specimens. Indeed, giving names to specimens is not the primary role of taxonomy, the discipline being devoted to the description of new species and to reconstruction of phylogenies, focusing on both genotypes and phenotypes. So, the use of metagenomics for routinary species identification is a welcome technological aid to the study of biodiversity, freeing taxonomists from the burden of sorting and identifying biological material.

Before this task is handed over to machines, however, some data validation is probably urgent. To genetically label a species and deposit the corresponding sequence in GenBank, in fact, specimens are assigned to nominal species through phenotype analysis (i.e., with traditional taxonomy). Genotypes are extracted from phenotypes that are given a name as such. If the determination of the phenotype is wrong, due to scarce taxonomic skills by those who conduct the polymerase chain reaction (PCR), the deposited sequence becomes the (wrong) reference for that nominal species.

If wrong information is stored in GenBank and is then used to compare sequences and to refer them to species, with metagenomics, then the taxonomic mistake is perpetuated and the ensuing species determinations are simply wrong.

Validation of data is essential to make GenBank sequences reliable. Even experienced taxonomists often quarrel about species identities according to different views of what is a species! If the sequenced

materials have not been obtained by experienced taxonomists, possibly during a taxon revision, wrong information can be crystallized in the open space of a database, and its handiness coupled with the illusion of the power of genetic approaches encourages people to believe that it is valid.

It is often the case that many of the sequences obtained with metagenomic screenings, furthermore, belong to unknown phenotypes. Moreover, the “actors” that make ecosystems functions are phenotypes, and not genotypes. So it is essential to know both types of information, in order to build up solid knowledge.

The *Italian Journal of Zoology* has now become the *European Journal of Zoology*, but it will still encourage a cross-cutting approach to zoology, without shortcuts that might give the illusion of objectivity, while being based on subjective determinations of phenotypes.

Revisions of taxa, with the aid of both phenotypic and genotypic approaches, are thus highly encouraged, in the hopes that possible mistakes in GenBank will be identified and corrected, so liberating taxonomists from the burden of routinary identification and giving them more time to develop their science with the aid of molecular techniques.

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