



Phenotypic vs genotypic approaches to biodiversity, from conflict to alliance



Ferdinando Boero^a, Giacomo Bernardi^{b,*}

^a University of Salento, CNR-ISMAR, Italy

^b Department of Ecology and Evolutionary Biology, University of California Santa Cruz, Santa Cruz, CA, USA

ARTICLE INFO

Article history:

Received 1 March 2014

Received in revised form 18 March 2014

Accepted 21 March 2014

Available online 2 April 2014

Keywords:

Morphological taxonomy

Genetic barcoding

Genomics

ABSTRACT

Taxonomy has traditionally been based on morphological characters. Such a “phenotypic taxonomy” has steadily been replaced by the advent of molecular approaches, culminating with the rapid sequencing of genetic barcodes. The convenience of barcoding and its relative ease has relegated “phenotypic taxonomy” to a historical status. The use of genetics is undeniably powerful. It has relatively few biases and DNA can be extracted from challenging groups, where forms are fragile, such as jellyfish, or where early life stages are difficult to connect with adult forms. The problem is that resources are finite, and the rise of one powerful method came with the demise of traditional taxonomy. In addition, genetic methods may be very sophisticated, requiring acute expertise to master its techniques. These two points in combination have resulted in less funding and attraction for traditional approaches. This is doubly unfortunate because, first we are quickly losing experts in organisms that have incredibly complex lifestyles, and second because in order to fully appreciate a molecular taxonomy, one needs to understand the organisms. In a time of rapid loss of biodiversity, time is ripe for traditional and molecular taxonomists to unite in order to better appreciate and understand the complexity of life forms.

© 2014 Elsevier B.V. All rights reserved.

1. Introduction

Biodiversity is a leading concept in biology. The unity of the hereditary material in a living form, based on the universal occurrence of genetic material, leads however to a very broad array of organisms and functions. Individual organisms can be ascribed to natural groups, i.e. species, that are sometimes liable of great phenotypic variability. The recognition of species is still a key problem (Bernardi, 2013). For centuries, species have been defined based on morphological characters, which is one aspect of the phenotype of the species. Hence, we are calling this traditional approach phenotypic taxonomy. With the advent of genetic sequencing, defining species on the basis of their genetic characters has become readily possible, thus it is called here genotypic taxonomy. Genetic barcoding (the main method used in genotypic taxonomy) is based on a standard portion of the genome common to all species, but different for each species. Specimens belonging to the same natural group (i.e. species) share the same sequence of that particular portion of their genome. Barcoding life is thus a very convenient practice to identify and recognize species (Ward et al., 2005). The shift from the phenotypic to the genotypic approach is a very convenient choice and allows to circumvent the complexity and ambiguity of phenotypes, linked to their plasticity. This revolutionary approach somehow led to the dismissal of traditional taxonomy, based on phenotypic

traits, and taxonomic expertise is slowly disappearing (Boero, 2010; Tautz et al., 2003). Why bother with cumbersome descriptions based on tiny details, often creating confusion and bitter disagreements among taxonomists (e.g. splitters vs lumpers)? Sequences, instead, are definitive and simple. Once a species is barcoded, and the barcode is deposited in a data bank, it is sufficient to “scan” specimens (or even portions of them) to confirm their identification. Massive scanning allows for species lists without even sorting the specimens.

1.1. The bright side

Barcoding of life requires collection and morphological identification, so as to assign a phenotype to a standard Linnean binomen, and then a barcode. By doing so, that name can be associated to a sequence that, once deposited in Genbank, can be the basis of future identifications. It is sufficient to insert the barcoded sequence in Genbank and, if the species has previously been barcoded, the sequence is matched to a name.

This is very convenient to produce species lists from specific locations, leading to biodiversity inventories. Furthermore, once barcoded, the stages of the life cycle of a species can be linked to each other, solving problems that have been afflicting taxonomy for centuries. In the Medusozoa (Cnidaria), for instance, the presence of a benthic polyp stage and a planktonic medusa stage, with much different morphologies, has led to great taxonomic confusion due to the difficulty of elucidating life cycles (Miglietta and Cunningham, 2012). Barcoding one

* Corresponding author at: 100 Shaffer road, Santa Cruz, California, 95060, USA.
E-mail addresses: boero@unisalento.it (F. Boero), bernardi@ucsc.edu (G. Bernardi).

stage allows matching stages with each other, thus solving a long vexing issue. The advantages are great and undeniable, there is no question that this is a powerful tool that should be part of the standard equipment of every taxonomist (Tautz et al., 2003).

1.2. The dark side

The problem behind all this is that expertise on phenotypes (i.e. traditional taxonomy) is rapidly vanishing and misidentified barcoded phenotypes are frustratingly common. To be sure, misidentifications are very common in traditional taxonomy too, therefore the issue is not confined to barcodes. Yet, the taxonomic problems are often so complex, that only a taxonomist expert in both phenotypic and genotypic taxonomy can clarify the issue by using the combined power of both approaches. Instead, once a species name is “frozen” into a barcode, the possible mistake is perpetuated. It is unfortunate that sequences deposited in Genbank might have been ascribed to the wrong nominal species, thus increasing confusion instead of clarifying issues.

1.3. Species roles

The easy way to species identification through the barcode, moreover, is giving the impression that with the genotypic approach the problem of biodiversity assessment is solved. Biodiversity, however, is not only a list of species. Each species gives a different contribution to ecosystem functioning, while playing an ecological role through the activities of its phenotypes (Piraino et al., 2002). The study of biodiversity is not simply the production of a list of names, and its linking to ecosystem functioning gives a meaning to these names (Costello et al., 2013).

1.4. The study of biodiversity

A modern taxonomist should be trained in morphology and genomics, but also understand well the physiology, including the life cycles, ecological niches, and biogeography of the organism groups studied. A species name is only the visible part of the iceberg. Behind each sequence there has to be a name, a phenotype (with all its variability and life forms), an ecological role, and a distribution. A modern “biodiversitologist” is a different kind of taxonomist. Unfortunately, the people who practice the genetic approach often do not master morphology, and those who master both morphology and genetics often do not master physiology and autoecology. Then, all this must be put in the framework of ecosystem functioning, passing from the physiology of individuals to autoecology and further to synecology, so as to close the circle that comprises biodiversity and ecosystem functioning.

1.5. Cooperation pays more than competition

So far, also due to different impacts of specific tribunes, the phenotypic and the genotypic approaches to the study of biodiversity have been competing, with the dismissal of phenotypic expertise based on the assumption that genotypic expertise is sufficient to solve biodiversity problems. We concur that, eventually, nobody is really claiming this, all recognizing that traditional taxonomy is very important, but the situation is nevertheless pushing phenotypes to the back. For some

popular groups (e.g. butterflies and shelled molluscs) the future of traditional taxonomy is passing to the amateurs (Fontaine et al., 2012), with the risk that they will use only morphology and disregard genetics, leading to an even messier situation than the present one. The two approaches must not compete but, instead, they should cooperate since none of the two does have logical primacy over the other and must be used in conjunction. This is still difficult also due to the features of journals, often focusing just on phenotypes or on genotypes.

1.6. Future work

All taxa need to be thoroughly revised, by using all available approaches, voucher specimens must be barcoded and safely deposited, to allow for future controls. Monographs must be set up in the form of databases where, species by species, each name must receive its barcode, an assessment of its morphology throughout the life cycle, and a reconstruction of its basic physiology (which includes its tolerance to physical and chemical features of the environment), its trophic niche (what is eaten by that species, and who feeds on it), its geographical distribution, and its presence in the recognized habitat types of the realm that it lives in.

A list of names, as that provided by the European Register of Marine Species, is just akin to a phone book that contains the names of all the people living in a town, but that does not provide their telephone number, their address, or what makes them unique.

The number of currently described species (especially from a phenotypic point of view) is about two million, but estimates of the number of species inhabiting the planet is at least four times that much (Mora et al., 2011).

There is still a lot of work to do to assess the biodiversity of planet Earth, and the alliance of phenotypic and genotypic approaches is promising exciting developments. New human capacities are to be built, to be given the most important scientific problem of all times: understand the variety of life forms that inhabit this unique planet and how they interact to make ecosystems function, and thus allow our survival, before it is too late.

References

- Bernardi, G., 2013. Speciation in fishes. *Mol. Ecol.* 5487–5502.
- Boero, F., 2010. The study of species in the era of biodiversity: a tale of stupidity. *Diversity* 2, 115–126.
- Costello, M.J., May, R.M., Stork, N.E., 2013. Can we name Earth's species before they go extinct? *Science (New York, N.Y.)* 339, 413–416.
- Fontaine, B., van Achenberg, K., Alonso-Zarazaga, M.A., Araujo, R., Asche, M., et al., 2012. New species in the Old World: Europe as a frontier in biodiversity exploration, a test bed for 21st century taxonomy. *PLoS ONE* 7 (5), e36881. <http://dx.doi.org/10.1371/journal.pone.0036881>.
- Miglietta, M.P., Cunningham, C.W., 2012. Evolution of life cycle, colony morphology, and host specificity in the family Hydractiniidae (Hydrozoa, Cnidaria). *Evol.: Int. J. Org. Evol.* 66, 3876–3901.
- Mora, C., Tittensor, D.P., Adl, S., Simpson, A.G.B., Worm, B., 2011. How many species are there on Earth and in the ocean? *PLoS Biol.* 9, e1001127.
- Piraino, S., Fanelli, G., Boero, F., 2002. Variability of species' roles in marine communities: change of paradigms for conservation priorities. *Mar. Biol.* 140, 1067–1074.
- Tautz, D., Arctander, P., Minelli, A., Thomas, R.H., Vogler, A.P., 2003. A plea for DNA taxonomy. *Trends Ecol. Evol.* 18, 70–74.
- Ward, R.D., Zemlak, T.S., Innes, B.H., Last, P.R., Hebert, P.D.N., 2005. DNA barcoding Australia's fish species. *Philos. Trans. R. Soc. Lond. Ser. B Biol. Sci.* 360, 1847–1857.