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Loosing the connection between the observation and the specimen: a by-product of the digital era or a trend inherited from general biology?

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Abstract

The original efforts of early naturalists are now placed in another context. Instead of adding lots of particulars to a catalogue of Life, the idea is now to contribute to an organized picture: comparative biology and general biology have merged. Systematics or the related sciences of Biodiversity employ a reasoning analogous to the one followed by early general biology when it separated from natural history and activities associated with collections in the early XXth century. There is a presumption one is already knowledgeable about laws or general patterns when studying biological processes or adding species: both contribute to the general picture. As a consequence of this state of mind, many authors do not feel the need for saving specimens. However, saving specimens is not only a way to keep records in a world which is still being discovered, it is also a very efficient way to store information and to allow one to return to the original specimens, thus generating additional data to answer other questions. We must be fully aware of both the rationale but also the present-day state of mind, in order to keep our motivation in the pursuit of an adequate sampling of Biodiversity.

Key words: General biology; comparative biology; collections; history of science.

Introduction

Many recently published studies or opinions have remarked that biological observations are increasingly disconnected from specimens and are following a trend leading to the virtualization of the biological sciences. For example, many DNA sequences have been made available without any relationship to a voucher (Pleijel *et al.* 2008). The occurrence of species may be recorded in databases exclusively on the basis of observations (Gaiji *et al.* 2013). And very recently, it has been argued that species descriptions and taxonomic name availability should be possible using a foundation that is limited to digital pictures (Minteer *et al.* 2014; Marshall & Evenhuis 2015). All these issues have provoked considerable controversies between two groups of scientists that could be tentatively grouped as modern versus old-fashioned scientists or as careless versus serious scientists, depending on which side the observer feels closest to (Rocha *et al.* 2014; Pape 2016;

Ceríaco *et al.* 2016). However, even if all these contributions disagree on how to use virtual data, they all share a common opinion that this trend can be explained by the development of the digital techniques that make everything virtual, including scientific data. It has become so easy to take a picture, to record a sound or to geolocate an occurrence, to save it on a server and to globally share it through the world wide web that it could become difficult to preserve the old standards of keeping voucher specimens. In addition, collecting specimens has also become problematical for ethical, conservation and legal reasons in some cases (e.g., Minteer *et al.* 2014). If indeed these are the reasons for such a disconnect between the observation and the specimen, we could hardly expect this trend to reverse but merely to increase.

Actually, I surmise that this trend is not necessarily a simple consequence of technological evolution. Digital techniques certainly facilitate the relative increase in virtual observations but they may not be the only and primary causes for such a trend. Identifying the causes of this trend is important, as it could allow for a better management of the problem from both methodological and practical points of view.

Following this line of thought, I argue that this trend could be traced back to the early origin of scientific approaches—the disciplines of general biology that separated from the pursuit of natural history collections and from comparative biology at the beginning of the XX^th^ century. Finding shared ways of thinking between the diversity sciences of the XXI^th^ century and the founders of general biology in the early XX^th^ century could seem quite surprising and I will briefly explore the causes behind such a similarity.

Disconnection from specimens in the early XXth century: the rise of general biology

The rise of natural history in the XIXth century provided an early foundation for comparative biology. The basic idea was to catalogue the diversity of Life and to organize it in a classificatory system, as seen for instance in Linnaeus' (1758) renowned work. From this system of classification arranged according to different subordinated groups, one which intuitively followed the model of patterns—the famous orderliness—of Life, evolutionary thinking eventually followed (Lecointre & Le Guyader 2006). At the beginning of this period and even after the early growth of evolutionary thought, scientists mostly took care of particulars, practicing an idiographic science where every natural item—particularly species—were considered in isolation as separate items (Mahner & Bunge 1997). These practices were also followed in the absence of any explicitly stated law that could explain the origin of different natural items/species. Later, after evolutionary thought had developed and strengthened, the focus of natural history remained fixed on particulars with the search for monophyly or for synapomorphies (Haeckel 1866; Hennig 1966). The notion of particulars just moved from species to higher-rank taxa or to clades. Comparative biology was born, including the various notions of biological species, relationships and homologies (Nelson 1970). The only assumption regarding the biological process behind these notions was descent with modification (Farris 1983).

Many other disciplines in natural history, such as ecology or genetics, developed after this early stage in comparative biology, around the beginning of XXth century. They immediately adopted another view concerning the study of Life: they focused on universals. From the beginning, and following Darwin's major contribution (Darwin 1859), the idea guiding such disciplines was to capture general laws that explained diversity, for example the laws of heredity or the principles of competition or those concerning the ecological niche (e.g., Fischer 1930; Gause 1934). Biology became a nomothetic science, a general biology. The immediate consequence of this great change in thinking is that one more “different” species does not change the picture of the whole, which is no longer organized according to species but instead according to the laws discovered by these disciplines. Looking at the metrics of biodiversity whose origin dated back to this period is enlightening: species richness for example is one of the most widely used measures in ecology, which does not consider the diversity of species but counts them all as equal (Pellens *et al.* 2016).

This intellectual process within general biology culminated in the development of iconic laboratory organisms, the so-called model organisms that were supposed to represent entire areas of Life (*Drosophila* for insects, *Arabidopsis* for plants, Zebra fish for Pisces, etc.) Knowing the processes at work in such organisms was supposed to provide sufficient insight regarding all of Life’s diversity (Jenner 2006).

Collecting different species was no longer useful for general biology, because the focus was not on their diversity but on their very general common traits. Why fill rooms with specimens of many different species when we only need to dig thoroughly within a few, in order to discover the laws that are supposed to drive the ecology, the functioning or the evolution of all existing species?

Comparative biology merges with general biology in the digital era

The main and recurrent argument cited in the relevant modern literature to justify the very low priority given to the collection of specimens is based on the speeding up of any kind of data collection process. Sadly, this is also the most common argument cited with regard to improvements in systematics (but see de Carvalho *et al.* 2008). Many authors have repeated this stance, basically arguing that we need to accelerate the information collection process before the extinction crisis has definitely crashed the biosphere. The idea is to complete the picture as fast as possible and to fill in the holes in the knowledge of biodiversity we have already organized (e.g., May 2004; Padial *et al.* 2010).

These kinds of description or sampling programs rarely incorporate scientific strategies on how and why to achieve this inventory but instead focus on procedures or tools that are supposed to speed up the process. So, the main idea is now how to finish building the database since a lot of information is already organized and available. Natural History and Comparative Biology were sciences of particulars and recently tended to become sciences of universals: species were no longer unknown entities described in isolation but instead small pieces of a huge puzzle that was already well-reconstructed (e.g., Mooers & Cotgreave 1994).

The idea entertained by some systematists or phylogeneticists is therefore that we continue to need specimens but occurrences or pictures or any other kind of digital record—which are so easy to procure instantaneously—become acceptable substitutes, because the species involved in these studies have already themselves been placed within a widely known context (e.g., Marshall & Evenhuis 2015). This is the core of the misleading concept of predictive classification (Grandcolas *et al.* 1997): the phylogenetic system should be complete enough to predict many characters within any species to be described in the future (Daly *et al.* 2012). Actually, a classification is not predictive sensu stricto but informative, a state of affairs that does not possess the same properties.

A conclusion and a perspective: collections and specimens are not just vouchers for studies in our present

These new conceptions in systematics refer to ideas that pertain to the general biology of the XXth century: contributing to an organized picture does not oblige one to keep specimens of everything. The problem behind this conception is that at first glance it looks reasonable and such that we might all agree to some extent. For example, who is willing to kill any specimen of common birds we observe every day in order to survey their populations? The rationale is that they are sufficiently well-known (in addition to obvious ethical obligations!), so we are not obligated to keep specimens. This rationale, though acceptable in some specific cases, cannot be taken as a general rule when we are dealing with poorly known organisms studied by only a few taxonomists in the whole world and obviously lacking faunistic or identification guides for any continent.

In addition, and most fundamentally, collection specimens are not only vouchers for checking the identifications performed in a given study, or for repeating analyses performed with other tools (e.g., molecular analysis performed after morphological identification).

Collection specimens become independent records of biodiversity, allowing for all kinds of future research (Suarez & Tsutsui 2004; Dubois & Nemésio 2007). Those few herbarium specimens sampled fifty years ago to revise a common European genus can now reveal invaluable data for the study of climate change as well as changes in phenology or species distribution, for example (Le Bras *et al.* 2017). In addition, we must understand that publishing an observation devoid of links to a specimen is already an outdated failure, which is missing the next boat of metagenomics and metabarcoding. In the case of those analyses that conflate DNA specimen and observation, the problem has already become how to connect global DNA with specimens (Pellens *et al.* 2016).

As a general conclusion, scientists studying biodiversity should not naively reiterate the dispute of particulars versus universals within their limited scientific domain. They should understand that a sound scientific strategy must be conceived to conduct the collection of specimens, one that must go beyond everyday taxonomic or any other forms of limited research activity. This strategy should incorporate the idea that the development of science is not linear and that new developments in totally different directions may be based on some earlier studies or specimens. Scientists should also keep the general picture of the History of Science in Biology in mind, with the aim of not repeating the mistakes made in earlier times in other contexts.

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