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The view of Systematics on Biodiversity

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1.1. Introduction

There are several ways to evaluate Biodiversity, which is a multi-level concept with multiple purposes. Each consideration of this concept generally involves the prism of a scientific discipline, a study level or a specific purpose [MAC 08]. Thus, scientists focus sometimes on intraspecific diversity, sometimes on interspecific diversity, or even on the diversity that can be studied at the level of ecosystems, etc. Disciplines usually concentrate on their study subject, such as genomics or population biology on diversity within genomes or populations, respectively.

For my part, I would like to share several general reflections on Biodiversity, which are inspired by the scientific contribution of a discipline, Systematics. The origin of this discipline is ancient and is still often assimilated in people's minds with description and classification tasks, as they were practiced at the time of the great naturalists of the 18th and 19th centuries. However, for over half a century, Systematics has been a major player in evolution biology, in particular with phylogenetic analysis, which appeared after the work of the systematist Willi Hennig in the 50s-60s and which spread throughout Biology [OHA 92].

Systematics contribution pertains to the field of comparative biology [NEL 70]: it compares organisms and their characteristics, and draw conclusions in term of evolutionary relationships (phylogenies, homologies); it establishes diagnoses (taxonomy). Far from denying the variability of the living world [DEB 01], which is especially integrated in species concepts, it studies it on the contrary to select

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invariants, which will make it possible to study the origin of Biodiversity, namely the way organism characters set up.

My goal is not to present Systematic case studies of biodiversity, but to highlight several significant points which Systematics can help us to understand or value regarding Biodiversity, and which are linked in a very interesting way to those uncovered by ecological approaches. The purpose of this presentation is obviously not to promote a discipline for its own sake, but to provoke reactions and reflections through the contrast between different points of views.

1.2. Species: all different

In the 80s, the creation of the concept of Biodiversity and the advent of phylogenetic analysis made it possible to reintroduce in people's minds a very valuable asset: the notion of diversity between species, which had faded away since the rise of General Biology[2] at the beginning of the 20th century [GRA 17].

In fact, General Biology and what we still call today Life Sciences (with components called System Biology[3] or Integrative Biology[4]) appeared and developed with the idea of seeking and defining main general principles common to all organisms, like for example the "laws of heredity". It is also at this time that organisms-models, which were supposed to represent on their own entire sections of the living world, emerged, such as the Thale Cress *Arabidopsis thaliana* for plants or the common fruit fly *Drosophila melanogaster* for insects. From the moment one focuses on the main constitution or operation principles supposedly common to all organisms, one is concerned far less with their differences and diversity. General Biology then contributes to the study of organism evolution, because it identifies general heredity or operation mechanisms of organisms. However, it does not then study the evolutionary History of different groups of organisms in interaction with the environment, which is the source of Biodiversity.

This eclipse of History (meaning evolutionary History), as the systematist Dan Brooks and the ethologist Deborah McLennan called it [BRO 91], then stopped in the 80s when the community of biologists became aware again of the importance to consider differences between species. At that time, the term biodiversity was coined

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[2] General biology studies in detail mechanisms in a few species and draws conclusions that can supposedly be generalized to the functioning of whole living world.

[3] System biology studies the functioning of living systems from the cell to the tissue, by focusing on cellular and molecular approaches.

[4] Integrative biology integrates physiological and biophysical aspects in the study of organism functioning.

by Thomas Lovejoy, Walter G. Rosen and Edward Osborne Wilson [WIL 88]. Phylogenetic analysis was formalized at the same time [WIL 81], which allowed it to benefit from the advent of molecular biology and its massive provision of data to study Biodiversity. The study of the living world thus regained not only intraspecific variation (population genetics in particular) and interspecific interactions (ecology), the study of which was well developed since the beginning of the 20th century, but also differences between species, the study of which was less advanced, especially at the evolutionary level. In all these ways, differences between species became again a subject of analysis and not a background noise to be removed in order to study the laws of the living world.

This awareness that the variety of living organisms must be a subject of scientific and societal concern, as much as the unicity of some processes in the whole living world was reflected in many different ways, including in Biodiversity sciences. For example, Biodiversity metrics changed, especially thanks to Systematics. We went from the rather universal use of specific richness, a traditional measure in ecology which considers all species as identical (a tribute to General Biology at the beginning of the 20th century), to more sophisticated metrics.

This way, Faith [FAI 92] offered phylogenetic diversity or PD, a measure taking into account for a set of individuals the total length of the phylogenetic tree branches connecting them: it thus expresses the quantity of common characteristics and differences characterizing them. Even though it is correlated with the specific richness (the more species are considered, the more the number of branches linking individuals in a tree increases, and therefore the sum of their lengths), PD provides much more information than a simple cardinal sum. It has the great advantage of being a potentially overall measure of genetic and phenotypic diversity, and thus goes beyond geographic, regional or local levels [VER 15; PEL 16-1].

We could mention another example with the first version of the "comparative method" of the 80s, which offered to calculate statistical causal relations between traits or environments [CLU 79]. This method considered species as equivalent here again and simply controlled that they were not statistically independent in case of close relationships (comparing ten squirrels and ten mice would statistically come to only comparing two groups!).

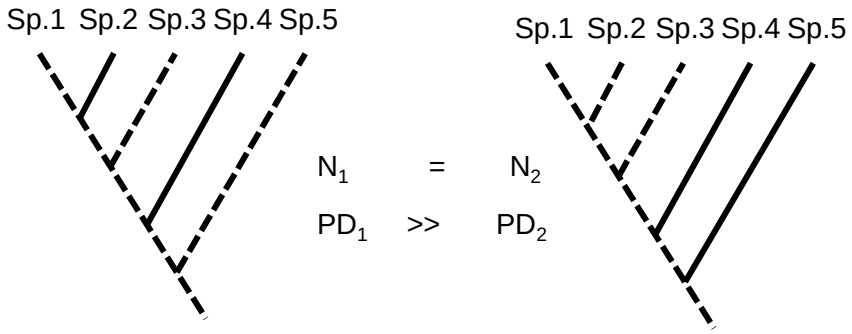


Figure N.1 *A theoretical phylogenetic tree in which two sets of 3 species are chosen (dotted lines). The specific wealth of the two sets is the same (N=3), but the PD of the left selection is much higher (with especially sp.5 which is the sister-group of the rest of the tree instead of sp.2, the sister-group of sp.1).*

This method then evolved into the phylogenetic analysis of evolution (with modern "comparative phylogenetic methods"), which compares several species evolutionary histories immediately considered as different, histories that are rebuilt by establishing potential homologies [BRO 91].

1.3. How about studying the other 90%?

This welcome awareness of the significance of the variety of living organisms certainly also helped to become fully aware of the terrifying disaster represented by the current crisis of Biodiversity. The Biodiversity crisis is serious, because individuals belonging to different species represent different values, functions and services: reducing their number and variety is equivalent to direct losses in all these aspects.

Nevertheless, there is still an intellectual frontier that Systematics can help us to cross, we mean understanding the significance of the 90 % of current Biodiversity still unknown. It is in fact a paradox to read the alarming numbers of extinctions, which are unfortunately already effective or to come within a few decades [BAR 11; REG 15] and which apply to what we know (10%), and which unintentionally bypass what we do not know (90%). Without being particularly concerned with cataloguing or inventory, we should still acknowledge that our sample of the living world is hardly representative in the light of the numerous issues raised, including the crucial issue of the extinction crisis.

Thus, do we really know what is going to disappear and, *a fortiori*, what was the role of the biodiversity that disappeared before we could know it [REG 09]? Can we be content with the possibility of a probable functional redundancy essential to the operation of ecosystems, without really knowing how many species are concerned and really redundant? From this point of view, and knowing that rare species can play significant parts in ecosystems [MOU 13], which serious consequences are going to have the extinctions of rare species that are still unknown? What would the 90% remaining Biodiversity provide in terms of knowledge, especially in the very current field of Biomimetics or Bioinspiration [BEN 16]? For the record, out of approximately one million known species, only 76,000 are concerned by patents [OLD 13]. What would it be with ten times more species known?

In view of this paradox - extinction of a mostly unknown set - the most common response is often only operational or logistic: we do not know enough about Biodiversity, never mind, let us use such and such tool or procedure and, in 20 years, we will have substantially increase our knowledge [MAY 04; DAL 12]. However, without neglecting the main programs of Biodiversity exploration, to which we can only subscribe with enthusiasm, it seems mainly important to realize that we should all address the issue of the still unknown Biodiversity and not leave it to the exploration programs of the living world alone (Systematics Agenda 2000, Barcode of Life, *La Planète revisitée*, and soon Planetary Biodiversity Mission). Almost as if the genomics discipline had only been built and practiced by consortiums composed for the sequencing of the first complete genomes.

This means that there is a requirement to improve ethics and to make taxonomic knowledge available, requirement that should be shared by all scientists studying Biodiversity. Let us not continue thinking in terms of general biology, as if knowledge research should only be content with the quest of universal aspects (laws, processes, etc.). We must realize that the increase in knowledge on Biodiversity specificities is also a key study subject. In this respect, the Nagoya Protocol and its national regulatory implementation are often seen as a restriction by scientists, whereas they helpfully remind us our ethical obligations. Laboratories studying biodiversity must train or house scientists competent in taxonomy, who are nowadays disappearing [GRA 12]: it is not enough to barcode, metabarcode, database, digitalize, geolocalize, etc. specimens to save information specific to a study or useful to society. It is also very often necessary to directly contribute to taxonomy, by describing or reviewing taxons. Information and knowledge access and sharing are only possible through a taxonomic system with reference specimens and names. The amazing molecular, digital and computer means, which are rapidly developing, only make this linkage even more vital [PEL 16-2]. This challenge is particularly crucial in the case of micro-organisms, whose accessibility is limited by

our powers of perception, and which are important in all respects, including through their omnipresence within other organisms, with which their interactions (for example, mycorrhizae, intestinal microbiome, etc.) are essential [SEL 17]. In their case, molecular data are directly integrated into a traditional taxonomy, which is very much alive. Nevertheless, beyond metabarcoding approaches, the ability to cultivate species or keep strains are significant issues, that microbiology laboratories have well understood.

1.4. Biodiversity changes

Systematic and comparative design of Biodiversity also reminds us that it is derived from a long evolutionary process, that it can be phylogenetically characterized, including at a specific level, and that it is not defined as such, in a kind of "fixist" or more specifically essentialist abstraction [ROB 17] as our short human perception level would suggest.

It is necessary nowadays to reconcile so-called functionalist, "microevolutionist" and "macroevolutionist" designs. There is no useful and significant microevolutionist evolution biology considering the population mechanisms to which we are confronted at our timescale (a few years or a few decades), and another quaint and "cultural" macroevolutionist evolution biology dealing with fossils and building phylogenies* for Platypus, Ginkgos and other Dodos at a timescale incompatible with our existence (millions of years).

We must know the origin and selective context of phenotypic traits to study them and understand the adaptive phenomenon at the population level. The great development of "tree-thinking" (*i.e.* the use of phylogenetic trees) in biology since the 90s has thus taught us that a lack of macroevolution contextualization often made us build the microevolutionary explicative model backwards [BRO 91]: for example, in some spiders, models trying to explain sexual dimorphism through male dwarfism strayed by not considering the gigantism of females [COD 97]. Not linking micro- and macroevolutionary studies would be like rejecting all the watches with no second hand, because we are disappointed not to see the movement of the hour and minute hands when quickly looking at the watch face. And yet, we need to tell time.

This level of - systematic and phylogenetic - Biodiversity macroevolutionary study is not only an essential explanatory foundation to conduct microevolutionary studies, it also helps to assess and perceive the living world in all its diversity. Once more, phylogenetic diversity is not only a good overall metrics, but it also allows us to ethically consider Biodiversity.

In a phylogenetic tree, no organism is superior to another. All current or fossil organisms, although they are very different, are the leaves of a tree, the root of which is an abstraction: there are only sister-groups within a tree, which does not show genealogies, but the kinship relationships between species [GRE 08; CRI 05; GRA 14]. Phylogenetic trees are then good media to explain that gradist[5] or anthropocentered reasoning is absurd, both for scientists and all publics [FOR 09; MAC 12].

1.5. Challenging decades

We are then at a crucial and paradoxical moment for the study and consideration of Biodiversity. It has never been so well known, but its greatest part still remains to be discovered. This whole biodiversity - known and unknown - is at risk of major extinction in the next decades. Our means to study it have never been so powerful but, paradoxically, the flood of data created by these means is in itself a challenge for knowledge access and sharing. This challenge has also a strong geopolitical component. Biodiversity is particularly significant in the South, and access and sharing must not only be an ethical concern common to the whole humanity, but also a desire to balance again knowledge, expertise and means between North and South political powers, in order to better share the environment common to all of us.

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[5] Misleading concept, the origin of which is often associated with Aristotle's Chain of Beings; it considers that the living world is graded according to complexity with the simplistic idea of an evolutionary progress that would result from adaptation; anthropocentrism is a form of gradism, because it puts human kind at the top of the grade.

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