



The galaxy of the non-Linnaean nomenclature

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Abstract Contrary to the traditional claim that needs for unambiguous communication about animal and plant species are best served by a single set of names (Linnaean nomenclature) ruled by international Codes, I suggest that a more diversified system is required, especially to cope with problems emerging from aggregation of biodiversity data in large databases. Departures from Linnaean nomenclature are sometimes intentional, but there are also other, less obvious but widespread forms of not Code-compliant *grey nomenclature*. A first problem is due to the circumstance that the Codes are intended to rule over the way names are applied to species and other taxonomic units, whereas users of taxonomy need names to be applied to *specimens*. For different reasons, it is often impossible to refer a specimen with certainty to a named species, and in those cases an *open nomenclature* is employed. Second, molecular taxonomy leads to the discovery of clusters of gene sequence diversity not necessarily equivalent to the species recognized and named by taxonomists. Those clusters are mostly indicated with informal names or formulas that challenge comparison between different publications or databases. In several instances, it is not even clear if a formula refers to an individual voucher specimen, or is a provisional species name. The use of non-Linnaean names and formulas must be revised and strengthened by fixing standard formats for the different kinds of objects or hypotheses and providing permanent association of ‘grey names’ with standardized source information such as author and year. In the context of a broad-scope revisitation of aims and scope of scientific nomenclature, it may be worth rethinking if natural objects like plant galls and lichens, although other than the ‘single-entity’ objects traditionally covered by biological classifications, may nevertheless deserve taxonomic names.

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1 Naming animal species, between Linnaean nomenclature and data aggregation in biodiversity databases

1.1 Naming matters

It is not difficult to imagine how seriously the scientific community is troubled when it is discovered that under the name of a popular model organism more than one species have been confused and are eventually recognized as distinct only after decades of studies and hundreds of publications. This happened, for example, with the ascidian (or sea squirt) *Ciona intestinalis*. Only 5 years after its genome sequence was published (Dehal et al. 2002), it was realized that the stocks used until then in the labs belong to two different species (Iannelli et al. 2007; Brunetti et al. 2015). Similarly, at least three species have been treated as one in the case of another popular model animal, the leech *Helobdella triseriatis* (Siddall and Borda 2003; Bely and Weisblat 2006; Kutschera et al. 2013). Problems are even more serious when organisms of economic importance are involved, as in the case of the whiteflies long confused under one name, *Bemisia tabaci*, this eventually explaining why different ‘strains’ of this agricultural pest differ in their use of the host plants and respond very differently to insecticides (Boykin et al. 2018), thus making it very difficult to compare the results of different studies (e.g., Legg et al. 2002; Sseruwagi et al. 2005; Mugerwa et al. 2012).

As the following analysis will show, there are good reasons for reiterating today in explicit terms a statement that Linnaeus already expressed in aphorism n. 240 of his *Philosophia Botanica* (1751): *Nomina si nescis perit et cognitio rerum*. The importance of names for the units of biological classification (technically known as *taxa*) is becoming increasingly prominent today, with the aggregation of biodiversity information from different sources into large, sometimes huge databases (cf. Leonelli 2016): “Without a stable and precise name as an identifier, it will be difficult to accumulate precise knowledge about exactly this species. A name is not an end to our understanding of a taxon, but a means and a beginning” (Ryberg and Nilsson 2018, p. 37).

The names or organisms, however, are both important¹ and problematic. As recently discussed by Sterner and Franz (2017), “data may lose their value when

¹ Unfortunately, nomenclatural curation does not seem to be high priority in otherwise well-managed data bases. For example, in the list of taxa to which are referred the entries of the BOLD database (about which more in Sect. 3.2.), several species are listed twice, under alternative combinations of the same specific epithet with two different generic names, but the taxonomic identity of these names is not flagged. The following examples where the first of the two Latin names corresponding to the same species is the one in current use according to the Roskov et al. (2019) show that duplicate names are found in that database also for popularly known animals, such as yellow-cheeked gibbon (*Nomascus gabriellae*=*Hylobates gabriellae*), pygmy marmoset (*Cebuella pygmaea*=*Callithrix pygmaea*),

taken out of context and aggregated together”. As we will see below, this is true both of the names of species taxa, the fundamental units of biological classification, and of the corresponding terms used as identification tags for individual specimens or sets of specimens. In either case (scientific names of species and species-level identification labels) these terms have usually the form (although not necessarily the meaning) of the names of the official scientific nomenclature, but sometimes depart from the latter in more or less obvious and more or less extensive way.

Even when the nomenclature is formally compliant with the official rules (more about this in the following Section), scientific names may become ambiguous when placed in contexts other than those for which they were originally proposed. In particular, as discussed below, names become ambiguous when used in a database in which are aggregated biodiversity data from sources that adopt alternative classifications for the same group of organisms. This is an example of the general principle illustrated by Piantadosi et al. (2012), that even the entries of a well-designed communication system will be ambiguous when placed in a new context. Again in agreement with Piantadosi et al. (2012, p. 282), ambiguity is intended here as “less than total specification of meaning within a unit” in a communication system.

Once acknowledged that “From Linnaeus onward, the efficiency, stability, and precision of communication have been leading motivations for the design and revision of practices and rules for biological nomenclature” (Sterner and Franz 2017, p. 107), we must accept that, as practices involving the use of species names have ever been changing, with a huge acceleration in our era of information technology, the adequacy of the Linnaean system deserves revisitation and new forms of disambiguation may require implementation.

This causes tremendous problems, only part of which can be solved by developing and implementing new solutions in the infrastructure of biodiversity databases (as recommended e.g. by Sterner and Franz 2017) and by careful filtering their input data; other problems, rather than emerging at the time individual sources are aggregated, are intrinsic to data: the solution will only be possible by the adoption of new rules to be followed at the time species-level labels are first used in publications or databases, as discussed in Sect. 4.

1.2 Linnaean nomenclature

Animal and plant species are usually given scientific names in accordance with sets of rules the current version of which are the fourth edition of the International Code of Zoological Nomenclature (International Commission on Zoological Nomenclature 1999), in force since 1 January 2000, and the International Code of

Footnote 1 (continued)

Malayan tapir (*Acrocodia indica*=*Tapirus indicus*), Bahia porcupine (*Sphiggurus insidiosus*=*Coendou insidiosus*), pygmy hippopotamus (*Hexaprotodon liberiensis*=*Choeropsis liberiensis*), alpaca (*Vicugna pacos*=*Lama pacos*), harp seal (*Pagophilus groenlandicus*=*Phoca groenlandica*), American mink (*Neovison vison*=*Mustela vison*), eyra (*Puma yagouaroundi*=*Herpailurus yagouaroundi*), ground pangolin (*Manis temminckii*=*Smutisia temminckii*), long-tailed pangolin (*Manis tetradactyla*=*Phataginus tetradactyla*), tree pangolin (*Manis tricuspis*=*Phataginus tricuspis*).

Nomenclature for Algae, Fungi, and Plants (Shenzen Code) (Turland et al. 2018), in force since 29 July 2017. The names of bacteria are also ruled by a Code (Lapage et al. 1990). Except when otherwise specified, in the following I will only refer to the names of the organisms traditionally treated as animals for the sake of nomenclature. I will also ignore the nomenclature for taxa above the species level, thus considering only species-group names, plus with a diversity of formulas more or less strictly comparable to the Code-compliant names for species-group taxa.

This system of names disciplined by the Codes is known as the Linnaean nomenclature; indeed, it continues the tradition established by Linnaeus, for plants with the first edition of *Species Plantarum* (1753), for animals with the tenth edition of *Systema Naturae* (1758). Linnaean nomenclature is based on the use of Latin binomials, e.g. *Homo sapiens*, as the names of the species, the basic units of a hierarchical classification that acknowledges ranks such as species, genus, family (not yet in Linnaeus), order and class, in ascending order.

1.3 How far is a Linnaean name reliable and informative?

As stated in the Preamble to the International Code of Zoological Nomenclature, “The objects of the Code are to promote stability and universality in the scientific names of animals and to ensure that the name of each taxon is unique and distinct”. However, universality and stability of nomenclature do not imply that the valid name for a species must remain unchanged forever: it will depend instead on the taxonomic context in which it is embedded, and this context has been changing since Linnaeus, and continues to change to date. For example, Linnaeus (1758), when introducing scientific names for the hippo and the Brazilian tapir, placed both species in the same genus, as *Hippopotamus amphibius* and *Hippopotamus terrestris*, respectively. Soon thereafter, Brünnich (1772) introduced the genus *Tapirus* and the valid name for the Brazilian tapir is since then² *Tapirus terrestris* and Linnaeus’ original binomen (*H. terrestris*) is reduced to a superseded combination (a combination of the same specific epithet—*terrestris*, in this case—with the name of a genus to which the species is no longer referred). A scientific name also ceases to be the valid name for a species when (or as long as) it is shown to correspond to a species for which a senior name is available: according to the Code, the senior name is the valid one and the junior synonym must not be used unless the synonymy is eventually refuted by a later taxonomic revision. Thus, for example, the fish described by Risso (1810) as *Raia punctata* is universally regarded to be the same as the fish previously described by Delaroche (1809) as *Raja*³ *asterias*, under which name it is currently known (Fricke et al. 2019). In taxonomic databases, synonymies are easily accounted for (e.g., Patterson et al. 2016), but names long regarded as junior

² And still currently accepted (Wilson and Reeder 2005; Roskov et al. 2019).

³ The original (valid) spelling of this genus name, introduced by Linnaeus (1758) is *Raja*; *Raia* is an incorrect subsequent spelling without separate status in zoological nomenclature, in the sense of Art. 33.3 of the Code (International Commission on Zoological Nomenclature 1999). Specifically, on *Raja* versus *Raia*, see Fricke et al. (2019), *ad vocem*.

synonyms (therefore, as names not to be used as valid) are sometimes resurrected because of changes in a group's taxonomy.

Changing taxonomy is indeed the source of standing ambiguity in the meaning of species names. For example, *Cervus elaphus corsicanus* (a name established by Erxleben 1777 for the small-size deer of Corsica) is usually regarded (e.g., Wilson and Reeder 2005; Roskov et al. 2019) as an insular subspecies of the European red deer, a species named *Cervus elaphus* by Linnaeus (1758), thus requiring that the continental form be named *Cervus elaphus elaphus*. However, the taxonomic status of *corsicanus* has been recently disputed by Groves and Grubb (2011). These authors recognize three species of European red deer: *Cervus elaphus* Linnaeus 1758 (West European red deer), *Cervus corsicanus* Erxleben 1777 (Corsico-Sardinian and North-African red deer), and *C. pannoniensis* Banwell, 1997 (East European red deer). This is not accepted by other zoologists (e.g., Zachos et al. 2013), who insist on recognizing only one red deer species in Europe. In other terms, '*Cervus elaphus*' in the sense of Groves and Grubb (2011) is not the same as '*Cervus elaphus*' in the sense of Zachos et al. (2013). As a consequence, aggregating information in a database by using the species name '*Cervus elaphus*' without further qualification would suggest a taxonomic agreement among the sources that does not exist in fact.

Even by restricting data aggregation to published and online sources of the last few decades, conflicting taxonomies for one and the same group of animals will be the rule rather than the exception. As a consequence, Linnaean names fail very often to perform the expected function of unique and universal label prescribed by the Code. As suggested by Berendsohn (1995), the best approximation to that target function is provided, rather than by Linnaean names, by *taxonomic concepts*, defined as the meanings of names as specified in a particular source: for example, *Cervus elaphus* Linnaeus (1758) sensu Groves and Gubb (2011). Aggregating data around taxonomic concepts and the semantic relationships among them [e.g., "*Cervus elaphus* Linnaeus (1758) sensu Groves and Gubb (2011)" is part of "*Cervus elaphus* Linnaeus (1758) sensu Zachos et al. (2013)"] would provide the necessary context for Linnaean names that, in the absence of qualification, are semantically instable because of changing taxonomies (e.g. Berendsohn et al. 2003; Franz et al. 2016, 2008; Franz and Peet 2009). A few authors remain skeptical about this issue and even defend the view that, "As concepts are little used and cannot be readily identified, we do not regard the practical challenges of managing concepts as currently tractable on a large scale, and so do not regard this area as ready for inclusion in a cyber-infrastructure" (Patterson et al. 2016, p. 52). Technical solutions, however, exist.

The problem has been addressed by the Taxonomic Databases Working Group (TDWG), known today as Biodiversity Information Standards, within its broad program devoted to developing, ratifying and promoting standards and guidelines for the recording and exchange of data about organisms (cf. <https://dwc.tdwg.org/>). Specifically, one of the TDWG standards is the Taxonomic Concept Transfer Schema (TCS), "conceived to allow the representation of taxonomic concepts as defined in published taxonomic classifications, revisions and databases. As such, it specifies the structure for XML documents to be used for the transfer of defined concepts" (<https://www.tdwg.org/standards/tcs/>).

An impressive example of large database built around taxonomic concepts is *Avibase* (Lepage 2019) in which more than 1.5 million taxonomic concepts for ca. 10,000 species and 22,000 subspecies have been organized, corresponding to the changing taxonomies of birds over the last 125 years, as illustrated by Lepage et al. (2014).

Once accepted that in data aggregation taxonomic concepts are less ambiguous than standard Linnaean names, producing and managing a database is largely a problem of information science, but the expert eye of the taxonomic specialist is nevertheless required as a quality filter for the data to be uploaded, because rules are not the same as usage: a perfectly Code-compliant species name found in a paper, in a database or on an identification label in a museum collection does not necessarily correspond to a specimen unequivocally referable to the named species.

Based on a survey of 567 papers published in entomological journals in 2016, Packer et al. (2018) have shown how difficult it is for the reader to evaluate the information actually carried by a cited Linnaean binomial. Most of those papers were silent about the methods or tools employed in the identification of specimens, and also failed to state whether voucher specimens supporting the identification had been preserved.

A different source of error plagues public databases when the entries are based on collection labels transcribed without previous taxonomic scrutiny. Even a trained clerk may become responsible for material errors, especially frequent when the source data are handwritten labels, often of difficult reading, or be unable to update the nomenclature if a specimen had been correctly identified but is still labeled with a superseded combination, or a name later found to be a junior synonym.

1.4 Intentional departures from Linnaean nomenclature

Current practice departs frequently from the Linnaean nomenclature as ruled by the Code. Quite often, this is not the mere effect of sloppiness or oversight,⁴ but the consequence of a critical (or adverse) attitude in respect to a specific rule of the Code, or even to its whole philosophy.

⁴ Little more than a curiosity is the survival of distinct names for the larva and the adult of the same animal. This double nomenclature was less exceptional in the XIX century, when knowledge about life cycles and metamorphoses was much less advanced than today. Thus *Phyllosoma* (described by Leach 1818), *Nectochaeta* (proposed by von Marenzeller 1892) and *Pelagosphaera* (introduced by Mingazzini 1905) were considered for a while to be independent genera (of crustaceans, polychaetes and peanut worms respectively), but were eventually recognized as larval stages of animals for which valid names had been previously established, based on adults. Things are admittedly less obvious when the name introduced for a larva is older than the name introduced for what eventually turns out to be the corresponding adult. Strict application of the Principle of Priority, one of the cornerstones of the Code, would fix the 'larval' name as valid for the adult too; but a ruling by the International Commission on Zoological Nomenclature might determine a reversal of precedence, as in the case of *Phoronis* Wright, 1856 (described on the adult animal) versus *Actinotrocha* Müller, 1846 (described on larvae), eventually suppressed (International Commission on Zoological Nomenclature 2015). The latter action should have terminated the paradoxical situation of both names being deliberately kept in use, one for the larva, one for the adult of the same animal, but this is practiced by some authors until now, e.g. with *Actinotrocha branchiata* and *Phoronis muelleri*, or *Actinotrocha sabatieri* and *Phoronis psammophila* (Conway 2015; Roskov et al. 2019).

Sometimes, intentional departures from the Code express the zoologists' dramatically decreasing familiarity with Latin. The most obvious deviation from strictly Code-compliant names are the binomials in which the specific epithet is frozen in its original spelling even if it is an adjective and has been subsequently transferred to a genus of grammatical gender other than the genus name with which the specific epithet was originally associated. Refusal to follow Art. 31.2 (gender agreement) is quite common among lepidopterists. This practice often generates curious results. For example, among the species of the genus *Megacraspedus*, belonging to the twirler moths or Gelechiidae, some adjectival epithets are given (e.g., by Huemer and Karsholt 1995) in the masculine, others in the feminine form, because of the gender of the genera in which the species were originally described. For example, *Megacraspedus binotella* is, according to these authors, the current combination for a moth first described as *Palpula binotella*, while in *Megacraspedus dolosellus* the specific epithet is masculine not in force of Art. 31.2, but because the species was first described as *Ypsolophus dolosellus*.

A different departure from the official nomenclature is the addition of a numerical code to the names formed in accordance to the rules. This was suggested in the early 1990s, to cope with a perceived deficiency of scientific names as keywords to retrieve information from databanks (Heppel 1991). Something of the actually never implemented concept of a numerical International Standard Taxonomic Code (ISTC)⁵ survives in the alphanumeric strings with which taxon names are registered in ZooBank (Pyle and Michel 2008; see www.zoobank.org/). Alphanumeric formulas were also recommended as a useful complement to the unconventional names suggested by Eric de Smet as a "new biological nomenclature" largely following the Linnaean hierarchy (except for the abandonment of the genus rank), but represented by terms based on Esperanto rather than Latin (e.g., De Smet 1991).

Radically alternative to the Linnaean nomenclature is the phylogenetic nomenclature first proposed 30 years ago to replace or at least to accompany the traditional nomenclature, as the latter was considered inadequate for an arrangement of taxa to which, as required by a strictly phylogenetic approach to taxonomy, absolute ranks (e.g., genus, family, order) should not be attributed (de Queiroz 1988; de Queiroz and Gauthier 1990). A new set of rules intended to apply to all kinds of organisms (the PhyloCode) was thus developed (see Cantino and de Queiroz 2010). This code does not rule on the names of species, but some phylocoders have completely disposed also of the latter rank, preferring to speak instead of Least Inclusive Taxonomic Units (LITUs; Pleijel and Rouse 1999), and a small number of new taxa have been actually described under uninominal LITU names, e.g. by Pleijel (2000) and Pleijel and Rouse (2000).

⁵ Unfortunately, this acronym, suggested by Heppel (1991) for the ill-fated International Standard Taxonomic Code, is actually in use for a different thing, the International Standard Text Code (see <http://www.istc-international.org/>, accessed August 1st, 2019). Ironic fate for the name of concepts intended to establish unique standards but also, as suggested by a reviewer of this article, an example of the fate of inadequately contextualized names.

2 Names for species, what else?

Species discovery (and formal description and naming) and specimen identification are two fundamentally distinct actions (Collins and Cruickshank 2012), but this distinction is often ignored in discussions about the format and use of scientific names. The diagnostic traits by which, in the judgement of its first descriptor, a newly discovered species differs from its closest relatives derive from the study of the type specimens, often limited to a singleton, on which the original description is based. Those traits are not necessarily representative of the whole range of variation, e.g. geographical, or by sex or age, of other specimens that at a subsequent time will be tentatively regarded as belonging to the same species. This may cause problems with the use of a Linnaean name.

It is too often overlooked that, while the Codes are intended to rule over the way names are applied to taxa, the users of taxonomy need instead names to be applied to *specimens*. This is probably true of all users other than professional biologists, but also of most biologists except for taxonomists in the strict sense. The zoological Code is explicit in stating (Art. 1.1) that “Zoological nomenclature is the system of scientific names applied to taxonomic units (taxa; singular: taxon) of extant or extinct animals”. Specifically (Art. 1.2.2.), “The Code regulates the names of taxa in the family group, genus group, and species group”.

Thus, strictly speaking, to use for individual specimens the names over which the Code rules, a number of conditions should be granted, among which

1. That the specimen can be referred to one of the species-group taxa for which a valid scientific name exists
2. That this species is currently treated as satisfactorily distinct from all other species hitherto described, and the person who identifies the specimen (provided that he/she is a knowledgeable specialist) has no reason to doubt its validity
3. That the specimen (or, documentation about the specimen, such as a photo) exhibits in an unambiguous way one or more traits enabling its distinction from individuals belonging to any other species.

In practice, one or more of these conditions fail very often to apply. The perhaps unwanted but unavoidable consequence will be that the so-called scientific names introduced by taxonomists—the names governed by the rules of the Code—do not match the semantic needs of the user. To address this mismatch between the available scientific names provided by taxonomists and disciplined by the Code and the names under which a specimen may be referred to, two options are available, namely (1) to use one of the existing Linnaean names nevertheless, or (2) to introduce a non Code-compliant name or formula.

Unfortunately, either behaviour runs against those ideals of stability and universality of zoological nomenclature so boldly declared in the second paragraph of the Code’s Preamble. We enter the dangerous and also poorly charted domain of names and formulas, more or less obviously departing from Linnaean names, that are in use either for individual specimens that cannot be obviously allocated to a named species, or for clusters

of specimens which, despite an objective delimitation from other, even closely related clusters, cannot be equated to species taxa as intended in traditional taxonomy. All these names and formulas are parts of an increasingly large and untractable *grey nomenclature*, the most obtrusive of whose members are, in the absence of widely adopted standards, those formulas of which it is not even clear if they refer to individual specimens or to hypothesized but formally unnamed taxa (Schindel and Miller 2010; Minelli 2017a).

However, simply declaring those practices the product of unprofessional, sloppy practice would seriously misappreciate the underlying problems, conceptual and operational alike, and miss a long-deserved rethinking that should eventually lead to an explicit negotiation about new rules of best practice between the taxonomists who describe, name and classify species and the users of taxonomy interested instead in the identification of specimens, i.e. to their allocation, as far as possible, to named taxa.

3 Exploring grey nomenclature

I will introduce this set of names and formulas not compliant with the Code under three headings: open nomenclature, provisional names for undescribed species, and mixed lists.

3.1 Open nomenclature

For reasons such as those listed in the previous Section, the identification of a specimen may remain uncertain even in the hands of a specialist.

Concealing this uncertainty under an unflagged Linnaean name would carry a wrong message. To avoid this, a number of formats have been put in use, as in the following examples: *Longitarsus* sp.; *Lumbricus* cf. *rubellus*. The relationship between the Code-compliant names of taxa and these names applied to individual specimens is generally clear; nevertheless, to flag the presence of specifiers such as ‘cf.’, of which there is no mention in the Code, the set of these names departing from pure Linnaean binomens is sometimes called *open nomenclature*. Matthews (1973), the first author to call the attention of the English-speaking world towards a notion introduced by Richter (1948) in a poorly accessible work in German, remarked that adopting an open nomenclature is not a way of abdicating taxonomic responsibilities. Careful and judicious use of open nomenclature reflects scientific honesty and “remains open to whatever possibility of improvement future findings might bring” (Matthews 1973, p. 714).

Despite the suggestions of Richter (1948), Matthews (1973) and Bengtson (1988) for a standardization of open nomenclature, the latter has never been regulated based on an official, or at least largely shared agreement, but its usage is widespread, especially in palaeontology and ecology. At last, Sigovini et al. (2016) have provided an articulated discussion, with a detailed glossary of the terms in use and some preliminary suggestions for their standardization. Table 1 summarizes the main levels or degrees of uncertainty in the identification of a specimen, with examples of how these can be expressed in open nomenclature.

Table 1 Open nomenclature. A summary of the main levels or degrees of uncertainty in the identification of specimens, with examples of how these can be expressed in open nomenclature [inspired by glossary and examples in Sigovini et al. (2016)]

1. No still undescribed and unnamed species is likely involved	
1.1. Identification at the species level uncertain because of contingent difficulties, e.g. incomplete specimens, identification not by specialist etc.	
1.1.1. Tentative identification at the species level not attempted	<i>Nucula</i> sp. <i>Didemnum</i> sp. A <i>Lekanesphaera</i> indet.
1.1.2. Tentative identification at the species level attempted	
1.1.2.1. Suggested identification limited to species group/complex	<i>Capitella capitata</i> (Fabricius, 1780) complex <i>Pseudocandona</i> ex gr. <i>eremita</i> (Vejdovski, 1882) <i>Pourtalesia</i> aff. <i>alcocki</i> Koehler, 1914
1.1.2.2. Suggested identification potentially (but not certainly) correct	<i>Polycera</i> cf. <i>hedgpethi</i> Er. Marcus, 1964
1.2. Identification at the species level uncertain because of inadequate taxonomy	<i>Maera aequimana</i> Ledoyer (1979) sp. dub. <i>Polycirrus pellucida</i> (Quatrefages, 1866) sp. inq.
2. New species involved, but description postponed	<i>Tisbe</i> sp. nov. <i>Petrolisthes</i> sp. nov. aff. <i>rufescens</i> (Heller, 1861)

3.2 Provisional names or formulas for undescribed species

The systematic comparison of gene sequences obtained from an exponentially increasing number of samples, either freshly collected or obtained from museum specimens, is revealing patterns of biological diversity that often do not match with any of the species described and named to date. Quite often, the results of molecular studies turn out to alert to the existence of previously undescribed species, hardly recognizable based on morphological characters, but separated at molecular level. In other instances, molecular evidence must be handled more cautiously. It may also happen that molecular analyses fail to differentiate between species that experienced taxonomists have good reasons to keep distinct anyway.

The most important contribution, by far, to the knowledge of biological diversity at the molecular level is the result of a large international effort intended to aid species identification and discovery known as *DNA barcoding*, that focuses on the analysis and comparison of short, standardized gene regions, a part of the cytochrome *c* oxidase I (COI) gene in the case of animals (Hebert 2003; Ratnasingham and Hebert 2007).

Following a suggestion previously floated online by Mark Blaxter, Floyd et al. (2002) proposed the acronym MOTU (Molecular Operational Taxonomic Unit) to indicate any diagnosable and operationally useful set of sequences recognized within the barcode sequences. Clusters of similar gene sequences are not necessarily

equivalent to Linnaean species (Blaxter et al. 2005), even if the algorithms used to generate these clusters are adjusted in order to maximize the correspondence between species and MOTUs. The problem is not limited to the animal kingdom. Writing about fungi, Ryberg and Nilsson (2018) have recently remarked that an increasing percentage of fungal diversity is known only from sequence data for which any correspondence to named species cannot be determined, even if it potentially exists. Among the mycologists, these are often referred to as *dark taxa* (Page 2016). To some extent, this produces two parallel taxonomies, because no simple or universal rule exists to ‘translate’ MOTUs into Linnaean species, or vice versa. Nevertheless, there are fine examples, such as the following one, that show how this can be obtained.

In a study of the tiny sea-slugs of the genus *Pontohedyle* only two taxa were recognizable according to morphology, but a genetic approach revealed a much larger, cryptic diversity that Jörger et al. (2012) classified as twelve MOTUs. In the same paper, three MOTUs were identified with previously described and named species, while the remaining ones, provisionally referred to as *Pontohedyle* sp. 1–9, were eventually described and named by Jörger and Schrödl (2013) despite the lack of morphological traits differentiating these cryptic new species from one another; the new taxa were thus established based on diagnostic nucleotides in the DNA sequences of four genetic markers and DNA samples have been preserved as holotypes (the name-bearing material vouchers that the Code prescribes must be deposited at the time a new species is described).

Different from Linnaean species are also the clusters of sequences labeled with Barcode Index Numbers (BINs), alphanumerical codes corresponding to partitions of the total set of gene sequences recorded in the Barcode of Life Data Systems (BOLD) database. Nevertheless, BINs are an excellent example of non-Linnaean formulas, because their meaning is defined by the algorithms through which they are generated (discussed in Minelli 2017a). These qualities are sadly lacking in other cases, when informal names, or formulas, are used to express the provisional character of the taxonomical assignment of a specimen, or the unresolved taxonomic distinctness of a putative new species. In an increasing number of papers in which the occurrence of cryptic species-level taxa is hypothesized, generally based on molecular evidence, those putative species are not described in full and named according to the Code, but are simply referred to using acronyms or other formulas.

Eventually, a number of these putative species will eventually find a place in the standard Linnaean classification (Trontelj and Fišer 2009; Pérez-Ponce de León and Nadler 2010; Minelli 2017b). We must expect, however, that a detailed taxonomic study of the hypothesized new species suggested by molecular studies will progress quite slowly, and possibly by steps. A good example is provided by Fišer et al. (2017, 2018) with their effort to accommodate into formally described and named taxa the lineages identified by molecular studies in the Swiss populations of freshwater crustaceans of the genus *Niphargus*. Of 22 clades emerging from the comparison of DNA sequences, 11 were found to correspond to previously named taxa, three were described as new in Fišer et al. (2017), another two in Fišer et al. (2018), while the taxonomy of the remaining

six clades was declared unresolved, and these are still referred to under formulas like ‘*Niphargus rhenorhodanensis* complex Schellenberg, 1997 lineage ABC’ or ‘*Niphargus* cf. *stygius*.’

In many cases, the time lag between the discovery of cryptic species and their formal taxonomic description is very long (Horton et al. 2017). For example, in a molecular study of the Central American species of the fish-parasitic worms of the genus *Neoechinorhynchus*, Pinacho-Pinacho et al. (2018) found nine previously described species plus 10 new lineages and/or candidate species, but abstained from describing the latter formally until a detailed taxonomic work will be performed, including morphology.

3.3 Mixed usage of names and formulas in the BOLD and GenBank databases

Names and formulas used in the largest sequence databases i.e. BOLD (the Barcode of Life Data Systems; <http://www.barcodinglife.org/>) and GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) are often ambiguous, or silent, about the kind of information they are intended to carry (Minelli 2017a, b). The main problem with this diverse set of labels is not that many of them do not follow the precepts of the Code, but the fact that most of those terms follow no standard at all (Schindel and Miller 2010; Minelli 2017a) and thus are not comparable between lists. Here, both formal Linnaean names and informal names and formulas are used to identify specimens, operational units and formal taxa, and no rules are visibly followed in this mixed usage. An example is given in Table 2.

4 Sustainable use of grey nomenclature: problems and solution

4.1 Problems

Dark taxa are often ignored in important contexts, both scientific (e.g., species list and related statistics in ecology) and not (e.g., legal documents), just because these taxa lack Linnaean names (Samyn and De Clerck 2012; Ryberg and Nilsson 2018).

But the worst aspect of grey nomenclature is the mixed nature of the objects and concepts for which it is used, often within one and the same list, where both open nomenclature entries and provisional names for dark taxa are included, often without unambiguous distinction. Two main problems must be addressed (Minelli 2017a, b).

First, is the alphanumeric specifier added to a genus name (e.g., *Cricetomys* sp. 3 PG2014), or even to a Linnaean binomen (e.g., *Marionina minutissima* PDW2010), intended to provide unambiguous labelling for a single specimen, a taxon, or both? This is often unclear, especially in database entries. The lack of rules for the creation and usage of these names or formulas precludes clear understanding of what the name or formula is for.

Table 2 List of ‘taxa’ referred to the nematode genus *Rhabditis*, corresponding to entries in the GeneBank database (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Tree&id=55887&lvl=3&lin=f&keep=1&srchmode=1&unlock>. Accessed 30 July 2019)

<i>Rhabditis belari</i>	<i>Rhabditis</i> cf. <i>longicaudata</i> Konza IIAB-27
<i>Rhabditis blumi</i>	<i>Rhabditis nidrosiensis</i>
<i>Rhabditis brassicae</i>	<i>Rhabditis rainai</i>
<i>Rhabditis colombiana</i>	<i>Rhabditis remanei</i>
<i>Rhabditis dolichura</i>	<i>Rhabditis terricola</i>
<i>Rhabditis</i> cf. <i>terricola</i> JH-2004	<i>Rhabditis</i> sp. BC7735
<i>Rhabditis</i> cf. <i>terricola</i> Konza IVAD-12	<i>Rhabditis</i> sp. D VSS-2017
<i>Rhabditis</i> cf. <i>terricola</i> Konza IVAD-144	<i>Rhabditis</i> sp. DF5059
<i>Rhabditis</i> cf. <i>terricola</i> Konza IVAD-41	<i>Rhabditis</i> sp. DW-2012
<i>Rhabditis</i> cf. <i>terricola</i> SWBT201226	<i>Rhabditis</i> sp. EM-2016
<i>Rhabditis tokai</i>	<i>Rhabditis</i> sp. F VSS-2017
<i>Rhabditis</i> sp.	<i>Rhabditis</i> sp. G VSS-2017
<i>Rhabditis</i> sp. 1 HMM2018	<i>Rhabditis</i> sp. H VSS-2017
<i>Rhabditis</i> sp. 1 MK-2017	<i>Rhabditis</i> sp. Hy CM-2010
<i>Rhabditis</i> sp. 1 TWN1422	<i>Rhabditis</i> sp. I VSS-2017
<i>Rhabditis</i> sp. 2 HMM2018	<i>Rhabditis</i> sp. J VSS-2017
<i>Rhabditis</i> sp. 2 MK-2017	<i>Rhabditis</i> sp. K CM-2010
<i>Rhabditis</i> sp. 2 TWN1423	<i>Rhabditis</i> sp. K VSS-2017
<i>Rhabditis</i> sp. 3 HMM2018	<i>Rhabditis</i> sp. LSU_7
<i>Rhabditis</i> sp. 3 MK-2017	<i>Rhabditis</i> sp. N CM-2010
<i>Rhabditis</i> sp. 3 TWN1998	<i>Rhabditis</i> sp. NISMZ
<i>Rhabditis</i> sp. 4 HMM2018	<i>Rhabditis</i> sp. NK-2011c
<i>Rhabditis</i> sp. 4 MK-2017	<i>Rhabditis</i> sp. NK-2011f
<i>Rhabditis</i> sp. 4 TWN1951	<i>Rhabditis</i> sp. OK-2011
<i>Rhabditis</i> sp. 5 HMM2018	<i>Rhabditis</i> sp. PS1130
<i>Rhabditis</i> sp. 5 MK-2017	<i>Rhabditis</i> sp. RA5
<i>Rhabditis</i> sp. 5 TWN1896	<i>Rhabditis</i> sp. Salt_Lake_E.4_apple
<i>Rhabditis</i> sp. 6 GVDU-2019	<i>Rhabditis</i> sp. Salt_Lake_Lib_D.1a_apple
<i>Rhabditis</i> sp. A VSS-2017	<i>Rhabditis</i> sp. Salt_Lake_Tom_A.1_tomato
<i>Rhabditis</i> sp. AW-2011	<i>Rhabditis</i> sp. Salt_Lake_WB.1a_pear
<i>Rhabditis</i> sp. B CM-2010	<i>Rhabditis</i> sp. Seattle_19A_tomato
<i>Rhabditis</i> sp. B VSS-2017	<i>Rhabditis</i> sp. Seattle_7A_fig
	<i>Rhabditis</i> sp. SSU1_7

Second, and most important, because of the inconsistency and arbitrariness of the criteria according to which these non-Linnaean names are formed and used, it is generally impossible to trace them across studies or databases (Schindel and Miller 2010; Pante et al. 2015; Morard et al. 2016; Minelli 2017a). In principle, there is no reason to expect that ‘*Lumbricus* sp. A’ listed in a given paper or database will be the same as ‘*Lumbricus* sp. A’ in another paper or database. As an example of ‘private’ label used in a publication, to denote a taxonomic unit whose identity was

destined to remain accessible to its ‘author’ only, Schindel and Miller (2010) quoted from Marks (1983) the following formula: “*Aedes (Finlaya)* ‘Marks sp. No. 104’. An undescribed species which has been studied in some detail by the author”. Other formulas listed in the same publication, hardly of more public use than the former, are “*Tripteroides (Rachisoura)* sp. nr *bisquamatus*. An undescribed species which will key out (either as larva or adult) to the species it is ‘near’. and “*Uranotaenia novaguinensis?* Identification of females or larvae tentative; specific distinctions best shown by males and/or larvae”.

4.2 Solution: rules for the non-Linnaean nomenclature

What set of rules should be enforced to overcome the current state of confusion may depend on a couple of basic choices.

First, should these rules become part of a revised version of the Code? Rules for the provisional naming of dark taxa could probably be accommodated without changing the Code’s aim in a radical way, but the apparently more innocent issue of open nomenclature would be much less tractable, unless we are ready to redefine the aims and scope of the Code. The Code has always ruled on taxon names, but open nomenclature is a set of names applied to individual specimens or individual samples of likely conspecific specimens.

This problem notwithstanding, a precondition for establishing a set of rules either for open nomenclature, for the names of dark taxa, or for both sets of names, is that unequivocally different formats (or sets of formats) be fixed for the two sets of non-Linnaean names or formulas.

Second, are current needs to handle scientific information still satisfied by the unique taxon names prescribed by the Code? Proposals to add a numerical or alphanumerical string to the Linnaean name have been mentioned above. Formal Linnaean names and alphanumerical formulas might also be thought of as distinct but complementary names in a kind of double nomenclature. This idea has been floated in recent discussions about possible strategies to overcome the problems of grey nomenclature; it has also been suggested that the kind of name to be used may depend on the identity of the communicating parties (Ryberg and Nilsson 2018): for example, digital object identifiers (DOIs) would be most suitable for communication between computers, but we should opt instead for binomials for use in the scientific literature and perhaps, additionally, vernacular names would be best for lay users. Mycologists have developed a large database for the molecular identification of fungi (the UNITE database; <https://unite.ut.ee/>), where clusters of molecular sequences are presented as species hypotheses tagged with unique DOIs to facilitate unambiguous communication (Kõljalg et al. 2016). But in mycology again, Hawksworth et al. (2016) have suggested that these fungal taxa should be eventually described and given valid names under the Code, although using as type a DNA sequence rather than the traditional herbarium specimen.

Complementing the Linnaean nomenclature with other kinds of names or formulas, however, will serve our needs for communication about the diversity of life only provided that the use of all these names and formulas will be formally disciplined.

Practical solutions to enable a sustainable use of names and formulas must be discussed elsewhere, let's however list here a set of points that future rules must fix:

- (a) Standard formats for the different kinds of objects (or hypotheses) we need to label, such as individual specimens, undescribed new species, or others,
- (b) Requirement for material vouchers (whole specimens and DNA sequences alike) to be preserved and exhaustively labelled and
- (c) Requirement of permanent association of each 'grey name' with source information, i.e. author and year for the names introduced in a publication, and equivalent information, in a format to be specified, for the non-Linnaean names and formulas used in database entries.

Sensibly, Schindler and Miller (2010), while describing as uniqueness and stability the properties that taxon labels must have, added that their format (including e.g. numerals or punctuation marks) must be such as to make it impossible to misinterpret them as taxon names.

5 Unconventional names for unconventional biological entities

If we accept that the Linnaean nomenclature must be complemented with the several kinds of names and formulas that are already in current use, but cause problems of communication because they are not disciplined by rules accepted by the whole community that needs to use them, we might also open the door to a revisitation of the nomenclature of other kinds of biological entities that are not covered by the Codes, mainly because they do not correspond to taxa at any level of the conventional hierarchy.

Among the entities that are excluded from the provisions of the Code are plant galls and lichens *as such*. To be sure, there are practical and uncontroversial ways to name them, but only in a circuitous way. The nomenclatural history of these two kinds of biological objects is otherwise very different. In the case of galls, terms have been only introduced to distinguish classes of galls according to the nature of the agent whose action on a plant is responsible for the production of the gall, for example nematoecidia, mycoecidia and entomoecidia for galls caused by nematodes, fungi or insects, respectively (Jolivet 1998). Within these broad taxa, however, galls are simply named with expressions such as 'the gall of *Andricus quercus-callicis* [a tiny wasp] on *Quercus robur* [the pedunculate oak]', or 'the gall caused by *Urophora cardui* [a tephritid fly] on *Cirsium arvense* [the field or Canada thistle]'.

The nomenclatural history of lichens is very different. Lichen species have been recognized and named since Linnaeus, who in the first edition of *Species Plantarum* (1753) listed 80 species of *Lichen* (as a genus of Algae!!) and another 8 lichen species in *Clavaria* (more sensibly classified with the Fungi). When Acharius (1810) published the first world monograph of lichens, not less than eight hundred species were already known. Lichen species (and genera, families etc.) continued to be described and named even after the discovery of their symbiotic nature (de Bary

1866; Schwendener 1868). But the algal or cyanobacterial partners (the phycobionts) of lichenic symbioses are quite uniform, compared with the diversity of the fungal partners (the mycobionts); moreover, many mycobionts are close relatives of non-lichenized fungi belonging to different lineages. Based on these circumstances, lichens have literally disappeared from the classification, as an independent group with its hierarchy of orders, families, genera and species, to show up again among the Fungi, but now scattered among the Ascomycetes (mainly) and the Basidiomycetes, following the phylogenetic relationships of the individual genera and species. As a consequence, a taxon like *Lecanora muralis* is better described today as a lichenized fungus, rather than a lichen.

Thus, strictly speaking, the ‘whole’ lichen, i.e. the symbiotic unit of mycobiont and phycobiont, actually lacks a name, similar to what happens to plant galls. Whether the current stand of the nomenclature of these natural objects should be regarded as satisfactory or not, it may be matter of dispute, but it should not be left unchallenged. In the case of plant galls, in particular, nomenclature reflects the way these objects are generally described—as abnormal plant structures whose production is stimulated, or caused, by a specific external influence (by an insect, mite etc.)—whereas the fidelity with which their specific and often elegant shapes are produced should invite to regard them as legitimate (not to say autonomous) targets of study in developmental biology, a perspective virtually unexplored till now (Minelli 2017c).

6 Conclusion

A walk through the galaxy of non-Linnaean kinds of biological nomenclature shows how remote is practice from the ideal of mutual independence of taxonomy and nomenclature loudly proclaimed in the Preamble of the zoological Code.

What happens if we try to freeze the rule of biological nomenclature in the terms of the current Codes or in a form only slightly modified in respect to them? Lack of flexibility in the way we name the units of biodiversity leads to unwarranted assumptions of ontology. So long as scientists consistently use Code-compliant Linnaean names that take for granted that the species is the unit of biodiversity, why should we question if, and in which sense, the taxa to which all these names are applied are in any sense equivalent? Statistics based on numbers of species, e.g. in ecology, biogeography and stratigraphy, implicitly take for granted that all taxonomic entities with a binomial name can be treated as equivalent, whereas these often have very little in common besides being described under similarly formed names (Minelli 2000). In the non-Linnaean galaxy, many clusters of names correspond to entities that defy pigeonholing into a neat Linnaean classification, and are best labelled with names other than those that the Codes currently allow to use.

Complementing the Linnaean nomenclature with other kinds of names or formulas, however, will serve our needs for communication about the diversity of life only provided that all these names and formulas are disciplined by rules, possibly accompanied by registration in an official database.

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