Bionomina, 7: 1–44 (2014)
www.mapress.com/bionomina/

Article

ISSN 1179-7649 (print edition)
BIONOMINA
ISSN 1179-7657 (online edition)

http://dx.doi.org/10.11646/bionomina.7.1.1
http://zoobank.org/urn:lsid:zoobank.org:pub:CFC4C697-0819-4CBF-BE8B-8BBD90BA8002

Proposal of an integrated framework of biological taxonomy: a phylogenetic taxonomy, with the method of using names with standard endings in clade nomenclature

Shun-Ichiro NAOMI

Natural History Museum and Institute, Chiba, Aoba-cho 955-2, Chuo-ku, Chiba 260-8682, Japan. <naostenus@hb.tp1.jp>.

Table of contents

Abstract

An integrated framework of biological taxonomy (IFBT) is proposed, in which the advantages of phylogenetic taxonomy and traditional, Linnaean nomenclature, together with the temporal banding methods (Hennig, 1966; Avise & Johns, 1999) are synthesized, without deteriorating the strength of theoretical coherence. The IFBT aims at achieving a completely rank-free reference system of the organismal group in question (i.e., phylogenetic arrangements of the names of clades as parts of timetrees); here, the whole area (all taxon names) of a reference system is called “general domain”, while its part (basic clade names) is called “particular domain”. Thus, the major task of IFBT is to precisely give names to those clades whose times of evolutionary origin are known; here, the categories of evolutionary clades that I recognize are “basic clade”, “holoclade” and “synclade”. Taxon names with standard endings can be used as components of a rank-free system created under the IFBT, when we interpret those taxon names as “meaningless symbols” under the Millian philosophy of language. Thus, introducing the method of using “names with standard endings” into the present clade nomenclature is logically possible. That is, by adopting the temporal bands of geological episodes (non-standard; standard) as the unique criteria for assigning the standard endings to some clade names in naming clades, we name the clades, so that we can create a particular domain of reference system that takes basically the same style as the Linnaean system (of taxon names), in that taxon names with standard endings are arranged in a hierarchical manner. The particular domain can be created by giving “names with standard endings” only to basic clades, out of the clades whose origins are located in one particular temporal band. The reference system is first reconciled with the evolutionary world view, because the taxon names precisely refer only to clades; and second, it also functions well as a convenient system for information storage and retrieval, because the mutual exclusivity of taxon names with standard endings in the particular domain is certain. The best way of practicing the IFBT at the present time is to create only the particular domain, by naming only the basic clades (extant, extinct), using non-standard temporal banding method. *The IFBT can construct the particular domains of (rank-free) reference systems, upon the particular Linnaean (ranked) systems of clade names*. The IFBT is proposed as the new framework for future biological taxonomy.

Key words. Linnaean nomenclature, temporal banding methods, reference system, convenience, rank-freeness, temporalness

Introduction

Carolus Linnaeus’s taxonomy (including nomenclature) and its revised versions are the scientific disciplines that biologists have adopted for classifying (or systematizing) and naming living things, and thus describing the biodiversity on Earth during the last ca. 250 years. The 1st edition of “*Species Plantarum*” (Linnaeus 1753) is regarded by convention as the starting point for botanical nomenclature, and the 10th edition of “*Systema Naturae*” (Linnaeus 1758) for zoological nomenclature.

In the Linnaean taxonomy of pre-evolutionary era, taxa recognized were abstract classes defined in terms of morphological similarities; and the Linnaean system of taxon names is a set of names of taxa (as classes) subjectively allocated to the hierarchical levels by naturalists. Darwin (1859) convinced biologists of the reality of evolution, which forms the basis of biological taxonomy, but the acceptance of evolution in the biologist community did little or nothing to change the practices of Linnaean taxonomy (Night 1981; de Queiroz 1988). What happened after the publication of *Origin of Species* is that taxonomists did reinterpret relationships expressed in the Linnaean systems (of taxon names) as the results of evolution.

The first, true Darwinian revolution of biological taxonomy occurred in the middle of 20th century, that is —the establishment of the theory of Phylogenetic Systematics by Hennig (1950, 1965, 1966), in which the principle of common ancestry certainly plays an important role in considering what the nature of biological taxa is. By equating higher taxa with monophyletic groups (clades), he aimed at creating the “phylogenetic systems” that reflect the phylogenetic relationships of organisms, under the Linnaean taxonomy. Since his “phylogenetic system” is an excellent approximation to the truly phylogenetic systems which reflect the continuous nature of nested series of clades, his approach to taxonomy has been widely accepted by contemporary systematists and phylogenetists (e.g., Eldredge & Cracraft 1980; Wiley 1981; Nelson &

Platnick 1981; Ax 1987). In his later works, Hennig (1969, 1981) adopted (literally rank-free) numerical prefixes in connection with the Linnaean names (e.g., 2.2.2.1.2. Odonata) to systematize the clade Insecta, whereas many researchers, though accepting Hennig's theory of *Phylogenetic Systematics* (1966), have used only the traditional Linnaean names connected with the names of nomenclatural ranks (e.g., genus, family) to systematize the organismal groups that they studied, as if Hennig's framework of phylogenetic systematics were theoretically compatible with the Linnaean nomenclature. Barkley *et al.* (2004*a*–*b*) went to the extent to contend that the Linnaean nomenclature does not prohibit taxonomists from creating a purely phylogenetic system (see also Wiley & Liebermann 2011: 252).

The Linnaean taxonomy and nomenclature have, however, some problems in naming living things and thus also in producing the systems of taxon names. One serious problem is that the nomenclatural ranks are not reconciled with the concept of phylogeny so that the Linnaean system of names has difficulty in conveying information about phylogeny (Griffiths 1973, 1974; de Queiroz 1997; de Queiroz & Gauthier 1990, 1992; Ereshevsky 2001; Härlin 2005). Another problem is that the Linnaean taxa with the same rank are not equivalent units (or entities), but because of adopting nomenclatural ranks, the Linnaean taxonomy seems to tempt biologists to do unwarranted comparisons across different taxa of the same rank (Mishler 1999; Minelli 2000; Pleijel & Rouse 2003; Kluge 2005; Bertrand *et al.* 2006). Given these problems, the ranks (which do not exist in Nature) caricaturize (or oversimplify) the fundamental structure of biological world when we try to understand it; and in the end, so do the Linnaean taxonomy and nomenclature.

Pointing out the out-dated conditions of traditional, Linnaean taxonomy (e.g., taxa are viewed as classes; taxonomy maintains independence from the concept of evolution), de Queiroz (1988) did a pressing plea for the necessity of a Darwinian revolution in the realm of systematics. In fact, the Darwin's axiom "*descent with modification*" has played a rather superficial role in taxonomy between 1859 and today. Evolution (or common ancestry) be taken as an axiom of systematics, from which taxonomic methods and concepts are deduced; and taking evolution as its axiom requires that preexisting taxonomic methods and concepts be reevaluated in its light (de Queiroz 1988). At once, he together with J. Gauthier started to create a new and highly original framework of nomenclature, or phylogenetic nomenclature (de Queiroz & Gauthier 1990, 1992, 1994; de Queiroz 1992, 1994), resulting in the *PhyloCode* as its codification (Cantino & de Queiroz 2000). They have devised their phylogenetic nomenclature, under which names are directly attached to clades by phylogenetic definitions (node-, branch- and apomorphy-based) that each include two or more specifiers, but do not make reference to a type and a rank. When a revised phylogenetic hypothesis is accepted, the stability of names is provided by the phylogenetic definition referring to the same ancestor, irrespective of the hypothesis; here common ancestry does certainly play a role as the central principle in clade nomenclature.

Their phylogenetic taxonomy is certainly excellent in that first, it aims at precisely naming clades without adopting nomenclatural ranks to form a rank-free system of clade names (de Queiroz & Gauthier 1990, 1992, 1994), and second, it also aims at naming all extant and extinct (fossil) clades in the Tree of Life that are worth naming (de Queiroz & Gauthier 1992; see also de Queiroz 2007*a*). Given this, some must have believed it brings a lot of promises for our future biological taxonomy. However, after the proposal of phylogenetic taxonomy by de Queiroz & Gauthier, a large variety of criticisms have appeared against their approach to phylogenetic nomenclature (e.g., Lidén & Oxelman 1996; Dominguez & Wheeler 1997; Moore 1998, 2003; Nixon & Carpenter 2000, 2003; Benton 2000; Forey 2001, 2002; Keller *et al.* 2003; Carpenter 2003; Schuh 2003; Barkley 2004*a*–*b*; Dubois 2005, 2011; Stevens 2006). The objects of those criticisms extend widely from difficulties with the taxonomic philosophy of de Queiroz (1992, 1994, 1995) that underlies the phylogenetic definitions of taxon names (Frost & Kluge 1994; Härlin 1998; Härlin & Sundberg 1998; Keller *et al.* 2003; Kluge 2005), to difficulties with the methods of naming clades with the phylogenetic definitions (Dominguez & Wheeler 1997; Moore 1998, 2003, 2005; Benton 2000; Nixon & Carpenter 2000; Kluge 2005; Härlin 2005; Platnick 2009, 2012), or to difficulties with the function of a rank-free reference system created under their phylogenetic taxonomy (Moore 2003, 2005; Platnick 2012; present paper). Out of them, one serious problem seems to be that taxon names should not change over time once they are defined phylogenetically (de Queiroz & Gauthier 1990, 1992), because this rule results in the rejection of a mutual exclusivity of taxon names brought by using standard endings (e.g., Platnick 2009, 2012). In short, the system of clade names created under their phylogenetic taxonomy does not seem to function well as a convenient system for taxonomic information storage and retrieval.

Both Linnaean and phylogenetic taxonomies (including nomenclatures) have problems, as mentioned above. Thus, biological taxonomy now no doubt faces a revolutionary turn, where biologists anticipate the arrival of a theoretically coherent framework of taxonomy that creates the system of clade names, which are reconciled with the evolutionary world view, and also that are useful and convenient for scientists and non-scientists alike. At the present stage no one knows what framework of biological taxonomy the systematist community will finally accept in the future. However, it seems to be adequate to say that the biologist community will espouse the view that the objects of study in biology are real entities in nature (i.e., clades and species), rather than human constructs. Thus, it seems to be also adequate to say that the systematist community will finally accept the view that *the biological units that merit recognition as formal taxa are clades and species*. Given that smaller clades are nested within the larger clades (see also first section), the systematist community will accept in the long run the rank-free framework in which the evolutionary clades are to be precisely named.

When taking seriously these things into account, I prefer the phylogenetic taxonomy to Linnaean taxonomy in spite of a lot of criticisms against the former; I certainly like the phylogenetic taxonomy which aims at precisely naming clades without recognizing nomenclatural ranks. However, this is not to say that I straightforwardly support de Queiroz and Gauthier's (QG-)phylogenetic taxonomy and *PhyloCode* (Cantino & de Queiroz 2010) as its codification, which cannot produce a scheme of words that functions as a convenient reference system. What I consider to be appropriate for naming clades is a theoretically coherent framework of taxonomy in which the advantages of phylogenetic taxonomy and Linnaean nomenclature are synthesized in a harmonious manner, that is, a phylogenetic framework which can create schemes of words (i.e., rank-free systems of clade names) that are both useful and convenient.

In general, ones may suppose that phylogenetic taxonomists cannot claim that they can avoid all the ranks and related problems while retaining all the information that the taxonomic ranks provide in the Linnaean system, but it seems to me that we can. Thus, I here propose an integrated framework of biological taxonomy (IFBT), into which the advantages of phylogenetic taxonomy and Linnaean nomenclature, together with the temporal banding methods (Hennig 1966; Avise & Johns 1999), are synthesized in a harmonious manner. Since I treat here a method of naming clades, first of all I will have to argue over the matter with clades and species as their parts. Second, I propose the IFBT, that is – a phylogenetic taxonomy, with the method of using names with standard endings in clade nomenclature. Third, I argue over the practices of naming clades under the IFBT. Fourth, I argue for the IFBT as the new framework for future biological taxonomy, and fifth, over compatibility between the traditional Linnaean taxonomy and IFBT. Sixth, I argue over a perspective on the phylogenetic taxonomy and nomenclature.

Clades and species as their parts

Two different kinds of living things exist on Earth, that is, species and clades, both of which are real entities; here the term "real" means that living things exist independently of human recognition and scientific activities such as naming clades and counting the number of species. These species and clades are impossible for human to perceive directly (de Queiroz 1988, 2007*a*), because of our brief temporal duration, and because of the relationships among their parts (e.g., organisms) which are sparsely located in space and time. Researchers can nevertheless ascertain their realities, by estimating them to be the parts of phylogenetic tree. Furthermore, since these species and clades are real entities that researchers can discover, it is reasonable to say that they cannot be constructed by lumping nor splitting by taxonomists; that is, they are not human constructs.

The clades are monophyletic groups, or complete systems of common descent (de Queiroz & Gauthier 1992; de Queiroz 2007*a*) that form parts of the Tree of Life. They each consist of an ancestor and all of its descendants (Hennig 1966; Farris 1974; Wiley 1981). A clade originates with an ancestor (an organism, a population, or a species) (de Queiroz & Cantino 2010: 28) because it derives from one of the three different incipient states of a species. First, when a species originates from a unisexual or asexual organism or a female organism with fertile eggs, and a clade derives from the species, then the ancestor of the clade is an organism eventually. Second, the ancestor of a (sexual, unisexual, asexual) species (e.g., species B) is a (local) population in cases where the species originates from a peripheral population of the ancestral species (e.g., species A); notice here that the ancestral species A does not become extinct at the speciation event where the species B originates. When a clade derives from the species, the ancestor of the clade is a (local) population. And, third, the ancestor of a (sexual, unisexual, asexual) species (e.g., species B and C) is the (whole) species (e.g., species A) in some cases of allopatric speciation; notice here that the whole ancestral species A becomes extinct at the speciation event where the new species B and C originate. When a clade derives from the species, the ancestor of a clade is a (whole) species. The first splitting of a species (derived from or as the ancestor) into the two just means the occurrence of a clade (Wiley 1980, 1981); and additional splittings of the species within the clade make it a larger clade that comprises more than two species. Thus, the smallest clade comprises two species, whereas the largest is virtually identical with the whole Tree of Life.

On the other hand, species are population-level evolutionary lineages (Wiley 1978, 1981; Frost & Hillis 1990; Frost & Kluge 1994; Mayden 1997, 1999, 2002, 2013; de Queiroz 1998, 1999, 2005*b*–*d*, 2007*b*, 2011; Wiley & Mayden 2000; Hey 2001; Wiley & Lieberman 2011; Naomi 2011). In other words, species are population-level lineage-forming entities. Many population-level lineages exist on Earth, including sexual, unisexual and asexual lineages; reproductively and/or geographically isolated lineages; and also lineages that originate from hybrid speciation. They are all species because they form lineages that evolve separately from other such lineages. This does not mean that all organisms belong to distinct lineage species. Namely, our biological world is not something like a factory that produces every days the same standardized soccer balls; and thus some species produce some organisms that do not belong to distinct lineage species (e.g., organisms that belong to microspecies in the dandelion *Taraxacum*; Grant 1981). The fate of a species rests just on evolutionary contingency (Wiley & Lieberman 2011). A species remains basically unchanged and goes extinct; or a species merges with another one to form a hybrid species. Otherwise, a species speciates into two or more species; and those species speciate at unexpected occasions and in various style (allopatric, parapatric, sympatric, etc.), because biological processes (e.g., selection, genetic drift) work on parts of the species (e.g., local population lineages, organisms, genes) in various manners at various times during the course of speciation events.

The occurrence of numerous speciation events results in the Tree of Life, which is continuous through time. Since the clades result from speciation events that occur at irregular intervals of time, there exist an innumerable number of clades at various levels of the Tree of Life (Fig. 1A), in a manner that smaller clades are nested within larger clades; that is, the clades form continuous nested series (de Queiroz & Donoghue 1990). This clearly shows that clades do not exist in principle *at the same universal level* within the Tree of Life, except for paired sister-clades that originate from the same ancestor, and thus have the same age. In many cases, those clades overlap, which means that a smaller clade forms part of a larger one; otherwise, they do not overlap at all, or are mutually exclusive. To be sure, many taxonomically important (i.e., distinct, with clear morphological gap) clades (e.g., Angiospermae, Coleoptera, Aves) do not overlap.

Researchers often mistakenly invoke arbitrary criteria (morphological gap, number of species, etc.) in order to taxonomically assign clades the same higher rank so that they can compare and/or count those clades. However, the taxonomic units so recognized are, as obvious from the above description, not the clades which are biologically meaningful, comparable units (except for sister clades). It would be also inadequate to consider that a group of clades that have evolved via a set of speciation events occurred quickly during a short period of geological time can be comparative units. This is because it is highly improbable in nature that an ancestral population (or species) lineage speciates simultaneously into several daughter species (Fig. 1C; Hennig 1966: 211) that finally result in several (young) clades that merit recognition as comparative units. The fact would be probably that those lineages have successively speciated (Fig. 1B) rather than having simultaneously evolved (Fig. 1C); and when depicted in the tree, the phylogenetic relationships among those clades seems to be hierarchical so that they are considered to form a nested set of clades. On the other hand, since species are independently evolving lineages, and are mutually exclusive in that they do not overlap their parts (e.g. local populations, organisms), they are comparable and countable units, except for the cases where organisms do not constitute distinct lineage species.

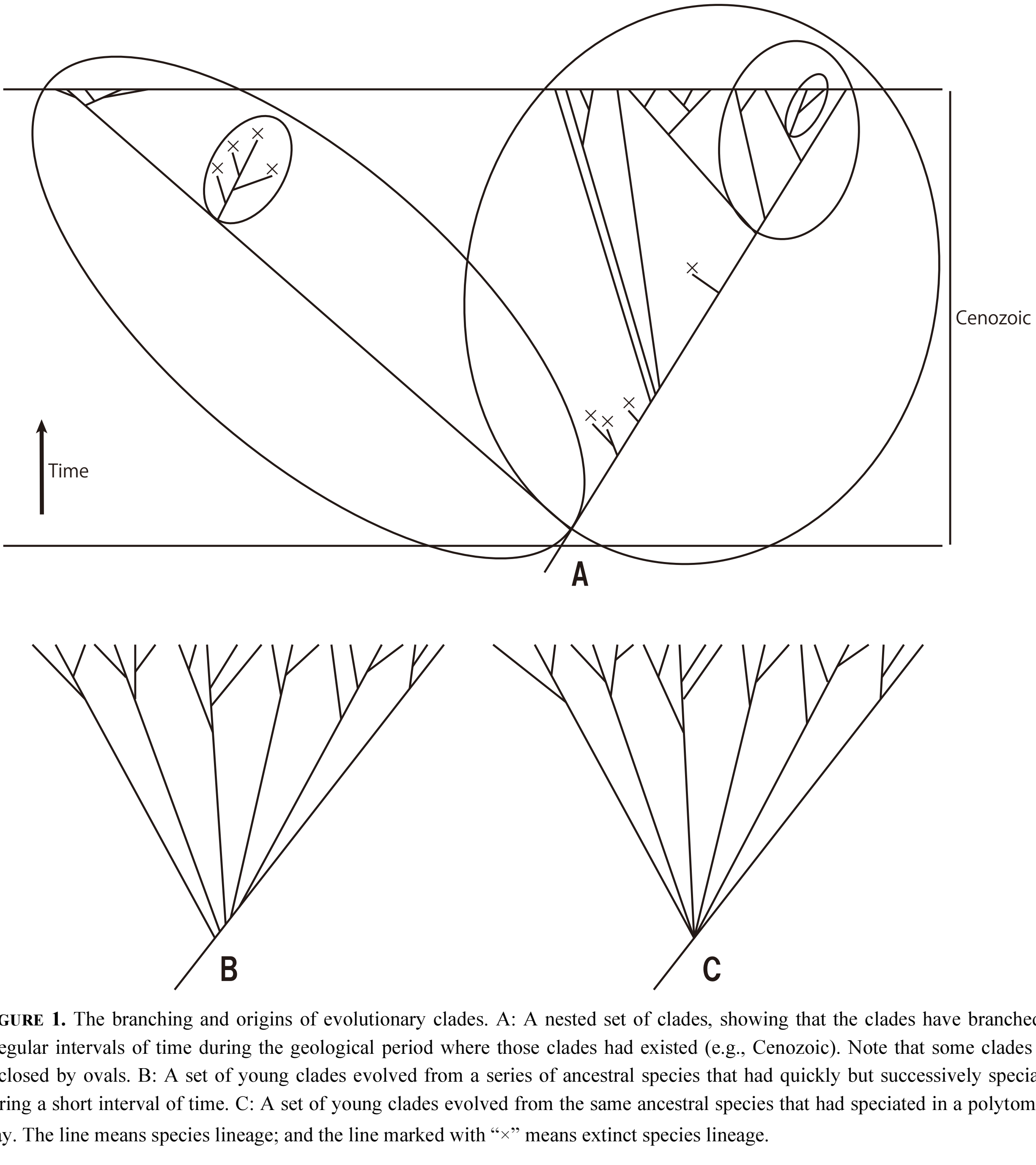

FIGURE 1. The branching and origins of evolutionary clades. A: A nested set of clades, showing that the clades have branched at irregular intervals of time during the geological period where those clades had existed (e.g., Cenozoic). Note that some clades are enclosed by ovals. B: A set of young clades evolved from a series of ancestral species that had quickly but successively speciated during a short interval of time. C: A set of young clades evolved from the same ancestral species that had speciated in a polytomous way. The line means species lineage; and the line marked with "×" means extinct species lineage.

Given the major biological properties of species and clades described above, what is obvious is that a species (as an evolutionary lineage) can be a member of a taxonomic category, while a clade cannot. The species category is a class whose members are all evolutionary lineages that merit recognition as species; and it can be logically defined by the necessary and sufficient property, that is, "*being a lineage*" (de Queiroz 2005*a*). Since the defining property of species category (i.e., "*being a lineage*") is accompanied by empirical contents actually represented by a variety of species criteria such as intrinsic isolation, ecological distinctness, diagnosability, phenetic distinctness, etc. (Mayden 1997; de Queiroz 1998), we can recognize the species level lineages separately in practice, with those biological properties. On the other hand, no clade category exists, except for the categories created by convenient ways of partitioning the continuous series of clades (de Queiroz 2007*a*: 957; this paper).

Viewed philosophically, species are considered individuals in the philosophical sense (Ghiselin 1966*b*, 1974) because they each are spatio-temporarily restricted, continuous through time, and have a unique origin and ending; and their names are proper so that the names can be defined ostensively by associating the names with species to which the names are attached. The same seems to be almost true of the evolutionay clades (Ghiselin 1974: 540; 1997: 54; see also second section). However, being different from the species, first, the clades are assumed to have unrestricted endings (O'Hara 1988) in cases where species (as their components) differentiate at the present moment rather than becoming extinct; but the clades seem to have the fate to finally decease when those species all become extinct. Second, the clades themselves do not participate in biological processes while at the same time they contain the species that do; thus Wiley (1980 1981) called the clades '*historical groups*'.

Proposal of a phylogenetic taxonomy, with the method of using "names with standard endings" in clade nomenclature

The reference system of taxon names with an organismal group serves dual purposes – practical and general ones. The practical purpose is that the reference system serves as the convenient[1] informational organization and retrieval system with the group, while the general purpose is that the reference system serves as the system of words (i.e., taxon names) that represents the phylogenetic relationships of organisms in the group. The existence of these two kinds of purposes of the reference system has led to a persisting controversy, because it has been seriously questionable whether the purpose of information retrieval is compatible with the purpose of generalization. When looking back at the debates over theory and practice of biological taxonomy in the last three decades, the taxonomist community does not seem to have reached a consensus as to what the purpose of taxonomy is (Mayr 1982: 148–149). In general, those who support the Linnaean taxonomy (e.g., Wiley 1981; Nelson & Platnick 1981; Mayr & Ashlock 1991; Benton 2000; Moore 2003; Schuh 2003), whether phylogenetic systematists or evolutionary systematists, seem to emphasize the practical purpose by evaluating the point that the Linnaean system can pack vast amounts of information into names by using a set of mutually exclusive taxon names that can be recognized with ease by their standard endings (see for example, Moore 2003; Platnick 2012). On the other hand, those who support phylogenetic taxonomy (e.g., de Queiroz & Gauthier 1990, 1992, 1994; Härlin 2005; Laurin 2010) seem to emphasize the general purpose by evaluating the point that a rank-free system is reconciled with the evolutionary world view.

However, to achieve both of those purposes simultaneously is, in my opinion, the prerequisite for making the reference system being espoused by many taxonomists and biologists, although it is certainly a difficult job. Motivated by those intellectual debates as to the matter with biological taxonomy and nomenclature, I here intend to propose, for achieving both purposes simultaneously, a phylogenetic taxonomy with the method of using names with standard endings in clade nomenclature. First, I argue over the taxon names used in the phylogenetic taxonomy, second over the categories of evolutionary clades, and third over naming clades by use of standard endings.

---

[1] The "*convenience*" (as a property of a reference system) means in this paper the practicality that is brought to a reference system by the mutual exclusivity of taxon names with standard endings that play a role as mnemonic symbols for users.

Taxon names used in the present phylogenetic taxonomy

First, I take a stance of individualism (Ghiselin 1966*b*, 1984, 1997) that taxa (clades) are individuals, and thus do not possess defining properties. Their names are proper names; and thus a name of taxon can be defined ostensively, connecting the name with the taxon to which the name is given, as at a christening. Regarding the nature of proper names, there are two philosophical approaches: the Russelian and the Millian. Under the Russelian approach, a proper name is an abbreviated description, and the description is considered equivalent to the meaning of the name (Härlin 1998; Härlin & Sundberg 1998). On the other hand, under the Millian approach, "*a proper name is but an unmeaning mark which we connect in our minds with the idea of an object, in order that whenever the mark meets our eyes or occurs to our thoughts, we may think of that individual object*" (Mill 1872: 22). If we adopt the Russelian approach in naming clades, as de Queiroz & Gauthier (1990) did, then the name is an abbreviated description; and it refers to whatever fits the description rather than the intended clade (Härlin & Sundberg 1998). This causes problems in the case of change of phylogenetic hypotheses, because we are to make language (rather than phylogeny) determine what clades to name, resulting in the primacy of names over clades. On the other hand, if we take the Millian approach, then the taxon name is but meaningless mark or symbol because it is a proper name. From the perspective of individualism, the name of a taxon (as individual) is a simple symbol not only in its initial ostension, but also in the following ostensions in cases where the phylogenetic hypotheses are changed, so that taxonomists can properly fix the reference of the name to the clade (Härlin 1998). Given this, the Millian approach is well reconciled with Ghiselin's thesis that taxa are ontological individuals (Härlin 1998; Härlin & Sundberg 1998; see also Wiley & Lieberman 2011). And thus, second, I here take the Millian approach regarding the nature of proper names.

If we take the stance that taxon names are meaningless symbols, then not only known taxon names with standard endings (e.g., Staphylinidae, Staphylininae, Staphylinini, Staphylinina) and without them (e.g., Insecta, Coleoptera, *Staphylinus*), but also random arrangements of letters (such as "Rdyfwgph" and "Tuqlijkm") all can be theoretically regarded as candidates for clade names in the rank-free systems created under the phylogenetic taxonomy, because those candidates (as meaningless symbols) can each firmly and equally point to a particular clade on the phylogenetic tree or timetree. The important point here is that, just like the names without standard endings and the random arrangements of letters, the names with standard endings can certainly be well reconciled with the theory of phylogenetic taxonomy or nomenclature (de Queiroz & Donoghue 2013: 170), and thus can be legitimately used as formal taxon names in the rank-free system. This means that the nomenclatures in which the standard endings are adopted in naming clades are not necessarily the Linnaean ones (i.e., IUMS 1992; ICZN 1999; IBCM 2012). Therefore, we should discard the idea that taxon names with standard endings can be effectively used only in the Linnaean (ranked) systems. In point of fact, I adopt here the method of using names with standard endings in naming particular clades. I am to do so, because in constrast with names without standard endings and random arrangements of letters, names with standard endings function well as mnemonic symbols. Specifically, I use names with standard endings as (meaningless) symbols that designate the *basic clades*, out of the clades whose evolutionary origins are located in one particular temporal band (see third subsection of this section).

Finally I show that basic clade names with standard endings can convey plenty of taxonomic information in a rank-free system as taxon names can do in the ranked system. The basic clade names in the (rank-free) reference system are arranged so that the mutual exclusivity of those basic clade names is certain; and thus the name of a small basic clade can convey taxonomic information not only about the clade itself, but also about the large basic clades whose parts are the small basic clade. Here, suppose that we have a reference system of Insecta, in which such names as *Staphylinus*, Staphylinidae, Coleoptera and Insecta are basic clade names. If so, then the name *Staphylinus* can convey information not only about the clade itself, but also about more inclusive clades such as Staphylinidae, Coleoptera and Insecta. When one knows that the *Staphylinus* belongs to the Staphylinidae within Coleoptera in Insecta, one can know with ease that the species of *Staphylinus* have in general short elytra (fore wings) that are contiguous along the mid line, have six legs and four wings, etc.

Given that those clades all are individuals (as historical entities that do not possess defining properties), the rich taxonomic information that the clade name (i.e., *Staphylinus*) conveys is descriptive information about those basic clades (i.e., *Staphylinus*, Staphylinidae, Coleoptera, Insecta); it is, however, never related to the organismal traits (as defining properties) that bring forth the meaning of the clade names as symbols. Users can obtain the information because of the particular taxonomic structure that the reference system has (i.e., a hierarchical arrangement of names [with standard endings] of the mutually exclusive basic clades). Thus, it follows that the basic clade names can convey plenty of taxonomic (or descriptive) information under the present phylogenetic taxonomy (that adopts the Millian approach to the nature of proper names). This is reasonable when considering that, even if a basic clade name serves as a symbol that conveys rich "descriptive" information, the name itself is still a meaningless symbol that was or will be used in ostension.

Categories of evolutionary clades

The categories of evolutionary clades that I recognize here are basic clades, holoclades and synclades. These three clade categories just represent convenient ways of partitioning the continuous nested series of clades, by using the different components (nodes and branches) of phylogenetic timetree (on which the temporal bands are overlaid) as reference points. First, I define the basic clades, holoclades and synclades, together with descriptions of some major characteristics of basic clades. I argue over the relationships of those three clades to the total and crown clades recognized in other phylogenetic taxonomies, and also over the wholly extinct clades. Second, I take up the matter with apomorphy clades and some problems related with them.

Basic clades, holoclades and synclades

In the part of a timetree located in one temporal band, there exist clades conceptualized as being represented by "one simple branch" that continues from a node to the upper temporal band (Fig. 2A), and has no intermediate nodes on the path from the basal node to the top transverse line of the temporal band (but the "branch" does not include the node at its base). This is to say that the "simple branch" in question means the clade that includes the ancestor species lineage represented by that simple branch, and all of its descendants including both extant and extinct subclades, species and organisms. Such clades all are here regarded as "*basic clades*". The "simple branch" (as part of a basic clade) is virtually the analog to the basal part (as stem lineage) of the total clade (e.g., de Queiroz 2007*a*: 958, fig. 2) (see also later discussion in more detail). A "simple branch" may have side branches although such side branches are not shown in Fig. 2A; here "side branches" mean extinct species or very small clades (that comprises several species). Thus, even if there are intermediate nodes (from which side branches split) on the path of the "simple branch" from the basal node to the top transverse line of the temporal band, "the simple branch" still represents one basic clade. Examples of basic clades are given in Fig. 2A. In the part of a timetree located in the temporal band "Oligocene", there exist five (extant) basic clades Ainae, Binae, Cinae, Dinae and Einae. Many known supraspecific taxa may be considered candidates for basic clades when they are monophyletic groups. The reason that they are called "basic" is that, as mentioned later, their names are fundamental components of a phylogenetic system in which they keep standard endings.

The major characteristics of the basic clades of the same temporal band (i.e., basic clades whose evolutionary origins are located in the same temporal band) are the following two. First, they have almost the same age. Second, they are mutually exclusive in that they do not overlap their parts; in other word, each basic clade does not form a more inclusive clade that comprises two or more basic clades, and all species and organisms that share a more recent common ancestor with those basic clades than with any other mutually exclusive basic clade. When considering these two points, it seems at first glance that the basic clades are comparable units just as species (as evolutionary lineages) are, and that those basic clades (as taxa) form an age class. In fact, some have developed similar ideas. For example, considering higher taxa at the same rank (defined by absolute age) to be comparable units, Hennig (1950, 1966) proposed to redefine the taxonomic categories as age classes (see also Griffiths 1976). And, although Dubois (2008: 57) indicated several basic problems with Hennig's approach, and rejected it for these problems for the time being, he thought that it could under certain conditions be appropriate to allocate a set of higher taxa defined by the absolute chronological criterion, to a given taxonomic category because they share some evolutionary meanings.

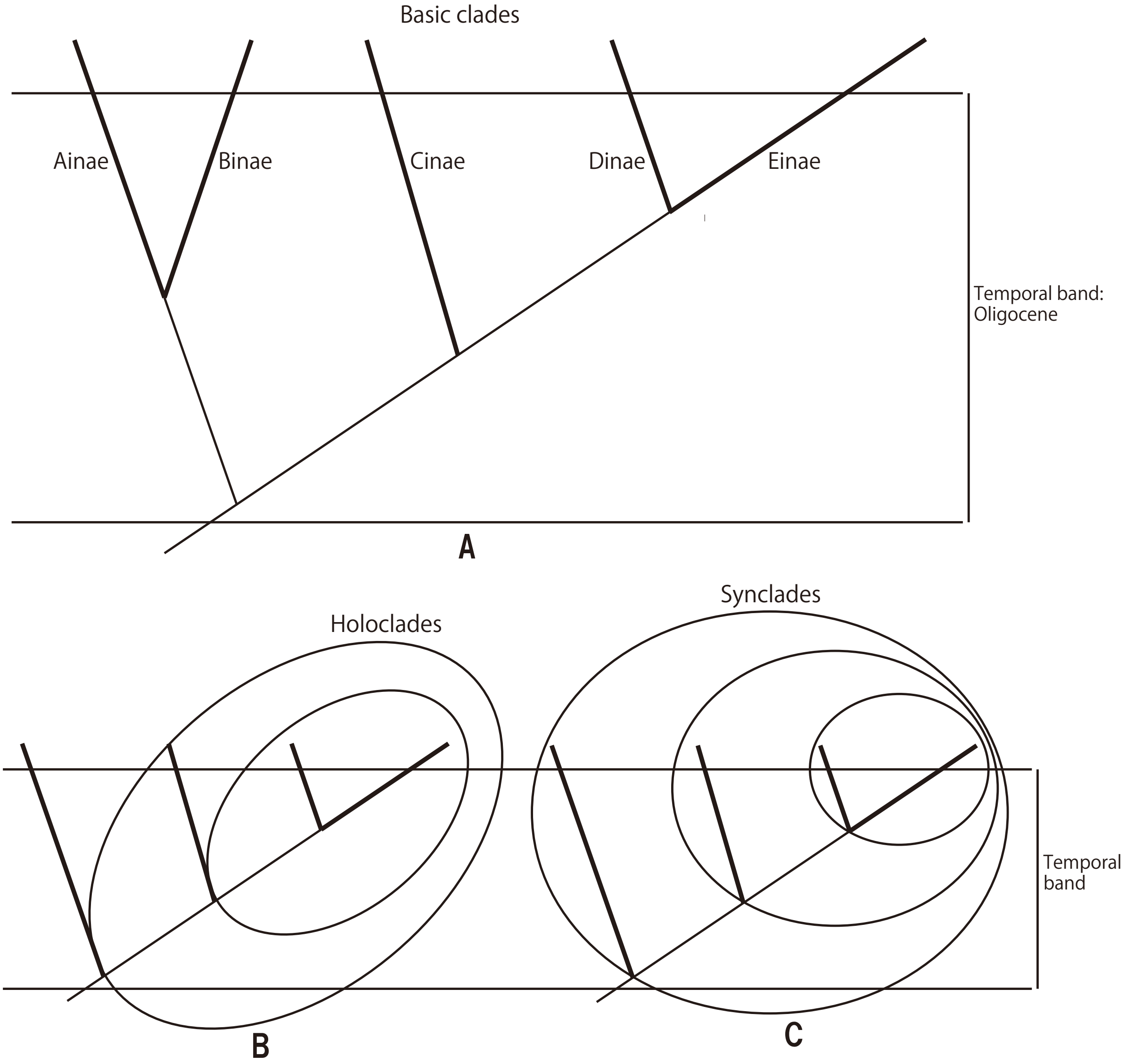

FIGURE 2. The evolutionary clades (basic clades, holoclades and synclades). A: Basic clades whose origins are located in the temporal band "Oligocene". Note that parts of the basic clades existed after the Oligocene are not depicted. B: A nested set of holoclades enclosed by ovals. C: A nested set of synclades enclosed by ovals. Note that in B and C, parts of the inclusive clades existed after the temporal band are not depicted. Thick lines represent the basic clades in A, B and C.

As pointed out in the first section, the equivalent (or comparable) clades are, however, the sister clades, because they differentiated from one and the same ancestor species lineage. Thus, whether the basic clades of the same temporal band are equivalent rests just on their phylogenetic relationship they have. If two basic clades happen to form sister clades, then they are equivalent (e.g., Ainae and Binae in Fig. 2A). If two basic ones do not form sister ones, then they are not. For example, Cinae and Dinae do not form sister clades (Fig. 2A), and thus they are not equivalent. The Cinae is equivalent only with its sister clade that comprises the Dinae, Einae and their common stem lineage, but not with the Dinae nor with the Einae, because the Dinae and Einae are each nested within (or constitute part of) the inclusive clade that is equivalent with the Cinae. Given the relationship of clades existing at various levels, the basic clades of the same temporal band cannot be considered equivalent (and countable) units; and thus they do not form a class nor belong to a taxonomic category defined in terms of absolute age. Nevertheless, when considering that the basic clades have the afore-mentioned two characteristics, we may be able to regard those basic clades of the same temporal band as "*semi-comparable*" units just from a point of convenience; and therefore they may be used in the biodiversity and other studies in biology as units that facilitate comparison.

Out of the clades that originate in the temporal band in which the basic clades exist, two categories of inclusive clades (holoclades and synclades) can be identified that include two or more basic clades. A *holoclade* is a clade comprising two or more basic clades (of the same temporal band), and all species and organisms that share a more recent common ancestor with those basic clades than with any other mutually exclusive basic clade (Fig. 2B). When depicted in the tree, the basal branch (that represents the stem lineage) of holoclade does not include the node at its base. As in the cases of basic clades, there are the cases of holoclades where side branches are split from the nodes on the basal branch. By definition, the clade comprising Ainae and Binae, and all species and organisms that share a more recent common ancestor with these two basal clades than with Cinae (Fig. 2A) is a holoclade. On the other hand, a *synclade* is a clade originating from the ancestor, from which a basic clade (or a holoclade) and its sister clade (as another basic clade or holoclade) differentiate (Fig. 2C); when depicted in the tree, the synclade includes the basalmost node, from which the branches (as its subordinate clades) are split. For example, the clade originating from the ancestor, from which Ainae and Binae differentiate (Fig. 2A), is a synclade.

This way of conceptualizing the inclusive clades (holoclade and synclade) is just for the sake of convenience for developing a framework of clade naming (see next subsection). The basic clades, holoclades and synclades do not represent fundamentally different kinds of evolutionary clades; and all of those clades are similar in that they each form a part of timetree, and consist of an ancestor and all of its descendants.

Let us take up also the topological sameness of, and difference between, the basic clade and holoclade drawn in the pictorial representation of a timetree (on which temporal bands are overlaid). The branch (as a basic clade) in any temporal band (except the latest temporal band) (e.g., Fig. 9: Ainae; Einae) has at least one or more nodes on the line in the subordinate temporal band(s). At each of those nodes, a subbranch (as a subordinate basic clade or holoclade) is split from the other subbranch (as its sister clade); here these subbranches mean the clades that are equivalent in that they have same ages. Thus, the simple branch as a basic clade in the temporal band (in which the origin of the basic clade is located) is part of the basal branch of the basic clade which means the stem lineage. Taking into account this aspect of the basic clade, together with the topological feature of holoclade described above, the basic clade and holoclade are topologically the same, in that they have the basal branch represented by the line as stem lineage. The difference between basic clade and holoclade is as follows. In the case of the branch (as a basic clade), the base of branch and the first node from the base are located in different temporal bands; that is, if the base of the branch is located in a temporal band, then its first node is located in one of its subordinate temporal bands. On the other hand, in the case of a branch (as a holoclade), the base of the branch and its first node are located in the same temporal band. The difference between basal clade and holoclade is so trivial from the phylogenetic point of view that they are basically considered to be the same kind of clades; and thus they should not be separately categorized. The reason that they should be here, is again closely related to developing a framework of clade naming (see next subsection).

Relationships of basic clades, holoclades and synclades to the total and crown clades

De Queiroz (2007*a*) developed an integrated system of clade names. He recognized the categories of crown, total, apomorphy, and some other (i.e., node-based, branch-based, apomorphy-based) clades, and considered that the former three are appropriate as the basis for a system of clade names; that is, they are the categories of clades that are worth naming. A crown clade (= * group: Hennig 1969, 1981; crown group: Jefferies 1979) is defined as a clade originating from the last common ancestor of two or more extant organisms or species (de Queiroz 2007*a*: 958). A total clade (= total group: Jefferies 1979; pan-monophylum: Lauterbach 1989; stem clade: de Queiroz & Gauthier 1992; panstem: Joyce *et al.* 2004) is defined as a clade composed of a crown clade and all species and/or organisms that share a more recent common ancestor with that crown than with any other mutually exclusive crown group. And, an apomorphy clade is defined as a clade originating with the ancestor in which a particular derived character state arose.

I here examine the relationships of basic clades, holoclades and synclades to the total and crown clades. All of these clades (basic clades, holoclades, synclades, total and crown clades) basically consist of the extant and/or extinct subclades comprising species and organisms (See also "Wholly extinct clades" in this paper; and de Queiroz, 2007*a*: 958–960). Out of these clades, the basic clades, holoclades and total clades are, when depicted in the tree, the same in their topology; they each have a basal branch. They are also the same in that they have often side branches split from nodes on the basal branch. Thus, the basic clades and holoclades are virtually equivalent to the total clades. On the other hand, the synclades and crown clades, when depicted in the tree, have the same topology in that they originate in a particular node of the tree. Furthermore, the topological relationship of a basic clade (or holoclade) to its subordinate synclade is the same as the relationship of a total clade to its crown clade. Since the basic clades (or holoclades) are equivalent to the total clades, the synclades are equivalent to the crown clades. It follows then that the clades (i.e., basic clades, holoclades, synclades) recognized in this paper are actually equivalent to the major ones (i.e., total and crown clades) in de Queiroz (2007*a*), putting apomorphy clades aside.

Wholly extinct clades

The wholly extinct clades that I take up here are not extinct clades that form side branches split off from nodes on the basal branches (as stem lineages) of extant clades (when depicted in the tree). They are extinct clades whose parts (i.e., subclades) merit recognition as objects for naming (e.g., large extinct clades such as Ammonoidea and Trilobita to small ones such as aardvark *Amphiorycteropus* [Lehmann, 2009]).

The question about how to name parts of wholly extinct clades has been controversial (e.g., Ax 1987; Meier & Richter 1992; Monks 2002; Donoghue 2005; de Queiroz 2007*a*). Ax (1987) advocated subdividing a wholly extinct clade into a stem and a crown, although those terms (stem and crown) have been previously used for extant groups. Following Ax, Lauterbach (1989) used the term crown for taxa comprising only extinct species. Meier & Richter (1992: 85) rejected Lauterbach's usage of term crown, because the term should explicitly refer to extant groups. De Queiroz (2007*a*), on the other hand, suggested that the terms crown and stem are generalized so that they can be used for wholly extinct groups. If so, then a definition of the term "wholly extinct crown clade" may be as follows: a clade stemming from an ancestor, from which a rapid species radiation (or differentiation) occurred, and the ancestor and descendants all have become entirely extinct, and do not survive to the present time – a definition, on which we can hardly identify the crown clade. Given the definition of the term crown clade mentioned above, there is no objective criterion, on which a wholly extinct clade is properly subdivided into a stem and a crown (Donoghue 2005: 556). However, the fact is that a clade whose component species all are extinct at present, has been certainly a crown clade at some earlier time, although it is not a crown clade in the context of present time (de Queiroz 2007*a*: 959). Furthermore, there is a need to name parts of wholly extinct clades in the paleontologist community (e.g., Ax 1987; see also Donoghue 2005: 556). Thus, following de Queiroz's way of generalizing the clade terms, I here consider that the terms basic clade, holoclade and synclade are generalized so that they can all be applied to wholly extinct clades as well as extant clades.

Apomorphy clades and related problems

Hennig (1965) recognized the existence of an ancestor of a clade with "typical character", at a point of the stem lineage between the age of the clade's origin and of its division, and conceptualized the ancestor of the clade in terms of the first appearance of its "typical character". Considering the "typical character" to be a typologically determined character, the use of which does not solve any phylogenetic problem, Hennig (1969, 1981: 26–27) withdrew his conceptualizing it. However, de Queiroz & Gauthier (1990: 310) recognized the apomorphy-based clade, which is virtually equivalent to a clade with "typical character" in Hennig (1965), by pointing out that the character used in defining the apomorphy-based clade name is (not the typologically determined character but) simply a means of specifying an ancestor. When de Queiroz (2007*a*) developed an integrated system of clade names, he recognized, as mentioned above, the categories of apomorphy clades, that is, apomorphy-based clades that are worth naming. However, regarding de Queiroz's stance that those apomorphy clades should be named, there seems to be some problems, as discussed below[2].

Although de Queiroz himself did not justify the reality of apomorphy clades in connection with de Queiroz's view on species, de Queiroz's (1999) lineage species concept seems to underlie the reality of apomorphy clades in nature. At first, he admits that a species lineage can change indefinitely during the course of its life, and still remain the same species, provided that the change is more or less gradual and continuous (de Queiroz 1999: 69). However, he also thinks that if a species lineage experienced a severe bottleneck, which is similar to a founder event, it is justifiable to regard the lineage segments on either side of the bottleneck as different species (de Queiroz 1999: 69). Thus, following his view on species, we can recognize with ease the clade originating from the ancestor with those apomorphies, as an apomorphy clade, in cases where the ancestor (i.e., a species lineage that evolved after a founder event) has acquired one or more apomorphies at this evolutionary event (Fig. 3). Given this, his concept of species is well reconciled with the concept of apomorphy clade, and thus actually endorses the reality of the apomorphy clade.

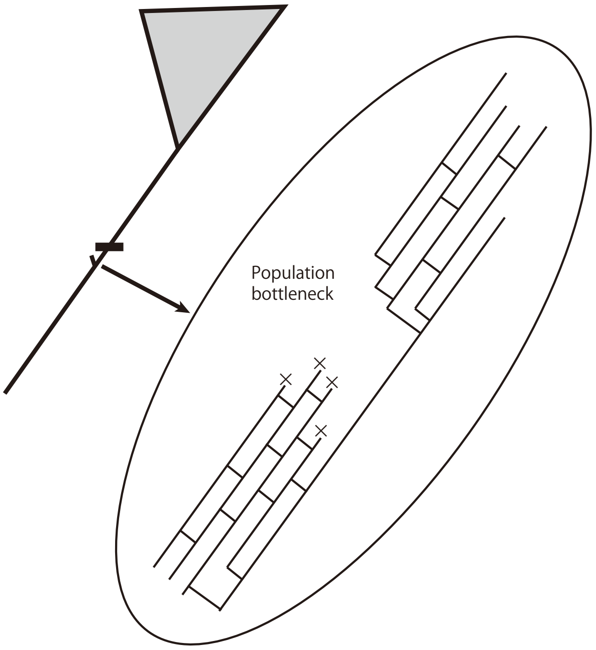

FIGURE 3. A total clade whose sister clade is difficult to recognize. The line marked with "×" means a wholly extinct sublineage of a species lineage.

De Queiroz virtually recognized the successional speciation without branching event, which the evolutionary or lineage species concept rejects (Wiley 1978, 1981). However, theoretically, the founder event recognized under his species concept is, if it occurred during the lifetime of a species, not a successional speciation, but a speciation, at which one sister species lineage become extinct during a very short period (Fig. 3). In short, it is a special case of speciation accompanied by branching event (e.g., allopatric speciation). Therefore, the clades originating from those ancestors with apomorphies can be regarded not as apomorphy clades, but as total clades whose sister clades are difficult to recognize. Given this, if they are named, then they are named not as apomorphy clades but as total clades.

---

2. Since the target for discussion in this part is evolutionary clades that are worth naming, the clades that I take up in the following discussion are only apomorphy clades.

Finally, let us consider the cases where species lineages as the ancestors of clades have changed anagenetically. Those species lineages have often experienced anagenetic (or phyletic) changes to a considerable degree, with the successive occurrence of apomorphies, as paleontological data show (e.g., Simpson 1953). In such cases, we may interpret every anagenetic stage of the species lineage with some apomorphies, as an ancestor of a clade with those apomorphies; thus we may also regard every clade originating from the ancestor with those apomorphies, as an apomorphy clade. Thus, if the nomenclatural rule that those clades with specified apomorphies can be named is approved, then the names given to the apomorphy clades may increase almost infinitely. Putting analogy to use, naming those apomorphy clades whose ancestors exist between the age of the clade's origin and of its division is similar to naming rational numbers in cases of the Dedekind cut, which means that if the real number line on a graph is cut by two different points, then infinite rational numbers exist between those two points. One of the reasons that de Queiroz considered the apomorphy clades to be those that are worth naming, may be from such practical point as facilitating communication among paleontologists about the phylogenetic relationships of the clades with rich fossil clades and species (see also de Queiroz & Gauthier 1992). However, because of the problem mentioned above, I do not recommend taxonomists to name those apomorphy clades in cases where researchers can see obviously that those apomorphies have occurred during the true anagenetic changes of the ancestral species lineage.

Naming clades with the use of standard endings

The method that I regard here as very important for naming clades, has developed in relation to Hennig's way of establishing the ranks of categories of monophyletic groups (clades) of various levels which have some evolutionary meaning (Hennig 1966: 154). Hennig (1966) considered that the monophyletic groups of a taxonomic category can be compared if they have almost the same age of evolutionary origin; and he tried to determine the absolute ranks of taxonomic categories according to the ages of evolutionary origin of the monophyletic groups (Table 1, upper). This idea has been rejected by not a few taxonomists (e.g., Crowson 1970; Eldredge & Cracraft 1980; Ax 1987; Scott-Ram 1990) in the last decades of 20th century when the task of reconstructing the timetrees was much more difficult than today, but Avise & Johns (1999) developed, by modifying Hennig's method, a standardized temporal scheme of biological taxonomy. They created the temporal bands of nomenclatural ranks, by assigning those ranks to the particular geological episodes (Table 1, lower); and thus a particular geological episode is associated with a particular rank. Under this temporal banding method, if the origin of a clade is placed in a particular temporal band, then the clade is treated as a taxon assigned to the rank, with which the particular temporal band is associated. For example, the time of evolutionary origin of the fruit fly genus *Drosophila* goes back to the Cretaceous, and thus *Drosophila* is a taxon at the level of suborder, because the temporal band Cretaceous is associated with the rank suborder (Table 1, lower; see also Avise & Johns 1999).

TABLE 1. Geological episodes, temporal bands, and taxonomic ranks as adopted by Hennig (1966) (upper table) and by Avise & Johns (1999) (lower table).

Geological episode	Temporal band	Taxonomic rank
Miocene	5–24 Mya	genus
Oligocene to Upper Cretaceous	24–100 Mya	tribe
Lower Cretaceous to Triasic	100–250 Mya	family
Permian to Carboniferous	250–350 Mya	order
Devonian to Cambrian	350–550 Mya	class
Precambrian	550 Mya-	phylum

...... *continued on the next page*

Geological episode	Temporal band	Taxonomic rank
Pleistocene	0–2 Mya	subgenus
Pliocene	2–5 Mya	genus
Miocene	5–24 Mya	tribe
Oligocene	24–33 Mya	subfamily
Eocene	33–56 Mya	family
Paleocene	56–65 Mya	superfamily
Cretaceous	65–145 Mya	suborder
Jurassic	145–205 Mya	order
Triassic	205–250 Mya	superorder
Permian	250–290 Mya	cohort
Carboniferous	290–350 Mya	subclass
Devonian	350–410 Mya	class
Silurian	410–440 Mya	superclass
Ordovician	440–500 Mya	subphylum
Cambrian	500–550 Mya	phylum
Proterozoic	0.55–2.5 Bya	kingdom
Archaean	2.5–3.6 Bya	domain

Hennig's and Avise & Johns' theories of taxonomy (which treat the monophyletic taxa at the same rank as "comparative units") cannot be adopted here, because their theories are closely linked with the nomenclatural ranks, which are not reconciled with the evolutionary world view (e.g., Zachos 2011). Their temporal banding methods, however, have a striking aspect with regard to the relation of standard endings (of clade names) to the temporal bands. That is, the particular standard ending corresponds to the particular temporal band (Table 1); notice here that the function that the standard endings have under the Linnaean nomenclature (namely, to designate particular ranks) is irrelevant here. The present phylogenetic taxonomy makes the best use of the association of standard endings with the temporal bands in naming clades; that is, it makes a particular standard ending of clade name have the function of associating the clade (whose name has a standard ending) with the temporal band to which the standard ending corresponds.

As mentioned in the first subsection, clade names with standard endings can be used as components of a rank-free reference system, when we interpret those names as meaningless symbols under the Millian philosophy of language. Thus, introducing the method of using "names with standard endings" into the present clade nomenclature is logically possible. That is, by adopting the temporal bands (to which the standard endings correspond), as the unique criteria for assigning those endings to some clade names in naming clades, we name clades so that we can create a reference system, in which taxon (clade) names with standard endings play a role as its fundamental components. The reference system created by this method is completely rank-free, but the particular domain of reference system has the same style as the Linnaean system of taxon names, in that those taxon names adopted all have standard endings, and thus the mutual exclusivity of taxon names is certain there. Let us describe in detail how we can obtain such a scheme of words under the present phylogenetic nomenclature.

What are the clades that are worth naming?

First of all, I take up and answer the taxonomic question as to what are the clades that are worth naming, or to which clades the names be given. The matters that we should consider when we answer such question are the following two. First, for the studies of diverse organismal groups in various fields of neontology and paleontology, biologists need reference systems of clade names, by which to obtain various information including the phylogenetic relationships between the organisms. Second, biologists encounter taxon name problems (i.e., confusion as to the usage of clade names) during the course of their studies. One major taxon name problem is that the same names are sometimes given to different clades in the traditional reference systems; and another one is that no name is given to the clade that they want to study. These taxon name problems seem to occur particularly in paleontology. For example, even if paleontologists agree on the reconstructed phylogeny of an organismal group (which actually forms a clade), they have often the problem as to whether the fossils discovered belong to the group, when the name has been applied to the group that comprises only extant species. Such problems frequently result in endless and fruitless debates about the taxonomic position of those fossils in the phylogenetic system (Hennig 1965). Furthermore, in cases where a rich set of fossils are discovered from the stem lineage of an extant clade, the same names are often given to the total clade, its crown clade and other clades originating at various nodes or branches (de Queiroz & Gauthier 1992; de Queiroz 2007*a*), causing difficulties in communication.

To achieve the goal of establishing such reference systems as adequate for taxonomic information storage and retrieval, and also as anchorage for solving various sort of taxon name problems including those that paleontologists have had, different clades in nested series be named differently (de Queiroz 2007*a*: 961) because of the following two reasons. First, this taxonomic option brings a rich taxonomic information to the reference system. That is, the larger the number of clade names that constitute a reference system, the greater is the bulk of information that the clade names convey, and thus the bulk of information that the reference system contains. This option obviously renders the reference system more useful both for communication and for the better understanding of nature. Second, this option also brings forth the precise reference of a name to a particular clade, resulting in avoiding those taxon name problems. Given this, as de Queiroz & Gauthier (1992: 457) stated succinctly, naming clades is no doubt preferable to leaving them unnamed. Thus, targets for naming under the present phylogenetic taxonomy are all (extant and extinct) basic clades, holoclades and synclades of a group in question.

Criteria for assigning standard endings to basic clade names: temporal bands of geological episodes

Temporal bands adopted in naming extant basic clades

The temporal bands of geological episodes (to which standard name endings correspond) play an important role as the unique criteria for assigning those endings to basic clade names in the present clade nomenclature; and the temporal bands for naming the extant basic clades are, if necessary, called "neontological temporal bands" (abbreviated as "N-temporal bands"). Hennig (1966) partitioned the geological age into 6 episodes (Table 1, upper), while Avise & Johns (1999) did it into 17 episodes (Table 1, lower). The set of 17 temporal bands proposed by Avise & Johns (1999) are here regarded as "*the standard temporal bands*", some of which are associated with the standard endings that the current Codes adopt in naming some higher groups (Table 2).

In Avise & Johns's version, however, no temporal band is associated with the subtribal rank; as a consequence, at present we do not have the temporal band that serves to assign the standard ending "-ina" (animals) and "-inae" (algae, fungi, plants and bacteria) (Table 2) to basic clade names. Thus, the temporal band "Miocene" (which is associated with the tribal rank in Avise & Johns's version) is here divided into two bands: The first is the temporal band "Early Miocene (or E-Miocene: ca 11-24 Mya)" which is, under the present nomenclature, associated with the standard ending "-ini" (animals) and "-eae" (algae, fungi, plants and bacteria); and the second is the temporal band "Middle and Late Miocene (or ML-Miocene: ca 5-11 Mya)" which is associated with the ending "-ina" (animals) and "-inae" (algae, fungi, plants and bacteria). Those two temporal bands are newly adopted here as components of the standard temporal bands (Table 2) in naming the basic clades of all organismal groups (i.e., animals, plants, algae, fungi and bacteria).

On the other hand, a set of temporal bands with a new partitioning of the geological age adapted for the phylogenetic taxonomies of groups (which are actually local clades) are here called "*non-standard temporal bands*". Such temporal bands are created by taking into account the relative ages of the local clades in the disparate organismal groups (Talavera *et al.* 2013), so that they only minimally disrupt the current reference systems of taxon names with those groups (Avise & Johns 1999: 7362). In the phylogenetic-systematic studies, using non-standard temporal bands, for example, Talavera *et al.* (2013) used the temporal band "Late Oligocene to Early Miocene (older than 15 Myr)" as the criterion by which to treat the clades whose origins are located in the temporal band, as subtribes for the butterfly family Lycaenidae; and Lim (2007) settled the temporal band "Oligocene", as the criterion by which to treat the clades whose origins are located in the temporal band, as tribes for the South American bat family Emballonuridae. In the present clade nomenclature, the non-standard temporal bands play a role as the unique criteria for assigning standard endings to basic clade names, as the standard temporal bands do.

TABLE 2. Geological episodes, standard temporal bands, and standard name endings that correspond to the standard temporal bands. The first and second lines show geological episodes and standard temporal bands, respectively, as adopted in this paper. The third, fourth and fifth lines show the standard name endings adopted in ICZN (1999), IBCM (2012) and IUMS (1992), respectively except for the following ones. The standard endings marked by * were suggested by Y. Hirashima; and the name ending marked by ** was adopted by Sibley & Ahlquist (1990); the name ending marked by *** is suggested by me; and the name ending marked by **** was adopted by Alonso-Zarazaga (2005). Note that the original name ending of "-zoes" in Alonso-Zarazaga (2005) is "-ozoes", which was originally adopted as ending for coining the names of higher taxa at the rank phylum under the Linnaean nomenclature.

Geological episode	Standard Temporal band	Standard ending (ICZN, 1999)	Standard ending (IBCM, 2012)	Standard ending (IUMS, 1992)
		Animals	Algae, fungi and plants	Bacteria
Pleistocene	0-2 Mya	—	—	—
Pliocene	2-5 Mya	—	—	—
Miocene (Middle & Late)	5-11 Mya	-ina	-inae	-inae
Miocene (Early)	11-24 Mya	-ini	-eae	-eae
Oligocene	24-33 Mya	-inae	-oideae	-oideae
Eocene	33-56 Mya	-idae	-aceae	-aceae
Paleocene	56-65 Mya	-oidea		
Cretaceous	65-145 Mya	[-i**]	-ineae	-ineae
Jurassic	145-205 Mya	[-iformes*]	-ales	-ales
Triassic	205-250 Mya	[-astra*]		
Permian	250-290 Mya	[-omedes*]		
Carboniferous	290-350 Mya	[-corphus***]	-idae; -phycidae; -mycetidae	
Devonian	350-410 Mya	[-morphes*]	-opsida; -phyceae; -mycetes	
Silurian	410-440 Mya	[-phytes*]		
Ordovician	440-500 Mya	[-nices*]	-phytina, -phycotina, -mycotina	
Cambrian	500-550 Mya	[-zoes****]	-phyta, -phycota, -mycota	
Proterozoic	0.55-2.5 Bya	[-regina*]		
Archaean	2.5-3.6 Bya	[-cosmos*]		

In order to name all extant basic clades existing in the Timetree of Life by the temporal banding methods under the present phylogenetic nomenclature, the name endings that correspond to all temporal bands, must be determined. However, determining those name endings for naming the basic clades (whose origins are located in the temporal bands, to which the standard endings do not correspond) is beyond the scope of this paper. Thus, just for the basis of further discussion I suggest here the 11 animal name endings that correspond to the temporal bands of geological episodes, to which standard endings do not correspond (Table 2), under the premise that the name endings that correspond to each temporal band can be some few or more, given the extraordinal biodiversity of living things that have evolved on Earth: Cretaceous: -i; Jurassic: -iformes; Triassic: -astra; Permian: -omedes; Carboniferous: -corphus; Devonian: -morphes; Silurian: -phytes; Ordovician: -nices; Cambrian: -zoes; Proterozoic: -regina; Archaean: -cosmos.

During their studies, taxonomists may face the situation where they need more than one standard endings for coining the names of basic clades whose origins are located within one geological episode – that is, the situation where they coin the names of basic clades whose origins are located at the several epochs or stages within one geological episode. One way to solve this problem is that taxonomists simply adopt new standard endings and use them in naming those basic clades. Another way is as follows: From a philological point of view, we can divide some of the suggested standard endings into two parts: connector and ending proper (Alonso-Zarazaga, 2005; Dubois 2006*b*: 211); for example, the standard ending "-morphes" can be divided into the connector "-morph-" and the ending proper "-es". Thus, as far as the standard endings can be properly divided into the connector and ending proper for naming basic clades, we can coin other standard endings (than listed in Table 2) by adding to the given connector such endings as "-ae", "-i" and "-idi", which were proposed by Alonso-Zarazaga (2005: 194). For example, to coin the names of basic clades whose origins are located at several epochs or stages within the Devonian, we may be able to use, if needed, such standard endings as "-morphae", "-morphi" and "-morphidi" in addition to "-morphes"[3].

In conclusion, the basic clade names coined with the use of standard endings under the present phylogenetic nomenclature are a mixed set of metarhizonyms (Dubois 2011: 57; i.e., names coined with the use of a second ending term; e.g. "Passeriformes") and rhizonyms (Dubois 2006*a*: 8; i.e., names based on the stem of lower clade names [i.e., generic names in the Linnaean nomenclature]; e.g., Staphylinina), as proposed in Sibley & Ahlquist (1990: 254).

Temporal bands adopted in naming wholly extinct basic clades

Temporal bands adopted in naming the extant basic clades are created by partitioning the entire or part of geological age into bands (to which standard endings correspond), but the temporal bands of geological episodes in the Cenozoic, whether standard or non-standard bands, always correspond to the standard endings designating the relatively lower nomenclatural ranks (e.g., "-ina", "-ini", "-inae", "-eae") (Table 2). Thus, taxonomists can adopt N-temporal bands (to which those endings correspond) also in naming some extinct basic clades in the Cenozoic (see, for example, those clades in Fig. 5). However, the N-temporal bands cannot be adopted for naming extinct basic clades whose duration is short (e.g., several epochs in one or two periods) in the Cenozoic (see, for example, the wholly extinct clade †Finae in Fig. 9). Furthermore, many extinct clades in various organismal groups had lived only in the limited duration of geological age in the Mesozoic and/or Paleozoic, but paleontologists have named many of the extinct clades and their subclades using the standard endings that designate relatively lower ranks. Given this, we cannot actually name those extinct clades and subclades, with the same method of using temporal bands as adopted for naming the extant clades; notice here that if we try to do, then the endings of almost all extinct basic clade names will drastically change.

We need, therefore, different type of temporal bands only for naming those extinct clades; here, the temporal bands used only for naming the extinct basic clades are, if necessary, called "paleontological temporal bands" (abbreviated as "P-temporal bands"). Logically, we cannot create standard P-temporal bands (that we can adopt for naming all extinct clades existing in the Timetree of Life) by partitioning the entire geological age into the bands (to which the standard endings correspond). This is because duration of the wholly extinct

---

[3] See Alonso-Zarazaga (2005: 194) regarding the name endings "-morphae", "-morphi" and "-morphidi"; and note here that he originally adopted those name endings in coining the names of some higher taxa under the Linnaean nomenclature.

clades in various groups in fact considerably varies (for example, from an epoch of the Paleozoic or of Cenozoic to several periods of the Paleozoic and Mesozoic), and thus does not overlap in many cases.

Thus, all P-temporal bands adapted for the phylogenetic studies of local extinct groups (which are actually clades) are non-standard temporal bands. An entire P-temporal band adopted here is composed of small-sized bands that we can find within the temporal band(s) of geological episode(s) where those extinct groups had lived. Specifically, the small-sized bands are, for example, epochs (e.g., those in Fig. 6) and stages of geological periods (recognized in the international stratographic chart), to which particular standard endings correspond. The way of partitioning part of the geological age into P-temporal bands in the study of a given extinct group, is arbitrary, but depends at base on how the clades and subclades existing in the group had evolved and thus become diverse in its duration. An important point here is that we must create the P-temporal bands such that we minimally disrupt the reference systems of extinct clade names with the group in question, in cases where those reference systems are constructed in an appropriate manner so that they reflect properly the phylogenetic relationships of organisms in the group (See also the discussion in "Practice of naming the extinct clades").

General method of naming clades

Naming extant clades

The first major rule in naming extant clades is that only the basic clades are named, using the standard endings by the temporal banding methods; and all extant basic clade names have standard name endings. If the origin of an extant basic clade is located in a temporal band, to which a particular standard ending corresponds, then the clade name is to have the particular ending. On the other hand, if the origin of an extant basic clade is located in a temporal band to which a particular ending does not correspond (e.g., "Jurassic"), then the basic clade must be named, using one of the newly suggested standard endings (Table 2) or others. For example, if the origin of an extant basic clade in the fish clade *Osteichthyes* is located in the temporal band Jurassic, then the standard ending "-iformes" is chosen. The second major rule is that all extant holoclades and synclades are named, without using standard endings; and all extant holoclades and synclades names do not have standard name endings. In order to create a complete reference system for a group, naming all extant holoclades and synclades (as well as basic clades) existing in the group is needed. However, the present phylogenetic taxonomy does not request taxonomists to name all of those inclusive clades; it just requests taxonomists to name some or all of them only when taxonomists need to do so.

These two major rules together claim that a name with a standard ending should not be used for a taxon nested into a taxon whose name has the same ending in a phylogenetic system; for example, the name Silphidae should not be used for a taxon nested into a taxon named Staphylinidae, without changing the name ending. Notice here that, if the extant holoclades and/or synclades are named, using standard endings by the temporal banding methods, then a taxon whose name has a standard ending is to be included into the other taxon whose name has the same standard ending. The reasons that the extant basic clades be named, using the standard endings are as follows: First, the basic clades only are targets for naming in the contemporary taxonomic studies using temporal banding method (e.g., Lim 2007; Talavera *et al.* 2013); and thus it is obvious that they are clades whose names should be fundamental components of reference system created under the present phylogenetic taxonomy. Second, the basic clades existing in a particular temporal band do not overlap each other (Fig. 2A); and when they are named with the standard endings, the mutual exclusivity of those names is certain, and thus those names serve as tools useful for human memory.

In order to preserve the extant clade names previously used in the traditional reference systems, the N-temporal banding method can take "*age threshold*" into account (Talavera *et al.* 2013). Consider the cases where an extant clade, when depicted in the timetree (on which temporal bands are overlaid), splits into several subclades before the end age of a temporal band where the origin of the clade is located. The rule of age threshold is that, if the origin of the first subclade of a clade in question is located within the age threshold, then the clade can be considered to be a basic clade, and thus named using standard endings. Suppose that three subtribal clade names (Aina, Bina and Cina) have been adopted in the traditional system; and the accepted timetree, however, showed that Cina is split into six subclades before the end age of the temporal band, in which the origins of Aina and Bina are located (Fig. 4A). The Cina is thus to be regarded as an extant clade with six basic clades in the temporal band; and the simple banding method requires taxonomists to give name to each of those basic clades, using standard endings. The rule of age threshold is adopted for this temporal band, such that the origin of the first subclade of Cina is located within the age threshold (Fig. 4A). Therefore, we can recognize the Cina as an extant basic clade; and we have those three clade names (Aina, Bina and Cina) in the rank-free system as before.

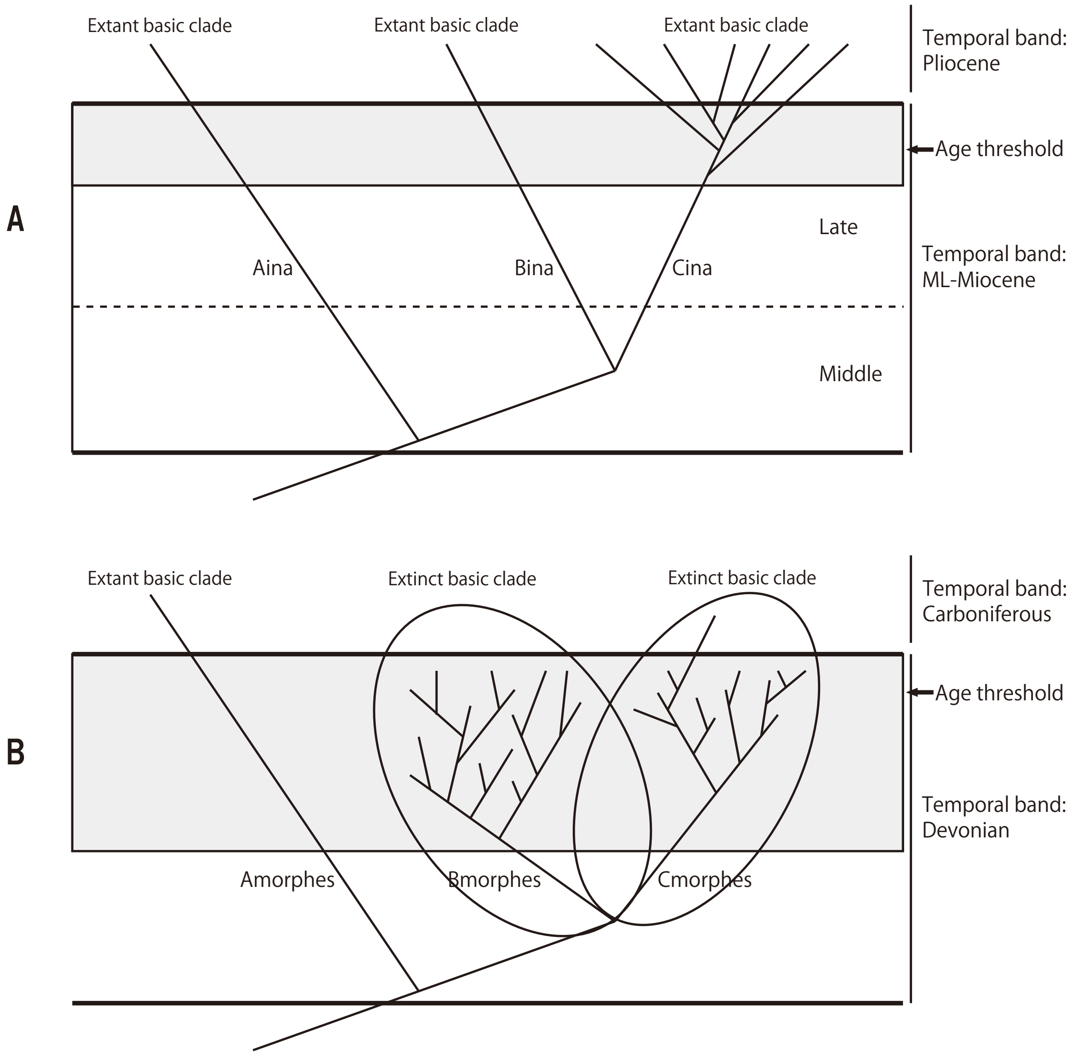

FIGURE 4. The examples of adopting "age threshold" for a temporal band. A: A time interval of late Miocene represented by the grey band is the age threshold in the temporal band "Miocene" specified to allow the extant clade Cina be recognized as a basic clade. B: About the upper half of Devonian represented by the grey band is the age threshold in the temporal band 'Devonian', specified to allow the extinct clades Bmorphes and Cmorphes be recognized as basic clades. Note that in A and B, parts of the extant clades existed after the temporal bands are not depicted.

Naming wholly extinct clades

The objects to be named that I take up here are wholly extinct clades and the subclades existing within the former ones. Those extinct clades are basically named with the use of temporal banding methods, by adopting the afore-mentioned two major rules, together with the rule of age threshold (Fig. 4B), as in the cases of extant clades, but the methods of naming extinct clades are clearly different from those of naming extant clades in several important points. There must be several valid ways of naming those extinct clades with the use of temporal bands, but the methods adopted here are the following ones. First, some Cenozoic extinct clades (e.g., those in Fig. 5) are named, with the same methods of using N-temporal bands (non-standard, standard) as adopted for naming extant clades. Second, the other Cenozoic extinct clades (e.g., those in Fig. 9) as well as all Mesozoic and Paleozoic extinct clades (e.g. those in Fig. 6) are named, with the use of P- and N-temporal bands. Since I described the first method above, I here take up and describe the second in detail.

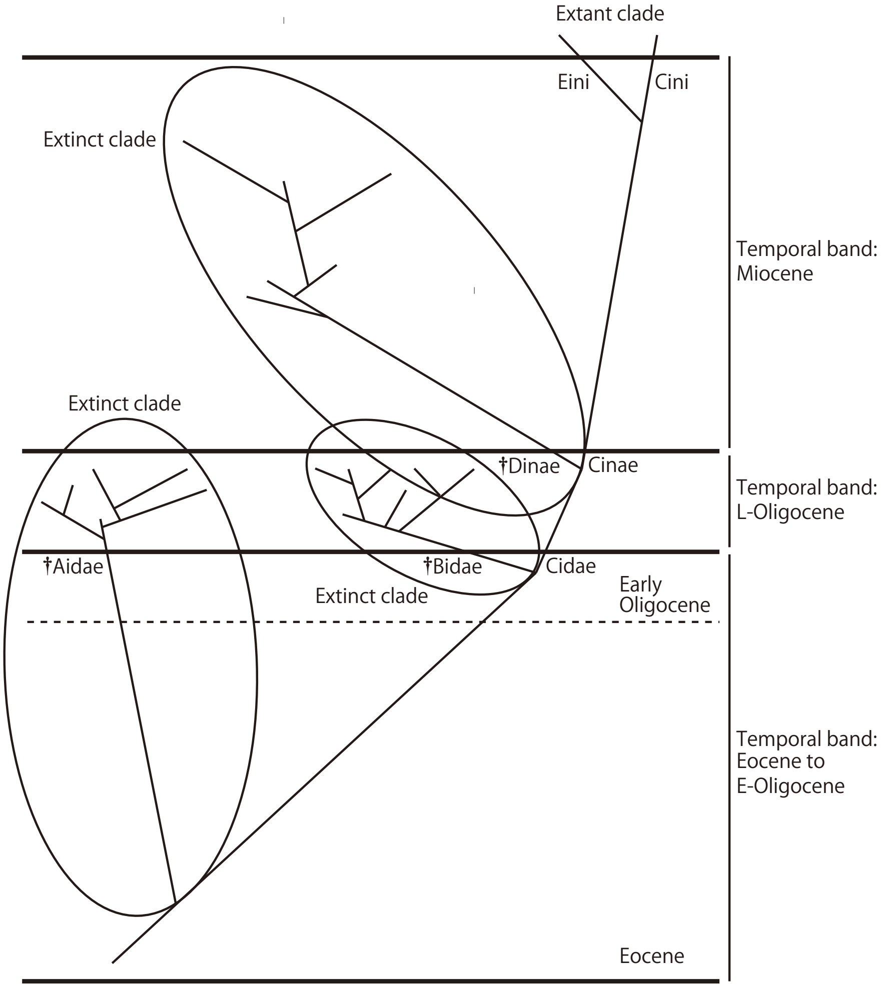

FIGURE 5. The case of naming an imaginary extant Cenozoic clade (with three extinct subclades), with the use of N-temporal bands. Note that parts of the imaginary extant Cenozoic clade existed after the Miocene are not depicted here.

The major rules for naming wholly extinct clades and their subclades, with the use of P- and N-temporal bands, are as follows: First, out of the extinct clades, only the wholly extinct clades are named, together with related extant clades, using the same N-temporal bands (non-standard; standard). If a wholly extinct clade in question is a holoclade (but not a basic clade) in the temporal band where origin of the extinct clade is located, then taxonomists should invoke the rule of age threshold (Fig. 4B) such that they can reinterpret the holoclade as a basic one. Note here that the rule of age threshold effectively serves to do the task (reinterpretation) with extinct clades (Fig. 4B), as in the cases of extant clades (Fig. 4A). The name of a wholly extinct clade has always the same standard ending as the ending of the names of extant basic clades whose origins are located in the temporal band where the extinct clade evolved. Thus, one can know the identical temporal origin of both the wholly extinct and extant clades by seeing the same standard ending.

Second, the subordinate basic clades in the wholly extinct clade are named, using the P-temporal band(s) that taxonomists created only for naming them; this is to say that they are named, using the standard endings of relatively lower ranks (e.g., "-ini", "-inae", "-idea"). The rule is that taxonomists name the larger basic clades existing in the wholly extinct clade, using the standard endings of higher ranks (e.g., "-idea") than ranks associated with the standard endings (e.g., "-ina") that they use in naming the smaller basic clades in the wholly extinct clade. If taxonomists cannot adequately recognize the subordinate basic clades of a wholly extinct clade in the P-temporal band(s), they should adopt the rule of age threshold (Fig. 4B) so that they may preserve known names of the basic clades in cases where those clades have been already given names under the traditional taxonomy. Third, the holoclades and synclades in the wholly extinct clade are named, without using standard endings. Fourth, to distinguish between the extant and extinct clade names, the dagger '†' be placed at the head of extinct clade names, at least when those extinct clades are depicted in the tree, and when their names are arranged in the reference system.

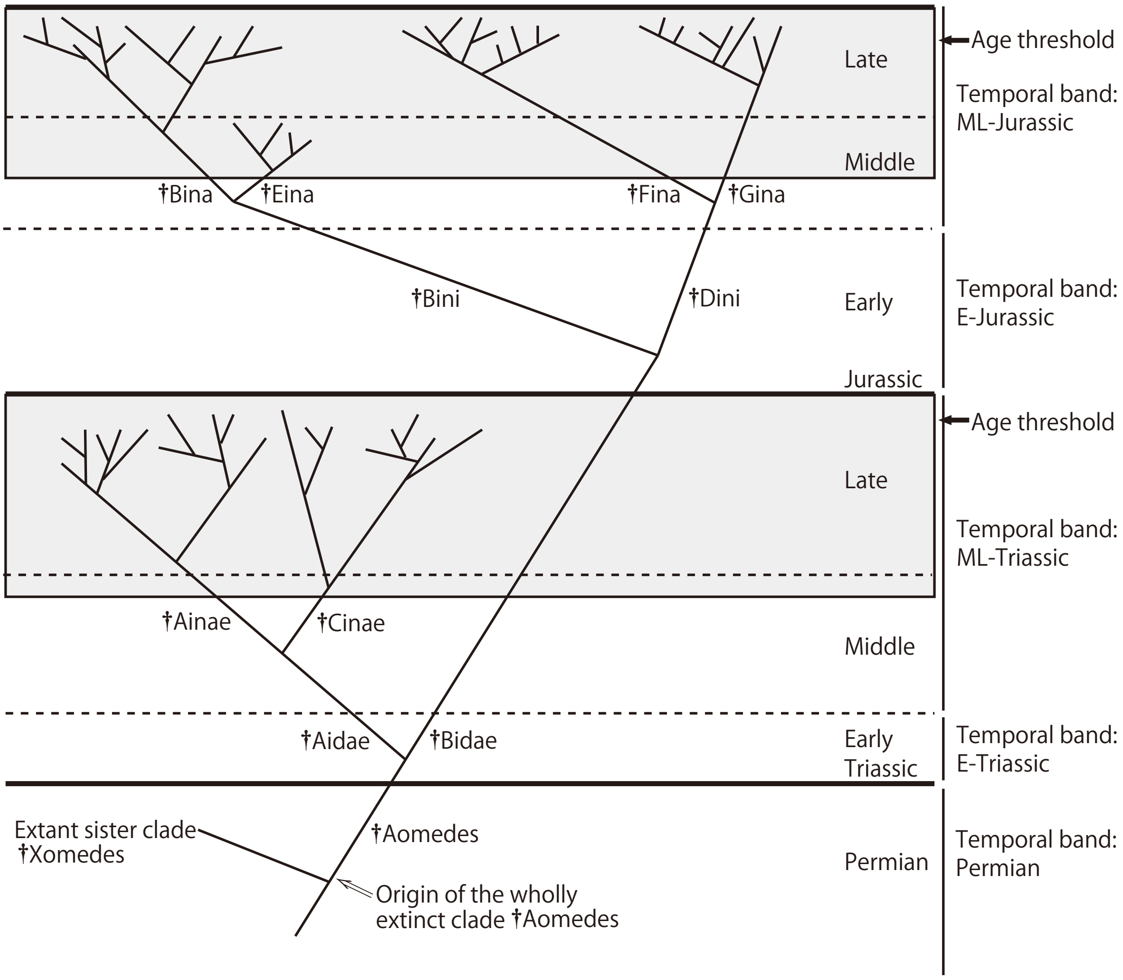

FIGURE 6. The case of naming an imaginary extinct clade "Aomedes" and its subclades, with the use of N- and P-temporal bands.

Two examples of naming extinct clades, following the major rules described above, are given. The first example is given in Fig. 5 of naming an imaginary extant Cenozoic clade (with three extinct subclades), whose evolutionary origin is in the Eocene, using N-temporal bands. Three N-temporal bands (non-standard) are created: "Eocene to Early (E- Oligocene" (to which the standard ending "-idae" corresponds), "Late (L-) Oligocene" ("-inae"), and "Miocene" ("-ini"). Based on these N-temporal bands, three extinct basic clades are named "Aidae", "Bidae" and "Dinae". Notice here that names of the extinct basic clades "Aidae" and "Bidae" have the same standard ending as the ending of name of the extant basic clade "Cidae" whose origin is located in the temporal band "Eocene to E-Oligocene" where "Aidae" and "Bidae" have evolved; likewise, the name of the extinct clade "Dinae" has the same standard ending as the ending of the name of the extant sister clade "Cinae".

The next example is given in Fig. 6 of naming an imaginary extinct clade with its subclades, whose duration extends to three temporal bands of geological episodes (Permian to Jurassic), using the N- and P-temporal bands. The wholly extinct clade is named "Aomedes", because the evolutionary origin of the clade is located in the (standard) N-temporal band "Permian", to which the standard ending "-omedes" corresponds (Table 2); notice here that the name of the extinct clade "Aomedes" has the same standard ending as the name of the extant sister clade "Xomedes". Four (non-standard) P-temporal bands are adopted: "E-Triassic" (to which the standard ending "-idae" corresponds), "ML-Triassic" ("-inae"), "E-Jurassic" ("-ini") and "ML-Jurassic" ("-ina"); and the rule of age threshold is adopted for two temporal bands "ML-Triassic" and "ML-Jurassic" that can adequately recognize 3 and 4 extinct basic clades, respectively. Consequently, we can recognize 10 (named) extinct basic subclades in the Aomedes.

Method of referring to the clades

The present phylogenetic taxonomy adopts the phylogenetic system of reference (Härlin 1998, 1999) regarding the definitions of taxon names (see also Kluge 2005: 8): That is, the name of a clade (as taxon) is defined ostensively by referring to the clade to which the name is given (Ghiselin 1966*a*, 1984). Logically, the action of fixing the reference ostensively can be accomplished by specifically pointing to the particular part of a graphic representation of the given timetree. For better clarification, however, the clade will *be described* by using words as in the style of the phylogenetic definitions of names with two specifiers (i.e., species); here the text accompanied by the names of specifiers is treated as a means of reference, but not as the definition of clade name (Härlin 1999: 2203).

The strict stability in clade names and content does not fit the taxonomic action of naming clades as historical entities in the long run, because hypotheses about the phylogenetic relationships may often change in revisional studies, when unknown clades and/or character data are added to the phylogenetic analysis. The taxon (clade) names (or name spellings) should be allowed to change in cases where the phylogenetic hypotheses change, so also should the taxon content. Thus, the present phylogenetic taxonomy also allows for a new circumscription of clade names, and for modification in reference and choice of specifiers. Both taxon name and reference should be allowed to change, while the history of changes of the taxon name and reference during a series of studies will be traced as in the Linnaean nomenclature (Härlin 2005), so that users can do unequivocal communication, using those taxon names that can change in revisional studies.

Changes of clade names (or clade name spellings)

Under the present phylogenetic nomenclature, all synclades (extant, extinct) are named, without using standard endings; and all synclade names do not have standard endings. Thus, once the synclades are named, even if the accepted phylogenetic hypothesis is changed, those synclade names (or name spellings) are not changed by changing the name endings, although the content of the synclades with which the names are associated, may be changed.

However, the names of basic clades and holoclades (extant, extinct) change. Let us consider the situation where all basic clades and holoclades are once named with a given group, based on an accepted phylogenetic hypothesis of the group (in the form of timetree). Following a change of phylogenetic hypothesis, a basic clade in a temporal band may be recognized as a basic clade in another temporal band. Furthermore, up to the position of the base and the first node (from the base) of the branch (as a basic clade) in a pictorial representation of the timetree, a basic clade may be reinterpreted as a holoclade, or a holoclade also may be reinterpreted as a basic clade. Thus, names (or name spellings) of these clades may be changed following change of the accepted phylogenetic hypotheses, because only the basic clades are named, using standard endings.

Three different kinds of name changes can be assumed there: First, a basic clade name is changed by changing the name ending as in the name ending changes of higher taxa under the Linnaean nomenclature (e.g., Quediinae to Quediini). Second, a basic clade name with a standard ending is changed into a holoclade name without any standard ending. Third, a holoclade name is changed into a basic clade name. These name changes are decidedly needed in order to keep the mutual exclusivity of those taxon (i.e., basic clade) names with the standard endings being certain in the particular domain of reference system, which form a unique nomenclatural rule for the present phylogenetic taxonomy. Representative samples of these clade name changes are given below (see Fig. 7, 8); and several basic clades whose names have the standard ending "-ini" or "-inae" (e.g., "Bini", "Binae") are used as sample cases of the basic clades whose names are to be changed following change of phylogenetic hypotheses.

The first is the cases where the basic clade name ending is changed as in the Linnaean nomenclature. Representative samples are as follows: The change of temporal band (where the basal node of basic clade was placed) to the subordinate (Fig. 7A→) or superordinate (Fig. 7A←) temporal band accompanies the change of position of the basal node of basic clade.

The second is the cases where a basic clade name be changed into a holoclade name. Some representative samples are as follows: (1) The change of temporal band (where the basal node of basic clade was placed) to the subordinate temporal band accompanies the change of position of the basal node of a basic clade (Fig. 7B→); (2) the change of position of the basal node of a subclade of a basic clade, with the change of the temporal band (where the basal node of the subclade was placed) to the superordinate temporal band (Fig. 7C→); (3) the change of position of the basal node of a subclade of the basic clade, with the change of the temporal band (where the basal node of the subclade was placed) to the superordinate temporal band, and also with the change of the sister clade of the basic clade by changing the position of the basal node of the basic clade in the timetree (Fig. 7D→); (4) the change of phylogenetic structure of the basic clade, by addition of a known subclade to the clade within the temporal band where the clade in question was recognized as a basic one (Fig. 8A→); (5) the change of phylogenetic structure of the basic clade, by addition of a newly discovered subclade to the clade within the temporal band where the clade in question was recognized as a basic one (Fig. 8B1).

The third is the cases where a holoclade name is changed into a basic clade name. Some representative samples are as follows: (1) The change of temporal band (where the basal node of basic clade was placed) to the superordinate temporal band accompanies the change of position of the basal node of holoclade (Fig. 7B←); (2) the change of position of the basal node of a subclade of the holoclade, with the change of the temporal band (where the basal node of the subclade was located) to the subordinate temporal band (Fig. 7C←); (3) the change of position of the basal node of a subclade of the holoclade, with the change of the temporal band (where the basal node of the subclade was placed) to the subordinate temporal band, and also with the change of sister clade of the holoclade by changing the position of basal node of the holoclade in the timetree (Fig. 7D←); (4) the change of phylogenetic structure of the holoclade, by separation of the known subclade from the holoclade to another position in the timetree (Fig. 8A←); and (5) the change of phylogenetic structure of the holoclade, by separation of the newly discovered subclade from the holoclade to another position in the timetree (Fig. 8B2).

In some cases of clade name changes, taxonomists are to give two different names (i.e., name with and without standard ending) to one and the same clade, which seems to be a difficulty in the present phylogenetic nomenclature. The first case occurs in some instances where the basic clade names be changed to holoclade names (e.g., Fig. 7B→, C→, D→). In order to avoid the confusion as to the method of naming the holoclades in these clade name changes, the nomenclatural rule is introduced that several "endings" ([e.g., "-acei[4]"] as the "endings" of holoclade names used only for the cases of the clade name changes) can be used; notice here that those "endings" are not standard name endings but name "endings" (*sensu* Alonso-Zarazaga [2005: 191]). If one coins, for example, the name of holoclade (whose origin is located in the temporal band Devonian), with which one should replaces a basic clade name "Amorphes", by using the ending "-acei", one obtains the holoclade name "Amorphacei". As a result, the basic clade names can be changed automatically

---

[4] See Alonso-Zarazaga (2005: 194) regarding the ending "-acei"; and note here that he originally adopted it in coining the names of some higher taxa under the Linnaean nomenclature.

into holoclade names, following this rule. The second case occurs in some instances where holoclade names must be changed to basic clade names (e.g., Fig. 7B←, C←, D←). In such cases, those holoclades can and thus should be renamed based on the criteria of the temporal banding methods that taxonomists adopted. Thus, those renewed basic clade names all are to have a standard ending.

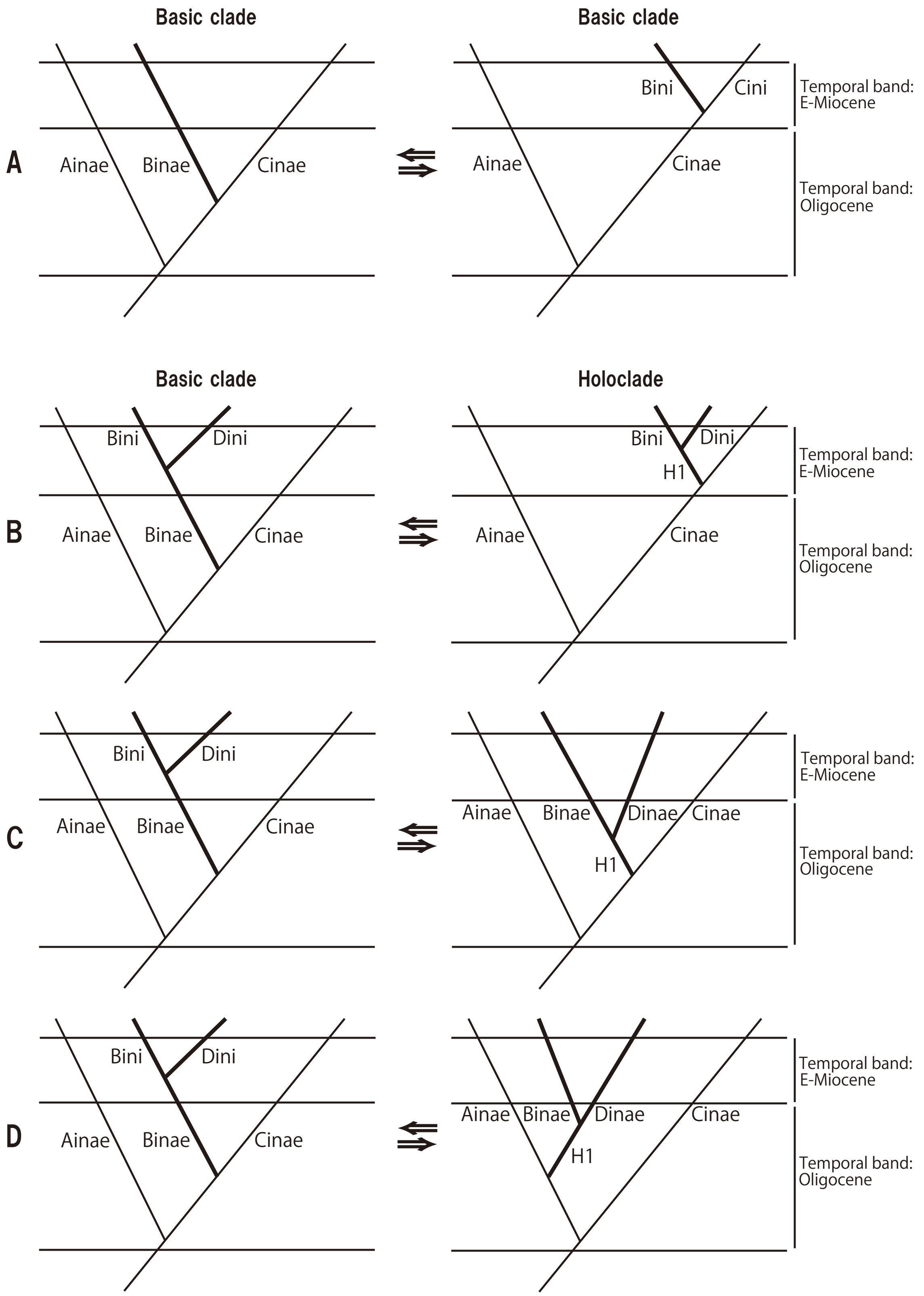

FIGURE 7. Examples of clade name changes (1). A: The basic clade names are changed by changing standard endings, as in the name changes in the Linnaean nomenclature. B–D: The basic clade names are changed to holoclade names, or vice versa (1). Note that in A–D, parts of the clades existed after the temporal bands are not depicted.

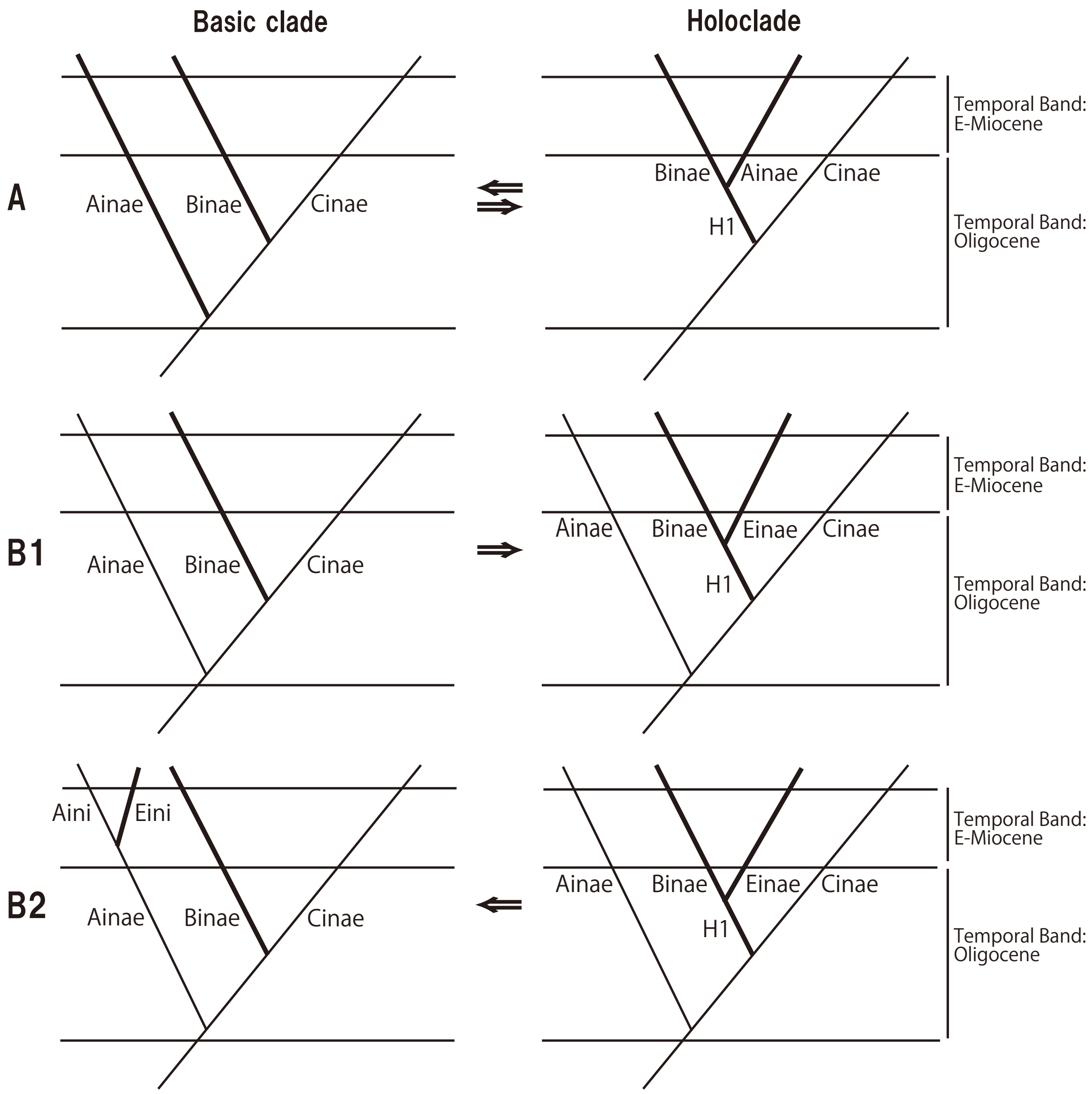

FIGURE 8. Examples of clade name changes (2). A, B1 and B2: The basic clade names are changed to holoclade names, or vice versa (2). Note that in A–B2, parts of the clades existed after the temporal bands are not depicted.

Consequently, the changes of basic clade names to holoclade names (and vice versa) under the present phylogenetic nomenclature are similar to name changes in the case of splitting or lumping under the Linnaean taxonomy, in that those name changes are virtually changes only with regard to the clade name endings.

Synonymy and homonymy

Under the present phylogenetic nomenclature, synonyms are names that are spelled differently but refer to the same taxon (clade) (see also Cantino & de Queiroz 2010: 60). If the type-specimen(s) of species (as specifiers) specifying a clade name are consistent with the diagnosis of the clade, then the name is the senior synonym that refers to the clade; and if the type-specimen(s) of species (as specifiers) specifying different (two or more) clade names are equally consistent with the diagnosis of a particular clade, then the oldest name is the senior synonym that refers to the clade, and other names are its junior synonyms (Kluge 2005: 35). Homonyms are names that are spelled indentically but refer to different taxa (clades) (see also Cantino & de Queiroz 2010: 58). Names with the same spelling cannot refer to different clades.

General and abridged reference systems

In the present phylogenetic taxonomy, the general reference system for a group is the scheme of words that represents the phylogenetic relationships of organisms in the group; specifically, it is the completely rank-free, phylogenetic system whose components are the names of all basic clades, holoclades and synclades (extant, extinct) in the group. When the basic clade names only are picked up from the clade names that constitute the general reference system, and are properly arranged in an indentation scheme, then its abridged reference system is completed. The whole area (all taxon names) of a general reference system is called here "*general domain*", while its part (basic clade names) is called "*particular domain*". As far as the abridged reference system (comprising the names of basic clades) is concerned, it is the same as the system created under the Linnaean taxonomy, in that all taxon names adopted have standard endings as if it were a ranked system.

Here, an example is given of constructing the general and the abridged reference systems with the parts of an imaginary clade Aidae. The objects to be named for constructing the reference systems are the clade "Aidae" and its subclades whose origins are located in the temporal bands "Oligocene", "Early (E-)Miocene" or "Middle and Late (ML-)Miocene" (Fig. 9). Based on the rules of clade nomenclature described above, the

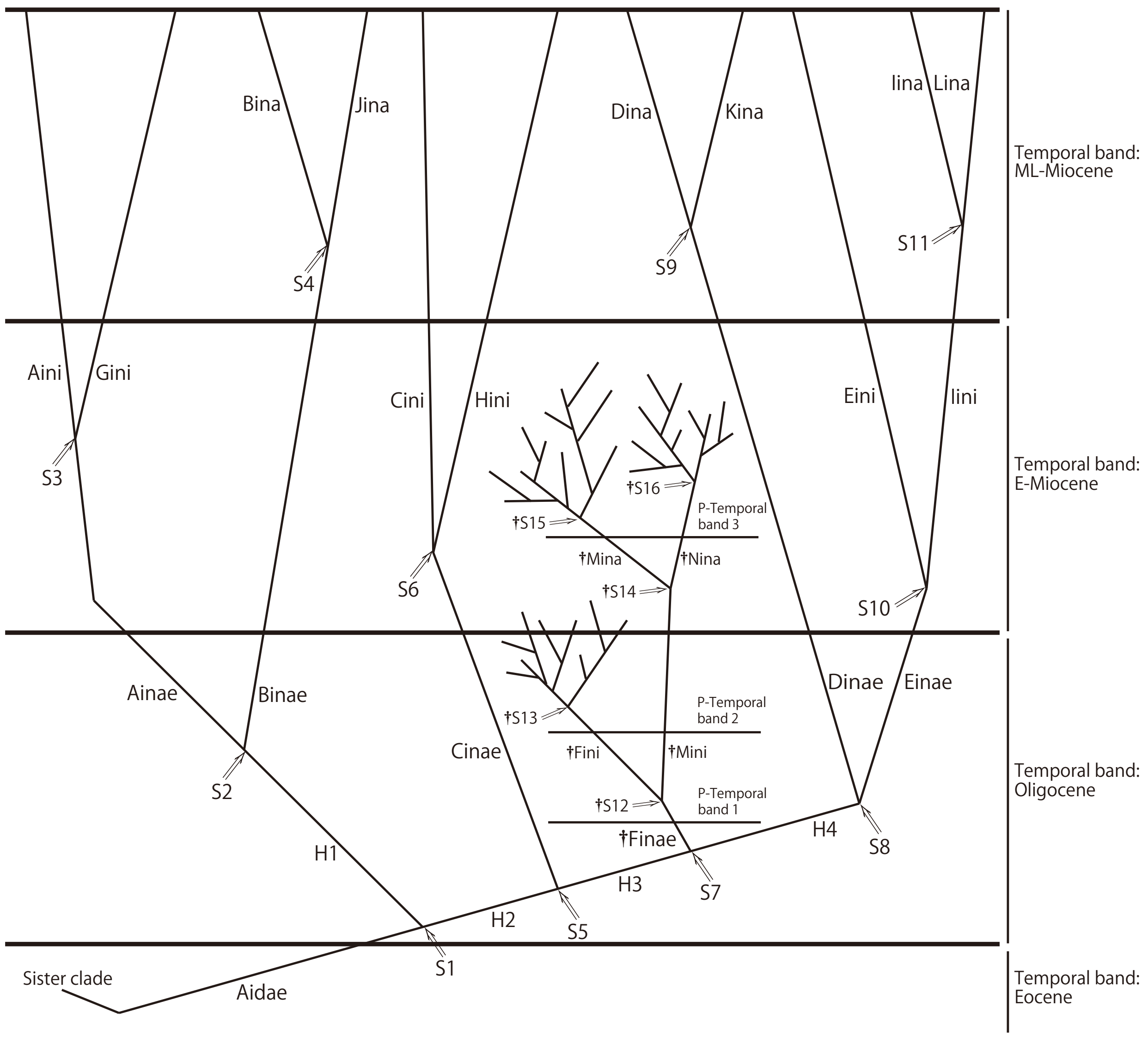

FIGURE 9. The case of naming an imaginary clade ("Aidae") and its subclades (extant, extinct), whose origins are located in the temporal bands Oligocene, E-Miocene or ML-Miocene. Note that the "Aidae" is an extant clade, but parts of the subclades existed after the Miocene are not depicted.

following clades are named. The five extant basic clades in the temporal band “Oligocene” are named “Ainae”, “Binae”, “Cinae”, “Dinae” and “Einae”; the six extant basic clades in the temporal band “E-Miocene” are “Aini”, “Gini”, “Cini”, “Hini”, “Eini” and “Iini”; the six extant basic clades in the temporal band “ML-Miocene” are “Bina”, “Jina”, “Dina”, “Kina”, “Iina” and “Lina”. The four extant holoclades recognized are named “H1”, “H2”, “H3” and “H4”; and the 11 extant synclades are named “S1”, “S2”, “S3”, “S4”, “S5”, “S6”, “S7”, “S8”, “S9”, “S10” and “S11”. The wholly extinct clade recognized is named “Finae”; the two extinct basic clades in the P-temporal band 1 are named “Fini” and “Mini”; the two extinct basic clades in the P-temporal band 2 are “Mina” and “Nina”; and the five extinct synclades recognized are named “S12”, “S13”, “S14”, “S15” and “S16”. Using these clade names as their components, the general (Fig. 10) and abridged (Fig. 11) reference systems may be constructed, following the conventions mentioned below.

- Aidae S1
  - H1 S2
    - Ainae S3
      - Aini
      - Gini
    - Binae S4
      - Bina
      - Jina
  - H2 S5
    - Cinae S6
      - Cini
      - Hini
    - H3 S7
      - †Finae †S12
        - †Fini †S13
        - †Mini †S14
          - †Mina †S15
          - †Nina †S16
      - H4 S8
        - Dinae S9
          - Dina
          - Kina
        - Einae S10
          - Eini
          - Iini S11
            - Iina
            - Lina

FIGURE 10. General reference system of parts of the imaginary clade Aidae depicted in Fig. 9. Note that it consists of the names of clade “Aidae” and its subordinate clades (basic clades, holoclades and synclades).

Conventions for constructing the general reference system

(g1) All names refer to clades (extant, extinct).
(g2) The names of subclades within each clade are indented to indicate hierarchical relationships.
(g3) No redundant name is used. If the part of a clade depicted in one temporal band is not split into two or more subclades (or, if it is completely represented by a simple branch), no name is given to the clade whose origin is located in the temporal band.

(g4) When two names are given on one row in the reference system, then the first is the name of basic clade or holoclade, while the second is the name of its subordinate synclade.
(g5) When a name represents an extinct clade, then a dagger † is placed at its head.

Conventions for constructing the abridged reference system

(a1) All names refer to basic clades (extant, extinct).
(a2) The names of the subordinate basic clades within each basic clade are indented to indicate hierarchical relationships except for the cases where the clade names are arranged according to the rules of (a3) and (a4).
(a3) Out of the names of the basic clades whose origins are located in the same temporal band, all basic clade names given by the same temporal banding method (i.e., basic clade names with a same standard ending) are lined up in the same indentation. For example, Ainae, Binae, Cinae, Dinae, Einae and †Finae all are lined up in the same indentation (Fig. 11); notice here that the wholly extinct clade †Finae is named, using the same N-temporal banding method as adopted for naming the extant clades whose origins are located in the temporal band Oligocene.

- Aidae
  - Ainae
    - Aini
    - Gini
  - Binae
    - Bina
    - Jina
  - Cinae
    - Cini
    - Hini
  - †Finae
    - †Fini
    - †Mini
      - †Mina
      - †Nina
  - Dinae
    - Dina
    - Kina
  - Einae
    - Eini
    - Iini
      - Iina
      - Lina

FIGURE 11. Abridged reference system of parts of the imaginary clade Aidae depicted in Fig. 9. Note that it comprises the names of clade "Aidae" and its subordinate basic clades.

(a4) No redundant name is used. Suppose, for example, that the sister clade of a clade is split into two subclades within a temporal band, where the clade is not split into the subclades, and also that in the subordinate temporal band, each of the split subclades is not split while the clade is split into two subclades; here the clades and subclades in question all are basic clades. In such cases, the names of the subclades of the sister clade whose origins are located in the temporal band can be lined up in the same indentation for saving the space, together with the names of the subclades of the clade whose origins are located in a subordinate temporal band. For example, Aini, Gini, Cini, Hini, Eini, Iini, Bina, Jina, Dina, and Kina all are lined up in the same indentation (Fig. 11).

(a5) When a name represents an extinct clade, then a dagger † is placed at its head.

Practice of naming clades with the use of temporal bands

Practice of naming extant clades with the use of non-standard temporal bands

Only in cases where explicit hypotheses about the timetrees of extant groups in question are available, the extant clades existing in the groups can be named with the use of temporal bands. Although such phylogenetic hypotheses are difficult to obtain indeed, at present we have a good prospect for reconstructing the timetrees in the different organismal groups (Hedges & Kumar 2009 [ed.]). According to Avise (2009: 21–22), major structural features and many finer details of the Tree of Life are quickly emerging, because vast amounts of molecular data are now gathered and analyzed phylogenetically; and since phylogenetic appraisals are in general based on unprecedented volumes of sequence information, estimates of the evolutionary origins of clades must be almost as secure as might ever become possible. In fact, in the recent volumes of such journals as *Molecular Phylogenetics & Evolution* and *Systematic Biology*, papers have appeared, in which explicit hypotheses about the timetrees of various extant groups are shown, suggesting that the academic circumstance seems to have been ready for practicing the phylogenetic taxonomy and nomenclature with those extant groups, using the temporal banding methods.

When naming extant clades existing in a group to create a rank-free reference system, taxonomists have options in the following items: First, there are two criteria for assigning standard endings to basic clade names (i.e., standard and non-standard temporal bands); second, there are three different categories of evolutionary clades (i.e, basic clades, holoclades and synclades) as the targets for naming; and third, the reference system that taxonomists create under the present taxonomy has a double structure (general and particular domains). How taxonomists name the clades in their group by selecting which option for each item, depends on, to which degree the group is studied taxonomically and phylogenetically (see also Fig. 12). However, since there are some nomenclatural difficulties in naming the extant clades under the present phylogenetic taxonomy, we cannot necessarily select any option for each item when practicing the phylogenetic taxonomy of the group in question at the present time. Thus I here argue over the best way, on the basis of which we should name the extant clades, using temporal bands.

One problem in naming extant clades concerns the adoption of standard temporal bands. According to Avise & Liu (2011), times of evolutionary origin of the clades (in the disparate groups such as plants, insects and mammals) recognized as taxa assigned to the same nomenclatural rank are different (or inconsistent) to a considerable degree. Thus, if those taxa are restudied taxonomically, using the standard temporal bands, there must be many cases where the endings of taxon names must be changed to those of names of taxa whose origins are located in the remote temporal bands. For example, the subfamilies (e.g., Piestinae, Omaliinae) of the family Staphylinidae originate in the Jurassic (Chatzimanolis *et al.* 2012); and thus, if they are re-named, using the standard temporal bands, their names are to have the newly suggested standard ending "-iformes", which has frequently been used as an ending of taxon names at the rank of order under the Linnaean nomenclature. At the present time, such drastic changes of the name endings of widely known taxa may not be warranted in the biological community. Thus, at the present stage, one important point in naming the extant clades is the adoption of non-standard temporal bands in order to minimally disrupt the current reference system of a given group, as in such taxonomic studies as Sibley & Ahlquist (1990), Lim (2007) and Talavera *et al.* (2013).

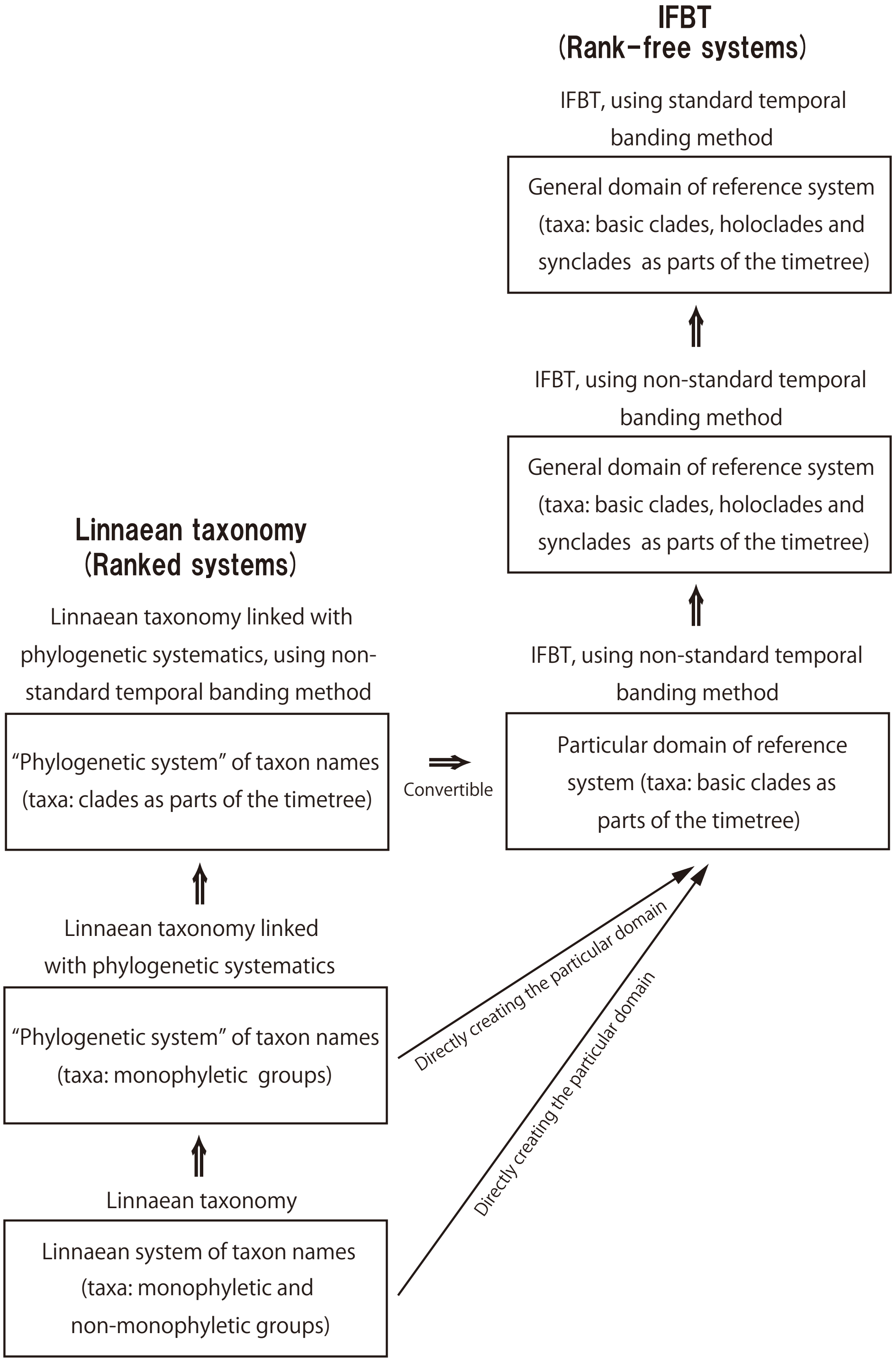

FIGURE 12. Developmental stages of the reference systems of clade names (left side: ranked systems created under the Linnaean taxonomy; right side: rank-free systems created under the IFBT). Note that the (ranked) "phylogenetic system" of taxon (clade) names created under the Linnaean taxonomy linked with phylogenetic systematics, using non-standard temporal banding method is actually convertible to the (rank-free) particular domain of reference system created under the IFBT, by reinterpreting the Linnaean clade names (as components of "phylogenetic system") as basic clade names under the IFBT.

The other problem in naming extant clades is caused by changing the clade names following changes of the accepted phylogenetic hypotheses. The troublesome problem is, as mentioned in the previous section, to change the basic clade names to holoclade names (and vice versa) in various cases (see Fig. 7 and 8). This may be especially true of the clade names in the groups to which a large number of unknown species and clades will be added in future, because a well corroborated timetree (which is necessary for clade naming under the present phylogenetic nomenclature) is very difficult to obtain for such a group at the present stage. If all extant clades (i.e., basic and inclusive clades) are named based on a temporarily accepted phylogenetic hypothesis, then changing the basic clade names to holoclade names (and vice versa) must be needed in many cases of future revisional studies. Given this, another important point in naming the clades is in principle naming only the basic clades in a given group, in order to avoid recurring clade name changes before we name the clades on a very well-corroborated phylogenetic hypotyhesis.

When considering the two problems mentioned above, *the best way of naming extant clades under the present phylogenetic taxonomy at the present time is to name only the basic clades of a group, using the non-standard temporal banding method, so that taxonomists can construct an abridged reference system (i.e., particular domain of reference system)*. In fact, in the cases of groups where no or a little fossils (that form side branches when depicted in the tree) have been discovered, naming the inclusive clades may not be needed at the present stage, because in such cases only the basic clade names seem to be enough for understanding the phylogenetic relationships of subclades within the group. Only in cases where researchers need a full general reference system for a group (for example, for a better understanding of the phylogenetic relationships of a group with rich fossils), taxonomists will name the inclusive clades as well as basic clades existing within the group, to create it; otherwise, they give names only to some important inclusive clades within the group.

Practice of naming extinct clades with the use of non-standard temporal bands

Although molecular data cannot be used in reconstructing the phylogeny of extinct groups, phylogenetic analyses of the parts of some large extinct groups (e.g., Ammonoidae: Moyne & Neige 2004; Hairapetian & Korn 2011; Trilobita: Hegna 2008; Sundberg 2008), or of the entirety of some small extinct groups, together with their related extant groups (e.g., aardvark Orycteropodidae: Lehmann 2009; carnivoran Felidae: Christiansen 2013) have been performed with the use of morphological data. In cases where explicit hypotheses about the timetrees of extinct groups are available, the extinct clades existing in the groups can be named, using the temporal banding methods proposed in this paper, as in the cases of extant clades. Since there are the same nomenclatural problems as in the case of naming extant clades, the best way of naming extinct clades is to name only the extinct basic clades in an extinct group in question, using non-standard temporal banding method. Practicing the present phylogenetic taxonomy of extinct groups even based on the best way, must results in drastic clade name changes in many cases, due to the traditional way of naming extinct organisms in paleontology. Some may consider this suggests the present phylogenetic nomenclature's inability to name the extinct clades, but I show below that the fact seems to be the opposite; that is, the present nomenclature can be appropriately applied also to extinct clades.

The important thing that we should first perceive here is that the traditional phylogenetic/taxonomic studies of extinct groups have adopted unique methods. Being different from the phylogenetic/taxonomic studies of extant organismal groups, paleontological studies are unique in that they recognize "temporal units" in the timetrees created. The "temporal units" are basic taxonomic units that are monophyletic, paraphyletic (or even polyphyletic) groups, and are depicted in the timetrees by straight lines or elongate ovals, which show the duration (and sometmes also size and morphological diversity) of those extinct groups. Those units are recognized in the particular geological episode(s), and thus described as formal taxa under the traditional paleontology. In such studies, the evolutionary history of a wholly extinct group has been reconstructed by simply connecting one "temporal unit" by lines to other ones, mainly using morphological criteria (e.g., Ammonoidea: Donovan & Callomon 1981). Although those "temporal units" are basic taxonomic units in the taxonomic studies of extinct groups, many distinct (good), wholly extinct clades have been known from the diverse organismal groups in paleontology, as represented by Ammonoidea and Trilobita and some subclades within them. Furthermore, there are cases where monophyletic "temporal units" (as subclades of a wholly extinct clade) have often lived during the discrete geological episode(s) (e.g., Devonian); and also, the duration of some monophyletic "temporal units" is distinctly different from that of some other such units existing in the same wholly extinct clade. They are, nevertheless, considered taxa of the same nomenclatural rank. In the Ammonoidea, for example, paleontologists have recognized the monophyletic "temporal units" in the late Devonian, the Permian-Triassic, and the Jurassic-Creaceous; and they all are assigned to the rank of order, named Clymeniida, Ceratitida and Lytoceratida, respectively.

Names of those monophyletic "temporal units" recognized in one extinct group have very often the same standard ending, although they have obviously lived during different geological episodes. Thus, when taxonomists try to recognize and name under the present phylogenetic nomenclature the clades and subclades existing in such extinct group, they will have to change many taxon names even if those taxa are monophyletic "temporal units". It goes without saying that taxonomists also have to change many taxon names, if they restudy under the phylogenetic nomenclature the wholly extinct groups, whose taxa comprise non-monophyletic as well as monophyletic "temporal units".

At first glance, such inescapable name changes seem to be due to the inappropriateness of applying the present phylogenetic nomenclature to those extinct clades. The difficulty in taxonomic paleontology we should notice here is, however, just that those wholly extinct groups have not yet been phylogenetically studied in an appropriate way, nor properly named based on the results of the phylogenetic studies. If they were studied, then many taxon names recognized in the current reference systems of those extinct groups would no doubt be drastically changed even under the Linnaean nomenclature; for example, Haploceratidae (a monophyletic temporal unit of Ammonoidea; House & Senior 1981: 119) will have to be undoubtedly downgraded to the subfamily rank, resulting in taxon name change. Given this, we should not mistake the nomenclatural problem (i.e., drastic name changes) caused by incomplete phylogenetic and taxonomic studies of the extinct groups, for the difficulty in applying the present phylogenetic nomenclature to the extinct clades in those groups. Since many of the clades and subclades recognized in extinct groups have lived, as noted above, during different geological episode(s), it is the present phylogenetic nomenclature that can properly name those extinct clades in an extinct group, using the N- and P-temporal bands, once we obtain a well-corroborated timetree of the extinct group.

Practice of naming clades with the use of standard temporal bands

In the previous subsections I discussed the practice of naming clades (extant, extinct), with the use of non-standard temporal bands. The problem that accompanies the practice of naming clades with non-standard temporal bands is that the same standard endings of basic clade names in disparate organismal groups actually refer to different geological episodes of temporal bands (made by the different way of partitioning the geological age). This means that the evolutionary ages are inconsistent to a considerable degree among those basic clades, whose names have the same standard ending. However, if we name the extant basic clades, with the use of the standard temporal bands, then the evolutionary ages are almost consistent among all extant basic clades, whose names have the same standard ending. Furthermore, if we name simultaneously both extant and extinct basic clades, with the method of using standard temporal bands, together with the P-temporal bands proposed in this paper, the evolutionary ages are almost consistent among the extant basic clades and the wholly extinct clades (but not the extinct subclades existing within the wholly extinct clades), whose names have the same standard ending. This means that those extant and extinct basic clades can be all considered to be semi-comparable units that are used in various studies of comparative biology as units that facilitate comparison.

In order to achieve this goal, the biologist community may proceed to the future step where taxonomists practice the phylogenetic taxonomy of whole living world, using standard temporal bands (Fig. 12). If so, then we need to have appropriate standard temporal bands (e.g., those shown in Table 2) for naming clades. The standard temporal bands are the criteria used for the purpose of assigning the standard endings to names of all extant basic clades and wholly extinct basic clades. Thus, partitioning geological ages into standard temporal bands is in principle arbitrary. However, because of the taxonomic inconsistency problem mentioned above, the drastic changes of endings of those basic clade names will accompany the practice of phylogenetic taxonomy with the standard temporal banding method. Given this, the decision about how we create the standard temporal bands is really a difficult task for individual taxonomists to carry out. Such task must be carried out only through a collective action of the international community in one or several international meetings (Dubois 2007, 2008); and the standard temporal bands be ratified by the biologist community at a certain stage in the near future. Once we acquire the standard temporal bands endorsed by the biologist community, the temporal bands will provide a universal yardstick to be applied to the diverse groups of organisms for objectively assigning the standard endings to basic clade names.

IFBT as the new framework for future biological taxonomy

The present phylogenetic taxonomy has three characteristics: First, it aims at creating a rank-free phylogenetic system of taxon names, which is the major characteristic of QG-phylogenetic taxonomy (de Querioz & Gauthier 1990, 1992, 1994). Second, it uses standard endings (e.g., -idae, -inae) in naming clades (i.e., monophyletic groups), which is a major characteristic of Linnaean nomenclature (although the current nomenclatural Codes allow taxonomists to name non-monophyletic as well as monophyletic groups). Third, it adopts the temporal bands of geological episodes (Hennig 1966; Avise & Johns 1999) as the sole criteria for assigning standard endings to basic clade names. Since the major characteristics of QG-phylogenetic taxonomy and Linnaean nomenclature, together with the temporal banding methods, are integrated in the present phylogenetic taxonomy, without deteriorating the strength of theoretical coherence, it is called here *integrated framework of biological taxonomy (IFBT)*, which is, however, actually *the IFBT with the use of non-standard temporal banding method* presented in this paper. The IFBT is, in my opinion, a version of the phylogenetic (but not traditional, Linnaean) taxonomy (which is equipped with a phylogenetic nomenclature) that aims at creating the rank-free system of taxon names. The fundamentals of IFBT are summarized as follows:

(1) *The reference system of clade names is completely rank-free*. Given that evolutionary clades form a nested series with smaller clades included in larger clades, nomenclatural ranks (to which those clades as higher taxa are arbitrarily allocated under the Linnaean taxonomy) caricaturize and oversimplify the fundamental structure of biological world. The ranks are incompatible with the nature of phylogeny (e.g., Griffiths 1974; de Queiroz & Gauthier 1990; Härlin 2005), suggesting that they must be discarded. Thus, the IFBT aims at creating a rank-free reference system, whose components are only the names of evolutionary clades, as the QG-phylogenetic taxonomy does. As a result, the theory of IFBT is well reconciled with the evolutionary world view.

(2) *Precisely naming clades is the basic task of IFBT*. Precisely naming clades is an important task in the QG-phylogenetic taxonomy (de Queiroz & Gauthier 1990, 1992), but the QG-taxonomy does not regard the time dimension (or temporalness) in terms of the duration of a clade (or the time of evolutionary origin of a clade), as a necessary element in the clade nomenclature. However, if precisely naming clades is an important task in phylogenetic taxonomy, then the names must be given to the clades as parts of the timetree (i.e., real 4-dimensional entities in nature). Thus, the IFBT considers that precisely naming the clades as parts of the timetree, with the use of temporal bands, is its basic task.

(3) *The reference system serves as a convenient system for information storage and retrieval*: Being different from those created under the Linnaean or QG-phylogenetic nomenclature, the reference systems created under the IFBT have a double structure: the general domain comprises all basic and inclusive clade names, while the particular domain comprises only the basic clade names. Of the two domains of a reference system, the particular domain takes basically the same style as the Linnaean system of taxon names, in that all taxon names adopted have standard endings, such that the mutual exclusivity of taxon names with those standard endings is certain there. The taxon names in the particular domain can convey information in similar

manner as the taxon names in the ranked system can do. Given the capacity of those taxon names in the particular domain to convey rich taxonomic information, the reference system created under the IFBT functions well as a convenient system for information storage and retrieval.

To sum up, when considering the above fundamentals, the IFBT is the taxonomic discipline whose end products are a rank-free reference system of clade names which serves as convenient system for taxonomic information storage and retrieval. In other words, the IFBT combines the advantage of phylogenetic taxonomy with that of Linnaean nomenclature. Given this, I propose here the IFBT as the new framework for future biological nomenclature.

A compatibility between the Linnaean taxonomy and IFBT

Constructing the rank-free reference system by two-stepped naming actions under the IFBT

When a "phylogenetic system" of taxon (clade) names with a group in question is created based on an accepted timetree of the group under the Linnaean taxonomy linked with phylogenetic systematics, using (non-standard) temporal banding method, all taxa recognized there are practically the basic clades, as empirical studies show (see, for example, the taxa recognized in the studies of Lim 2007; Talavera *et al.* 2013). When considering this, together with the structure of particular domain of a rank-free reference system discussed above, we see the following two common points between the "phylogenetic system" and the particular domain (e.g., that in Fig. 11): First, the taxon names adopted both in the "phylogenetic system" and the particular domain are names with standard endings. Second, the "phylogenetic system" and the particular domain have in principle the same taxonomic structure (i.e., hierarchical arrangement of taxon names). Therefore, putting aside the semantical problems with regard to the taxon names given under the different taxonomic philosophies, first, Linnaean taxon (clade) names are equivalent to the components (basic clade names) of the particular domain of rank-free reference system; and second, the "phylogenetic system" is practically equivalent to the particular domain.

Given this, taxon (clade) names as components of the Linnaean (ranked) system *can be used to* form the particular domain of a rank-free reference system. Thus, the particular domain of reference system with a group in question can be created using Linnaean taxon names by reinterpreting them as basic clade names under the IFBT (and also by newly naming unnamed basic clades if there are any in the group). On the other hand, the names of holoclades and synclades existing in the group are usually not found in the "phylogenetic system" created under the Linnaean taxonomy, with the temporal banding method (see, for example, the reference systems created in the studies of Lim 2007; Talavera *et al.* 2013). Thus, the general domain of a rank-free reference system can be created by naming holoclades and synclades and adding those inclusive clade names to the particular domain which consisted only of the basic clade names. In sum, constructing the rank-free reference system of the group is completed by the two-stepped naming actions: first, naming the basic clades; second, naming the inclusive clades (holoclades and synclades).

IFBT can construct the abridged (rank-free) reference systems upon the particular Linnaean systems of taxon names

As a rule, the Linnaean taxonomy and IFBT are not compatible with regard to method of creating reference systems (except that they have a major common point in that they adopt the method of using standard endings in nomenclature) and thus also to the end results of taxonomic practices (i.e., reference systems of taxon names). However, when the "phylogenetic system" of taxon (clade) names of a given group is created under the Linnaean taxonomy linked with phylogenetic systematics, using (non-standard) temporal banding method, then, as pointed out above, it is actually compatible both in taxonomic structure and components, with the particular domain of rank-free reference system of the group created under the IFBT (Fig. 12). Two important points we should notice here are the following ones. First, the particular domain of reference system with the group can be created, as pointed above, using Linnaean taxon names by reinterpreting them as basic clade names under the IFBT. Second, since those Linnaean names can be used, as they are, as components (basic clade names) of the particular domain, creating the particular domain by using those Linnaean names under the IFBT can be carried out without changing the endings of previously used Linnaean names. Given these points, there is a *peculiar compatibility* between the Linnaean taxonomy (including nomenclature) and IFBT specified above; and thus *the IFBT can directly construct the abridged (rank-free) reference systems, upon the particular (ranked) systems of taxon names*. For example, we can directly construct the abridged reference systems of the butterfly clade Polyommatina, upon those Linnaean subtribal and generic names recognized in Talavera *et al.* (2013), by simply reinterpreting them as basic clade names under the IFBT.

A perspective on the phylogenetic taxonomy and nomenclature

At the present time, many taxonomists are creating Linnaean systems of taxon names for diverse organismal groups under the traditional taxonomic/nomenclatural framework, or creating the "phylogenetic system" under the phylogenetic-systematic framework, without adopting the temporal banding methods, while some phylogenetic systematists start to create quasi-phylogenetic systems of clade names, based on the accepted timetrees for disparate groups, with non-standard temporal banding method (e.g., Crustacea: Tinn & Oakley 2008; Insecta: Talavera *et al.* 2013; Aves: Sibley & Ahlquist 1990; Mammalia: Lim 2007). No one knows what framework the taxonomist community will choose in the future. However, as aptly pointed out by Härlin (2005: 221), any taxonomic system intended for the future will need to get rid of ranks; and the IFBT will achieve the goal of obtaining the rank-free systems of clade names with various groups.

When current phylogenetic studies are taken into consideration, let alone such form of studies as carried out under the phylogenetic systematics with temporal banding methods, the more general phylogenetic studies aiming at producing the "phylogenetic systems", without using the temporal bands, are also considered to be useful for creating the base for a rank-free system of clade names, because many of the clade names given under those general phylogenetic studies are actually candidates to become basic clade names as components of the particular domain of a rank-free system (see, for example, a review for generic names adopted in Talavera *et al.* 2013: 185–188). Thus, at the first (present) stage, *we continue to do these phylogenetic systematic studies, without making amendments to the Code-compliant ways of naming clades*. We can do indeed, given the peculiar compatibility of Linnaean taxonomy (including nomenclature) and IFBT specified above. In parallel with these phylogenetic and taxonomic studies, phylogenetic taxonomists can create rank-free, abridged reference systems (i.e., particular domains), using the non-standard temporal bands under the IFBT (Fig. 12). Those rank-free systems will be created by converting the previously used Linnaean clade names to basic clade names, and also by newly naming the unnamed basic clades if there are any in the group. These taxonomic studies will not suffer from the taxon name problems caused by drastic name changes, because they adopt the non-standard temporal bands adapted for the phylogenetic studies of local groups; and thus the biological community will have no difficulty accepting the end results of these studies (i.e., rank-free, abridged reference systems of basic clade names).

In almost all "phylogenetic systems" created under the Linnaean taxonomy, with the temporal banding method, the inclusive clades (holoclades and synclades) of the groups in question have not been named. Thus, in the second stage, taxonomists, if needed, also give names to some inclusive clades of the groups in question under the IFBT. And, they may also go further to creating the full reference system, by naming all inclusive clade names of the groups, and adding those names to the particular domains they have already constructed (Fig. 12).

The IFBT needs the timetrees of the group in question, in order to name the clades, and to create the rank-free reference system of the group. Not a few taxonomists may be anxious about the difficulties in obtaining reliable timetrees of a given group, but it is highly likely that the time will certainly come soon or later where we obtain the "standard" version of timetrees of the group in question, when considering the recent rapid progress in reconstructing the timetrees for the diverse groups of organisms based on both molecular and palaeontological data (e.g., Hedges & Kumar 2009). Thus, the methodological problems with regard to reconstructing the timetrees are not considered here to be substantial.

If the taxonomist community goes along with the IFBT (with non-standard temporal bands), then we will be able to create step by step the rank-free system of the groups in which we are interested (Fig. 12), probably without confronting the serious confusion of clade names caused by changing the name endings. The IFBT has advantages with regard to producing the rank-free reference systems of clade names. To sum up, first, the names explicitly refer to the clades (i.e., real entities) as parts of the timetree, so that the names surely play a significant role in the theories of evolutionary biology and ecology. Second, the mutual exclusivity of taxon names with standard endings is certain in the particular domain so that the reference system can pack vast amounts of taxonomic information into the clade names in that domain, as in the Linnaean systems. Thus, the biological community will finally achieve the goal of acquiring a rank-free phylogenetic system of clade names that is well reconciled with the evolutionary world view and also serves as a convenient system of information storage and retrieval, although it probably takes a long duration for doing it.

The taxonomist community has at present the *PhyloCode* (Cantino & de Queiroz 2010) as a codification of the QG-phylogenetic taxonomy. Thus, those who support the theory of QG-phylogenetic taxonomy can take the option of creating a rank-free system of clade names under the *PhyloCode*. The difficulties in creating a rank-free systems of names under (the present version of) the *PhyloCode* are the following two. First, the *PhyloCode* creates the rank-free system of clade names for a given group, not by adding the necessary clade names to the existing Linnaean systems of the same group, but by newly constructing an alternative phylogenetic system, under the new phylogenetic nomenclature that rejects the Code-compliant way of hierarchically arranging the taxon names with standard endings in the rank-free systems of names. Thus, for example, it is logically possible in the rank-free system created under the *PhyloCode* that the taxon named Silphidae is included within the taxon named Staphylinidae, without changing the name ending. This means that two different systems of taxon names for the same organismal groups will exist in parallel for a long time, which obviously causes confusion in communication. Second, since the mutual exclusivity of taxon names with standard endings is no longer certain in the rank-free system created under the *PhyloCode* (Moore 2003; Platnick 2012), the system of names does not function well as a convenient taxonomic information storage and retrieval system.

It is obvious that naming the clades of a given group is more easily practiced with the *PhyloCode* than with the IFBT, because the latter requires a timetree, in addition to a phylogenetic tree of the group. However, when considering the above difficulties the *PhyloCode* has in naming clades, I think, the biological community, sorry for PhyloCoders, will not be happy with the end products of (the present version of) the *PhyloCode* .

Conclusions

When looking back at the current debates about the theory and practice of biological taxonomy, we can see that there are three important properties with regard to the reference systems of taxon names (i.e, "convenience", "rank-freeness" and "temporalness"), which may be properly called the trinity of properties of reference systems. These three properties have existed separately in the different frameworks of previous biological taxonomies, as if each were the property that is destined to relate itself to the particular taxonomic system: that is, the convenience is closely related to the Linnaean system; the rank-freeness to the phylogenetic system; and the temporalness to the Hennig's and Avise & John's versions of temporal banding methods.

Considering all of these three properties to be must-have ones for the reference system created under the future biological taxonomy, I here developed the theory of IFBT, whose end products (i.e., reference systems of clade names) have the trinity of properties. Creating reference systems simultaneously characterized by these three properties is in fact logically possible under the theory of IFBT, as demonstrated in this paper. Looking retrospectively, however, this way of creating a rank-free system has been a hidden aspect of biological taxonomy; and thus we may fail to notice it. (Note however that at least until 2002, K. de Queiroz has already conceived a similar idea of a phylogenetic systems of clade names characterized by both convenience and rank-freeness [de Queiroz & Donoghue 2013: 171–172]: "*one of us (KdQ) raised the issue of incorporating rules into the PhyloCode to preserve the hierarchical relationships [both nesting and mutual exclusivity] implied by Linnaean endings*".)

The IFBT or its like will be, I hope, accepted and espoused by the biological community in the near future. If so, then we can stop the endless debates about which system of names, the traditional Linnaean or the phylogenetic, is better; furthermore, we can use the standard endings of taxon names in the particular domains of reference systems, so that the mutual exclusivity of those taxon names are certain there. Thus, we will finally achieve the goal of obtaining a rank-free reference system of names convenient for users to obtain the taxonomic information they want to know.

Acknowledgements

I would like to express my sincere gratitude to Dr. Alessandro Minelli (University of Padova, Padova) for his constructive comments on various draft versions of this paper, and also for his fruitful advices for preparing the manuscript, and also to Dr. Alain Dubois (Muséum National d'Histoire Naturelle, Paris) for his careful reading and important comments on the manuscript of this paper. I sincerely thank Dr. Yoshihiro Hirashima (Fukuoka) for suggesting the excellent set of animal name endings marked by * in Table 2. I also thank Dr. Hiroyuki Yoshitomi (Ehime University, Matsuyama) for his encouragement and advice.

References

Alonso-Zarazaga, M. A. (2005) Nomenclature of higher taxa: a new approach. *Bulletin of zoological Nomenclature*, **62**: 189–199.

Avise, J. C. (2009) Timetrees: beyond cladograms, phenograms, and phylograms. *In*: S. B. Hedge & S. Kumar (ed.), *The timetree of life*, New York (Oxford University Press): 19–25.

Avise, J. C. & Johns, G. C. (1999) Proposal for a standardized temporal scheme of biological classification for extant species. *Proceedings of the national Academy of Sciences of the United States of America*, **96**: 7358–7363. <http://dx.doi.org/10.1073/pnas.96.13.7358>

Avise, J. C. & Liu, J.-X. (2011) On the temporal inconsistencies of Linnaean taxonomic ranks. *Biological Journal of the Linnean Society*, **102**: 707–714. <http://dx.doi.org/10.1111/j.1095-8312.2011.01624.x>

Ax, P. (1987) *The phylogenetic system: the systematization of organisms on the basis of their phylogenesis*. New York (Wiley-Interscience): i–xi + 1–340.

Barkley, T. M., DePriest, P., Funk, V., Kiger, R. W., Kress, W. J. & Moore, G. (2004*a*) Linnaean nomenclature in the 21st Century: a report from a workshop on integrating traditional nomenclature and phylogenetic classification. *Taxon*, **53**: 153–158. <http://dx.doi.org/10.2307/4135501>

Barkley, T. M., DePriest, P., Funk, V., Kiger, R. W., Kress, W. J., McNeill, J., Moore, G., Nicolson, D. H., Stevenson, D. W. & Wheeler, Q. D. (2004*b*) A review of *the International Code of Botanical Nomenclature* with respect to its compatibility with phylogenetic classification. *Taxon*, **53**: 159–161. <http://dx.doi.org/10.2307/4135502>

Benton, M. J. (2000) Stems, nodes, crown clades, and rank-free lists: in Linnaeus dead? *Biological Reviews*, **75**: 633–648. <http://dx.doi.org/10.1111/j.1469-185x.2000.tb00055.x>

Bertrand, Y., F., Pleijel, F. & Rouse, G. W. (2006) Taxonomic surrogacy in biodiversity assessments, and the meaning of Linnaean ranks. *Systematics & Biodiversity*, **4**: 149–159. <http://dx.doi.org/10.1017/s1477200005001908>

Cantino, P. & de Queiroz, K. (2000) *PhyloCode: International Code of Phylogenetic Nomenclature*. 1–46. <http://www.ohio.edu/phylocode/>.

Cantino, P. & de Queiroz, K. (2010) *PhyloCode: International Code of Phylogenetic Nomenclature. Version 4c*. 1–101. <http://www.ohio.edu/phylocode/>.

Carpenter, J. M. (2003) Critique of pure folly. *The botanical Review*, **69**: 79–92. <http://dx.doi.org/10.1663/0006-8101(2003)069[0079:copf]2.0.co;2>

Chatzimanolis, S., Grimaldi, D. A., Engel, M. S. & Fraser, N. C. (2012) *Leehermania prorova*, the earliest staphyliniform beetle, from the Late Triassic of Virginia. *American Museum Novitates*, **3761**: 1–28. <http://dx.doi.org/10.1206/3761.2>

Christiansen, P. (2013) Phylogeny of the sabertoothed felids (Carnivora: Feridae: Machairodontinae). *Cladistics*, **29**: 543–559. <http://dx.doi.org/10.1111/cla.12008>

Crowson, R. A. (1970) *Classification and biology*. London (Heinemann educational books Ltd.): 1–350.

Darwin, C. (1859) *On the origin of species by means of natural selection; or the preservation of favored races in the struggle for life. Reprinted first edition*. Cambridge, MA. (Harvard University Press): i–ix + 1–513. <http://dx.doi.org/10.5962/bhl.title.2106>

De Queiroz, K. (1988) Systematics and the Darwinian revolution. *Philosophy of Science*, **55**: 238–259. <http://dx.doi.org/10.1086/289430>

De Queiroz, K. (1992) Phylogenetic definitions and taxonomic philosophy. *Biology & Philosophy*, **7**: 295–313. <http://dx.doi.org/10.1007/bf00129972>

De Queiroz, K. (1994) Replacement of an essentialistic perspective on taxonomic definitions as exemplified by the definition of "Mammalia". *Systematic Biology*, **43**: 497–510.

De Queiroz, K. (1997) The Linnaean hierarchy and the evolutionalization of taxonomy, with emphasis on the problem of nomenclature. *Aliso*, **15**:125–144.

De Queiroz, K. (1998) The general lineage concept of species, species criteria, and the process of speciation. *In*: D. J. Howard & S. H. Berlocher (ed.), *Endless form: species and speciation*, New York (Oxford University Press): 57–75.

De Queiroz, K. (1999) The general lineage concept of species and the defining properties of the species category. *In*: R. A. Wilson (ed.), *Species: new interdisciplinary essays*, Cambridge (The MIT Press): 49–89.

De Queiroz, K. (2005*a*) The definitions of species and clade names: a reply to Ghiselin. *Biology & Philosophy*, **10**: 223–228. <http://dx.doi.org/10.1007/bf00852247>

De Queiroz, K. (2005*b*) A unified concept of species and its consequences for the future of taxonomy. *Proceedings of the California Academy of Sciences*, **56**, Supplement 1 (18): 196–215.

De Queiroz, K. (2005*c*) Ernst Mayr and the modern concept of species. *In*: J. Hey, W. M. Fitch & F. J. Ayala (ed.), *Systematics and the origin of species*, Washington D. C. (The National Academies Press): 243–263.

De Queiroz, K. (2005*d*) Different species problems and their solution. *BioEssays*, **27**: 1263–1269. <http://dx.doi.org/10.1002/bies.20325>

De Queiroz, K. (2007*a*) Toward an integrated system of clade names. *Systematic Biology*, **56**: 956–974. <http://dx.doi.org/10.1080/10635150701656378>

De Queiroz, K. (2007*b*) Species concepts and species delimitation. *Systematic Biology*, **56**: 879–886.

De Queiroz, K. (2011) Branches in the lines of descent: Charles Darwin and the evolution of the species concept. *Biological Journal of the Linnean Society*, **103**: 19–35. <http://dx.doi.org/10.1111/j.1095-8312.2011.01634.x>

De Queiroz, K. & Donoghue, M. J. (1990) Phylogenetic systematics or Nelson's version of cladistics? *Cladistics*, **6**: 61–75. <http://dx.doi.org/10.1111/j.1096-0031.1990.tb00525.x>

De Queiroz, K. & Donoghue, M. J. (2013) Phylogenetic nomenclature, hierarchical information, and testability. *Systematic Biology*, **62**: 167–174.

De Queiroz, K. & Gauthier, J. (1990) Phylogeny as a central principle in taxonomy: phylogenetic definitions of taxon names. *Systematic Zoology*, **39**: 307–322. <http://dx.doi.org/10.2307/2992353>

De Queiroz, K. & Gauthier, J. (1992) Phylogenetic taxonomy. *Annual Review of Ecology & Systematics*, **23**: 449–480. <http://dx.doi.org/10.1146/annurev.ecolsys.23.1.449>

De Queiroz, K. & Gauthier, J. (1994) Toward a phylogenetic system of biological nomenclature. *Trends in Ecology & Evolution*, **9**: 27–31. <http://dx.doi.org/10.1016/0169-5347(94)90231-3>

Dominguez, E. & Wheeler, Q. D. (1997) Taxonomic stability is ignorance. *Cladistics*, **13**: 367–372. <http://dx.doi.org/10.1111/j.1096-0031.1997.tb00325.x>

Donoghue, P. C. J. (2005) Saving the stem group – a contradiction in terms? *Paleobiology*, **31**: 553–558. <http://dx.doi.org/10.1666/0094-8373(2005)031[0553:stsgci]2.0.co;2>

Donovan, D. T. & Callomon, J. H. (1981) Classification of Jurassic Ammonitina. *In*: M. R. House & J. R. Senior (ed.), *The Ammonoidea: the evolution, classification, mode of life and geological usefulness of a major fossil group*. London (Academic Press): 101–155.

Dubois, A. (2005) Proposed rules for the incorporation of nomina of higher-ranked zoological taxa in the *International Code of Zoological Nomenclature*. 1. Some general questions, concepts and terms of biological nomenclature. *Zoosystema*, **27**: 365–426.

Dubois, A. (2006*a*) Proposed Rules for the incorporation of nomina of higher-ranked zoological taxa in the *International Code of Zoological Nomenclature*. 2. The proposed Rules and their rationale. *Zoosystema*, **28** (1): 165–258.

Dubois, A. (2006*b*) Incorporation of nomina of higher-ranked taxa into the *International Code of Zoological Nomenclature*: some basic questions. *Zootaxa*, **1337**: 1–37.

Dubois, A. (2007) Phylogeny, taxonomy and nomenclature: the problem of taxonomic categories and of nomenclatural ranks. *Zootaxa*, **1519**: 27–68.

Dubois, A. (2008) Phylogenetic hypotheses, taxa and nomina in zoology. *Zootaxa*, **1950**: 51–86.

Dubois, A. (2011) The *International Code of Zoological Nomenclature* must be drastically improved before it is too late. *Bionomina*, **2**: 1–104. <http://dx.doi.org/10.11646/bionomina.2.1.1>

Eldredge, N. & Cracraft, J. (1980) *Phylogenetic patterns and the evolutionary process*. New York (Columbia University Press): i–vii + 1–349.

Ereshefsky, M. (2001) *The poverty of the Linnaean hierarchy: a philosophical study of biological taxonomy*. Cambridge (Cambridge University Press): i–x + 1–316.

Farris, J. S. (1974) Formal definitions of paraphyly and polyphyly. *Systematic Zoology*, **23**: 548–554. <http://dx.doi.org/10.2307/2412474>

Forey, P. L. (2001) The PhyloCode: description and commentary. *Bulletin of zoological Nomenclature*, **58**: 81–96.

Forey, P. L. (2002) PhyloCode – pain, no gain. *Taxon*, **51**: 43–54. <http://dx.doi.org/10.2307/1554962>

Frost, D. R. & Hillis, D. M. (1990) Species in concept and practice: herpetological applications. *Herpetologica*, **46**: 87–104.

Frost, D. R. & Kluge, A. G. (1994) A consideration of epistemology in systematic biology, with special reference to species. *Cladistics*, **10**: 259–294. <http://dx.doi.org/10.1111/j.1096-0031.1994.tb00178.x>

Ghiselin, M. T. (1966*a*) An application of the theory of definitions to systematic principles. *Systematic Zoology*, **15**: 127–130. <http://dx.doi.org/10.2307/2411630>

Ghiselin, M. T. (1966*b*) On psychologism in the logic of taxonomic controversies. *Systematic Zoology*, **15**: 207–215. <http://dx.doi.org/10.2307/2411392>

Ghiselin, M. T. (1974) A radical solution to the species problem. *Systematic Zoology*, **23**: 536–544. <http://dx.doi.org/10.2307/2412471>

Ghiselin, M. T. (1984) “Definition”, “character”, and other equivocal terms. *Systematic Zoology*, **33**: 104–110. <http://dx.doi.org/10.2307/2413135>

Ghiselin, M. T. (1997) *Metaphysics and the origin of species*. Albany, New York (State University of New York Press): i–xi + 1–377.

Grant, V. (1971) *Plant speciation*. New York & London (Columbian University Press): i–x + 1–435.

Griffiths, G. C. D. (1973) Some fundamental problems in biological classification. *Systematic Zoology*, **22**: 338–343. <http://dx.doi.org/10.2307/2412942>

Griffiths, G. C. D. (1974) On the foundations of biological systematics. *Acta biotheoretica*, **23**: 85–131. <http://dx.doi.org/10.1007/bf01556343>

Griffiths, G. C. D. (1976) The future of Linnaean nomenclature. *Systematic Zoology*, **25**: 168–173. <http://dx.doi.org/10.2307/2412743>

Hairapetian, V. & Korn, D. (2011) Phylogenetic analysis of the family Beloceratidae (Ammonoidea; Late Devonian) and a new *Beloceras* species from eastern Iran. *Bulletin of Geosciences*, **86**: 675–682. <http://dx.doi.org/10.3140/bull.geosci.1261>

Härlin, M. (1998) Taxonomic names and phylogenetic trees. *Zoologica scripta*, **27**: 381–390. <http://dx.doi.org/10.1111/j.1463-6409.1998.tb00469.x>

Härlin, M. (1999) Phylogenetic approaches to nomenclature: a comparison based on a nemertean case study. *Proceedings of the royal Society of London*, (B), **266**: 2201–2207. <http://dx.doi.org/10.1098/rspb.1999.0909>

Härlin, M. (2005) Definitions and phylogenetic nomenclature. *Proceedings of the California Academy of Sciences*, **56**, Supplement 1 (19): 216–224.

Härlin, M. & Sundberg, P. (1998) Taxonomy and philosophy of names. *Biology & Philosophy*, **13**: 233–244. <http://dx.doi.org/10.1023/a:1006583910214>

Hedge, S. B. & Kumar, S. (ed.) (2009) *The timetree of life*. New York (Oxford University Press): i–xxi + 1–551.

Hegna, T. A. (2008) Cladistic analysis of ptychaspidid trilobites (Upper Cambrian), and a new hypothesis of ingroup relationships. *In*: I. Rábano, R. Gozalo & D. García-Bellido (ed.), *Advances in trilobite research*, Madrid (Instituto Geológico y Minero de España): 167–169.

Hennig, W. (1950) *Grundzüge einer Theorie der phylogenetischen Systematik*. Berlin (Deutscher Zentralverlag): i–vii + 1–370.

Hennig, W. (1965) Phylogenetic systematics. *Annual Review of Entomology*, **10**: 97–116. <http://dx.doi.org/10.1146/annurev.en.10.010165.000525>

Hennig, W. (1966) *Phylogenetic systematics*. Urbana, Chicago (University of Illinois Press): i–vii + 1–263.

Hennig, W. (1969) *Die Stammesgeschichte der Insekten*. Frankfurt am Main (Verlag von Waldemar Kramer): 1–436.

Hennig, W. (1981) *Insect phylogeny*. Chichester, New York (John Wiley & Sons): i–xxi + 1–514.

Hey, J. (2001) *Genes, categories, and species: the evolutionary and cognitive causes of the species problem*. Oxford, New York (Oxford University Press): i–xvii + 1–217.

IBCM (International Botanical Congress Melbourne) (2012) *International code of nomenclature for algae, fungi, and plants (Melbourne Code)*. Königstein (Koeltz Scientific Books): i–xxx + 1–208.

ICZN (International Commission on Zoological Nomenclature) (1999) *International code of zoological nomenclature, 4th edition*. London (International Trust for Zoological Nomenclature): i–xxix + 1–306.

IUMS (International Union of Microbiological Societies) (1992) *International code of nomenclature of Bacteria, 1990 Revision*. Washington, DC. (ASM Press). <WWW.ncbi.nlm.nih.gov/books/NBK8807/>.

Jefferies, R. (1979) The origin of Chordates – methodological essay. *In*: M. House (ed.), *The origin of major invertebrate groups*, London (Academic Press): 443–477.

Joyce, W. G., Parham, J. E. & Gauthier, J. A. (2004) Developing a protocol for the conversion of rank-based taxon names to phylogenetically defined clade names, as exemplified by turtles. *Journal of Paleontology*, **78**: 989–1013. <http://dx.doi.org/10.1666/0022-3360(2004)078<0989:dapftc>2.0.co;2>

Keller, R. A., Boyd, R. N. & Wheeler, Q. D. (2003) The illogical basis of phylogenetic nomenclature. *The botanical Review*, **69**: 93–110. <http://dx.doi.org/10.1663/0006-8101(2003)069[0093:tibopn]2.0.co;2>

Kluge, A. G. (2005) Taxonomy in theory and practice, with arguments for a new phylogenetic system of taxonomy. *In*: M. A. Donnelly, B. I. Crother, C. Guyer. M. H. Wake & M. E. White (ed.), *Ecology and evolution in the tropics: a herpetological perspective*, Chicago (The University of Chicago Press): 7–47.

Laurin, M. (2010) The subjective nature of Linnaean categories and its impact in evolutionary biology and biodiversity studies. *Contributions to Zoology*, **79**: 131–146.

Lauterbach, K.-E. (1989) Das Pan-Monophylum – ein Hilfsmittel für die Praxis der Phylogenetischen Systematik. *Zoologischer Anzeiger*, **223**: 139–156.

Lehmann, T. (2009) Phylogeny and systematics of the Orycteropedidae (Mammalia, Tubulidentata). *Zoological Journal of the Linnean Society*, **155**: 649–702. <http://dx.doi.org/10.1111/j.1096-3642.2008.00460.x>

Lidén, M. & Oxelman, B. (1996) Do we need "phylogenetic taxonomy"? *Zoologica scripta*, **25**: 183–185. <http://dx.doi.org/10.1111/j.1463-6409.1996.tb00158.x>

Lim, B. K. (2007) Divergence times and origin of neotropical sheath-tailed bats (tribe Diclidurini) in South America. *Molecular Phylogenetics & Evolution*, **45**: 777–791. <http://dx.doi.org/10.1016/j.ympev.2007.09.003>

Linnaeus, C. (1753) *Species plantarum, exhibentes plantas rite cognitas as genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natabilis, secundum systema sexuale digestas*. Holmiae (Laurentii Salvii): 1–1200. <http://dx.doi.org/10.5962/bhl.title.669>

Linnaeus, C. (1758) *Systema Naturae per regna tria naturae, secundum classes, ordines, genera, species, cum characteribus, differentiis, synonymis, locis*. Editio decima, reformata. Tomus I. Holmiae (Laurentii Salvii) : [i–iv] + 1–824. <http://dx.doi.org/10.5962/bhl.title.542>

Mayden, R. L. (1997) A hierarchy of species concept: the denoument in the saga of the species problem. *In*: M. F. Claridge, H. A. Dawah & M. R. Wilson (ed.), *Species: the units of biodiversity*, London (Chapman & Hall): 381–424.

Mayden, R. L. (1999) Consilience and a hierarchy of species concepts: advances toward closure on the species puzzle. *The Journal of Nematology*, **31**: 95–116.

Mayden, R. L. (2002) On biological species, species concepts and individuation in the natural world. *Fish & Fisheries*, **3**: 171–196. <http://dx.doi.org/10.1046/j.1467-2979.2002.00086.x>

Mayden, R. L. (2013) Species, trees, characters, and concepts: ongoing issues, diverse ideologies, and a time for reflection and change. *In*: I. Y. Pavlinov (ed.), *The species problem-ongoing issues*, (InTech): 171–191. <www.intechopen.com/books/the-species-problem-ongoing-issues/>

Mayr, E. (1982) *The growth of biological thought: diversity, evolution, and inheritance*. Cambridge (Harvard University Press): 1–974.

Mayr, E. & Ashlock, P. D. (1991) *Principles of systematic zoology, second edition*. New York (McGraw-Hill, Inc.): i–xvi + 1–475.

Meier, R. & Richter, S. (1991) Suggestions for a more precise usage of proper names of taxa: ambiguities related to the stem lineage concept. *Zeitschrift für zoologische Systematik und Evolutionsforschung*, **30**: 81–88.

Mill, J. S. (1872) *A system of logic, ratiocinactive and inductive: being a connected view of the principles of evidence and methods of scientific investigation*. New York (Harper & Brothers Publishers): i–xvi + 17–659.

Minelli, A. (2000) The ranks and the names of species and higher taxa, or a dangerous inertia of the language of natural history. *In*: M. T. Ghiselin & A. E. Leviton (ed.), *Cultures and institutions of natural history: essays in the history and philosophy of science*, San Francisco (California Academy of Sciences): 339–351.

Mishler, B. D. (1999) Getting rid of species? *In*: R. A. Wilson (ed.), *Species: new interdisciplinary essays*, Cambridge (The MIT Press): 307–317.

Monks, N. (2002) Cladistic analysis of a problematic ammonite groups: The Hamitidae (Cretaceous, Albian-Turonian) and proposals for new cladistics terms. *Palaeontology*, **45**: 689–707. <http://dx.doi.org/10.1111/1475-4983.00255>

Moore, G. (1998) A comparison of traditional and phylogenetic nomenclature. *Taxon*, **47**: 561–579. <http://dx.doi.org/10.2307/1223578>

Moore, G. (2003) Should taxon names be explicitly defined? *The botanical Review*, **69**: 2–21. <http://dx.doi.org/10.1663/0006-8101(2003)069[0002:stnbed]2.0.co;2>

Moore, G. (2005) A review of past and current debates in nomenclature: 250 years of progress or going around in a circle? *Symbolae botanicae Upsalienses*, **33**: 109–117.

Moyne, S. & Neige, P. (2004) Cladistic analysis of the Middle Jurassic ammonite radiation. *Geological Magazine*, **141**: 115–223. <http://dx.doi.org/10.1017/s0016756804009082>

Naomi, S.-I. (2011) On the integrated frameworks of species concepts: Mayden's hierarchy of species concepts and de Queiroz's unified concept of species. *Journal of zoological Systematics & evolutionary Research*, **49**: 177–184. <http://dx.doi.org/10.1111/j.1439-0469.2011.00618.x>

Nelson, G. & Platnick, N. (1981) *Systematics and biogeography: cladistics and vaicarience*. New York (Columbia University Press): i–xi + 1–567.

Night, D. (1981) *Ordering the world: a history of classifying man*. London (Burnett Books): 1–215.

Nixon, K. C. & Carpenter, J. M. (2000) On the other "phylogenetic systematics". *Cladistics*, **16**: 298–318. <http://dx.doi.org/10.1111/j.1096-0031.2000.tb00285.x>

Nixon, K. C. & Carpenter, J. M. (2003) The PhyloCode is fatally flawed, and the "Linnaean" system can easily be fixed. *The botanical Review*, **69**: 111–120. <http://dx.doi.org/10.1663/0006-8101(2003)069[0111:tpiffa]2.0.co;2>

O'Hara, R. J. (1988) Homage to Clio, or, toward an historical philosophy for evolutionary biology. *Systematic Zoology*, **37**: 142–155. <http://dx.doi.org/10.2307/2992272>

Platnick, N. I. (2009) Letter to Linnaeus. *In*: S. Knapp & Q. D. Wheeler (ed.), *Letters to Linnaeus*, London (The Linnean Society of London): 171–184.

Platnick, N. I. (2012) The poverty of the Phylocode: A reply to de Queiroz and Donoghue. *Systematic Biology*, **61**: 360–361.

Pleijel, F. & Rouse, G. W. (2003) Ceci n'est pas une pipe: names, clades and phylogenetic nomenclature. *Journal of zoological Systematics & evolutionary Research*, **41**: 162–174. <http://dx.doi.org/10.1046/j.1439-0469.2003.00236.x>

Schuh, R. T. (2003) The Linnaean system and its 250-year persistence. *The botanical Review*, **69**: 59–78. <http://dx.doi.org/10.1663/0006-8101(2003)069[0059:tlsaiy]2.0.co;2>

Scott-Ram, N. R. (1990) *Transformed cladistics, taxonomy and evolution*. Cambridge (Cambridge University Press): i–xi + 1–238.

Sibley, C. G. & Ahlquist, J. E. (1990) *Phylogeny and classification of birds: a study in molecular evolution*. New Haven (Yale University Press): i–xxiii + 1–976.

Simpson, G. G. (1953) *The major features of evolution*. New York (Columbia University Press): i–xx + 1–434.

Stevens, P. F. (2006) An end to all things?—Plants and their names. *Australian systematic Botany*, **19**:115–133. <http://dx.doi.org/10.1071/sb05011>

Sundberg, F. A. (2008) Potential outgroup for the oryctocephalids, a cladistics analysis of Cambrian trilobite hypostomes. *In*: I. Rábano, R. Gozalo & D. García-Bellido (ed.), *Advances in trilobite research*, Madrid (Instituto Geológico y Minero de España): 381–387.

Talavera, G., Lukhtanov, V. A., Pierce, N. E. & Vila, R. (2013) Establishing criteria for higher-level classification using molecular data: the systematics of *Polyommatus* blue butterflies (Lepidoptera, Lycaenidae). *Cladistics*, **29**: 166–192. <http://dx.doi.org/10.1111/j.1096-0031.2012.00421.x>

Tinn, O. & Oakley, T. H. (2008) Erratic rates of molecular evolution and incongruence of fossil and molecular divergence time estimates in Ostracoda (Crustacea). *Molecular Phylogenetics & Evolution*, **48**: 157–167. <http://dx.doi.org/10.1016/j.ympev.2008.03.001>

Wiley, E. O. (1978) The evolutionary species concept reconsidered. *Systematic Zoology*, **27**: 17–26. <http://dx.doi.org/10.2307/2412809>

Wiley, E. O. (1980) Is the evolutionary species fiction – a consideration of classes, individuals, and historical entities. *Systematic Zoology*, **29**: 76–80. <http://dx.doi.org/10.2307/2412628>

Wiley, E. O. (1981) *Phylogenetics: the theory and practice of phylogenetic systematics*. New York (John Wiley & Sons): i–xv + 1–439.

Wiley, E. O. & Lieberman, B. S. (2011) *Phylogenetics: the theory and practice of phylogenetic systematics, Second edition*. New Jersey (Wiley-Blackwell): i–xvi + 1–406.

Wiley, E. O. & Mayden, R. L. (2000) The evolutionary species concept. *In*: Q. D. Wheeler & R. Meiner (ed.), *Species concept and phylogenetic theory: a debate*, New York (Columbia University Press): 70–89 (position paper), 46–158 (critique paper), 198–208 (reply paper).

Zachos, F. E. (2011) Linnaean ranks, temporal banding, and time-clipping: why not slaughter the sacred cow? *Biological Journal of the Linnean Society*, **103**: 732–734. <http://dx.doi.org/10.1111/j.1095-8312.2011.01711.x>

■ *Submitted: 5 January 2014. Accepted: 13 April 2014. Published: 6 June 2014.*
Corresponding Editor: Alessandro Minelli.

APPENDIX 1. GLOSSARY. Some important terms used in this paper are defined here because there is no consensus as to how those terms are defined in the taxonomist community.

Systematics: The discipline that studies the diversity of organisms and the relationships among them, and orders (or systematizes) them into taxa (named groups of organisms) for constructing the reference systems of taxon names. Subdisciplines of systematics are as follows:

- **Taxonomy:** See "Taxonomy".
  - **Descriptive (Linnaean) taxonomy**: See "Descriptive (Linnaean) taxonomy".
  - **Phylogenetic taxonomy**: See "Phylogenetic taxonomy".
- **Phylogenetics:** See "Phylogenetics".

Phylogenetics: The discipline that estimates or reconstructs the phylogeny of organismal groups on Earth, and ultimately the timetree of life.

Taxonomy, biological (in general): The discipline that describes and names the groups of organisms, and orders the taxa for constructing the reference system of taxon names. Taxonomy consists of two sections: taxonomy proper (taxonomic system; de Queiroz 1997: 126) and nomenclature (nomenclatural system; de Queiroz 1997: 126). Taxonomy proper is a set of conventions specifying how reference systems are constructed, while nomenclature is a set of conventions (principles and rules) for naming taxa and regulating the use of those names (de Queiroz 1997: 126). Since the nomenclature is a section of the discipline taxonomy, we cannot discuss or compare at base the theories and activities of nomenclature and taxonomy as if they were the disciplines of equal ranks.

Descriptive (Linnaean) taxonomy (Linnaean system of taxonomy): A subdiscipline of taxonomy that aims at creating the Linnaean (ranked) system of taxon names, by assigning taxa to the ranks in the Linnaean hierarchy. The Linnaean taxonomy consists of two sections: taxonomy proper comprises a set of conventions specifying how the Linnaean system is created; and nomenclature (see "Linnaean nomenclature").

Quasi-phylogenetic taxonomy: A version of Linnaean taxonomy that aims at creating the Linnaean (ranked) system of clade names under the Hennigian framework of phylogenetic systematics (i.e., "quasi-phylogenetic system of taxon names").

Phylogenetic taxonomy (phylogenetic system of taxonomy): A subdiscipline of taxonomy that aims at creating the rank-free (phylogenetic) system of clade names (that represent the phylogenetic relationships of organisms in a group in question), by giving names only to clades (existing in the group), without using nomenclatural ranks. At present, there are various versions of phylogenetic taxonomy: e.g., de Queiroz & Gauthier's (1990, 1992, 1994), Härlin's (1998, 1999), Kluge's (2005) and my own version (this paper). Each version of phylogenetic taxonomy consists of two sections: taxonomy proper comprising a particular set of conventions specifying how the phylogenetic system is created, and a particular phylogenetic nomenclature (see "Phylogenetic nomenclature" and "Phylogenetic system of clade names").

Nomenclature, biological (in general): A unified body of principles and rules governing taxon naming and the use of taxon names.

Linnaean nomenclature (Linnaean system of nomenclature): Linnaean nomenclature adopts the method for naming taxa based on the Linnaean hierarchy, and determines the application of names according to rank assignments and nomenclatural types. The Linnaean nomenclature is codified in ICZN (1999) for zoology, IBCM (2012) for algae, fungi and plants, and IUMS (1992) for bacteria.

Phylogenetic nomenclature (phylogenetic system of nomenclature): De Queiroz & Gauthier's (1990, 1992, 1994) version of phylogenetic nomenclature adopts the phylogenetic definitions of taxon names which specify the meanings of taxon names in terms of common ancestry. Härlin's (1998, 1999) version of phylogenetic nomenclature adopts the phylogenetic system of reference, that is, a system in which names only refer to clades under the premise that clade names cannot be defined in terms of defining properties. Kluge's (2005) and my (present) versions of phylogenetic nomenclatures adopt Härlin's phylogenetic system of reference. De Queiroz & Gauthier's version of phylogenetic nomenclature has been codified as the *PhyloCode* (Cantino & de Queiroz 2000, 2010).

Reference system (a taxonomy; a classification): A reference system is an end product of (practicing) taxonomy; it is in general a hierarchical arrangement of taxon names. In this paper, "Linnaean system" and "phylogenetic system" mean "Linnaean system of taxon names" and "phylogenetic system of taxon names", respectively.

Linnaean system of taxon names: A hierarchical (ranked) arrangement of names of taxa (monophyletic, paraphyletic, polyphyletic groups) created under the Linnaean taxonomy.

Quasi-phylogenetic system (or "phylogenetic system") of taxon (clade) names: A ranked arrangement of names of taxa (monophyletic groups or clades) created under the Linnaean taxonomy linked with phylogenetic systematics.

Phylogenetic system of taxon (clade) names: A rank-free arrangement of clade names created under the phylogenetic taxonomy. This can be also called "truly (or genuinely) phylogenetic system of clade names".

Discussion. Phylogenetic system is a term that has been previously used with at least three different senses. First, it means a phylogenetic system of taxa (clades); second, a phylogenetic system of taxon (clade) names; and third, a phylogenetic system of taxonomy (see "Phylogenetic taxonomy"). Here I discuss briefly the reason why researchers use the term "phylogenetic system" in the first or second sense, before making clear that in this paper I use the term in the second sense.

In order for understanding what the components of phylogenetic system are, one thinks of symbols such as Staphylinidae or *Giraffa* in a phylogenetic system. Given that a name is a word or term by which an entity is designated and distinguished from other, we must understand that each symbol is the name of taxon (clade). Specifically, a particular arrangement of letters (i.e., a symbol) as used in the phylogenetic system is the name that represents a clade. However, when we say that "Staphylinidae has short elytra", or "*Giraffa* eats leaves", then the Staphylinidae or *Giraffa* is not a clade name but it means a clade (or living things). In general, when one talks about the phylogenetic system and its components (for example, in discussions of biological taxonomy), those symbols are (clade) names. On the other hand, when one talks about living things, to which those symbols refer, those symbols mean the living things themselves. Thus, those symbols appeared in a phylogenetic system play two different roles: first, they are names that represent (or refer to) the clades; and second, they just mean the clades. We can consider thus that in the former case, the phylogenetic system means a "phylogenetic system of (clade) names", while in the latter case, the phylogenetic system means a "phylogenetic system of clades".

This suggests that whether a phylogenetic system means a phylogenetic system of clades or a phylogenetic system of clade names, depends on how we understand the components of phylogenetic system under what situation. Since this paper treats the matter as to how the phylogenetic system be created, I should use here the term phylogenetic system as "phylogenetic system of clade names". Therefore, even if a researcher apparently used a phylogenetic system as a phylogenetic system of clades in his or her paper, I can and should here reinterpret the phylogenetic system, for making the discussion be consistent, as a "phylogenetic system of clade names". The phylogenetic system created under the Linnaean taxonomy linked with phylogenetic systematics is here called *quasi-phylogenetic system* or "*phylogenetic system*" (e.g., Hennig 1966: 9), while the phylogenetic system created under the phylogenetic taxonomy is simply called *phylogenetic system*, or *truly (or genuinely) phylogenetic system* (e.g., de Queiroz & Gauthier 1994: 452).