

**PHILOSOPHY, EVOLUTION, AND TAXONOMY, OR:
WHAT BIOLOGICAL CLASSIFICATION IS FOR?
(PRACTICISING BIOLOGIST'S COMMENTS
ON SOME RECENT PAPERS BY PODANI)**

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ABSTRACT: Recently PODANI (2009; 2010a, b) published some papers promoting several (individually not novel, but composed into – to my knowledge – rather original complex) ideas from the notoriously controversial “triple junction” area between philosophy, evolution, and taxonomy. His main (at least in my evaluation) implicit thesis (that biological facts should be interpreted according to philosophical theorems) led him to several explicit conclusions, the two most important from the practising taxonomist’s point of view being: 1) that diachronic classifications are ambiguous, incompatible with either Linnean hierarchy or Darwinian evolutionary postulates, and therefore only synchronic systems are sound; and 2) that binomial nomenclature is illogical and unnecessary, therefore genus names should be abandoned or fixed as parts of uninomina. As in my opinion these ideas should not be left uncommented, I wish to present some critical remarks here.

KEY WORDS: Classification, evolution, nomenclature, paraphyly, philosophy, taxonomy.

It is time that taxonomists find their backbones. A series of compromises and accommodations in the 20th century only served to further marginalize taxonomy. WHEELER 2007

While towards the end of XX century advocates of strictly cladistic (based on the HENNIGIAN dogma of unacceptability of paraphyletic taxa) classifications seemed to have almost completely overrun at least the declarative “surface” of taxonomy (consistent implementation in the taxonomic **practice** – except in some groups – has been modernistic extravagance rather than rule...), in the last years the defenders of the synthetic (“evolutionary”, recognizing the priority of information content and truth to biological reality – cf. HOŁYŃSKI 2005 for introduction of, and/or argumentation for, the terminology used here and in my other publications) systems begin to regain the voice in the dispute (e.g. BRUMMITT 2006; HOŁYŃSKI 2005, 2008, 2010; HÖRANDL 2006, 2007, 2010; HÖRANDL & STUESSY 2010; MAYR & BOCK 2002; NORDAL & STEDJE 2005; STUESSY 2009; STUESSY & KÖNIG 2008, 2009). Acceptation of one or another of these approaches [some more or less intermediate suggestions do also exist, but from the perspective of our present considerations all of them are but insignificant “varieties” of this or that “main” idea] has various far-reaching theoretical, methodological, and practical consequences, and in this sense the “paraphyletic contest” is arguably one of the most fundamental controversies in contemporary biology. Recent papers by PODANI (2009; 2010a, b) may serve as a good illustration of the kind of conclusions rigid application of the cladistic principles leads to, and as such they are certainly worthy of critical comments.

Beatty (1982) acknowledges that he is uncertain “under what circumstances, if any, scientists should take philosophers seriously”. I am equally uncertain.

PLATNICK 1982

PODANI's argumentation (like those – even if not always so explicitly stated – of other cladists) is evidently (and admittedly: e.g. “*I do not think in science there is stronger argumentation than what results from a clear logic*” – PODANI, 2010a) based on his firm conviction that consistency with logical/philosophical theorems should be considered absolutely decisive in solving taxonomic (and scientific in general) problems. At the first glance this looks uncontested, and indeed **in abstract philosophical sense** it is – but scientists do not work in abstract philosophical “environment”, and their aim is not to solve abstract philosophical questions! Logical inference is reliable **only inasmuch** as reliable (and applicable to particular problem!) are the initial premises; as the basic philosophical theorems represent by far too “*different phenomenological levels*” [to use ELDREDGE & CRACRAFT's (1980) phrase] to make their applicability to biological issues directly assessible, the premises of argumentation must be based on **observed biological facts**, observed facts must be considered decisive in evaluation of results (and then – if somebody is interested – the final conclusion may be interpreted in terms of philosophical tenets – see HOŁYŃSKI 2005 for more extensive explanation). Proceeding in the opposite direction amounts to invitation for errors (“*Logic has prompted many geologists, that ... humid periods – pluvials – should correspond to glacials of higher latitudes, but the same logic suggested to others, that pluvials should match warm, and thence humid, interglacials. Alas, hypotheses based only on logic, however ‘iron-firm’ may it be, often lead astray*” – VAN ANDEL 1991 [my retranslation from Polish]).

A natural system of classification seeks to build groups based on many congruent characters and character states. The more congruent characters that are employed successfully, the greater the information content of the system, and the more robust and stable it should remain even in the face of new information being added to it.

STUESSY 2009

So, although PODANI arrived at his conclusions by deduction from several preconceived assumptions, I will follow the opposite way: evaluating first his final stipulations in light of observed biological reality and only thereafter analyzing particular arguments set forth by him to substantiate his claims. But first of all we must answer the – very rarely discussed or even posed, but absolutely fundamental – question: **what is biological classification and what is it for?** My views have been formulated and argued in detail in several earlier publications, so here some brief quotations from one of them (HOŁYŃSKI 2005) will suffice: “*classifications are taxonomic hypotheses*”, and – as “*the most essential property of a hypothesis is its predictive power*” [“*prediction is the very hallmark of science – indeed, ... a science isn't really a science if it lacks the power to predict*” (ELDREDGE 1989)] – “*they also should be evaluated on the same basis: according to the extent to which the (morphological, ecological, physiological, genetical, or any other) characteristics of an organism may be predicted from its placement in the system*”. Having said this, how can we judge PODANI's proposals?

Phylogenetic nomenclature ... offers many opportunities for interesting philosophical debate, but it is patently an absurd proposition as a practical system.

BENTON 2000

Let me start with the simpler one: the call for uninominal nomenclature. Nomenclature is a [component of] the language of taxonomy, a **tool** enabling taxonomists (or anybody speaking about living organisms) understand what are they speaking about. The most important property expected from any tool is to be **functional**; in case of language this means to enable as easy, as exact, and as unequivocal exchange of views and ideas as possible. And it was just the effort to maximally approach this goal that prompted the “father” of modern biological nomenclature to invent the binomial system! In the pre-Linnean times nomenclature was basically uninominal (“*vulpes*”, “*cuculus*”, “*apis*”, “*lilium*”), but even then the majority of less well-known animals were not given separate “one-unit” names, being rather “attached” to a more popular one with some words added as characters distinguishing them from the “model” [*Homo diluvii testis*], [*Elephas marinus sibericus*], [*Hirudo cauda utrinque pinnata*], &c.] – in principle exactly the same practice that was later formalized by LINNAEUS as obligatory binomina consisting of a “*Genus proximum*” and a “*differentia specifica*” [that both the “*genus*” and “*differentia*” were frequently erroneous – “Siberian marine elephant” has been proven a “composite” of walrus and mammoth, “man who witnessed the deluge” was in fact a salamander living, at that, much-much earlier than the “deluge”, “leech with the tail feathered on both sides” is now known as a parasitic copepod – is of course a completely different story]. Indeed, in the “compound” names used by pre-Linnean authors the added, distinguishing part often consisted of only one word (so the entire name was a binomen) thus many of them have been later simply adopted (and so made “available”) by LINNAEUS or his contemporaries and are “officially” used today. Also the vernacular names used by laymen all-over the world are very frequently of the same structure (“flying fox”, “white stork”, “honey bee”, “sugar cane”, “red oak” &c.); similarly, almost everywhere in the world the time of “uninominal” names of people (Imhotep, Hypatia, Attila, Beowulf) has passed long ago and we changed to “binominal nomenclature”: Francesco PIZARRO, Margaret THATCHER, Maria [CURIE-]SKŁODOWSKA... Such nearly universal tendency is, of course, not accidental: LINNAEUS knew very well why to adopt this, so widely established and tested scheme: to remember the meaning of even those few thousand names of the then known species of organisms separately, “out of context”, was practically impossible, they must have been added a “sign-post” pointing to the group (“*Genus proximum*”) the particular taxon belongs to. But by now biologists have described and named not thousands but millions of species (and scores of subspecies...), and these represent but a fraction of those really existing (to be – hopefully before they become **non-existent**... – described and named in future), so the (to say it very mildly...) impracticability of uninominal nomenclature is more than evident [and the – reasonable by themselves – suggestions of “*harmonization of the three codes*” (PODANI, 2010a) would further underscore its worthlessness...]: even the mere invention of tens of millions of unique (non-homonymous) pronounceable combinations of letters would be a formidable task, but their proper application to the actually meant taxa by the speaker or writer, and then correct “re-translation” by listener or reader, would demand supernatural abilities!

Taxonomic hierarchies allow for retrieval of vastly more information on an included taxon (even if only by inference from knowledge of relatives) than the isolated species name alone.

NEW 1999

Well, one can say that also now nobody can know and remember the genus-names of all the animals and plants; indeed, the decades of efforts of indefatigable followers of “*current fashion of ‘split first and think later (if at all)’*” (HARVEY 2001) have produced such a multitude of “microgenera” that even within the group of one taxonomist’s special interest (e.g. in “my” **Coleoptera: Buprestidae**) it is very difficult to remember them all... This is true, but, on the one hand this is a problem created by some taxonomists, not “original sin” of binominal nomenclature, and on the other it is anyway much easier to remember several hundred generic names than fifteen or twenty thousand (in jewel-beetles – HOŁYŃSKI 2001) of specific uninomina. And do not forget the information content: even if I would have never heard of *Metataenia longicollis* (KERR.), the very fact that the first part of its name is *Metataenia* gives me a general knowledge about this species: that it is a buprestid, lives somewhere in SW-Pacific, is about 15–25 mm. long, &c. (and if also the subgeneric – *Cyphogastrella* – name is mentioned, my acquaintance with the beetle is further augmented); from an uninominal epithet I know nothing...

The PhyloCode rests on arguments that range from the misguided (e.g. that names should be immutable for hypotheses that change; ...) to the false (e.g. that the PhyloCode is more stable than the Linnaean system; ...) to the absurd (e.g. that the Linnaean system cannot convey evolutionary schemes because it predates Darwin). ... it may be fairly concluded that what the PhyloCode seeks to do does not need to be done and what it claims to do it does not.

WHEELER 2004

So, what are PODANI’s arguments against the Linnean system? The main objection seems to be “*that genera have no meaning in the context of evolution*”, and “*if species are the only entities which have ... more or less sharp boundaries, while genera and those above do not, why do we attach the name of a species to the name of a higher taxon if the contents of that taxon varies in time?*” (PODANI, 2010a). These reproaches are untrue both as regards genera (they **do have** evolutionary meaning, even if different from what the author has apparently in mind) and species (they **not always** have sharp boundaries), but even if true they are irrelevant: contrary to PODANI’s logic (that “*using binominals ... goes back to pre-evolutionary thinking and is therefore* [emphasis mine – RBH] *in serious conflict with evolutionary theory*”), not everything “*pre-evolutionary*” is necessarily “*in conflict with evolutionary theory*” even if both refer to the same objects (LINNAEUS’ **pre-evolutionary** classification in which wolf is closer to elephant than to sparrow or lizard fully agrees with modern **evolutionary** conclusions), and especially when their scopes **do not** overlap! The function of a language is not to describe or reflect our changing concepts but to enable communication between people; the function of biological nomenclature – as an element of language – is not to reflect evolutionary theory but to provide unequivocally understandable names to the objects of biologists’ interest. Whether these objects – groups of organisms, taxa – developed in the process of evolution, have been separately created by God, appeared independently from each other as a result of *ludus naturae*, or even are but a product of our imagination without real existence, is in this context perfectly immaterial: the only question that matters is how efficiently (exactly, unequivocally, easily) they can be recognized by their names: nomenclature is a **tool**, not a theory!

Whatever species concept or better stated whatever set of criteria for recognizing species taxa one accepts, this concept or set of recognizing criteria must be applied consistently to all organisms if species taxa are to have any meaning in describing biodiversity or in comparative studies in biology.

BOCK 2004

As signalized above, the allegations of “*sharp boundaries*” of species and “*no meaning*” of genera are not true, but the question of their justness being irrelevant to the matters of nomenclature, it will be better to discuss them in the context of taxonomy – so let us now turn to PODANI’s other stipulation: that of synchronous classification. Had this proposal been put forward by a dogmatic creationist, I would not be surprised: indeed, if “*tot sunt species quot creavit ab initio infinitum Ens*”, then we can classify only those species living today and need not bother with those of geological past because they either did not exist (fossils are but a result of Nature’s joke, *ludus naturae*, as it was explained in Middle Ages), or were the same which we observe now. Or, if – as according to CUVIER-D’ORBIGNY’s “theory of catastrophes” – in each epoch of its history the Earth was inhabited by separately created set of organisms, then the idea (quoted from CROWSON 1970) “*to construct a separate classification of each era of the geological past*” (PODANI, 2010a) would make sense. But how can such concepts be fitted in the **evolutionary** context is totally beyond my comprehension... If we accept that all species have evolved from common ancestor; that the features of their structure, life and reproduction are variations traceable to the same fundamental “groundplan”; that extinction is as immanent aspect of phylogeny as speciation; &c., then we must also accept the fact that *Hallucigenia sparsa*, *Lepidodendron obovatum* or *Archaeopteryx lithographica* is perfectly “legitimate”, “full-right” element of the System of Life, exactly equivalent to *Boletus edulis*, *Dynastes hercules* or *Alligator mississippiensis*, and any classification excluding them would be atrociously distorted and misleading. As to separate classifications for each geological epoch, it is an evidently unrealistic proposal for the evolving organisms: since the origin of life, continuously throughout millions of years, some taxa become extinct, some others transform, new ones originate, so we would need at least thousands – not several tens (demanded by as many CUVIERIAN catastrophes) – of different systems, each of them fragmentary, unnatural, and no more reasonable or serviceable than separate classifications for organisms inhabiting each one-degree-of-longitude “lith” of the Earth or those described in each particular year...

The proximal aims of systematic biology are not to determine which of the many processes that shape evolution were operative in a particular instance, but to recognize the end-products of that history and to analyze the relationships among them.... insistence on the nonconspecificity of mother and daughter species that are identical in every respect is simply a belief divorced from evidence.

WHEELER & PLATNICK 2000: 93

PODANI’s main (as I understand him) argument against diachronous classification consists of what he calls “boundary paradox”: “*morphological and genetic gaps between higher taxa are the result of evolution; they are apparent only at a horizontal cross section of the phylogenetic tree*”, i.e. “*the classification itself evolves*” (PODANI, 2009) and so, what an “*imaginary taxonomist*” at some “*Time 1*” in the past would consider a pair of closely related species, later on could develop into what another “*imaginary taxonomist*” at the “*Time 2*” would recognize as two genera, and for a recent specialist (“*Time 3*”) appears as distinct

families; “obviously, our taxonomist at Time 1 did not put them into separate families because he could not **predict** [emphasis in the original] that divergence would be so strong” (PODANI, 2010a). All this is of course true but – again! – irrelevant! We are taxonomists of the “Time 3”, we **do know** (or, at least, assume to have known) the phenetic, genetic, taxonomic and evolutionary relationships between studied taxa, and based on this: on **our present** knowledge – **not on the knowledge of any “imaginary taxonomist” at any time in the past!** – propose our classification of the taxa known **to us** (we do not classify the organisms of “Time 4, 5, 6” or any other in the future)! Similarly true but irrelevant is that “single classification, ... cannot reflect faithfully the process of evolution, only the results of it. ... a phylogenetic tree can” – yes, of course! **just this** is the difference between their respective functions and purposes: to reconstruct and illustrate (e.g. in the form of trees) the process (or, more exactly, the course) of evolution is the task of **phylogeny**, while that of **taxonomy** is to discover and present as maximally informative (predictive) classification[-s] the **observed** pattern of “biodiversity” [and “once the order has been found, we may, if we wish, assume that it’s the result of evolution” (PLATNICK 1979 as quoted by PODANI, 2009)!]. By the way, the reproach of “ambiguity” against “pattern cladists” (“who maintain that evolutionary pattern is central to their version of cladistics, while they dismiss the entire field of phylogeny reconstruction” as the base for their classifications – PODANI, 2009) is apparently a result of confusion between the **search for** the natural patterns and their **interpretation** (the distinction so clearly formulated by PLATNICK’s remark quoted above); it is just this, unfortunately frequent, confusion what allows creationists to claim that evolution is not a **fact** established as a **result** of scientific research, but on the contrary: scientific research (at least in biology) is **based on “preconceived dogma”** of evolution...

Unfortunately living organisms do not readily submit to our attempts to neatly categorize them. POOLE & VAN BERGEN 2006

Another alleged shortcoming of diachronous classification is that it “can at best be a fuzzy one (i.e. without crisp boundaries)” (PODANI, 2009). Again, it seems to me a rather strange reproach in a publication by an author constantly adducing evolution as the basic “axiom” in any consideration: nothing would have pleased creationists more than the discovery that “crisp boundaries” separate all, or the majority of, taxa: this would be the best imaginable proof that evolution does not occur! In fact, the boundaries are “fuzzy” because the **true** relationships between **natural** taxa **are** fuzzy – they are such (as, by the way, the Author himself admits at several other occasions) also among “synchronous” species! – and if we wish our classifications to be natural, we must accept the fact and fit the “fuzziness” into them (or, for purely practical reasons, divide the **real**, fuzzy “border zones” by **admittedly conventional** “demarcation lines” – we do so frequently everywhere: the boundaries between colours, languages, oceans, biogeographical regions, between fluids and gases, planets and stars, &c., &c., &c., are all “fuzzy” (even if **artificially represented** as sharp) because such is the “nature of the Nature” that **natural** boundaries are rarely “crisp”!

Dividing up an evolutionary tree into mutually exclusive families, genera, and species, which are all strictly monophyletic, is a logical impossibility. ...The insistence on monophyletic taxa is increasingly causing unnecessary chaos in taxonomy.

NORDAL & STEDJE 2005

And here we arrive at the question of paraphyly. First of all, I use this term in its traditional, the only meaningful and logical sense: it denotes the situation where ***all the ancestors of any member of a group, back to – and inclusive of – the last common ancestor, belong to that group, but one or more side-branches do not***; so, it is the antithesis of holophyly, while that of polyphyly is monophyly (including ***both*** holo- and paraphyly – ASHLOCK 1971, 1984; HOŁYŃSKI 2005; HÖRndl & STUESSY 2010). The “*various definitions*”, of which PODANI (2010b) quotes three and which allegedly are source of confusion demanding “resolution” in form of introduction of additional terms (“*paraclady*”, “*parathety*” and their analogues for “*mono-*” – i.e. holo- – and poly-relationships) are in fact the ***results*** of confusion generated by HENNIG’s “ban” of paraphyletic taxa: his own – HENNIG (1966), quoted by PODANI (2010b) as “*definition P2*” – formulation “*A group of species that has no ancestor in common only with them*” is a glaring nonsense (according to it, a group consisting of colibris, sharks, anemones and roses is paraphyletic...), and NELSON’s (1971) “*An incomplete sister-group system lacking one species or one monophyletic species-group*” – “*definition P3*” (PODANI, 2010b) is not much better (would the group become holophyletic if ***more than one*** species[-group] is removed???). All such “modified” definitions – like philosophical sophistications to the effect that “*supraspecific taxa are not evolvable entities*” or that “*taxa cannot ‘occur’ anyway*” (PODANI (2010a) – lack any ***biologically relevant*** substantiation, having been invented in the (anyway futile...) attempt to smother the evident absurdity of the consequence (“ancestral taxa do not exist”) of cladistic “paraphylophobia”: they ***do not justify*** the rejection of paraphyly but, to the contrary, preconceived dogma of unacceptability of paraphyletic taxa is the only justification ***for them*** (“*the need for a term to describe the condition now called paraphyly originated from the cladistic school of classification and not from the workers studying the evolutionary process*” – HÖRndl & STUESSY 2010)! As in science just dogmas are unacceptable, and as this particular dogma leads to illogical assertions and unnatural (uninformative) classifications (see HOŁYŃSKI 2010 for more detailed comments), there is no reason to consider cladistic taxonomy as valid alternative to synthetic (“evolutionary”) approach.

Farris' claim that cladistic classifications also convey the most information about phenetic similarity ... is true only by its own criterion, one which is not related to overall similarity, ...

BOTTJER 1980

Some statements in these works are apparently based on terminological misinterpretations, being incongruent with the Author's own arguments. So, e.g., in one of the papers (PODANI, 2010b) he quotes (as I understand, approvingly) FARRIS' explanation that “... a valid monophyletic taxon can be polythetic ...” to assert in the other (PODANI (2010a) that “*evolutionarily minded biologists cannot say that 'Boraginaceae occurred, say, 80 million years ago'*” because “*we do not know if the combination of defining characters was possessed at all by the last common ancestor population of any recent taxonomic group*”! First of all, we ***can*** – at least in principle – know (“reconstruct”) the characters of the ancestor: this is one of the aims of phylogenetic analyses. But, more importantly, whether or not in the “first boraginaceous” ***all*** the “defining characters” of recent representatives had already been developed is, of course, utterly irrelevant ***both from the cladistic and from the “evolutionary” point of view***: for a cladist what matters is only that the ***clade*** he calls “Boraginaceae” had occurred 80 million years ago; for a synthetic taxonomist – that at that particular time the

Earth was inhabited, among others, by plants which, **based on their characters**, would be, if found today, classified as belonging to **Boraginaceae**, and so there is no reason to exclude them from the family only because they had later become extinct. Even among recent organisms not all subtaxa (often **none** of them!) show all the characters typical for the group they belong to: several **Hexapoda** have four instead of six legs (or even do not have any), some **Carnivora** are specialized on plant food, we know apterous **Pterygota**, egg-laying mammals, non-segmented arthropods – and certainly many such examples could be quoted by any botanist, too! The meaning of the word “polythetic” is just “taxon defined by a set of characters, **none** of them being diagnostic **alone**”!

Although the Script is pure truth, nevertheless if scientific facts seem to contradict it, the interpretation of the respective fragment should be reconsidered. MAJMONIDES, teste KRAUSS (1999)

Similarly misconstrued is PODANI's (2009, 2010a) “*hierarchy conflict*”: “*Linnaean classification corresponds to a so-called **inclusive hierarchy***” where “*all species are of equal rank, all the genera are equal to one another, and so on*”, while “***exclusive hierarchy** ... is a partition of objects such that there is an ordering relation among the classes*”. “**The relation between members of a higher taxon cannot be at the same time equivalence relation and subordinate relation**” but, although most taxonomists “*strive for a ... basically Linnean, ... inclusive hierarchy*” concepts of subordination (“*“lower plants” vs. “higher plants”, “primitive” vs. “advanced”, etc.*”) “*are still present in our biological thinking*” (PODANI, 2010a – emphasis in the original). All this reasoning is based on misinterpretation. First of all, there is no logical impossibility in two (or more) “*objects*” being co-ordinate in one respect but at the same time one of them being sub-ordinate to the other from a different point of view, and the relation may even be opposite in still another hierarchy: when I was university student, the professor of systematic zoology (A) was the Head of Zoology Department while professor of animal physiology (B) was the Dean of the Faculty of Biology; so, as a member of staff of the Zoology Dept. B was subordinate to A, while as a lecturer in the Faculty of Biology A was subordinate to B, and at the same time they were equal as professors of their respective subjects! And similar is the situation with taxa: all extant species are evidently equal as tips of terminal branches of the evolutionary tree; all genera (orders, classes and so on) are equivalent **as units of classification**; but at the same time – if our ideas of evolution are more or less true – the common ancestor of herring, frog, snake, colibri and gorilla was a fish (if survived and found today, it would be classified as a fish), *i.e.* (notwithstanding the cladistic-philosophical objections of the Author against taxa as ancestors) **Pisces** are the group from which **Amphibia**, **Reptilia**, **Aves** and **Mammalia further** evolved: **in this sense – as a stage of evolutionary development** – fishes are “lower” than other classes of **Vertebrata**. And similarly other taxa can be considered equal as genera or families being simultaneously “lower” or “higher” according to the “*exclusive*” hierarchy based on their place in phylogeny or degree of structural development – there is no contradiction: simply the “categories” of “lower” and “higher” (or “primitive” and “advanced”) on the one hand, and “ranks” of taxonomic classification on the other, are “levels” of **different hierarchies**!

If we opt for paraphyletic grades such as Invertebrata and Pisces, then the system is ... at least noncommittal as to the branching sequences. In which case it is of no use for anyone who needs that

particular kind of information. On the other hand that particular kind of information can be clearly and unequivocally expressed in the form of a tree-like diagram. And since the tree does the job perfectly well, the arguments for a strictly genealogical arrangements are by no means compelling.

GHISELIN 1997

To sum up: if our classifications are to be natural, *i.e.* informative, predictive, reflecting true taxonomic relationships among organisms, then

- there is no biologically relevant reason to eliminate fuzzy border areas from classifications, so there is no biologically relevant justification to consider systems enforcing strict holophyly as valid alternative to those accepting paraphyletic taxa;
- there is no biologically relevant reason to treat extinct taxa differently from those living today, so there is no biologically relevant justification to consider synchronous classifications as valid alternative to those including all known representatives of the studied group;
- there is no biologically relevant reason to remove the generic “sign-post” component from names of species, so there is no biologically relevant justification to consider uninomina as valid alternative to well tested, efficiently functioning, traditional Linnaean binominal nomenclature.

Quod erat demonstrandum.

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