



doi: 10.15407/ukrbotj73.01.003

R.B. HOŁYŃSKI

PL-05822 Milanówek, ul. Graniczna 35, skr. poczt. 65, Poland
rholyński@o2.pl

FALLACIES AND FALSE PREMISES: A PLEA AGAINST THE DISSOCIATION OF TAXONOMY FROM BIOLOGY

Hołyński R.B. **Fallacies and false premises: a plea against the dissociation of taxonomy from biology.** Ukr. Bot. J., 2016, 73(1): 3–10.

Abstract. The virtual extinction of the doctrinally phenetic school in biological systematics has left two principal competitors on the battlefield: adherents of the synthetic («evolutionary») approach argue for classifications based on all available (reconstructed pattern of evolutionary development as well as its observed genetic/phenetic results) evidence, whereas according to the advocates of cladistic («phylogenetic») principles taxonomy should exactly mirror the phylogenetic branching pattern, with no regard to anything else. The debate, often vehement and harsh, lasts already for half a century, but mostly without mutual understanding: the concrete biological arguments posed by synthetists are typically being left unaddressed by cladists who, instead, respond with some preconceived philosophical concepts or formally technical divagations. This paper is an attempt to turn the discussion back to biology by replying specifically, one by one, to the points raised in some recent, very typical of cladists' attitude, papers by Zachos (2011, 2014) and Schmidt-Lebuhn (2012, 2014), and evaluating their claims in light of observable or deducible biological facts.

Key words: taxonomy, classification, cladistics, synthetic approach, paraphyly, holophyly, predicting power, information content.

The discussions on acceptability of paraphyletic taxa – *i.e.* on cladistic («phylogenetic») *vs.* synthetic («evolutionary») classifications – are going on already for half a century both in botanical/zoological as «general biological» publications [Bock (1974), Bottjer (1980), Brummitt (2003, 2006), Christoffersen (1995), Crowson (1971), Hörandl (2006, 2007), Mayr (1974), Nordal & Stedje (2005), Podani 2010, Richardson & Oberprieler (2007), Rieppel (2009), Stuessy (1997), Wiley (1981) are but few examples], but, unfortunately, from the cladists' side the same reasonings (mostly of philosophical or «technical» nature) are being repeated, with almost full disregard of the factual, biological meaning of the counter-arguments posed by the «synthetists» (whose articles are usually cited rather selectively...), what on the one hand allows avoiding the necessity to answer rationally to the «inconvenient» questions, and on the other hand creates the false appearance of nearly universal acceptance of cladistic dogmas in classification. The recent papers by Zachos (2014) and Schmidt-Lebuhn (2014) are «school-bookish» examples of such – to use the latter author's

(Schmidt-Lebuhn, 2012) formulation – fallacies and false premises, providing an excellent opportunity for the attempt to clarify the deep basic «ideological» differences (as to, *e.g.*, what biological classification is for?) that prevent understanding of the very meaning of each other's argumentation. Thus, in the following text I will refer specifically to their misconceived reproaches, using them as a framework for discussion.

To avoid confusion, I begin with two important but notoriously neglected or misinterpreted terminological questions.

(1) I am discussing here cladistic **classifications**, not cladistic principles of **phylogenetic reconstructions**. Zachos' (2014) «*plea against the dissociation of taxonomy and phylogenetics*» is not necessary, since no such danger (at least from the side of «synthetists») really exists: the very epithet «synthetic» refers to their close **association!** But association (requirement for taxonomy to be **compatible** with phylogeny) does **not** mean identity: taxonomy and phylogenetics are closely related, but **different** fields of research, and their results need not, and **should not**, be the same – otherwise one of them would be simply superfluous.

(2) I strongly suggest (and do in this and my other publications — e.g. Hołyński, 2005, 2010, 2011 *etc.*) to avoid application of the misleading «marketing-motivated» epithets «evolutionary» vs. «phylogenetic» to «classification» or «taxonomy» (all — except the currently almost never used strictly phenetic — are **both** evolutionary **and** phylogenetic: nothing can be «evolutionary» not being «phylogenetic» or *vice versa!*) and replace them with the adequate terms: «synthetic» (synthetising total available evidence: on genealogy **and** results of evolution) and «cladistic» (based exclusively on a hypothesized branching pattern), respectively.

Another terminological question, reinterpretation of which by Hennig (1950) and his followers has introduced enormous confusion making a meaningful dispute very difficult, is the definition of monophyly. The term was coined by Haeckel in the early 1860s (Ashlock; 1984) simply to denote common ancestry, and for the next hundred years it was universally so interpreted: a group is monophyletic if all included taxa have a common ancestor; it is polyphyletic if there is no single common ancestor. Schmidt-Lebuhn (2014) tries to ridicule this definition [«*The currently preferred assumption appears to be that any two randomly chosen species on Earth have a common ancestor*»] but I find it difficult to believe that he himself takes such reproach seriously: pre-Hennigian biologists were, and modern «synthetists» [I propose to introduce this term — in lack of another adequate — for the followers of the synthetic school] are, not idiots and used the criticized formulation simply as a convenient, easily understandable shortcut for the otherwise unnecessarily lengthy and cumbersome description («*the last common ancestor of all members of the group and all intermediate taxa between them and the common ancestor*»)!

Stuessy & Hörandl's (2014) «*claim*» that paraphyly is a type of monophyly is by Schmidt-Lebuhn (2014) evaluated as «*simply factually wrong*»; instead (according to him) «*there is very little difference between paraphyla and polyphyla*», because it is «*trivially possible to select a non-monophyletic group of extant species and call it either paraphyletic or polyphyletic merely by changing the inferred ancestral state of the character used to diagnose it*». This is an excellent example of the type of the abstract formal logic used by cladists as arguments with disregard of the biological reality. Indeed, «*by changing the ancestral state*» of the common ancestor of birds and mammals a cladist can make homoioterms [birds+mammals] «paraphyletic» in relation to some groups of «polyphyletic» poikilotherm reptiles, but living

(recent or extinct) organisms are neither products of artistic imagination nor artificial constructs whose «character states» can be changed according to our convenience: they are **real** plants or animals with **real**, independent of our preferences, traits. It is indeed easy to juggle (as done by Schmidt-Lebuhn) with a «*set of four plant species*» arbitrarily defined as white- or yellow-flowered, also arbitrarily assuming accelerated or delayed transformation; however, biological reality is not arbitrary, characters of (terminal or ancestral) taxa cannot be changed at will but must be either based on observation or (as it is usually the case with extinct organisms) inferred from available evidence (e.g. phylogenetic reconstruction), and consequently they are **objectively** (according to our best actual knowledge) **either** paraphyletic **or** polyphyletic. So, «*simply factually wrong*» is the alleged «*very little difference between*» paraphyly and polyphyly: while the former is indeed «*a type of monophyly*» [«*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)*» — Hołyński, 2011], the opposite conclusion of Schmidt-Lebuhn (2014) is evidently a result of cladists' inability to distinguish between the more inclusive term «monophyly» and more restrictive «holophyly».

Another example of «*fallacies and false premises*» is Schmidt-Lebuhn's (2014) assertion that «*the existence of long branches is an illusion brought about by extinction and an incomplete knowledge of the fossil record*», as «*any newly discovered intermediate species and, especially, intermediate fossil breaks the long branches*». In fact, such discovery may eliminate the **effect** of long branch **attraction** in phylogenetic reconstruction, but the length of the branch [«*evolutionary divergence*» of Stuessy & Hörandl (2014): the distance — in terms of the sum of genetic (and consequently phenetic) transformations — between its base and the tip of the longest «twig»] will remain unchanged. From the taxonomic perspective, the intermediates would probably make the definitions of the respective taxa more «fuzzy ... (i.e. without crisp boundaries)» (Podani, 2009), but «*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' ... such is the 'nature of the Nature' that natural boundaries are rarely 'crisp'!*» (Hołyński, 2011). It is obviously true that «*striking*

macroscopic morphological differences are not necessarily correlated with similar differences in biochemistry or microstructure», but very often they are (as evidenced e.g. by supraspecific taxa established in the 19th century whose validity has usually been confirmed by modern anatomical, biochemical and/or phylogenetic studies), and anyway synthetic classifications – contrary to cladistic ones! – are (at least in principle) based on total available evidence, not just on one or two «striking» traits.

And so we have arrived at what Schmidt-Lebuhn (2014) – justly! – evaluates as the «*central argument*» in the discussion: the question of information content. According to him (and this is the usual claim posed by cladists) the «*phylogenetic system ... obviously contains information about phylogenetic relationships*». Yes, it obviously does! But is it the information provided **by the classification**? – evidently **not**: cladistic classification is a simple (usually inexact) translation of the cladogram, so «*it is not cladistic classification that predicts genealogical relationships, but the opposite: cladistic classification is nothing more than the pattern of genealogical relationships (as previously reconstructed!) presented in words (taxon names)*» (Hołyński, 2005); whereas, until the phylogenetic reconstruction has been done, no «*information about ... relationships*» existed, thereafter the resulting cladogram presents it in much more exact and much more convenient form, so the cladistic classification is glaringly superfluous: «*If we opt for paraphyletic grades such as Invertebrata and Pisces, then the system is ... at least noncommittal as to the branching sequences ... 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).

«*The primary goal of general purpose («natural») classification is to provide groupings of maximum predicting power: 'high information content' (i.e. highly correlated suites of characters)*» (Jensen, 2009), so what about informations obtainable really **from the classification** (i.e., from the place of the taxon in the system), which can only be gained by the assumption that the traits (morphological, ecological, physiological, geographical or any other) of an animal or plant can be deduced from those of other members of the group? There are two possibilities: either (as in the case of e.g. **Coleoptera**, **Trochilidae** or **Gorilla**) the «cladistic»

taxon is identical to that proposed by «syntheticists» and so identical is also its information content, or they are different (as for **Osteichthyes** or **Dinosauria**) and the «predictive power» of the cladistic classification is (often drastically) lower and less reliable. What of use (except «*few 'synapomorphies' important for phylogenetic analysis but usually trifling from any other point of view*» – Hołyński, 2010) can be said of *Latimeria* on grounds of its belonging to the «**Sarcopterygii**» (or whichever name is attributed to the «non-fish» **Vertebrata**)? It «*looks like a fish, tastes like a fish, behaves like a fish* [not like a warbler, monkey, turtle or toad – RBH], and thus – in some legitimate, exceeding narrowly understood tradition, sense – *it is a fish*» (Gould, 1991).

Cladists «*usually adduce, as the paramount advantage, the fact that – while all deductions from a synthetic classification are «only approximate» (the information that an animal belongs to the **Insecta** strongly suggests, but does not prove, that it has three pairs of legs) – cladistic systems **exactly** «predict» genealogical relationships*» (Hołyński, 2005); to support this reproach Schmidt-Lebuhn (2014) «examines» the information content of the imaginary classification of four imaginary taxa: «*Family A = (genus B, genus C, genus D, genus E)*», and concludes that in «*phylogenetic*» interpretation the «*B, C, D, and E are reciprocally monophyletic*» and thus «*the system obviously contains information about phylogenetic relationships*» and that information «*can be useful for downstream* [what does it mean in this context? – RBH] *studies in biogeography, evolutionary biology, biochemistry, plant breeding and various other fields*». First of all, what is the really useful (even if only cladistic: restricted to the branching pattern) information in the «reciprocal monophyly» of B, C, D, and E? Is their **true** relationship B(C(DE)) or ((BE)(CD)), or D(B(CE)) or anything else? What makes them different genera (or why are they not further split)? Are they grouped into the «*Family A*» (to the exclusion of the – also «*reciprocally monophyletic*» – genera F, G, H and all the others) based on the fancy of the author (so what about «information content»)? on some formal convention? or on the so scornfully excommunicated phenetic similarity? Even this imaginary example, specially invented by Schmidt-Lebuhn (2014) to show the superiority of cladistic classifications, in fact makes it obvious that also strictly cladistic information is «translated» from the cladogram so inexactly as to be practically worthless. As to the «*various other fields*», I cannot imagine what important information of use for e.g. biogeography, biochemistry or plant breeding could be derived from the hypothesis

of the taxa being «reciprocally 'mono'phyletic» (i.e., to use the unambiguous term, holophyletic)? In what important respect the interpretation of distributional history or recent biogeographical pattern of, say, **Hippopotamidae** is dependent upon whether they are holo- or – as suggested by some recently proposed phylogenies – paraphyletic (in relation to **Cetacea**)? The only truly confusing and potentially misleading factor would be **polyphyly**, but this is not allowed by either «school»!

Schmidt-Lebuhn's (2014) attempt to negate the information content of synthetic classifications [*«Because the taxa in an evolutionary classification are partly defined based on common ancestry, it does not contain reliable information on phenetic similarity or dissimilarity either»*] is also by no means convincing. The very formulation «partly based on common ancestry» is misleading, suggesting some contradiction between genealogical and phenetic aspects of synthetic classification, something like «some dissimilar taxa have been included based on phylogenetic relationships and some phylogenetically unrelated on grounds of similarity» – of course nothing like this is true: all «synthetic» taxa are strictly «phylogenetic» (no polyphyly is allowed), and only **within this constraint** phenetic similarity becomes decisive! Probably the Author refers to the situations where the genealogical constraint separates superficially similar groups like **Bivalvia** and **Brachiopoda** or ichthyosaurs and dolphins, but **just in such situations** similarity concerns only what he dismisses as «small but human eye-catching set of morphological characters». Good synthetic taxonomy – contrary to Schmidt-Lebuhn's (2014) accusation (and unlike **cladistic** systems, taking only one/two/three «synapomorphies» into consideration!) – is not based on «few striking macroscopic morphological differences» but on **all available evidence**, and such is almost by definition congruent with phylogeny, generally no contradiction could exist [*«Arguably, even in the most striking cases of convergent evolution, the accumulation of differences overwhelmingly surpasses the development of similarities (albeit occasionally few superficial resemblances can make the appearance of the opposite). That is to say, the disparity between any two lineages always increases in time (the respective species are more different now, than their ancestors were at any time in the past) – overall convergence does not exist!»* (Holyński, 2005)].

To sum up, the information derivable from **both** types of classification – like **any** scientific (or other) statement, whether presented as «fact», «theory»,

«hypothesis» or «supposition» – is more or less «unreliable» (possibly wrong) and limited (offering but a «subsample» of potentially knowable characteristics of the included taxa) – the difference lies in the «originality» (whether the classification is **itself** the source of information or is it only a redundant crippled «translation» of that provided by the cladogram), degree of reliability, and «amount» of the derivable («deducible», «predictable») data. In all three respects the synthetic classifications perform better: the degree of originality is here nearly 100% as compared to 0% for cladistic ones (where all informations derivable from classification is already present in the cladogram – but not the opposite!); reliability of the derivable genealogic information is usually somewhat higher (based on the same phylogenetic reconstruction but further verified phenetically); and information content (extending to all characteristics of the taxon vs. mere hypothesis on its holophyly) often simply incomparable!

«A system containing a genus *B* that is paraphyletic to genus *C*» – argues Schmidt-Lebuhn (2014) – «invites the end user to search for breeding partners to a species in *B* only among other members of *B*, potentially missing all its closest relatives». I am not convinced that breeders bother very much with classification or phylogeny, but if they do, the «invitation» to search mainly from among members of *B* would, in most cases, be perfectly right: reproductive isolation is largely based on, and so correlated with, the evolutionarily accumulated genetic and phenetic differences between taxa; the correlation is, of course, not absolute but anyway definitely positive, so an aberrant «offshoot» of the clade *B*, so much differentiated that it has been separated into a distinct genus (*C*), is almost certainly **less** appropriate as a breeding partner than are other members of *B*! The reproach (continuation of the above) that «it invites them to conduct a study on the biogeography or of character evolution in *B*, never realizing that none of this makes evolutionary sense without including *C*» is still less understandable: would the understanding of the geographical distribution or character evolution of true cormorants (*Phalacrocorax*) make less sense if their descendant, Galapagos flightless cormorant (*Nannopterum harrisi*), remains unknown? Of course we must know what are we speaking about: whether the object of our study is the genus *Phalacrocorax* in the «broad cladistic» (including «*P.*» *harrisi*), or synthetic (paraphyletic, excluding the Galapagoan offshoot), or «narrow cladistic» (*P. carbo* and its closest relatives, after splitting off – «to avoid paraphyly» – the

«genera» *Leucocarbo*, *Microcarbo* etc.) meaning – any interpretation confusing these concepts must, naturally, «make no evolutionary [or any other...] sense», but this is a totally different question.

Thus, first of all, there is the fundamental question of *what is the aim of scientific research?* Is it, as seems to be nowadays generally believed, the study of the *real* world, «systematic observation of facts and seeking to formulate general explanatory laws and hypotheses that could be verified empirically» (Garmonsway, 1969), or construction of abstract, philosophically perhaps sound but having little in common with observable reality, «ideal systems»? Should we study the *genuine* facts, or – as some mathematicians say – «interesting is not what the world is like, but what it should be like» (Lánczos Kornél, see Marx, 2000)? We are biologists, not mathematicians or philosophers, so – I hope, evidently – we are primarily interested in the real world, not in any idealistic utopia, and if so, arguments in our discussions should be based on observed facts, not on philosophical concepts.

Therefore I will not enter into discussion with Zachos (2014) as to whether or not biological concept of taxa does or does not fit into any of the philosophical «types of group formation: classes and individuals»: for a non-philosopher classes are classes, individuals (Roman Hołyński, Donald Duck, the oak-tree in front of my window) are individuals, and taxa (*Homo sapiens*, *Aves*, *Fagaceae*) are taxa (distinctive, internally homogeneous groups of genealogically related organisms). Such groups do really exist and may be studied – there is no necessity (and little sense) to ask philosophers what attributes taxa *should* have: these attributes are open to empirical ascertainment by simple observation.

Of course, «internally homogeneous» does not mean that every individual has every particular feature of the set making its taxon distinctive, so «if a female cat gave birth to a kitten with only one or two auditory ossicles or without hair» this will certainly not be considered a reason to exclude it from the class *Mammalia*. Paraphyletic taxa are *not* simply «defined by similarities ('reptilian grade')»: they are ultimately «defined» by their maximum information content (= predictive power), approached by similarities *within common ancestry*. But, as Zachos (2014) justly admitted, «taxa ... are always hypotheses, and if and when these hypotheses are refuted ..., then they will have to be replaced by a new taxonomic hypothesis. This is how science works, it is not a weakness of taxonomy but vital evidence of its scientific character», so even if (what, however, seems

very unlikely...) he some time proves right in assertion that turtles are as «derived» (as distinctive) as birds, this would only mean that, in order to assure the maximum information content of the vertebrate classification, *Chelonia* should be «upgraded» to the rank equal to that of *Aves* – no problem in the frames of the synthetic system! By the way, while Zachos (2014) accuses «evolutionary taxonomists» of the «anthropocentric» belief in «progress in evolution», his evaluation of paraphyletic taxa as «grades» suggests that he himself is a believer: speaking of a «reptilian grade» means that *Reptilia* are considered higher (occupy a higher rung on the *scala naturae*) than representatives of «pre-reptilian» but lower than «post-reptilian grades» [grade: «degree of quality, rank etc.» – Garmonsway, 1969]...

Apparently the central (anyway returning again and again) point in Zachos' (2014) argumentation is that taxa must be «non-arbitrary», «rigorously defined», while paraphyletic taxa are not. It is true, «definitions» of paraphyletic taxa are to some degree arbitrary – but so (indeed, *even more* so!) are cladistically formed holophyletic ones as well! «Taxa ... are always hypotheses», and – having been formed according to other hypotheses – they cannot be anything else. In synthetic classifications taxa are recognized and delineated based on two hypotheses: the general, of monophyly («all the ancestors of any member of a group, back to – and inclusive of – the last common ancestor, belong to that group» – Hołyński, 2011), applicable to all taxa; and the specific, of maximum information content («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» – Hołyński, 2005), used to select which of the millions of monophyletic lineages should be demarcated as a genus, family, order etc. Cladists also define their taxa according to the phylogenetic hypothesis (that of holophyly), but their criteria to select the actual rank and limits (why this or that particular «node» in the basic cladogram, rather than one below – more «inclusive» – or one above, is «designated» to define the particular taxon) are left mysterious (surely, «there is no non-arbitrary way of defining it», predictive power or even superficial similarity being evidently unapplicable under cladistic dogmatism...).

More importantly, the very demand of «rigorous» and «non-arbitrary» definitions is out of place: such exist only in mathematics and, perhaps, philosophy – as mentioned above, in nature everywhere (even in physics, though there they are relatively narrow) «fuzzy

border areas» dominate, and any attempt to «rigorous» delimitation must unavoidably be arbitrary. Indeed, as regards taxonomy, the very possibility to define taxa rigorously and non-arbitrarily would be the best imaginable proof that creationists are right: the theory of evolution is false...

One of the notorious problems with cladistic «taxonomic ideology» is the glaring contradiction between the **demand** for a common ancestor and the dogma of its... non-existence («*no taxon can be the ancestor of another taxon*») because such ancestor would be **by definition** paraphyletic, and paraphyletic taxa **by definition** «do not exist»! Cladists usually carefully avoid this question, but if they nevertheless must invent some solution, one of the following two is offered. Some say that it is but a convention allowing to keep classifications «objective» [but what is the value of a convention (or objectivity) that is both illogical and contradictory to the observed reality: dinosaurs are evidently ancestors of birds, and the «trick» of «lumping» them together – «*colibris are flying dinosaurs*» – does not solve anything because the common ancestor of the so constructed **Dinosauria sensu lato** and **its** sister-group is also paraphyletic, and so back to the *primaeva* coacervate!]. Another subterfuge is to exempt species from the ban on paraphyly («*the concept of paraphyly does not apply to the species category*»), so the «actual common ancestor is (or was) a species, but it does (did) not belong to any supraspecific subdivision of the descendant group» – again a destructive (making classification cripple, with millions – one for each «accepted» non-monotypic taxon! – of species «not belonging anywhere») and illogical «convention» designed only to defend the indefensibly harmful dogma [*That the common ancestor of insects, crustaceans, cheliceratans must have existed – does not matter: it did belong to the Arthropoda but not to any class, order, family, genus or species [once in Precambrium there lived a primitive arthropodan, say, Protarthropodus verus, member of the family Protarthropodidae, order Protarthropodomorpha, class Protarthropoda; later on some of its populations evolved further into divergent lineages, and at that very moment... the class, order, family, genus and species retroactively disappeared: not only they did not exist any more in Cambrium and thereafter, but their existence has been «erased» even from the Precambrian past!!!]. Maybe it is good philosophy, but good biology it is certainly not...*» – Hołyński, 2005].

Zachos (2014) accuses synthetists of adherence to the «pre-evolutionary» typological thinking and «historically

fascinating philosophical but scientifically obsolete idea» of *scala naturae* ascending from «lower» to «higher» groups; in fact, just the cladistic classifications are evidently typological [«rigorously» based on particular (sets of) «important» characters («synapomorphies» – as contrasted to «unimportant plesiomorphies») and pre-evolutionary (indeed, even pre-scientific!). Synthetic taxonomy has nothing to do with *scala naturae* or «ranking» organisms according to the degree of their «lowness» or «highness» – instead, its basic assumptions are very simple: (1) «mono- (holo-, para-)phyletic» means «having a common ancestor»; (2) if mono- (either holo- or para-)phyletic taxa do exist, common ancestors must have also really existed; (3) such an ancestor was evidently a [group of] population[-s]; (4) each population belongs to a series of hierarchically arranged («nested») taxa (species>genus>family *etc.*); (5) so, a common ancestor of two or more descendant taxa is a really (at least in the past) existing taxon; (6) that taxon is by definition paraphyletic; (7) thus, **acceptance of paraphyletic taxa is logically unavoidable**. And indeed, a great part (perhaps the majority) of **natural** (homogeneous in morphological, physiological, ecological, or any other respect, and distinct from other such groups) species, genera, families, orders *etc.* are paraphyletic (becoming natural only **after exclusion** of one or more «dissident» lineages descending from the same ancestor); even among the recent species paraphyly is a common situation (Ross, 2014).

Thus, under closer examination all claims of superiority of cladistic classifications raised by Schmidt-Lebuhn (2014) and Zachos (2014) prove fallacious, all their reproaches against paraphyletic taxa based on false premises and/or biologically irrelevant abstract imaginary constructs. The best natural, general-purpose classification is that with the highest information content (and, consequently, of maximum 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), which in case of cladistic systems is, as regards branching pattern, no more than a redundant imperfect «translation» of what is easier and more exactly derivable from the respective cladogram, and in any other respect it is at most (for well-defined holophyletic taxa accepted by both schools) equal to, but in most cases curtailed and less reliable than, that provided by synthetic classifications.

So, how cladists can defend their «anti-paraphyletic» dogma? Apparently, it is only possible by resort to casuistic loopholes. Paraphyletic taxa must not exist,

but both logic and observation prove their existence – no problem, let's merge some totally different groups together, or divide the homogeneous one into several «reciprocally monophyletic» parts! But such «improved» taxa also must have had ancestors – well, so let's declare that the «real» ancestor was only the respective species, and that species did not belong to any higher taxon! But ancestral species are also by definition paraphyletic – so other quibble must have been conceived: the distinction between «mono-» and paraphyly «does not apply» to species... Every inconsistency can be «resolved» by some ingenious jink – but should we, 21st century biologists, turn back to the Middle Ages? Throughout the ancient and medieval times science and philosophy were considered synonyms, and interpretation of observed and (on almost equal footing...) imagined «facts» meant usually attempts to «press» them into the frames of some preconceived philosophical concepts. Even if the story of hot theoretical disputes on how many legs a crayfish «must» have is but an anecdote, scholastic (based – like cladistic taxonomy.. – on «*rigorous conceptual analysis*» rather than direct examination of facts) reasoning dominating the attempts to describe and understand the world led to a wide spectrum of more or less strange conclusions from the belief in the real existence of dragons or unicorns («*Under the principle of plenitude, God had created all possible species, including all those already known and all those that could be imagined*» – Anderson, 2013) to the geocentric Universe. Man lives on the planet Earth, so the Earth «must» be placed at the very center; circle is the most «perfect» figure, therefore orbits of planets «must» be exactly circular; *etc.* And what if we clearly see that the orbits are not circular? – then «evidently» other circular orbits («epicycles») «must» be conceived. And if this is still not enough to make philosophy and observations agree? – «of course» introduction of other «beings» («deferents», «equants») is needed, *etc.* I certainly do not wish to underestimate the Ptolemaic system: it was an excellent work at the «cutting edge» of the «state of the art» almost *two thousand years ago*, but do we really wish to work *now* according to such «principles»? Or, perhaps, it is the time to dissociate taxonomy from philosophical dogmatism and re-associate it with biology? – otherwise, indeed, «*we might soon have to say farewell ... to the whole taxonomic system*» (Flegel, 2013) and return to the concepts like *scala naturae* with its «*fundamental principles: plenitude, continuity and gradation*»... Zachos (2011) asks «*why not slaughter the sacred cow?*»; unfortunately, he has misidentified it – yes, let's slaughter the sacred cow, **but the proper one!**

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Recommended for publication by S.L. Mosyakin Submitted 03.11.2015

Голинський Р.Б. **Хибні уявлення та помилкові передумови: заперечення проти від'єднання таксономії від біології.** — Укр. ботан. журн. — 2016. — 73(1): 3–10.

вул. Гранична, 35, пошт. скр. 65, PL-05822 Мілянукв, Польща

Фактичне зникнення класичної фенетичної школи в біологічній систематиці призвело до існування двох основних конкурентних груп у цій дискусії: прихильники синтетичного («еволюційного») підходу виступають за класифікацію на основі всіх доступних свідчень (реконструйованих шляхів еволюції, а також її генетичних/фенетичних наслідків), тоді як послідовники кладистичних («філогенетичних») принципів вважають, що таксономія має точно віддзеркалювати послідовність

філогенетичного галуження, без будь-яких застережень. Ці дискусії, часто різкі й жорсткі, тривають уже протягом півстоліття, не призводячи, проте, до взаєморозуміння: кладисти не зважають на конкретні біологічні аргументи, які висувають прихильники синтетичної теорії, і, в свою чергу, відповідають певними упередженими філософськими концепціями або формальними технічними міркуваннями. Ця стаття є спробою повернути дискусію в бік біології шляхом надання послідовних конкретних відповідей на питання, порушені в деяких нещодавно опублікованих типових кладистичних роботах (Zachos, 2011, 2014; Schmidt-Lebuhn, 2012, 2014), а також оцінки цих тверджень у світлі як наявних біологічних фактів, так і висновків, що з них випливають.

Ключові слова: таксономія, класифікація, кладистика, синтетичний підхід, парафілія, голофілія, прогностична здатність, інформаційний вміст.

Холинский Р.Б. **Заблуждения и ошибочные предпосылки: возражение против отделения таксономии от биологии.** — Укр. ботан. журн. — 2016. — 73 (1): 3–10.

ул. Граничная, 35, почт. ящик 65, PL-05822 Милянукв, Польша

Фактическое исчезновение классической фенетической школы в биологической систематике привело к существованию двух основных конкурентных групп в этой дискуссии: сторонники синтетического («эволюционного») подхода выступают за классификацию на основе всех доступных свидетельств (реконструированных путей эволюции, а также ее генетических/фенетических последствий), в то время как последователи кладистических («филогенетических») принципов считают, что таксономия должна точно отражать последовательность филогенетического ветвления, без каких-либо оговорок. Эти дискуссии, часто резкие и жесткие, продолжаются уже в течение полувека, не приводя, однако, к взаимопониманию: кладисты не учитывают конкретные биологические аргументы, которые выдвигают сторонники синтетической теории, и, в свою очередь, отвечают определенными предвзятыми философскими концепциями или формальными техническими соображениями. Эта статья является попыткой вернуть дискуссию в сторону биологии путем предоставления последовательных конкретных ответов на вопросы, поднятые в некоторых недавно опубликованных типичных кладистических работах (Zachos 2011, 2014; Schmidt-Lebuhn, 2012, 2014), а также оценки этих утверждений в свете как имеющихся биологических фактов, так и выводов, вытекающих из них.

Ключевые слова: таксономия, классификация, кладистика, синтетический подход, парафилия, голофилия, прогностическая способность, информационное содержание