

IS PARAPHYLY INDICATION OF POOR TAXONOMY? – OPEN LETTER TO DRS. CARVALHO AND EBACH

Roman B. Holynski*

* 05-822 Milanówek, ul. Graniczna 35, skr. poczt. 65, POLAND. E-mail: holynski@interia.pl

Dear Dr. CARVALHO, Dear Dr. EBACH,

I have recently read a series of your papers (CARVALHO 2009, CARVALHO et al., 2007, 2008; CARVALHO & EBACH, 2009; EBACH & CARVALHO, 2010; EBACH & HOLDREDGE, 2005) on various aspects of contemporary trends and policies relevant to taxonomic research. I will not expatiate on those your opinions and arguments (the majority: concerning “*taxonomic impediment*”, detrimental role of “*cybertaxonomic-automation paradigm*” or “*DNA-barcoding enterprise*”, etc.) which I perfectly agree with – I have also published several papers [HOLYŃSKI, 2001, 2005, 2008a,b,c, 2010] expressing similar views – there is, however, one important aspect heavily emphasized by you where I am not only unable to agree with your attitude, but find it so glaringly incongruent with your approach to other questions (see above) that it is difficult for me to understand how they “fit together” in your minds? These remarks were initially intended as a “private” letter to you (I quote almost exclusively from your publications and address only the formulations used by you), but as the problem is very important, as it concerns all systematists, and as in this case also – like in that of “barcoding”... – almost totally silent majority has been increasingly dominated (and forced to accept poor scientific practice...) by influential eloquent minority, I decided to publish it as “open letter”.

Of course I am speaking of your dogmatically cladistic attitude: depreciation of synthetic (“evolutionary”) classifications, negation of paraphyletic taxa. How can you so clearly see that e.g. “*barcoding enterprise*” or other parataxonomic “shortcuts” and technocratic tricks produce only a formal, unnatural “parataxa”, “*nothing more than a hedgepodge of names that may not refer to any real units in nature*” [CARVALHO et al., 2008: 153], and at the same time not realize that exactly the same is true of cladistic (adhering to strict **holophyly**) classifications (please note that I am referring to cladistic **taxonomy**: reconstructions of **phylogeny** must, of course, be essentially cladistic!)? What scientific or biological is in splitting a homogeneous, **monophyletic** taxon into two or more – in all respects identical – ones only because a part of it has become detached and evolved separately? or, alternately, in “cramming” evidently disparate group into another one with which it has already little in common, only because somebody **supposes** that it had split off later than some parts of its “*not monophyletic*” (in fact, **monophyletic**, only not **holophyletic**) “mother”-taxon? It is like the allegation that a hen becomes another individual every time she lays an egg, or that the egg – and then the bird developed from it – remains still a part of its mother... “*Conservation efforts should be aimed ... not on binomials devoid of real existence*” [CARVALHO et al., 2008: 153] – indeed! but taking cladistic dogma seriously we should concentrate our conservationist efforts at... preventing speciation (and cladogenesis in general): each such event would mean **extinction** of one “*monophyletic unit*”, i.e. one taxon! By the way, I am unable to imagine how “*paraphyly may lead astray even the most well-intentioned ecologist*” [CARVALHO et al., 2007: 142], unless that ecologist is **unaware** of the existence of paraphyletic taxa!

Generally: what is the scientific (or even only biological) value of a “classification” containing [**by definition**: see the detailed discussion in HOLYNSKI, 2005] **no** information beyond that (on few “synapomorphies” important for phylogenetic analysis but usually trifling from any other point of view) provided already (**in more exact form!**) in the “original” (cladogram: somebody’s current idea about **one aspect** – branching sequence – of evolutionary history) from which the uncritical “translation” (cladistic “classification”) has been automatically made?

You write [EBACH & CARVALHO, 2010: 165] that “*paraphyly*” [*i.e.* acceptance of biological **facts** – “*Latimeria looks like a fish, tastes like a fish, behaves like a fish, and thus – in some legitimate, exceeding narrowly understood tradition, sense – it is a fish*” (GOULD, 1991)] “*is nothing more than an indication of poor taxonomy*” – don’t you see that **really poor** taxonomy, a kind of religion rather than science, is just such formalistic, rigid adherence to some preconceived dogmas (interpreted, at that, on shifting sands of one of actually fashionable phylogenetic hypotheses!) with scornful disregard to biological reality? You write – justly! – that taxonomy is not just a service to “*end-users*”, why do you wish to reduce it to nothing more than a technique of describing in words (names) the (partial) results of phylogenetic studies? It is a separate independent branch of science whose main purpose is to formulate, in form of natural classifications, hypotheses on the structure of living world (the **results** of evolution). “*Taxonomists must ... remain focused on substantiating the ‘general reference system’*” [CARVALHO et al., 2008] – and the reference system to be “*general*” must maximize the information content: the only meaningful definition of “*natural*” classification is “*that of maximum predictive power*”!

However, rejection of treating taxonomy as only a service to end-users does not justify disregard to the situation with the **object of our own research**, so it is impossible to agree with such statements as “*cataloging all life because of a biodiversity crisis is sensationalist and defeats the purpose of taxonomy and systematics*” [EBACH & CARVALHO, 2010: 166]: the “*purpose of taxonomy and systematics*” **is**, indeed, the study of biodiversity – including *cataloging* [possibly] *all life* – and so we **must** “*hurry up*” to catalogue as many taxa as we can before they disappear forever [of course, by “*cataloguing*” I mean “*discovering and describing what is not yet known*”, rather than simply preparing a list (like “*ZooBank*” proposed by nomenclaturists) of names already introduced!]. By the way, I do not think it fair and correct to stigmatize the opponents and their views with brands like “*sensationalist*”, “*fundamentalist*”, “*instrumentalist*”, *etc.* – having criticized [EBACH & CARVALHO, 2010: 167] the style of argumentation where “*ideas diverging from the held belief are immediately labeled as ‘typology’*” you would be expected to avoid this style yourself.

As mentioned above, information content (and consequently predictive power) of simplistic, mechanically translated from cladograms, cladistic classifications amounts to zero, so they are evidently not “*natural*” what makes the application of CEM [“*Cladistic Enterprise Model*”] to **taxonomy** (or anywhere **beyond phylogenetics**) – to apply your (EBACH & CARVALHO, 2010: 176 resp. 171) formulations – “*anti-intellectual ... characterized by non-scientific aims and methods*”, using “*scientific arguments to justify what is essentially poor practice*”! Those who adhere to the truly informative synthetic classifications are usually – contrary to your [EBACH & CARVALHO, 2010: 166] accusal – no less “*trained on phylogenetics*” than advocates of cladistics, and have no problems with “*understanding why the groups they wish to preserve are not holophyletic*” [**monophyletic** these taxa are!]; they only wish to produce meaningful “*general*”

reference system' allowing the (morphological, ecological, physiological, genetical, or any other) characteristics of an organism to be predicted, as reliably and exactly as possible, from its systematical position. Of course no such **general** reference system can be ideally informative for any **specific** question, maximization of the "summary" predictive power unavoidably compromises precision of information on some peculiar characteristics of some aberrant taxa, but this is anyway incomparably more than what can be offered by cladistic classification, "exactly predicting" [in fact only – imperfectly! – translating from the respective cladogram] the single "trait": the branching pattern... It is also true that synthetic systems are subjective, not "rigorously" substantiated, *etc.* – indeed, as you [CARVALHO & EBACH, 2009: 467] aptly observed, "*systematics is an intuitive activity in which knowledge is acquired through experience ... through interactive observation of organisms. ... This "gained experience" will then accrue into an intuitive appreciation of an organismal collective, in embryonic conception of relationship (i.e., homology, taxa)*", and just this involvement of "learned intuition" makes it not "anti-intellectual"); as "no two specialists are entirely alike" [CARVALHO & EBACH, 2009: 468] it is natural that we typically have several competing classifications of any group simultaneously.

You are right, due to "*cost-cutting and time-saving advances*" followed by "*losing specialists and the resultant knowledge of organism*", there indeed seems to be "*an inverse relation between knowledge and molecular data – with every new molecular systematic analysis it seems as if we know less about the organisms we study*" [CARVALHO & EBACH, 2009: 468], but spreading of cladistic dogmas [by the way, often motivated similarly to barcoding: to paraphrase your statement (CARVALHO et al., 2008: 154), "*recent criticisms of [synthetic – RBH] taxonomy appear to be self-serving, concealing an agenda – the promotion of 'quicker', mechanized methods for taxonomic research*"] has similar effects! As noticed by WINSOR (2009: 43) "*nowadays some students receive the impression that little of value was understood about systematics before the revolution begun by Willi Hennig*"; in my opinion, the "HENNIGIAN revolution" has been just one of the factors **undermining the position and hampering the development** of systematics, and we would now know **more** of value about studied organisms had the German author **not** introduced confusion in clear adequate rules based on the Modern Synthesis. HENNIG's work, being – to paraphrase Samuel JOHNSON's words (as quoted by WILL et al., 2005: 844) – "*both new and good, but what's new [cladistic classification – RBH] is not good and what's good [cladistic principles in phylogeny – RBH] is not new*", has (contrary to common belief) not changed very much in **phylogenetic** analyses [*"the most dramatic departure of cladistics from previous systems has not at all been on phylogeny reconstructions"*] (STUESSY, 2009: 72); currently applied computerized phylogenetic procedures – the only, partial, exception known to me being my MICSEQ – are in fact almost purely phenetic: we do not use previously discovered synapomorphies to disclose the ways of evolution, but identify synapomorphies from previously reconstructed phylogeny...]; however, its impact on **taxonomy** has been truly revolutionary – and, as such (revolutions are generally much more efficient in destruction than in building the promised "better"), **disastrous**. 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: 54); depriving classification of this most important quality, cladists in fact deny its very *raison d'être* (cladistic classification which – by definition! – does not convey **any** information beyond that already, **more clearly and more exactly**, readable from the cladogram it

is rigidly based on, is patently superfluous...!) There are also two “side-effects”: 1) all that makes our disputes – in the eyes of non-systematists – remind of those between medieval scholastics as to how many devils can stay on tip of a needle, our conclusions (sparrow is a dinosaur, *Latimeria* is more closely related to elephant than to herring or salmon, *etc.*) bizarre and ridiculous, and all systematics an *art pour l'art* without much relation to reality; 2) acceptance of simplistic formalism (automatic translation of cladogram into classification) in one aspect of taxonomic research paves the way for simplistic formalisms in other situations (*e.g.* DNA Barcoding Enterprise), leading by common effort to following (or similar)

Non-luddite recipe for a modern efficient taxonomy

[compiled from commentaries of funding agencies, editors, peer-reviewers etc.]

Collect one-one specimen of two-three (out of 100 known) species, send to a laboratory to obtain partial sequence of this or that gene, download from GenBank more or less equivalent sequences of yet three allegedly (even if uncontrollably) well determined species, put them into computer; after performing the alignment with PerhapsFit2009 choose the Abrakadabra version 3.ac, command preprapro*xy to obtain 123456 equally parsimonious trees: apply Tratatretre 5.2a for a full consensus tree, then Hurumburum-test with Maybegood correction for Whynotthis model selected by Iknowbetter(spec) will tell you that the Makebelieve's sigma-tt is 0.73 what corresponds to 132% support for the clade Q; print it out with Hokeypokey ZW, describe the cladogram with words and call the result “classification” (don't bother with information content or predictive power: the assumedly apomorphous curvature of seta on last antennal joint is “predictable” from the cladogram, all the other characteristics of involved taxa being by definition not interesting). Don't think (thinking is subjective), don't take external evidence into consideration (this would be preconception), don't try to reconstruct ancestors (ancestors do not exist, only descendants do!), this will release you from any temptation to ponder whether these (non-reconstructed because non-existent) ancestors could have ever been viable or where they might have occurred (modern scientist does not dabble at subjective *ad hoc* conclusions), don't present any own interpretation (speculative scenarios are unscientific), don't question results disagreeing with commonsense (commonsense? – oh, how primitive...), proudly proclaim that you have just falsified the old-fashioned view (resulting from two centuries of useless archaic activity of “morphological” taxonomists) that tiger is a member of **Felidae (Mammalia)**, as your rigorous analysis has shown that it cladistically belongs to flatworms where – together with green hydra and swallowtail – it should be grouped into a new phylotaxon **Paranormalomorpha**. Now submit the paper to SkyreachingImpactFactor journal from the newest Philadelphia-list, and wait for the well deserved Nobel Prize!

Caricature? – of course! But already long ago LEVINS & LEWONTIN (*teste* WILLIAMS, 1988: 417) stated that “... *most science in the western world is already merely a caricature of what science should be, ..., and that in the non-western world is simply a caricature of a caricature*”; now the difference between West and East largely disappeared: everywhere dominates a caricatural version of the caricature of a caricature...

Unfortunately – and here again you [CARVALHO et al., 2008: 155] are perfectly right! – “... *systematists must bear some blame ... as well – qui tacet consentire videtur (he who keeps silent is assumed to consent). ... coherent remarks of Crisci (2006a, p. 219) ... ‘... the climate of opinion depends upon who speaks and who keeps quiet, ... editors, peers, administrators, and policy-makers become enforcers of a vox populi vox dei [in support of] molecular systematics’, ... leading to a ‘new kind of superficiality ... where technological advance is equated with conceptual progress’*”.

Indeed, “*how is it possible, in science, for superficiality to be so in vogue? For propaganda to outfox common sense?*” [CARVALHO, 2009: 18]???

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