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Taxonomy and the Mediocrity of DNA Barcoding – Some Remarks on Packer et al. 2009: DNA Barcoding and the Mediocrity of Morphology

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> Abstract

The paper is a reaction to that published by Packer et al. (2009, Molecular Ecology Resources 9, Suppl.1: 42–50), depreciating the value of traditional – especially morphological – data in taxonomical studies as "mediocre" and boosting instead the simplistic 'barcoding' procedures as "obviously efficient". Having explicitly stated my – as a 'traditional' taxonomist – 'decalogue', I show that accusation of "lust for monopolization of knowledge" and "vociferous hostility" towards the adherents of an alternate approach is glaringly misdirected by Packer et al. and in fact fits much better the attitude of 'barcoders' themselves; while point-by-point evaluation of the arguments and examples set forth by them allowed to refute both their main claims and confirm once again that morphological data, far from being accusable of "mediocrity", still usually (some special situations excepted) provide the most reliable source of evidence for taxonomic conclusions, whereas simplistic 'barcoding' is obviously inefficient in basic research (as opposed to some practical applications) and thence unqualified for the role of anything more than occasional preliminary 'proxy'.

> Key words

Barcoding, basic research, morphological data, taxonomy.

To paraphrase a once heard '*bon mot*': if you, taxonomy, have friends like Packer et al., you need no enemy… Nowadays taxonomists interested in entire organisms, and not only in their molecules, everyday read and hear more or less open, more or less coarse, more or less clever attacks on their work and on taxonomy in general, but I have rarely met a so craftily constructed one as this! The authors (apparently to avoid eventual accusation of partiality) several times declare that they appreciate the importance of 'traditional' taxonomy, consider DNA-barcoding as a supplement and help rather than replacement of morphological studies, and do not wish or expect elimination of taxonomic education and research – but these empty words are made here and there deeply in the text, while at prominent places marketing slogans of quite different meaning are displayed: "*mediocrity*" of morphology in the title, "*small but vocal community*" of "*critics*" in the abstract, demagogical 'strawmen fight' throughout the paper!

The favourite trick of Packer et al. is what Polish people call "*turning the cat with its tail forwards*": vehemently attacking morphologists for what in fact is the typical behaviour of '**molecular**' (and other 'modern') biologists. One characteristic example is just the frequently repeated phrases like the above-mentioned "*small but vocal community*", "*vehemence of criticisms*", "*rancour of the debates*" etc., presenting them as the attitude of traditional taxonomists hostile to modern techniques and wishing to eliminate them from scientific practice. In fact [as is easy to ascertain by reading taxonomic publications or – still much more convincingly – 'peer-reviews' of submitted manuscripts (or especially of applications for grants)], if 'molecularists' would be only as "vociferous" and "hostile" as are defenders of morphology, the two 'camps' would have lived in peaceful coexistence, fruitfully cooperating, and no "rancour" whatsoever would have ever developed! Of course, when a 'morphotaxonomist' heard or read hundred times that his work is "*XIX-century philately*", when he tried many times to publish his paper in a well-known journal but always in vain because his work was not based on molecular characters, when his grant applications are se-

rially rejected as "*outdated hobby*" "*not worth spending tax-payers' money*", no surprise that he becomes 'hostile' and sometimes makes spiteful remarks – but even so I have never met anybody who would seriously propose to dismiss, cease to support, or otherwise discriminate molecular studies: contrary to 'barcoders', we only try to defend our own right to perform ***honest, sound*** taxonomic work from – alas! increasingly successful! – lust of 'molecule-worshippers' for "*monopolization of knowledge*"!

The 'body' of PACKER et al.'s paper consists of a mixture of demagogical formulations, strawmen, true but misdirected statements, disdainful invectives ("*old-fashioned eccentrics working away in dusty museums*"), etc. It is difficult, e.g., to believe that the authors do not grasp the difference between the ***science*** of taxonomy and ***application*** of its achievements to identification of disease-virus vectors or crop pollinators (the less so that they even emphasize the distinction where it is convenient to them, as on p. 48), but most of their arguments for the superiority of barcoding or "*mediocrity*" of morphological taxonomy are supported just with such 'practical' examples! Equally hard to believe is that they are truly unable to understand that selection of a single invariable and/or otherwise most suitable feature ***for the identification key*** does not mean that other characters were disregarded or that "*the range of intraspecific variation … is ignored entirely*" ***in taxonomic considerations***: such is indeed the attitude ***of barcoders***, glorifying the "*obvious*" "*efficiency of using a minimalist, standard fragment approach*", while among 'morphological' taxonomists this became 'outmoded' since at least half a century: selection of a key character is typically the result of examination of (and assessment of variability among) ***all*** observable features of ***many*** (often thousands) specimens of ***many*** (often hundreds) of species from ***throughout their distribution areas***! Or are the authors indeed unable to distinguish between ***discovering*** a difference between few representatives of two populations and ***interpretation*** of this difference as proof of ***specific*** distinction, do they really believe that e.g. American Indians and Europeans belong to different species because they differ in many ways, or do they think that ***intraspecific*** differences do not occur among molecules? Reading their comments, one could suspect that PACKER et al. do not really know what they are speaking about – as this is evidently not the case, how can we interpret their claims?

Let me begin with the statement of my own 'decalogue' (similar, to my best knowledge, to the position of almost all 'traditional' taxonomists):

(1) For some ***practical*** purposes like routine discrimination between few morphologically similar species in ecological studies, medical diagnostics, etc., 'barcoding' ("*using a minimalist, standard fragment approach*") may certainly be helpful; what the "*vociferous critics*" claim is only that this is ***not*** taxonomical ***research*** but ***application*** of its ***results*** to other tasks (including ***other*** – non-taxonomical – research).

(2) Identification of fragmentary material (e.g. subfossil 'debris', decomposed content of a bird's stomach, etc.) is indeed often very difficult to reliably do based on morphological traits; in such cases analysis of molecular sequences (or even, in routine work – mainly when but few species come into account – single-sequence 'barcoding') may, of course, be very helpful; but these also are ***not*** cases of ***research in*** but ***applications of*** taxonomy to ***other*** problems.

(3) Sometimes molecular analysis may be the most convenient way to clarify the taxonomical assignments between sexes, developmental stages, castes etc., and then the proper – as established on the ground of these studies – 'barcodes' may, if necessary, be applied as in (1) above.

(4) In some cases the observed difference between 'barcodes' might be the first ***suggestion*** that our actual taxonomic interpretations (as to e.g. conspecificity of two populations) ***may*** be wrong – but this must be tested with ***more comprehensive*** evidence (crossbreeding, ecological, ethological, biogeographical, other molecular, and/or any available data, of which in the majority of situations morphology is the most convenient and reliable).

(5) In some groups (e.g. bacteria or nematodes) taxonomically useful morphological characters seem very scanty and unconvincing – there also molecular analysis may be the most promising tool, but the studies should be based on ***as extensive*** sequences of ***as many*** genes from ***as many*** individuals representing ***as many*** populations as possible, and results tested against other (ecological, biogeographical, available morphological) information, not just restricted to comparison of few 'barcodes' and counting of 'percents of bp difference'!

(6) The same applies to 'sibling species', allegedly indistinguishable by morphology [though this in most cases means only insufficient observation: more detailed study usually reveals – often very clear-cut and stable – (sets of) diagnostic characters. As a good example may serve the Cyclopidae (Crustacea: Copepoda): until the mid-1980's the genus *Mesocyclops* was considered to include some 40 species, less than 10 were known from the Indo-Pacific Region, and even the majority of these were treated as synonyms of *M.*

leuckarti; then VAN DE VELDE (1984a,b), in her revision of African species, introduced the pattern of distribution of small setulae and spinules as diagnostic traits, and application of these 'microcharacters' by other students revealed that *M. leuckarti* occurs only in the Palaearctis, that SE-Asia is inhabited by more than 30 species (HOŁYŃSKA 2000), and that not only the genus *Mesocyclops* but also other Cyclopidae are much more speciose than hitherto believed (e.g. in *Mesocyclops* ca. 70 species are currently distinguished – HOŁYŃSKA et al. 2003) – all this by the "*mediocre*" morphology: no 'barcoding' (or any sophisticated molecular analysis whatsoever) was necessary!]

(7) In the overwhelming majority of actual cases, morphological characters (based on examination – by ***many*** students since the time of Linnaeus or even before – of ***all*** visible traits of ***scores*** of individuals from ***all*** the known distribution area of ***all*** representatives of the group in question, and interpreted according to the experience gathered during ***centuries*** of taxonomic work) are even 'by definition' evidently more reliable than few sequences of one-two-three (rarely more) genes (to say nothing of ***one 'standard'*** sequence of ***one*** gene...) from rarely more than few (and ***anyway*** less than is available for morphological observations) specimens of rarely more than a small 'sample' of relevant taxa, evaluated according to the (for a while fashionable but frequently changing – see e.g. BALLARD & RAND 2005; BIÉMONT & VIEIRA 2006; CHECK 2006; TINN & OAKLEY 2008; WHITE et al. 2008; etc. as examples of various aspects) allegations of a very young discipline! As morphological traits are also incomparably more convenient (in 'my' **Buprestidae** I can check the 'state' of an 'average' character on tens or even hundreds of specimens in a minute; specialists of other taxa may need more time, but anyway much-much ***less*** than is conceivable for DNA sequencing), the 'supremacy' of morphology ***in taxonomical research*** is in case of most groups of animals and plants incontestable (CAMERON et al. 2006; LÜCKING 2008).

(8) The cause of slow (in relation to the needs) progress in taxonomic studies is not the alleged "*mediocrity*" of morphology but its ***discrimination***: even now – in the time when "*museum tradition is not dying – it is being killed*" (OLSON 1981); when most 'high-ranked' journals do not accept taxonomic (especially descriptive) papers for publication; when evaluation of scientists' work is based on completely irrelevant (and especially disadvantageous for taxonomists) formal 'indexes' like the ill-famed Impact Factor [see e.g. GUERRA-GARCÍA et al. 2008; KRELL 2000, 2002, 2006; VALDECASAS et al. 2000; WERNER 2006 (biodiversity studies), WIŚNIEWSKI 2006 (humanities); etc.]; when taxonomy is practically eliminated from university education; when answer to the question "*how many taxonomists are employed*" in a major Natural History Museum is usually something like "*20 years ago we were 30, 10 years ago 15, now remained 5*"; when more and more restrictions make collection, transport, exchange of specimens costly, difficult, and often impossible [to the point of total absurdity, as in the case of that "*group of entomologists*" collecting for study "*some dangerous groups of mosquitoes, especially those responsible for dengue fever*" that "*was taken to jail in handcuffs while working on Palawan ... Their ambassador had to travel down from Jakarta to secure their release. They left behind 22 vials of dead mosquitoes in alcohol – which presumably now are in the "black museum" of the environment department as a major triumph*", while "*At the same time Manila was plastered with posters on how to kill as many mosquitoes as possible in dozens of ingenious ways*" – LARSEN 2005]; when it is easier to receive 500 000 (in whichever currency) support for molecular 'phylogeography' of (say) Polish populations of *Ixus ypsilonius* than one tenth of that for comprehensive revision of a family containing hundred species; etc., etc., etc. – even in this situation most of the taxonomic work is done by 'morphologists', most of the progress in biodiversity knowledge is the effect of their work, and indeed even the most valuable taxonomic results of ***molecular*** studies are almost invariably those evaluated on the background of (simultaneously or separately performed) analysis of ***morphological*** data (cf. e.g. BROOKS et al. 2007; FREUDENSTEIN et al. 2003; GATESY et al. 1999, or case studies by BRÜSTLE & MUONA 2009; GATESY & ARCTANDER 2000; MEIER et al. 2006; MESSENGER & MCGUIRE 1998; SEIFERT & GOROPASHNAYA 2004; TREWICK 2008; WYNGAARD et al. 2008; etc.); "[in] *all molecular systematic studies, the strength of interpretation relies on comparative morphological data to make biological sense*" – HUYS et al. (2006)!

(9) Taxonomy is not only the starting point for any other research in biology (the results of our work are evidently meaningless if we do not know what plant or animal are we speaking about), but is also the Great Synthesis of all biological research: classifications are (or at least should be…) 'natural', i.e. maximally predictive (HOŁYŃSKI 2005), and to be such they must be based on ***all*** available knowledge; attempts to reduce taxonomic studies to counting 'molecular distances' between small fragments of DNA-sequence transform one of the most fascinating branch of science into "*what is our little Johnnie's idea of scientific research*".

(10) DNA-barcoding – like its commercial 'elder brother' – may be useful to provide a 'label' mark-

ing the 'product' previously identified, analysed and evaluated with appropriate more reliable methods, eventually as a 'key character' used in a ***well-studied*** group where its diagnostic value had been established and verified as a result of ***comprehensive*** ('total evidence') taxonomic research, but 'in itself' may at most be considered as a first signal suggesting the need for closer examination of the case ("*Molecules give added scope, but will never serve as a replacement for a taxonomy based on two centuries of careful examination of phenotypes*" – Kannan 2007).

To sum up: neither I, nor any of the 'traditional taxonomists' whose opinions are known to me (from publications or personal contacts), consider molecular studies (or even 'barcoding') ***as such*** useless or dangerous (either for science or – despite Packer et al.'s insinuations – for ourselves); none of us wishes to deride or disdain molecular studies (the "*mediocrity of DNA-barcoding*" in the title is also only a 'paraphrased quotation' from the ***intentionally offending*** expression used by Packer et al.). We are only convinced that each approach should be applied ***where it is appropriate*** but becomes ***dangerous*** (both to some scientists and to ***science***!) if applied ***elsewhere*** – especially if used to "*monopolize the knowledge*": to discredit and eliminate others! ("*New idea that DNA barcoding can replace normal taxonomy for naming new species and studying their relationships is worse than bad, it is destructive*" – Will et al. 2005.)

Let me now turn to some specific questions raised, or formulations used, by Packer et al. (2009).

"*DNA barcoding now seems … a threat because it has the potential to dissociate the morphological taxonomist from the entire process of organismal identification*". Barcoding has ***no*** such potential [it "*can function only as an identification* ***tool*** *– a* ***by-product*** *of a classification system* ***established in a traditional way*** *– but not as a taxonomic system itself*" (Vogler & Monaghan 2006; bold-face added by me: RBH)]. Unfortunately, however, 'decision-makers' have (and make use of! – Hołyński 2008) the potential to ***replace taxonomy with barcoding***, i.e. to transform science into a formal 'game' (like playing patience), pushing it back by centuries to the time of "VIC-taxonomy" (Hołyński 1993; VIC for Very Important Character) when taxonomic decisions were based on single feature (now it would be an arbitrarily chosen DNA-sequence), and even the basic taxonomic unit – species – was not a "*fragment of evolutionary lineage*" but assemblage of individuals differing in a VIC from others to the arbitrarily fixed degree (in case of barcoding: 'molecular distance')!

"*For the better-known taxonomic groups … surprisingly large sequence divergences within 'species' generally occur where subspecific differentiation have been postulated or where previously differentiated species had been (incorrectly) synonymized by other workers*". Exactly as expected: ***molecular*** differences of potentially taxonomic significance are most often found where ***morphological*** ones had long before been established – only (perhaps because of insufficient information as to e.g. reproductive isolation) there are various opinions as to their (easier for 'barcoders', who largely ignore such 'subtleties'…) ***interpretation*** as of specific *vs*. infraspecific value (*Hybridisierungen, ökologischer Ausschluss und/oder kleinräumige Sympatrie und/oder Allopatrie sagen über den biologischen Status ... neu definierter Arten erheblich mehr aus als ... eine DNA-Sequenz allein, nach der letztlich zu oft entschieden wird*" – Martens & Bahr 2007).

"*Deep divergences indicate a lack of genetic cohesion among reproductively isolated taxa*". "Deep divergence" ***may***, but ***not always*** does, indicate reproductive isolation; 'traditional taxonomists' have long since been aware of this fact…

"*Traditional taxonomic methods have been remarkably successful in describing the diversity … In the past 250 years, the number of known animal species has increased from about 4400 … to approximately 1.5 million … our understanding of the higher-level classification … is both impressive and fascinating*". Stunningly efficient is this "*mediocre*" discipline…

"*This biodiversity crisis has been recognized by traditional taxonomists and armies of newly trained experts have been called for … These calls have largely been ignored*". And ***this*** is the problem! If molecular biologists do ***earnestly*** wish the acceleration of biodiversity studies, they should immediately switch by 180^0 from proclaiming "*mediocrity of morphology*" to joining the 'traditional taxonomists' in the call for ***more jobs, more funds, more opportunities*** for those able and willing to do ***sound*** systematic work (Ebach & Holdredge 2005; Hołyński 2001, 2008; Wheeler 2008)! "*We need only remove the obstacles from taxonomy, fund and encourage its independent practice, enable its logical international and inter-institutional connections, and get* [out] *of its way in order to witness the greatest advance on our knowledge of species and characters in history*" – Wheeler (2009).

"*This* [rarity of repeated revisions] *suggests that the taxonomic community considers re-revising a previously studied group to be an unnecessary duplication of effort*". Sorry for the 'invective', but this is so glaring nonsense that I do not know how to com-

ment… The only thing that this (justly!) suggests is that there is a ***too little number*** of sufficiently experienced taxonomists to be able to perform ***even the first*** revision of all large groups, the more so that e.g. an application for support is more often than not put off as "*low priority project*" ("*Instead funds flow to the latest molecular techniques that we seem to do only because we now can, not because they offer improved estimates of species or reference systems*" – Wheeler & Valdecasas 2007)!

"*Nonetheless, when subsequent researchers re-examine a species or a group of species, they often make different decisions from those of earlier researchers*". An extremely strange 'reproach'! This is ***normal*** situation in ***all*** sciences (successive molecular-based phylogenetic analyses on the same taxon usually also differ in at least part of their resulting trees, and often differences are even fundamental): scientific 'decisions' are not dogmas to be worshipped but hypotheses to be tested and further developed. Darwin arrived at different conclusions than Lamarck; Einstein modified the 'laws' formulated by Newton; what few years ago was considered 'junk DNA' is now known to play a very important role (Andolfatto 2005; Check 2006, 2007); in 2000 one eminent geologist (R. Hall, pers. inf.) told me that between New Caledonia and New Zealand no extensive land existed in the last 50 million years, in 2006 another team (Meffre et al. 2006) published the opinion that a large island was there emergent, one year later still another scientist (Schellart 2007) wrote that it was not one large island but a chain of small islands. It would be extremely strange if just in taxonomy opinions of subsequent students would be always the same as those of their predecessors [or even their own views formulated earlier: "*If somebody shows me a scientist who wrote something in 1968, and now still writes the same, I will say that he had met a fool*" – Paul R. Ehrlich (quoted – in my retranslation – after Lewis 2000)]!

"*That different individuals come to different conclusions with the same material at hand is particularly worrying when one considers that whole large groups of taxa have often been revised by only one author. … This suggests that the idiosyncrasies of individual taxonomists are likely to have a large impact …*". So, ***what*** is "*particularly worrying*": that "*idiosyncrasies*" of ***one*** taxonomist may cause a ***single*** opinion to "*have a large impact*", or that in other groups ***several*** workers express ***disparate*** opinions? By the way, the "*material at hand*" is very rarely the same: usually the later student (even if the same person!) has access to some material (e.g. newly collected) not accessible to the previous one, sometimes the opposite is true, often both; moreover, their background knowledge is different, they use different methods, etc. – these are just the sources of progress in science! As to the single expert in a group – see above remarks on biodiversity crisis and rarity of repeated revisions!

"*The independent data that barcoding provides is … a useful calibration of the inherent taxonomic uncertainty*". If used as ***one of many*** 'calibration points' it of course may be useful, but as 'the' (or main) calibration point it is obviously no more qualified than e.g. single word in various languages for 'calibration' of linguistic hypotheses.

"*DNA barcoding often speaks loud and clear while morphology is mute*". If "loud and clear" would be synonymous (or even but highly correlated) with "reliable", this would be a very nice argument – unfortunately more often the opposite is true (e.g. Seifert & Goropashnaya 2004; Song et al. 2008; etc.)! In cases where morphology is ***indeed*** "mute" [but see above point (6) of "my decalogue"] an extensive analysis of ***as many*** as possible ***carefully – for that specific purpose – selected*** DNA sequences from ***many*** specimens may indeed be most appropriate, but certainly not (in such situation ***especially not***!) a minimalistic, 'standard' VIC-barcode!

"*In other instances, morphology has something to say, but stating it in a key is often less elegant than with a good DNA sequence*". DNA sequence as an "*elegant*" key character??? Somewhat strange notion of elegance, but… *la question de goût*! However, a key must be first of all ***reliable***, then it should be ***convenient***, and only when these conditions are satisfied we can consider the 'elegance'…

"*Species level identification of fish fillets*", "*monitoring water quality*", etc. These indeed are problems for which 'barcoding' may be appropriate – but have glaringly little to do with ***taxonomic research***!

Halictus ligatus as "*an impressive example of the failure of morphology*" – see above points (5) and (6) of the 'decalogue' and e.g. the remarks on "*deep divergence*"!

"*Bad taxonomy is often all we have available*". Yes, sometimes we are in such situation. However: **(a)** this is the failure of some ***particular taxonomist***, not of ***morphology***; **(b)** poor ***molecular*** works are at least as common [and can lead to disastrous results, as exemplified by Buhay's (2009) somewhat surrealistic but highly symptomatic experiment "*I used a subset of*" a dataset from a published phylogenetic analysis "*and added my favourite recipe for pumpkin pie (imagine it is a numt sequence or junk DNA) to the nexus*

file ... executed the file and"... 'demonstrated' (***with 100% bootstrap support!***) that her pumpkin pie belongs to the genus *Orconectes* (Crustacea: Decapoda: Cambaridae) and is the sister species of *O. burri*!!! I cannot imagine a similar result of, however (inadvertently or purposefully) erroneous, analysis of ***morphological*** data...]; **(c)** one of the main causes of poor work is lack of serious taxonomic education at universities, the other – policy of 'science managers' promoting 'rat race', short-time grants (three years is almost the upper limit, while ***good*** revision of a "*large genus … with 600+ species*" evidently cannot be done within this time) and ridiculously inflated bureaucracy (detailed applications, justifications, reports, accounts, etc.) robbing the scientist of a great part of his time. "*Competition is a cheap measure of whatever performance ... and science is too serious a matter for racing contests*" – Rohrer (2006).

"*If morphological variation in a single genitalic structure is necessary for the identification of a large proportion of species in a taxonomic group, is a 5% sequence divergence in a DNA barcode really that much simpler?*". Yes, ***it is!*** Firstly, in the overwhelming majority of cases difference in genitalia is ***not*** "*necessary*", but only ***sufficient*** and considered most ***convenient*** as a ***key*** character among ***several*** (often many) interspecifically variable features on which its ***specific distinctness*** has been evaluated. Secondly, it has typically been checked on ***many*** specimens. Thirdly, the particular trait has been selected, and particular degree of difference evaluated, ***specifically*** for the particular 'couplet'. Fourthly, genitalic characters (and others involved in the SMRS – Specific Mate Recognition System – like nuptial plumage of birds or horns in some mammals and beetles) are very special just because their principal ***biological role*** is to distinguish between closely related species; this is why they usually make the ***first*** difference that appears between a pair of newly evolved 'sister' species (especially when they become sympatric), and often provide the only diagnostic character to identify them. Arbitrarily designated percent of difference in a relatively minute segment of DNA selected as a 'jack-of-all-trades' for identification of everything, evidently ***does not*** satisfy ***any*** of these conditions…

"*The possibility that intraspecific genitalic variation causes trouble for identifications has received almost no attention, although such variation does exist*". Gospel truth! Some 'morphologists' have also the tendency to consider this or that fashionable character-set as the 'all-decisive' VIC, and genitalia are among those most frequently chosen for this role. But exactly the same can be said of molecular characters, e.g. barcodes ("… *it is important to point out that although gene homogenization appears to be the rule, intragenomic variation is known* [what] *may have implications for the extent and mechanisms of concerted evolution and will introduce some degree of caution in using rDNA for phylogenetic analysis*." – Carranza et al. 1996; "… *in recently published molecular analyses usually data quality is not evaluated independently of tree construction*" – Bäcker et al. 2008; see also e.g. Meyer & Paulay 2005)!

"*It is perhaps ironic that new species are readily described on the basis of subtle morphological variation, yet there is general reluctance to describe species on the basis of genetic evidence alone, which suggests that data chauvinism … is alive and well within the taxonomic community*." First of all, we must clarify what are we speaking about: Packer et al. – like other molecular biologists – misuse the term "genetic", which originally means "*referring to genes and effects of their action*", but here it is meant as a synonym of "*concerning base-pairs*", i.e. in fact ***phenetic*** at the molecular level! Molecular characters ***alone*** are not considered sufficient to make taxonomic decisions **(a)** because reliance on single type of features is to be ***generally*** avoided; **(b)** because "*even a single morphological character in most cases is likely a summary of many genes and thousands of base pairs, filtered by eons of natural selection and canalized by the hierarchy that results from a history of common ancestry. Such a rich, highly predictive, broadly explanatory understanding of species ... offer an imminently more interesting and powerful approach to taxonomy than the comparatively easy but relatively uninformative and phenetic barcoding alternative*" – Will et al. (2005); **(c)** because – as already explained at several occasions above – they are almost always based on much less extensive [target- and – especially – comparative] material, represent an incomparably smaller part of potentially evaluable characters, and mainly are practically uninterpretable in terms of function, potential convergence, 'concerted evolution', etc., and thus the relation between molecular difference and reproductive isolation is much more difficult to establish! This is not "*chauvinism*", but wise prudence and realistic evaluation of the ***taxonomic*** value of these types of data ("*taxonomy needs evolution, not revolution*" – Knapp et al. 2002, and our experience and knowledge of the 'behaviour' of molecular features is still far from being even roughly comparable to those concerning morphology).

"*Even the necessary genitalia preparation for a single lepidopteran identification can take a well-trained technician an hour*". And how many hours takes the preparation, sequencing, and nucleotide interpretation of a DNA sample for 'barcoding'???

In fact, genitalia are among ***the most*** time-demanding, but at the same time ***only in some groups*** – and even in most of these ***not always***! – "*necessary*" morphological characters.

"*This* [possibility of quick routine determinations for practical purposes] *suggests the role of DNA barcoding in providing societally useful identifications that will free up traditional taxonomists to do what they alone are exquisitely qualified to do: perform taxonomic revisionary studies*". Well, well!!! So, at last we have arrived at the correct conclusion: ***traditional taxonomists alone are qualified to do taxonomic studies*** and – what is but the straightforward, though unfortunately not always understood, logical consequence of the previous statement – to ***select the most appropriate*** (usually morphological, in some situations molecular, frequently both) type of characters for their studies! Would the authors have ***begun*** with such distinction between taxonomy and 'barcoding', nobody would oppose and neither 90% of their further divagations nor my comments would have been necessary!

And this seems to be the most appropriate conclusion of my remarks.

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