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THE MYTH OF OBJECTIVE TAXONOMY AND CLADISM: MUCH ADO ABOUT NOTHING

Abstract — The Author, taking the opportunity to comment on a paper by Weigoldt, maintains that there can not be objective criteria in taxonomy and suggests that some new rules of nomenclature are necessary to deal with populations which are distinguishable on non-morphologic characters.

Riassunto — *Il mito della tassonomia obbiettiva ed il cladismo, molto rumore per nulla.* L'autore prendendo spunto da un lavoro di Weigoldt discute alcuni aspetti della tassonomia cladistica e conclude che, mentre non è possibile una sistematica puramente oggettiva, sono necessarie alcune nuove regole di nomenclatura per descrivere le popolazioni distinguibili in base a caratteri non morfologici.

Key words — Cladism / taxonomy.

In these last years I have been led by my work on the evolution of Arthropods (SIMONETTA, 1975; SIMONETTA e DELLE CAVE, 1981a, 1981b) to give some attention to the current issue about cladistic systematics. I was and am unconvinced by cladism, but I have long hesitated to write anything on the subject, as I wondered whether it was worth while to record my opinion, as opinions on which I almost entirely concurred were advocated by a number of authorities (cfr., for instance, the recent paper by MAYR, 1981). I have finally decided to write something just because it offered an opportunity to make some practical suggestions in the field of formal taxonomy.

Let us first consider the question whether systematics and taxonomy, this last in the narrow sense of formal classification, may be equated. The obvious answer is emphatically negative and it appears that while systematics is a truly scientific endeavour,

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and possibly the ultimate task of Biology, formal taxonomy is merely a tool or rather one of the languages of Zoology.

Lest this last statement seem outrageous to some fellow taxonomist, we may consider what the systematist is actually doing: he deals with a number of animals, quite often in the literal sense of specimens, and by using all the evidence that he may gather, and this is often quite poor especially for fossils, he tries to assess the mutual relationships and evolutionary past of them. Since evolution and adaptation are the essential features of living things and the systematist should whenever possible use all sorts of available evidence concerning the animals he is studying, he is doing an essential part of Zoology and that which subsumes all the other branches of this science.

But is the systematist bound to classify animals in a formal taxonomic arrangement? This is customary and necessary indeed, but, more often than not, the systematist does not find that any taxonomic arrangement will precisely express his ideas and has recourse to dendrograms and other graphic techniques, to appropriate discussion etc., briefly he writes a paper. This goes far to prove that formal taxonomy is but a sort of « basic » language of systematics, but that, like telegrams, is not suitable to convey complex thoughts and feelings.

We shall come back to the problems of formal taxonomy, but I think that we can be satisfied that systematics and its basic problems may be discussed separately from it.

It is a tautology that systematics is the science (or art?) of arranging taxa in a reasonable order thus improving our understanding of zoological phenomena *sensu latu*. However it is seldom realized that some of the problems that anger many systematists are problems of semantics, that is that we are led into traps by our use of the same words to mean substantially different concepts.

Taxonomists striving for an « objective taxonomy » should realize that there is no way to define what a taxon is. There are indeed blatant differences in what concept is subsumed by the term « species » when we speak of animals which reproduce sexually, purely asexually or only by parthenogenesis, or when we deal with fossils; but it is moreover by no means exceptional that the concepts subsumed may change within the same « taxon » as, e.g. when we deal with the mictic and amictic populations of, say,

Bacillus rossii; the former obviously forming « gene pools », the second as many clones as there are genotypes and new clones arising at any mutation. This is significant also from the evolutionary standpoint as in the mictic population selection operates on gene recombination + mutants, while in the amictic population this works generally only on mutants.

Moreover it is generally agreed that taxonomy deals with populations and not with individuals, but is it always clear what we mean by population? Usually it may be taken to denote an actual genetic pool and/or a number of interacting individuals of the same taxon.

This second criterium may lead to circularity, as the Taxon is precisely what we wish to define, but both criteria may be the object of occasional restrictions and qualifications. So, for instance, both are valid for a species such as *Taeniarhynchus saginatus*, whose adults usually occur in numbers in a single host and whose proglottids may cross-mate with those of different individuals, but they are not for the related *Taenia solium*, which forms self-fertilizing clones and which interaction with other members of its own species consists in preventing them, albeit indirectly, from becoming established in the same final host, so that one might eventually have to speak of a species consisting of one-individual populations! In like manner in the many animals which yearly die just after laying eggs, each year's population is technically a gene-pool of a nature considerably distinct from that of those animal species where there is generational overlap and cross-breeding. And finally, just to make the puzzle more complicated: what shall we think of parasitic birds such as *Vidua paradisaea*, which consist of seven reproductively isolated gene-pools, which however are separated only by a learnt ability: the love song that the males learn from their hosts while juveniles and that allows the females, who also learn it, to recognize the males of their own gene pool, in the meantime they also learn which is the proper nest to lay their eggs, so that the juveniles will have the proper, genetically determined, gular pattern to induce their hosts to feed them, as it mimics that of their offsprings.

We shall see further on other implications of the fact that in different animal groups taxa have a different meaning and that even within the same higher taxon the concepts subsumed in the recognition of the various taxa by which it is formed vary also as a

mere consequence of how much or how little is known about each one of them. Anyhow not only supraspecific taxa, but also these of the species level must be considered to be categories which are subjectively defined.

I strongly doubt that any logician may be able to show that we may have an objective classification of anything that is first subjectively grouped into basic units, except in the sense that it will be possible to attain an arrangement that is not self-contradictory and that is consistent with the subjectively chosen premises.

We may have objective knowledge of facts or rather we may test the objective validity of hypotheses concerning facts and their connections. Thus we may hope to be able to test the objective validity of a supposed phylogenetic sequence, as this may or may not have actually occurred, and we may equally hope for an increasing knowledge of the mechanisms of evolution, as, again, that is something happening; but a classification, unless it purports to be a phyletic classification, is nothing of the sort: it is simply a convenient way of naming and grouping things or, rather, classes of things.

Cladism is actually supposed by its advocates to be a system of classification based on phylogeny, but as it is put by Weigoldt, himself a cladist, in a recent paper (WEIGOLDT, 1979) « the cladistic method was devised for the classification of taxa of a particular geological time level, usually recent taxa. If understood in this way, the statement (\overline{ABC}) has only one meaning; A and B share a common ancestor which is not shared by C. No recent taxon can be the ancestor of another recent taxon, just as an ameba cannot be the ancestor of its sister, even if it looks exactly like that ancestor. By splitting a taxon gives rise to two new taxa, but gives up its existence ».

Now either Weigoldt is wrong in his assumption that the splitting of taxa and their extinction by splitting are assential to the cladistic method, and he is not, or, as this is a false assumption, the cladistic method is necessarily false. *Tertium non datur*.

Most zoologists will no doubt hardly consider seriously extinction by splitting, but, since there is a fair number of cladists, it is worth spending a few words on this point.

Let us first eliminate the comparison with the Amoeba, which is irrelevant and misleading; the Amoeba in this case is an individual while a taxon is a collective entity or-with the qualifications

necessary in some instances — is made up by one or more populations.

The taxa neither do necessarily evolve by « splitting » nor do they become extinct by splitting, as can be demonstrated by a number of examples and I shall quote but a few of them.

In recent years and in a variety of animals, caryological analysis has shown that Robertsonian fusions may well lead to the reproductive isolation of populations, which are unquestionably « taxa » of some sort ⁽¹⁾. It is usual (CAPANNA, 1980, for mice, WHITE, 1978, for Grasshoppers, and many others) to find such « Robertsonian taxa » as islands, or rather as more or less completely isolated demes within or bordering the parent, non-Robertsonian population. True, while Robertsonian taxa were evolving, it may be presumed that also the parent population has evolved somehow, but there are sound reasons to presume that it may still be considered as belonging to the same gene-pool from which the Robertsonian demes have split.

I wish to add that we should also consider the possibility, I think the probability, that some of these reproductively isolated demes may still have a « gene-pool » which is closer to that of some population of the non-Robertsonian demes, than are the gene-pools of some populations of the non-Robertsonian ensemble itself, and that in spite of their not being reproductively isolated.

Robertsonian evolution is just one of the many ways by which a taxon may split from a parent taxon, as it has been shown by a number of geographical, ecological and ethological modes of speciation, and in most cases the «parent species» is happily still living at the same time as many of its « daughter species »; classical examples being provided, for instance, by the well studied insular speciation of the *Drosophils* in the Hawaii Islands or by the different pathways to speciation in Mosquitoes studied by COLUZZI (1979) ⁽²⁾.

Obviously, determined cladists may claim that what we call the « parent species » is itself a « daughter species » identical with the true parent species, but that would be a *petitio principii* and needs not be taken seriously.

(1) They would rank as species according one of the more widely accepted definition of what a « biological species » is. In some instances these populations show peculiar eco-ethological adaptations.

(2) In some instances the daughter taxa underwent ecological specialisation so that they now occupy different niches within the same area at the parent taxon.

Last but not least to dispose of cladism: Henning was not adamant that speciation went always by dichotomies, but most cladists take dichotomies for granted. Anyway in cladism a taxon to evolve must split; now we have some very good records, mainly in Molluscs and in the Oreodonts, of considerable orthogenetic evolution in isolated populations which were subject to constant selective pressure, and which changed their morphology to such an extent that the starting and terminal members of a series are often classified in different genera, *but which did not split at all*.

An incidental problem which I have been unable to solve is to understand how do cladists manage with the, admittedly very rare, taxa which arose by introgression.

That much for cladism as a system of evolutionary classification, but what of some other aspects of this method? To quote again Weigoldt, « If all intermediate forms were not extinct, but alive, there would be no need for an evolutionary or typological classification, because the only method by which a continuum can be classified is the cladistic approach ».

Now a continuum can not be made into discrete units except by arbitrary subdivision, the criteria used being purely subjective or pragmatic or otherwise conventional. Dividing a given length in centimeters rather than inches is anything but a scientific operation leading to the discovery of some objectively testable truth.

We may grant that for some phyla the fossil evidence is either lacking or so poor as to be useless, and what we do are phyletic inferences based on comparative anatomy, embryology, molecular biology and so on; could cladism be useful at least in these cases? Quite apart the consideration that a method based on false assumptions has little to recommend itself, that cladistic taxonomy may be useful even in these cases and in the limited field of « formal taxonomy » is more than doubtful, at is has a sort of built-in drive to splitting, and any excessively « split » classification is quite noxious to zoologists other than some museum-keepers and old fashioned beetle collectors.

Although I feel that the previous arguments should be sufficient for disposing of cladism, it is still worth examining a somewhat sophisticated approach, which has been mainly developed by Platnick (PLATNICK, 1978a, 1978b) in criticism to Bock's defence of classic phylogenetics and of the validity of induction (BOCK, 1977) Platnick's argument runs like that:

- 1) We must reject the notion that systematics is a useful art and not science, as proposed by SIMPSON (1961) and rather strongly maintained by ACKERMAN (1976), or that is merely a technical enterprise as advocated, for instance by SOKAL (1969) and that on two grounds: « A) that it would be difficult to see how a paid professional scientist could then justify spending the bulk of his time on systematics, any more than he could on other useful arts (such as glassblowing) or technical enterprises (such as computer or electron microscope operation) ». B) that « it is possible to make statements that (1) are intended to apply to all organisms, wherever in the universe they may occur, and (2) do not suffer from tautology » and that, under certain conditions and formulations, such statements and hypotheses may be tested by « Popper's paradigm » of falsifiability, thus being qualified to be called scientific theories.
- 2) that we must assume that the only method permissible in science is the hypothetico-deductive method and testing by falsifiability, induction having always to be rejected as being incapable to lead to objective knowledge.

We may well skip as irrelevant Platnick's worries about being paid to produce useful artifacts. Why should they not be paid if they are useful? One feels that what lays behind Platnick's statement is the feeling that taxonomy as an art would be ancillary to the science of Zoology and that would hurt the feelings of a pure taxonomist.

Platnick's points 1B and 2 may be taken together. One must agree that, at least in many instances, it is possible to formulate zoological hypotheses that are both general and not tautological.

However that does not lead us very far, as in all the immense field of comparative morphology and paleontology, typical experimental evidence, such as ordinarily used to test an hypothesis, is barred by the nature of the evidence itself ⁽³⁾. Moreover it will be very rare that only two contrasting theories may be proposed, so that by falsifying one, the other may be considered to be proved.

So, for instance, if we take the positive statement « Evolution has occurred and occurs » it has been argued that it can not be

(3) Obviously this evidence can be considered « experimental » in the sense advocated by WATSON (1951).

either inductively « proved » — by Popper's paradigm — nor it can be disproved. On the other side, as this is one instance of a situation which allows for only two possibilities, as evolution either has or has not occurred, one may think to prove it by falsifying the reciprocal statement « evolution has not occurred ». Indeed the fact that we have a succession of faunas, or, more precisely, a succession of biological taxa through the ages can be taken to falsify any anti-evolutionist statement, provided we use Occam's razor to choose between the hypothesis of countless creations and evolution. This is satisfactory for practically all biologists, as the evolutionary hypothesis satisfies also all genetic, biochemical, etc. evidence, which multiple creationism fails to do, but can not be considered as completely satisfactory from a purely logic standpoint. Briefly the systematic usage of the « Popperian paradigm » will be useful in ruling out a number of theories, but, especially in the field of phylogenetic hypotheses, will leave us with a host possible alternatives.

Moreover is really induction to be rejected as scientifically unsound? I think not and that for reasons that, I concede, somewhat beg the point, but which nevertheless appear worth of consideration. My arguments for induction are briefly the following ones: 1) all that we know about learning in animals (possibly with qualifications as far as man is concerned) is by trial and error and by reinforcement on the evidence of past positive experience⁽⁴⁾, that is by a basically inductive mechanism. This way of operating choices has been selected for more or less in all animals capable of learning even to the extent that, by mechanisms which are difficult to envisage, we have instances of what must have been originally a learnt knowledge being incorporated into the genetic pool, such as, e.g., the recognition of hawks by unexperienced chickens.

Now if selection, operating through hundreds of thousands of years over countless individuals, has just privileged induction, this may only mean that induction, when properly used, provides a sufficiently reliable probability of accurate knowledge.

2) The formulation and selection of testable hypotheses is

⁽⁴⁾ This is disputable in many instances of classical imprinting, as the learned ability is put to test much later in life and, though it has a reproductive advantage, it is perfectly neutral for the survival of the individual.

always based on induction. The mere fact that even in deductive sciences scientist have never worked by screening and testing random hypotheses, goes far to prove that induction is an essential and irreplaceable instrument in scientific thinking and that, while it can be used alone with some measure of success, the hypothetico-deductive system and testing by falsiability are unconceivable divorced from preliminary induction.

The anxious search by many zoologists for objective methods in taxonomy may have some psychological urge; maybe they have not sufficient confidence in their judgement and therefore they strive for a mechanism to substitute for it, so that their conclusions may be safe from challenge and need not conform with facts, but rather with set rules (this applies not only to cladism, but also to numerical taxonomy, biochemical taxonomy etc.). This, however, reminds me that Franz Joseph Haydn, to answer what was apparently in demand in fashionable circles, devised what he called « the play of the menuet »: a simple set of rules by which, taking four notes at random, a complete and correct menuet might be written by anyone. However Hydn's play did not turn parlour amateurs into composers.

In the beginning of this paper I said that I had some constructive proposals and let us now come to them.

Let us then start by the consideration that there is no doubt that efforts towards a « natural » classification of animals have been periodically hampered by the very progress of knowledge, so that a « natural » taxon became increasingly difficult to define, and recently by the realisation, that « taxonomic », or rather « Linnean », species are often, and probably, save perhaps for a few instances of very rare and local species, always made up by a number of subunits of very different significance.

If we agree that real living groups of beings, or « natural taxa », are very complex ensembles with considerable and as yet poorly understood essential differences from one to another, and that the taxa of formal taxonomy may be considered to be the nature of logical operators, the need to devise them such a way as to make them semantically unambiguous is obvious.

Indeed, if the nature of formal systematics is that a language, by which we formalize certain ideas, we may well think how to improve and enrich it. Language being a tool and there being usually a positive feedback between technological and scientific

progress, we may even hope that any improvement in formal taxonomy may pay dividends in the truly scientific field.

Our main problem is the fact that the traditional Linnean species is made of a number of subunits of different nature, which often will not fit with our concept of geographical subspecies.

I feel that what is needed is to recognize the Linnean « species » as a useful convention for grouping a number of more or less known, presumably closely related subunits which may be either geographic or caryological, biochemical, ethological etc. « subspecies » as well as « subspecies » determined by any combination of these factors. Then there is the absolute need to agree to a system by which we may specify, within any context, to which kind of these « subspecies » belong the biological units with which we are dealing, and this could be made clear by different conventional ways of writing or marking the third, subspecific, name of any taxon ⁽⁵⁾, such as using different typographical characters, adding symbols to mark the degree of reproductive isolation etc.

There would obviously remain the problem of how old types and therefore names, can be linked with real individual « subunits », as museum specimens are obviously not liable to the many tests which would be necessary for the purpose. This, however may be done, albeit conventionally, by the traditional method of restricting the type locality, as once this has been restricted to a particular ecological niche in a very precisely and restricted locality it is highly improbable that more than one biological subunit will occur there. This is, I think, the only way to avoid throwing 99% of our nomenclature into the *nomina dubia*.

All that may be attained by limited amendments in the « Rules of Nomenclature ».

To conclude, if a conclusion is permissible, zoologists should recognize that, with such a varied ensemble as the animal kingdom, subject to a multitude of different selective and therefore evolutionary constraints, while the traditional, let us say « common sense » or pragmatic approach to phyletic classification may lead in many cases to testable systematic arrangements, it is highly improbable that there may be any fixed set of rules by which we may hope to get a valid classification.

Figure 1 shows one possible situation and its consideration shall evidence the essentials of our problem.

⁽⁵⁾ Admittedly under this concept « sibling species » will usually merge as kinds of « subspecies » into the « Linnean species ».

Geographical range of supposed Linnean species <u>Xus xus</u>								
Geographical-morphological subspecies	A		B		C		D	
Cariotypes (reproductively isolated types underlined)	T ₁				<u>I₂</u>		T ₃	T ₄
Gene-enzyme patterns	α		β		γ		δ	
Eco-ethological segregation	X		X		X		X	X
	Y		Y		Y		Y	Y
Fossil subspecies							M	

Fig.1 - A hypothetical example of the complicated pattern of taxa which could be shown to exist within a traditional species by using different kinds of evidence. Areas where the species does not occur or is unrecorded: ; areas for which no evidence is available:

Briefly that the old dictum that a valid taxon is that which has been established by a good taxonomist is to remain true.

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