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CIRCUMSCRIBING THE CONCEPT OF THE GENUS

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Summary

The present paper suggests that, despite its conceptual weakness, the cladistic approach to the delimitation of genera contains a valuable logical formalism. This logic could be applied to the dendrogram of the informational (genetic) similarity between the taxa to be classified. Even if this leads to a departure from a purely phyletic model of classification — that cannot be always maintained in a classification because of the internal limitations of the concept of classification — this approach corresponds much better to what we want a classification to be. A logical justification is given to phenetic taxonomy, when properly done.

Résumé

Malgré la faiblesse de son concept de base, le cladisme contient dans sa logique interne des éléments très valables. Cette logique peut être appliquée au semi-treillis représentant la similarité de l'information génétique des taxa à classifier. Une classification ne peut toujours être un modèle évolutif, à cause des limites intrinsèques du concept de classification. Par conséquent, même si l'application de cette logique nous fait nous éloigner du modèle purement phylétique, elle nous rapproche de ce que nous voulons intuitivement que soit cette classification. De ces considérations, nous concluons que les méthodes phénétiques de taxonomie sont justifiées logiquement, lorsqu'appliquées avec discernement.

In a recent paper (Legendre and Vaillancourt, 1969) we tried to show the logical structure of the categories species and genus. The genus was then defined as a monophyletic group of species that occupies a given adaptive zone. However, in order to be logical, we introduced the concept of phyletic closure, by which all the species descending from a common ancestor have to be included in the same genus. We did not realize then that we were falling into the cladistic tendency when applying the notion of closure to the phyletic dendrogram, or evolutionary tree. Many of the following remarks are also applicable to categories above that of the genus.

A biological classification is not intended to be a perfect representation of an evolutionary tree. Such a tree, to be perfect, would have to be drawn in a multi-dimensional, non-euclidian space. On the contrary, a classification is a two-dimensional representation of the relationship between organisms that defines on them a series of partitions of the organisms (vertical axis) in which the groups are ranked hierarchically (horizontal axis), as in the following example:

Family	Genus 1	Species 1
		Species 2
		Species 3
	Genus 2	Species 1
		Species 2
	Genus 3	Species 1

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The classification can be intended to carry infomation on the closeness of taxa, saying for instance that genus 1 is closer to genus 2 than it is to genus 3 (often the case with higher categories); or it shows simply a relation between taxa that allows grouping of them under the next higher category, as is often the case with species that are ranked alphabetically under their common genus.

But what is the relationship that we are referring to, in taxonomy? It is not always a relationship based on recency of common descent. For instance, the modern apes are more closely related by descent to man than to the monkeys. However, we want to group the apes and monkeys in one taxonomic group, and man in another, since man has become fit to a completely different adaptive zone, thus modifying considerably its gene pool.

This example shows that a relationship, which we want to express in a classification, is based not on phylogeny but rather on genetic content or information content of the individual. It is preferable to use "information content" as a general term, since the importance of mutations is difficult to weigh in terms of change in the information-adaptive content of the individual. We do not refer here to genic and chromosomal mutations: the latter group does not necessarily have a major adaptive effect even if it is the type of mutations that lead to internal reproductive isolation, or speciation. We refer rather to mutations in the sense of the geneticist, and not in the sense of the cytologist, as we did in the paper mentioned above.

In the course of evolution, when a group evolves fast to a new adaptive niche, it looses and gains some information in the process. So, its similarity with phyletically related groups decreases.
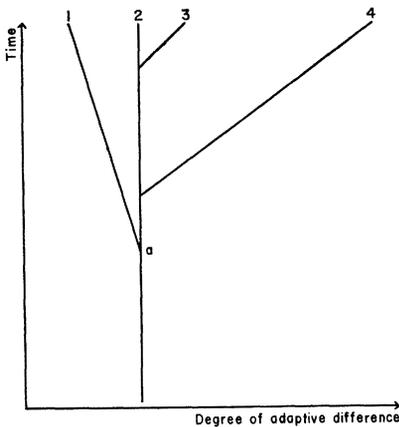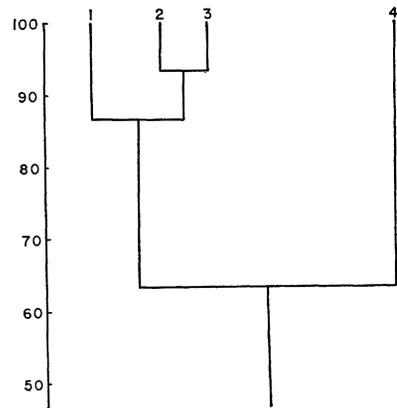

Fig. 1.
Phyletic dendrogram (phylogram).

Fig. 2.
Dendrogram showing in ordinate the degree of similarity between the information content of the taxa 1 to 4.

An example is given in figures 1 and 2. Figure 1 shows the phyletic tree that led to the formation of four species from a common ancestor *a*. According to the generic criterion of phyletic closure, species 1 to 4 would have to be included in the same genus. However, the phylogram shows that species 4 has reached an adaptive zone different from that of species 1 to 3. In the differentiating process, the gene pool of species 4 has gone through a certain

138   TAXON VOLUME 20

amount of change, that allows us to draw figure 2. This figure can be drawn in such a way that the horizontal distance between the taxa is arbitrary, or it can be made proportional to the degree of adaptive difference, as it is drawn here. One has to note that in this case, the supplementary information given about the adaptive difference is redundant to the information carried by the ordinate, since the degree of adaptive difference is proportional to a large extent to the genetic differentiation. Furthermore, assuming that the genetic basis of the difference of the information content is expressed phenotypically, it becomes legitimate to equate the dendrogram of figure 2 to a phenogram based upon the study of many characters.

In this example, we assumed that we knew the phyletic branching pattern of species 1 to 4, even if this information is not available most of the time. We showed however that we do not need this information, since it is not relevant when we are looking for a classification: only the difference in the information content of the gene pools under study is important. If we say now — what seems to be a legitimate assumption — that two closely related gene pools are also closely related in their phylogeny, we can change the expression "monophyletic group of species" in the definition of the genus to "a group of species with a genetic information content sufficiently similar". On the dendrogram of figure 2, we can apply legitimately the concept of phyletic closure that may now be called "informational closure", and then allow the arbitrariness of the worker who will decide about his preference of a big or small genus (in the example, he has the choice of making his genus with species 1 to 3, or with species 1 to 4), considering the material under study. The taxonomist will also tend to make his genus small enough so that the species will show the closeness of their gene pool by a possibility of rare hybridization of each species with at least one other species of the genus.

Most of the time, the material on which the taxonomist works gives information mainly as to its morphology. Assuming as above that there is a phenotypic expression of the difference in information content of the gene pools of the species under study, then, if we make certain that we select sufficiently many characters to cover the phenotypic differences, the methods of phenetic taxonomy can be applied. A remarkably good dissection of this method, extendable to the higher categories, has recently been given by Rogers and Appan (1969).

From these remarks, we may conclude that the evolutionary taxonomist is not looking for a classification that follows exactly the phylogeny: in order to be formal, such a taxonomist would have to be cladistic. Rather, he is concerned with the information content of the genetic program shared by the organisms, the pattern of which can depart from the phyletic tree in some cases. This is, however, what we want intuitively a classification to be, and also what has been formalized by the phenetic taxonomists whose work is legitimate when they consider a large enough number of characters, carefully weighed.

References

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