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Toward a definition of the genus in mycological taxonomy

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Abstract: The author's concept of genus as a biological unit in Agaricales (and presumably in fungi) is stated and discussed with a view of arriving at a general definition of the term. A caveat is added not to underestimate the importance of correct species identification when modern taxonomic methods are presented.

Since more than fifty years I have been particularly interested in the status of the genus in Basidiomycetes. In my last effort, a generic monograph of the Agaricales (Singer 1986), I did not achieve a definition of the word - nobody else did - but I had a concept that served me for the purpose. When I said (in Cléménçon 1977) "my point is that every author is free to use his set of taxa as long as he defines them", I wish to extend that statement from the infraspecific taxa to the genus. He who manipulates generic taxonomy should indicate his or her concept of the term genus. My own concept must have become clear to those who read and use "The Agaricales in Modern Taxonomy", but I shall resume shortly:

A genus, aside from its hierarchical position in botanical nomenclature, is a taxonomic unit containing one to many species; it must, in the first place, be strictly natural (not only in the sense of being homogeneous, but also in the sense that it must not remain separated from other genera which are structurally identical and distinguishable only by a single character state, especially if there are intermediate forms); furthermore it should be separated from other genera by a significant hiatus which, especially in uni-specific genera, must be at least as significant as the hiatus between it and other genera of the same family; its species should be more closely related to each other than to any species belonging to other genera. The main diagnostic characters of genera (or at least one of them) should be normally different from those involved in the separation of its species. Intrageneric hybrids are not known in fungi.

The most important requirement is naturalness. Heterogeneous genera like *Cantharellus*, *Armillaria* or *Trogia* (all in the sense Fries-Saccardo, not to speak of *Agaricus* Fr. 1821) cannot enter in any modern genus concept; they have only historical (and nomenclatorial) meaning. Modern literature carries still a few non-natural genera, but they are either already controversial or will become so on the basis of additional knowledge not now available. But most have been separated (or combined) in such a way as to meet the principles of

natural classification. Since mostly mycologists are familiar with these and generally respect them I think it unnecessary to enumerate them here. The solution of many problems in generic taxonomy has been found to be simply general application of the respective rules.

Other elements of my concept as outlined above suffer from a lack of precision and from a lack of biogeographical and palaeological data. Yet, the rule that generic characters should be different from specific characters in the species of the same genus, as mentioned above, brings in a time factor. Evidently the characters of the ancient form to which the ascendance of the recent species of a genus leads back, were acquired much earlier than the specific characters of its descendants.

Likewise, the words "significant hiatus", more (or less) close affinity or relatedness, cry out for quantification. Quantification would give us the basis for a shorter and precise definition of the genus in the non-nomenclatorial sense in mycology. Such a definition would make it possible to decide whether a genus is just that or rather an infrageneric taxon. It would bring to an end the constant change in the sense of the word genus which is caused by the trend to elevate sections or subgenera to genera, or genera to higher ranks (status), even if the new rank does not make any visible impact on the progress of science. The quantification would set an end to unnecessary discussions about the rank of any putative genus (or subgenus). The only possibility of future changes in rank, then, would be new evidence, for example a taxon or taxa filling in the gap between two putative genera which between them, now, show no more the large hiatus we believed existed. When a modern system of classification with often smaller genera was introduced in the first half of this century, some of the critics expressed fear that many of the newly introduced genera would be of limited value since eventually newly discovered taxa would fill out the presumed hiatus between them and older genera. Fifty years of watching did not produce more than a few exceptional cases of genera becoming obsolete because of such reasons. We do not expect that another fifty years will create a significant number of such cases.

The question is: How can we come to a definition of genus in mycology? With numerical systems being more laborious, less apt to direct quantification, and more likely to lead to errors, based, as they are, mainly on morphology, and frequently at odds with a DNA-based phylogeny (cf. for example Crawford et al. 1991 p. 217), we prefer to set our hopes on DNA analysis and related work. In mycology, Jahnke (1984) has found its temporary limit insofar as it was not workable on ranks higher than species. In his case DNA/DNA hybridization of species of the same genus was used and the combined

denaturalized DNA was renaturalized (paired) to a certain point (100% or near indicating identical, much lower percentage figures different species). It is now necessary to find, for fungi, a method which provides us with a clear range of numbers for affinity and/or hiatus in connection with the genus. I have (Singer 1986) expressed the hope that this will happen (maybe it has already happened).

I wish to end my remarks with a word of caution. It will be easier to overcome some technical difficulties in the development of molecular biology than to correct some exaggerated assumptions about the easiness of fungus identification, particularly that of Higher Fungi. Frequently (fortunately not in the cited work by Jahnke), no data on the place where material studied has been deposited is indicated. In some of the very modern studies, the identification and/or description is antiquated or inadequate. American dried material is identified, it seems, with the help of Michael's popular book or Moser's key for Central European Agaricales and Gastromycetes. Both these works are valuable, even irreplaceable, but for the purpose they are not sufficient. For DNA analysis (and other similar work) increasingly important in taxonomic mycology, it should be understood that identification - unless the specimen is a type - is the work of responsible scientists, competent specialists in the group at hand, capable of providing full modern descriptions of both young and mature, fresh and dried material, so that not the slightest doubt about the identity of the respective fungi may linger in the mind of the reader. Only if this assistance of "old-fashioned" taxonomy is guaranteed will DNA analysis and related methods be of immediate usefulness for systematics - the definition of taxa.

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