The road to stability

Stability and progress are antagonists. Having both at the same time in a developing science is impossible, and consequently that also goes for nomenclature. Nevertheless, the users require the highest possible nomenclatorial stability in order to facilitate the access to related data. The transit from an anamorph-teleomorph system to the one-fungus-one-name principle will have consequences for fungal names, and the mycological community is taking its responsibility and is working towards a solution with as little changes as possible.

Nearly all changes are caused by the definition of the generic concepts, and – as the generic concept is based on the characteristics of the type specimen – in order to avoid later corrections with nomenclatorial consequences, sufficient details of the type species (including molecular data) have to be known. Ideally before implementing the one-fungus-one-name principle a full analysis of all type specimens should be made in order to establish the relations between the type specimens and as a consequence of the minimal generic concepts.

The first logical step is to have a complete set of the available genera with their type species. This project is nearing completion and the results will be made available to the mycological community for comments, additions, and corrections. This will be an on-going process and feed into the development of a list of generic names with their type species for consideration foreventual protection. It is anticipated that a first draft of that list will be available shortly. This will result in a list where the combination 'generic name - type species of the genus' on that list will be protected. That protection does not extend to the circumscription of a genus. It only means the generic name is tied to its generic type species, and that can generally only be changed by conservation of the name with a different type or in some cases a different specimen. The protection of any subset of genera – even when considered in current use – should be discouraged when the type species are insufficiently characterized. If that is not the case, a black box situation is created, where the types of different protected genera may turn out to be congeneric.

The second step consists of collecting the available data of the type specimen in a database. That would include, for example, the location, habitat, host or other substrate, herbarium, culture collection (where appropriate), descriptions, illustrations, and molecular data. When no type specimen has been designated or when it cannot be located, a neotype has to be selected or collected, preferably from or close to the original location on the original host or substrate. If the type material is unsuitable for molecular research, an epitype can be designated to integrate the type into molecular databases. When it is evident that type material does not agree with the current concept of the genus, it may be desirable to change the type by conservation or the protected lists themselves.

It is clear that the ideal situation – sufficient knowledge of all type specimens – is not within reach. It is also clear, that supposed generic anamorph-teleomorph associations are only valid when the type specimens of these genera are congeneric, and that – in case sufficient molecular data on the type species of these genera are lacking – such associations are not *a priori* acceptable. That means that mycologists, provided they want short- to medium-term results, have to find a practical solution. This can be found in the critical mass concept:

- All data on type specimens present in the database are compared, and nomenclatorial decisions are made on synonymous genera represented by congeneric type specimens.
- Specialists of well-studied groups (families, orders) can judge that the material available is sufficient for the classification they have in mind, even if the data on type specimens of potential genera of that group are not complete. They may consider that the available data have reached the critical mass for this group, and that the clades they consider to have generic status are provided with generic names with well-researched type specimens. The names in that group will then be declared protected and any type specimen from the remaining pool, that after examination threatens an accepted generic name will not get the protected status and will be rejected (i.e. reduced to synonymy). If the material is not competitive with a protected genus, its data will be added to the database and the generic name will be acceptable.
- As soon as the total of available type specimens is considered to have reached the critical mass, the list can be proposed for protection and othergenera, including ones newly described, can only be considered for inclusion if their type specimens do not threaten genera that are already protected.
- As generic concepts change, as they inevitably will in some cases, through differing taxonomic opinions of mycologists, or more often when new data are obtained, the priority rules will remain effective within the group of protected names.
- Changes afterwards will still be possible, but they will require either an act of conservation or a revision of the protected lists.

The advantages of this system are:

- Only genera with well-characterized type species will occur on the list of protected genera.
- Generic names not on the protected list remain available for use unless they are synonyms of protected genera (assuming proposals to grant them that status are approved).
- No generic names will be invalidated through not being listed, as was the case for bacterial names not on the *Approved List of Bacterial Names* (1980).
- The system can be applied to protect specific groups, such as families or orders, before a full list receives protected status.
- The status of a protected generic name can only be changed by conservation or revision of the protected list.
- This way sizeable results can be obtained and produced for consideration and approval by the IMA at IMC10 in 2014.

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Keys to genera

I write as an Assistant Professor in the Department of Biotechnology in the University of Pondicherry, India.

The Fungi (vols. IV A & B, 1973, Ainsworth GC *et al.,* eds) are classic volumes and have served fungal taxonomists for several generations in identification of different genera of fungi. It is now four decades since these volumes were published. A huge amount of information has accumulated during this period, with numerous new genera described, and others transferred or redisposed[1]. Though, in recent times, molecular sequencing data has been relied upon in many laboratories for identification of fungi, many genera are not represented in the DNA databases and workers throughout the world still depend on morphology for identification. Hence, I feel that an updated treatise on all accepted fungal genera, with identification keys, is not only wanting, but also much-needed. This would go a long way in helping both budding and established fungal taxonomists in making identifications.

Experts should be encouraged to come forward for such a new venture, with a view to publishing a series of keys to all accepted fungal genera (including lichen-forming genera) at an affordable price. I would like to see the IMA facilitate such an initiative.

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[1]The number of accepted genera has risen from 5 100 in the 6th edition of *Ainsworth & Bisby's Dictionary of the Fungi* (1973,) to 7 533 in the 10th (2008) [Ed.]

Equipment for molecular mycology needed

I am a lichenologist studying the lichen symbiosis, and focus on the genetic diversity of the fungal and photosynthetic bionts and their phylogenies.

On 1 October 2013, I will move from the University of Graz, Austria, to start a new unlimited research position at the University of Trieste, Italy, shortly, but the laboratory where I will work is still not set up for my molecular biology research with fungi. I will need to equip this with to enable me to continue my studies. Therefore, if any readers have machines which are no longer used, but are still operable, and could donate them to my new laboratory, that would help enormously in initiating new research in Trieste.

These are the items that that the laboratory lacks:

1. PCR thermocycler (possibly with heated lid)
2. Running chamber for agarose gels
3. Pipette set(s)
4. Culture chambers/incubator for fungal (algal) cultures
5. Heating plate
6. Magnetic stirrer (possible also coupled with the heating plate)
7. Thermomixer
8. Heating
9. Drying chamber/drying cupboard/ cabinet dryer
10. UV light for DNA gel visualization
11. Camera/digital camera system to recorder gel photos
12. DNA analyser
13. Tissuelyser machine (for fragmenting environmental samples into powder)
14. Computer(s) McIntosh or PC
15. Stereo-microscope
16. Light-microscope
17. Digital camera for light/ stereomicroscope

Any assistance you are able to give would be deeply appreciated.

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