IN THIS ISSUE

An exciting new mathematical model of hyphal growth, the Neighbour-Sensing model, and a computer program realizing that, was described in the April number of Mycological Research (108(4): 341–353) and showed how it could explain the growth of fungal fruit bodies. Fast-tracked in this issue, the model is refined further to enable it to be applied to colony growth on semi-solid substrates such as agar and soil, and shown to simulate actual colony and cord formation in Phanerochaeta velutina (pp. 1241–1256). The model has immense potential for modelling and so predicting the effects of multifarious factors on fungal growth and their development in silico using ‘cyberspecies’, which can then be checked by in vivo experiments, and it is therefore not surprising that this work has been highly acclaimed.

While enormous progress has been made in resolving the phylogenetic relationships of basidiomycetes in the last few years, as pointed out by Michael Weiß in the September Mycological Research News (Mycological Research 108(9): 979–981, 2004), the use of sequences from additional genes can be supportive or lead to some reconsiderations. β-tubulin gene sequences have been hardly studied in basidiomycetes, but now 36 such sequences from representatives of the major lineages in the group have been compared; the gene is highly conserved as are intron positions and there were few surprises, the Hymenomycetes and Ustilaginomycetes being resolved as monophyletic groups (pp. 1257–1263).

Five papers consider relationships and variation on and around the population and species levels using various molecular, morphological and VCG approaches. Although the dry rot fungus Serpula lacrymans is extremely common in Europe and includes five VCGs, AFLP analysis of 308 strains showed that only 1.6% were polymorphic, in contrast to S. himantioides where 31.3% of 268 strains exhibited polymorphisms (pp. 1264–1270). In the grey snow mould, Typhula incarnata, a causal agent of diseases in cereals, data from 115 markers using 37 RAPD primers indicated 48% polymorphism over 40 sites in the northern USA (pp. 1283–1290). Mycosphaerella punctiformis may comprise several cryptic species, but while the situation...
could not be adequately resolved in an ITS rDNA study, the application of the name is now secured by epitypification and the synanamorphs are described in culture (pp. 1271–1282). Morphological and molecular data establish that ‘Cephalosporium careudens’, used for over 40 years in industrial fermentations to produce cerulenin and helvolic acid, is actually Sarocladium oryzae, a genus now shown to belong the hypocrealean family Ceratostomataceae (pp. 1291–1300). Species complexes in Colletotrichum are especially hard to resolve, and in some cases isolates with different genetic compositions appear able to arise rapidly; studies of anastomoses formed between conidia show that these may occur between different species of the genus, which may explain at least part of the variation (pp. 1320–1326).

A third part of a revision of the Hygrophoraceae in the Greater Antilles is included, previous parts having been published in 2000–2001 (Mycological Research 103: 215–224, 104: 873–878); 17 species are treated here, including five new to science and five new to the region (pp. 1301–1314). Species of Laboulbeniales occurring on different parts of their insect hosts showing some differences in the thalli have often been regarded as separate species. However, studies of a new Laboulbenia species found on a South American fly suggest that at least in this host the different thalli are better interpreted as ‘growth forms’ of a single species (pp. 1315–1319).

The fungi associated with birch shoots where the trees are exhibiting crown die-back in Scotland have been compared with those on shoots of healthy trees, and the pathogenicity of the fungi isolated has been tested against birch seedlings; while detailed information on the biology and points of entry of the predominant species is presented, their role in relation to the disease requires further study (pp. 1327–1334). In the entomopathogenic Metarhizium anisopliae, the effects of water stress and washing treatments in relation to the sugar alcohol content (especially erythritol) and the germinability of conidia are reported, generating information that will need to be considered in relation to the production and storage of inoculum for use in biocontrol (pp. 1337–1345).

AN ONLINE DATABASE OF NAMES AND DESCRIPTIONS AS AN ALTERNATIVE TO REGISTRATION

Taxonomists should spend their time meaningfully with the study of organisms and the publication of novel observations rather than wasting time determining if names are available for use or not (Hawksworth 1992). A compulsory registration of new names and their accessibility on the Internet seemed to be the solution, but the idea of a registration system, which entailed sending copies of publications to a documentation centre, was first mooted in a nomenclature meeting organized under the auspices of the International Union of Biological Sciences in Geneva in 1954 (Hawksworth 1992). After years of preparation (Brummitt et al. 1986, Greuter & von Raab-Straube 1998, Wilson 1997, 1998), proposals were made in the years 1991–1998 with the aim of making the registration of names of new taxa and other nomenclatural novelties compulsory before they are accepted as validly published (Faegri 1991, Borgen et al. 1997, 1998, Greuter & Hawksworth 1999). It was thought that this registration mechanism would help solve frequent problems encountered in determining which names are effectively published (Art. 29.1) and when (Art. 32.1). Proposals made by a special committee on registration and formulated by Faegri (1991) were not approved at the meeting of the nomenclatural section preceding the Tokyo Botanical Congress (Greuter, McNeill & Barrie 1994: 138–156, 168–169), but a sentence forecasting such a procedure was included in the Tokyo Code (Greuter et al. 1994: Art. 32.1, last sentence). After publication of vivid objections (Egli 1998, Turland & Davidse 1998), and the proposals concerned with registration having failed in the mail vote, these were withdrawn at the beginning of the St Louis Congress (Barrie & Greuter 1999). Following a motion from the floor, the clauses concerned with registration were removed from the St Louis Code (Greuter et al. 2000).

A related proposal was made to recognize nomenclatural novelties published in doctoral theses as validly published (Farjon 1998) only if an ISBN number was printed in the book. In spite of some friendly amendments, this proposal received only 50% support, too little to be accepted (Greuter et al. 2000: 141–154). In the time of laser printers it is often impossible to decide what has been sufficiently multiplied and what are single prints of a manuscript. As a consequence, there is still a grey area of doubtfully published work, and many questions concerning criteria of effective and valid publication remain unanswered. Whether publications on the Internet or on CD-ROM can ever be recognized as appropriate for nomenclatural novelties is still debated (Zander & Wilson 1998). A new special committee was established at the St Louis congress to look into this matter, and proposals of some amendments to the Code have been published (Zander 2004). The earlier proposals for the registration of nomenclatural novelties foresaw the establishment of numerous national nodes to whom authors were supposed to send published material containing nomenclatural
novelties. These distributed registration centres would, without further screening, pass on the material to central institutions responsible for generating indexes. At present the date of effective publication establishes priority, but with the registration system, the date of registration would have determined priority of a name. However, serial publications could choose to be vehicles of nomenclatural novelties and supply copies of all issues as they appeared to indexing centres to be screened automatically for any novelties (Borgen et al. 1997, 1998, Greuter & von Raab-Straube 1998), thus relieving the authors of papers published in those journals of this task.

To the benefit of the biological community, central institutions generate indexes, for example, the International Plant Name Index (IPNI, produced by collaboration between the Royal Botanic Gardens Kew, Harvard University Herbaria, and the Australian National Herbarium), and Index Fungorum (maintained by CAB International under the auspices of CABI Bioscience, UK, and the Centraalbureau voor Schimmelcultures, The Netherlands). These highly beneficial indexes covering all nomenclatural novelties published for angiosperms and fungi are indispensable sources of information, the content having been screened for validity, legitimacy and orthography (implicitly in IPNI, and explicitly in Index Fungorum). These indexes are accessible on the Internet: the International Plant Names Index at http://www.ipni.org/ and Index Fungorum at http://www.indexfungorum.org/. However, the current workload of these centres is becoming insurmountable because of the extremely voluminous and intricate extracting work, which requires access to an ever increasing amount of literature. Furthermore, this type of work has little priority in the minds of scientific boards and funding agencies, and consequently is not financially well-supported. Defraying the costs to the customer who has to pay what appears to be exorbitant prices for the hardcopies is not a good solution.

In contrast to this situation, we see databases of DNA sequences (GenBank, EMBL, etc.) growing almost automatically with the spontaneous on-line input from individual contributors who, after a minimal screening of their submission, receive an accession number for each deposited sequence that must be cited in the ensuing publication, a requirement now imposed by many scientific periodicals. This mechanism works well, although the source of the sequenced material is often insufficiently documented. The sequence banks are, however, an indispensable source of information and have gained worldwide appreciation.

We propose a similar procedure, possibly with a subsequent modification of the Code, to ensure the effective and valid publication of nomenclatural novelties for fungi. A two-step procedure is necessary. (1) At the time a paper is editorially accepted by a journal (or book editor/publisher), the author submits the relevant protologue (Latin diagnosis, a description in another language, illustrations (optional but recommended) and typification, or proposed recombinations with basionsynoms and indication of types), electronically to the indexing centre. This can be one central institution, or several interconnected nodes. The proposed name(s) will be screened with respect to validity, legitimacy and orthography and placed in the on-line database, but without public access to unpublished names. Each nomenclatural entity will receive a MycoBank accession number, analogous to a GenBank number issued for each sequence submitted, that is communicated to the author and should be cited in the final version of the paper. In cases where the proposed names do not fulfill the requirements of the Code, the author will be informed and invited to make a correction. (2) Immediately after effective publication, the author responsible informs the indexing centre of this fact and communicates the exact date and bibliographic details, so that the numbered database entry with the associated information (text and, if permitted, illustrations) becomes freely accessible. The direct communication of nomenclatural novelties to MycoBank by the publishing journals at the very moment of publication would of course speed up the procedure further.

The responsibility for submitting details of proposed new taxa rests with the author(s), and this kind of submission should be imposed by high standard journals as a good practice policy. This could become a mandatory requirement, if the botanical Code and other codes were to be modified.

The date for priority purposes will remain, as in the present situation, the date of effective publication, assuming the name complies with all requirements for valid publication. The indexing centre will include all nomenclatural novelties in their indexes.

Although this procedure requires some extra activity by author(s), it will not be more cumbersome than the submission of DNA sequences (already an accepted practice), and it has substantial advantages. The indexing authority can inform the author in time about inadequacies of the submission in order to ensure valid publication. No censorship will be exerted on the publication. The indexing centre will be greatly relieved from bibliographic search that is otherwise necessary to keep the index up-to-date and which is always bound to be incomplete. The biological community, however, gets immediate access to all novelties on-line.

The arguments put forward by Turland & Davide (1998) and Eggli (1998) against registration can now easily be rebutted:

A clumsy, bureaucratic fallible system: The proposed system is straightforward with a minimum of bureaucracy. There can be a short time between submission of the final data and publication on the web.

Duplication of efforts: This is no longer the case, because the indexing centres, and the central GBIF Taxonomic Name Service (ECAT), are already
interlinked, and doing this work. Their efforts can be reduced when the proposed system works.

*A clumsy remedy for a few ‘troublesome bibliographic citations’,* i.e. publication of invalid or illegitimate names: The percentage of such incorrect publications is not negligible. It causes irritation and contributes to the existing disrepute of nomenclature. If the results of the screening are communicated to an author before publication, the percentage can be reduced significantly.

*Inadequate access:* The Internet is now significantly more accessible (especially in less developed countries) than it was three years ago. More biologists consult the net than read either *Taxon* or the *Code*. Because of increasing prices and declining budgets, access to the literature by individuals diminishes. GenBank is consulted hundreds of times a day and the on-line version of Index Fungorum has hundreds of unique visitors each day.

*Who would pay?* The indexing institutes are now putting tremendous effort into screening periodicals and other publications. With the proposed system, less effort will be required for effective functioning of the indexing institutes, assuming that the time needed to scan publications for nomenclatural novelties is substantially reduced. Nevertheless, competent staff to check validity, legitimacy and orthography of names at the indexing centre remains indispensable. To ensure their continued existence, international bodies will have to consider investing in the project. The increased recognition and importance of the indexes may in itself be an incentive for scientific boards and responsible authorities to continue the financing.


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DOI: 10.1017/S0953756204231550

ENZYME DISPENSABILITY IN SACCHAROMYCES CEREVISIAE

Previous studies have shown that as much as 80% of yeast genes are not essential for viability under laboratory conditions. Using a flux model, Papp, Pál & Hurst (2004), studied the optimal use of the metabolic network to produce major biosynthetic components for growth and the effects of gene deletions, testing these experimentally. The model indicates that 37–68% of the dispensable genes might be important under different environmental situations, although not in the laboratory conditions used; in some cases it was possible to predict conditions where these could become important. In addition, 15–28% of the genes are
compensated for by a duplicate, although duplicates were not more common for indispensable reactions, and 4–17% are buffered by metabolic flux network reorganization.


**CONCERN OVER THE STATE OF MYCOLOGY IN SPAIN**

Spain is undoubtedly amongst the strongest countries in the world for the extent of its mycological activities. About 50% of the publications on fungi of the Iberian Peninsula to have been published since 1762 have appeared since 1980. But is even that amount of activity commensurate with the need? Now three leading Spanish mycologists suggest this may not be so. Heykoop, Llarandi & Moreno (2003) trace the history of mycology in Spain and progress in its exploration. While 9867 species were known from the Iberian Peninsula in 2002, the authors estimate that this represents only about 25% of a total of probably 40,000 species (including lichen fungi). Examples illustrating the extent of the knowledge gap are presented, and little-explored habitats are highlighted – some of which are restricted and under threat or being destroyed. The mycological group in the University of Alcalá alone has described 83 species new to science from Spain in the period 1992–2002.


**DO FUNGAL BIOCONTROL AGENTS POSE A THREAT?**

Brimmer & Boland (2003) drew attention to the theoretical and potentially the actual risks posed by fungal biocontrol agents against non-target organisms. Now, Kiss (2004) has responded by analyzing the data the first authors presented, concerned with *Trichoderma virens* (wrongly as ‘*G. virens*’ [sic!]). *Ampelomyces quisqualis*, and other *Trichoderma* strains, and finds the case for serious warnings to be unsupported. This is especially so for natural ecosystems as opposed to agricultural or forestry systems where critical published information is lacking. Boland & Brimmer (2004) responded by pointing to problems caused by invasive plant and animal species, and acknowledged that much of the available evidence on effects of fungi on non-target organisms has not been published, sometimes because of confidentiality associated with commercial registration. They also draw attention to the lack of experiments on interactions in the case of *A. quisqualis*, and the taxonomic confusion that has abounded over the identity of the *Trichoderma* species involved in the ‘green mould’ disease of *Agaricus bisporus*. The need is not to over-react on the grounds of possible theoretical problems that might arise, but to come to a balanced risk assessment, weighing the benefits of using fungal biocontrol agents of insects, weeds, and plant pathogens, etc., against the damage that would occur with no control, and also the effects of applications of chemical pesticides in particular on non-target organisms. The situation is clearly not a black vs white one, but as in the case of the release of genetically modified organisms, it is research on a case by case basis that is required, not sweeping generalizations. The use of fungi as biocontrol agents of plant pathogens is an expanding field, and lessons could perhaps be learned from the extensive experience of testing regimes used by entomologists using parasitoids in particular against insect pests. It is perhaps no coincidence that some of the largest programmes in biocontrol using fungi against insect pests, such as those against locusts (Prior 2004), are based in organizations with extensive experience in the use of insects as biocontrol agents.

This debate has been useful in bringing the issues requiring testing agent by agent to the fore, and should serve to encourage more thorough studies of possible impacts on non-target organisms in agricultural as well
as in natural ecosystems. Perhaps this is an area where a more elaborate series of tests needs to be devised and agreed as necessary internationally, for example under the aegis of FAO with inputs from other pertinent international bodies (e.g. IUCN, IUSMS, IUBS, and UNEP); such an agreed list of tests would then become a prerequisite for any agent being registered and approved for use.

DOI: 10.1017/S095375620426155X

CONVERGENCE OF INVASIVE GROWTH IN FUNGI AND STRAMINIPILES

One reason that the straminipilous fungi (kingdom Straminipila) were traditionally included amongst the true fungi (kingdom Fungi) was the presence of invasive filaments or hyphae that penetrate potential food sources. Now, Money et al. (2004) have shown a remarkable extent of convergence in how invasions into the tissues of other organisms are accomplished. The hydrostatic forces developed in the hyphae of one basidiomycete, three ascomycetes, two zygyomycetes, one chytrid, and six straminipilous fungi (referred to as ‘Oomycota’) were measured using a miniature strain gauge. Remarkably, the hyphae of species in both kingdoms were found to be able to exert pressures of up to two atmospheres as they extend their tips. This parallel is quite remarkable, providing a common approach to overcoming the problem of ‘mining calories from solid food sources’ – and one which is not known in any other groups of eukaryotes.


DOI: 10.1017/S0953756204271556

ADHESINS: CELL-SURFACE PROTEINS OF ADAPTIVE VALUE IN MEDICALLY IMPORTANT FUNGI

Adhesion is a key factor in enabling fungi such as Candida species to gain access to and proliferate in human tissues in particular, but also in biofilms, and further on plastic materials such as catheters, prosthetic heart valves, and dentures. Verstrepen, Reynolds & Fink (2004) have reviewed the occurrence and variation in the adhesion cell-wall glycoproteins that are crucial to this effect, but also to routine interactions between hyphae. They detail the conserved nucleotide sequences of the flocculation genes (FLO) and of the generated adhesins, and describe a diversity of adhesins which is considered to arise through recombination. The extent of recombination poses problems for the control of fungi expressing the gene in hospital environments. Conservation is taken as evidence of the functional importance of these proteins. In the case of Saccharomyces cerevisiae, the need for the adhesion-producing FLO1 gene is demonstrated in colour on polystyrene wells and in Petri dish cultures. The authors emphasize that the variation in cell-surface adhesins arising from recombinations is important in relation to possible treatments for fungal infections in humans. Such infections pose mounting clinical problems, and are often hospital-acquired via biofilms on instruments.

The occurrence and role of adhesins in filamentous fungi, to supplement the information now available from human pathogenic yeasts, is clearly a topic ripe for further investigation.