Lichen thalli are a rich source of unusual fungi, but little is known of the biology of obligately lichen-inhabiting (lichenicolous) fungi. The host-parasite interfaces in different members of the Dacomiaceae have been studied for the first time and the fungal partner of the lichen proves to be the main target for the parasites (pp. 1348–1353). Fungi isolated from another unusual habitat, marine sponges, have a high proportion with biological activities and structurally diverse secondary metabolites (pp. 1354–1365). A range of ectomycorrhizal fungi tested in vitro against various heavy metals showed a strong variability in responses within isolates of the same species, but whether these came from polluted or unpolluted sites was not significant (pp. 1366–1371). The association between Pinus sylvestris and two ectomycorrhizal species commonly found together, Gomphidius roseus and Suillus bovinus, has been examined by molecular and anatomical approaches; the Gomphidius may actually function as a parasite (pp. 1372–1378).

The development of cruciate basidiospores in the tricholomatoid mushroom Tricholosporum laeteviolaceum has been examined by scanning electron microscopy (pp. 1379–1383). Studies of ultrathin sections show that chitin localisation varies in the different spore stages of the blister rust Cronartium ribicola (pp. 1384–1388).

A monographic revision of the genus Amorphomyces, a member of the Laboulbeniales, leads to the recognition of ten species which are illustrated and keyed (pp. 1389–1398). Another new genus of ascomycetes, named Torrentispora, and which has ascospores with a fibrillar sheath has been discovered on submerged wood in tropical streams (pp. 1399–1403), and two new dematiaceous hyphomycetes have been found on leaf litter in Spain (pp. 1404–1407).

**BLACK BOXES AND MISSING SINKS: FUNGI IN GLOBAL CHANGE RESEARCH**

Global change research focuses on potential effects of climate and land use change on factors such as productivity of the biosphere, carbon dioxide ($CO_2$) emission from soil, decomposition of organic matter, nutrient transformations, and soil development. We have every indication that a very diverse array of fungi (along with bacteria and soil fauna) is involved in each of these processes. Nevertheless, ecosystem ecologists who study these large-scale fluxes often consider the below-ground community as a ‘black box’. Dead plant tissues enter this box, and inorganic nutrients such as ammonium, nitrate, and $CO_2$ exit after a well-documented time unless they don’t. Actually, field studies to date have indicated that we are not able to successfully predict how these black box processes will respond to perturbations like elevated atmospheric $CO_2$ and anthropogenic nitrogen (N) deposition (a by-product of car exhausts and agricultural practices). Fortunately, recent advances in genetic analyses and stable isotope techniques can be combined with traditional approaches to connect the identities of fungal groups with their ecological functions in natural systems. The next crucial step is to establish strong connections between ecosystem ecologists, who are comfortable thinking at large scales, and mycologists, who have often focused on the physiology and function of individual fungal groups at smaller scales. Such interactions are likely to improve our predictions of how the biosphere will respond to global change, and at the same time provide valuable insights to unresolved issues in ecosystem ecology.

Several unanswered questions in ecosystem ecology were recently noted in a special issue of the New Phytologist (147(1), July 2000) entitled ‘Root dynamics and global change: an ecosystem perspective’. One central focus in this issue is the potential effects of global change on soil microbes and carbon (C) dynamics (Norby & Jackson 2000). This question has received much attention because evidence from experimental and modeling studies suggest that soils may form a sink for C under elevated $CO_2$, and in the process, slow rising atmospheric $CO_2$ levels and mitigate global warming to some extent (Harrison & Bonani 2000). In fact, current budgets of global C have been unable to account for a ‘missing’ C sink of about 2 Gt C per year (Schimel et al. 1995), and one hypothesis is that a portion of this sink may be hidden in microbial tissues and by-products in the soil. Indeed, Treseder & Allen (2000) reported several studies in which mycorrhizal standing crop or components (e.g. glomalin) actually increased in soils under elevated $CO_2$. Mycorrhizal fungi are also a rapid conduit for the transfer of C from the plant to the soil and atmosphere (Fitter, Heinemeyer & Staddon 2000). Approaching from a larger scale, Zak et al. (2000) reported that in response to elevated $CO_2$, many studies find increases in C fluxes both entering and leaving the soil. However, microbial biomass, N mineralization (i.e. release of ammonium or nitrate), and immobilization of N in microbial tissues, can strongly increase or decrease, with high variation in response among studies. The authors suggested that differences among plant species in root longevity and biochemistry may be responsible, to some extent, for this unpredictability. By the same token, physiological differences among microbial groups could play a role as well. The community composition of ecto- and arbuscular mycorrhizal fungi can change under elevated $CO_2$ and N deposition, with potential consequences for C and N immobilization and/or mineralization (Fitter et al. 2000, Treseder & Allen 2000).

Mycorrhizal fungi vary in chemical composition (e.g. N, phosphorus, and chitin) of their tissue (Treseder & Allen 2000) and the degree to which they transport nutrients to plants (Fitter et al. 2000). In addition, many mycorrhizal studies in global change ecology are plant-centered and tend to overlook the biology of the fungal component (Fitter et al. 2000). Non-mycorrhizal fungi have received less attention, but a recent laboratory study has indicated that fungal community composition can affect changes in the decomposition rate of
litter under ambient versus elevated CO$_2$ (Conway et al. 2000)$^2$. The identity, as well as abundance, of fungi may be critical in determining responses of ecosystems to elevated CO$_2$.

Thirty years ago, in his Presidential Address to the British Ecological Society, Harley (1971) asserted that fungal groups should be considered independently when investigating their contributions to nutrient dynamics. He stated that one of the main difficulties in assessing the ecological roles of fungi is ‘determining what species occur in any ecological substrate and their state of vegetative activity’. This challenge has indeed limited ecological studies until very recently. Molecular and immunolabelling approaches are being used to assess the composition of fungi in situ in response to CO$_2$ or N treatments (Fitter et al., 2000, Treseder & Allen 2000).

Radajewski et al. (2000) have presented a newly-developed technique that may prove an additional breakthrough for microbial and ecosystem ecologists. By introducing a given isotopically-labeled substrate (e.g. $^{13}$C-labeled methane) into soil for microbes to metabolize, the DNA of the specific microbial groups that use that substrate will become labeled itself. After extracting bulk DNA from the sample, a centrifugation step separates labeled DNA from unlabeled DNA. The labeled DNA is then sequenced and compared to known sequences in a gene sequence databases. The identity of microbes that use a given substrate can thus be determined. Techniques such as this, when used by mycologists and ecosystem ecologists working in concert, may allow us to address comprehensively the role of fungi in the response of nutrient dynamics to global change, and more importantly, to eliminate the notion of a black box.


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**MYCOBIOTA, MYCOTA OR FUNGA?**

As fungi are not animals or plants, mycologists have been seeking for an appropriate word for the fungi in a particular geographical location or ecological niche to parallel ‘fauna’ for animals and ‘flora’ for plants. To continue to speak of a ‘fungal flora’ or a ‘microbial flora’ perpetuates the deep-rooted idea that fungi are still plants. ‘Mycobiota’ has much to commend it as ‘biota’ is a familiar concept to ecologists and biologists generally, and the prefix ‘myco-’ is also well known. ‘Mycota’ has also been widely taken up, but has the disadvantage of being a suffix indicating the rank of phylum (or division; e.g. Basidiomycota) and is also sometimes used (arguably incorrectly) as Mycota or Eumycota as the name for the kingdom Fungi. Mycological ecologists want a word to encompass all organisms studied by mycologists, including groups like the Myxomycota, Oomycota, and not just the kingdom Fungi.

Now a new proposal has been made, the term ‘funga’. ‘The word “Funga” [the original author’s italics] is a newly established concept since fungi now have their own kingdom corresponding to the plant and animal kingdoms’ (Gravesen 2000: 76). The word is used in phrases such as ‘the associated funga’, but the alternatives of mycobiota and mucota already in use are not discussed.

My personal preference is to avoid having to use such words. Why speak of, for example, ‘the mycobiota of North America’ when ‘the fungi of North America’ is equally clear and immediately understandable by non-mycologists — provided that fungi is used unitalicised to make clear it does not signify the mycobiota of North America? (cfr. Hawksworth et al. 1995). Where a special word seems essential, I would commend ‘mycobiota’, but it remains to be seen what consensus will emerge.

The Executive Editor is grateful to Brian Flannigan for drawing the word ‘funga’ to his attention.


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$^2$ See also Mycological Research News in Mycological Research 104(2): 129–130 (February 2000).