

the following steps: (1) retrieving specimens of fungal genera unrepresented in GenBank from the Kew collection; (2) selecting 2–3 of the largest, youngest and most geographically diverse specimens of one species of each genus; (3) removing a small fragment of each selected fungal specimen; (4) carrying out DNA extraction, purification, hot-start proofreading PCR and direct DNA sequencing or cloning from PCR products; and (5) comparing the DNA sequences generated against existing GenBank accessions to identify any matching environmental unknowns, and (6) submit representative DNA sequences to GenBank.

We were able to generate at least one DNA sequence from each of 30 target genera (GQ981488–981532). These included a few well-known fungal genera (e.g. *Mutinus*, *Clathrus*, *Albatrellus*). Only one of the 30 genera had entered GenBank by the time we analysed the data (i.e. *Albatrellus*). Twenty-one had significant similarity within the highly variable ITS to fungi in the databank, and 12 of these matched best DNA sequences from unknown fungi generated from a variety of sources including house dust, soil, roots, soil, hyphae, and mycorrhizas. The latter included a new *Royoungia* specimen with a mycorrhizal *Anisoptera*, a *Podohydangium* of *Nothofagus*, and a *Picoa* of *Epipactis*.

These results highlight that: (1) similarly to the small proportion of the fungal biodiversity in the environment currently represented in GenBank, of the fungal biodiversity represented in collections only the tip of the iceberg is currently represented in GenBank; and (2) fungi are not truly unknown unless we know they are not represented by a vouchered named specimen in a collection.

Brock PM, Döring H, Bidartondo MI, 2009. How to know unknown fungi: the role of a herbarium. *New Phytologist* **181**: 719–724.

Rinaldi AC, Comandini O, Kuyper TW, 2008. Ectomycorrhizal fungal diversity: separating the wheat from the chaff. *Fungal Diversity* **33**: 1–45.

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Homo- and heterothallic mating in *Candida albicans*

Cryptic mating in *Candida albicans* occurs between different strains with α and α cells which are linked to pheromone production genes, i.e. heterothallic mating takes place. Now Alby *et al.* (2009) have demonstrated that in this species and in *Saccharomyces cerevisiae*, the Bar1 protease produced by α cells inactivates mating pheromone α typically secreted by α cells. Further, they have shown that in strains with cells able to produce both pheromones self-mating occurred, i.e. homothallic mating was taking place. Pheromone production by α strains also promoted same-sex mating in wild-type α strains. The process is shown diagrammatically neatly by Heitman (2009) in a thoughtful and thought-provoking commentary on the paper which also compares the situation with that in *Cryptococcus neoformans* and *Schizosaccharomyces pombe*.

It is therefore evident that there is potential for genetic exchange even within unisexual populations of *C. albicans*. This ability may contribute to the ability of the species to survive

and adapt to different conditions, not least challenges from antifungal compounds.

Alby K, Schaefer D, Bennett RJ, 2009. Homothallic and heterothallic mating in the opportunistic pathogen *Candida albicans*. *Nature* **460**: 890–893.

Heitman J, 2009. Love the one you're with. *Nature* **460**: 807–808.

Recreational use and sporocarp production of ectomycorrhizal fungi

The question of the impact of recreational activities, such as roaming in woodlands and camping, on the ectomycorrhizal fungi present is a key issue in fungal conservation. In order to investigate this in subalpine forests, Trappe *et al.* (2009) studied six camp or maintenance sites in the Crater Lake National Park with current or historic usage, paired with six similar sites without such usage, using 1000 m² plots which were studied for three years. Sporocarps of 166 species were found, but many were either too frequent or infrequent to be informative. The final data set comprised 38 species subjected to ordination analysis in relation to soil density, chemistry, fuels (litter mass and woody debris), and stand age and elevation. Surprisingly, at the macrosite scale, vegetation, fuel levels and compaction appeared to have no significant effect. However, at the microsite level the effects were profound as almost no sporocarps occurred in the most disturbed areas, i.e. those with bare and trampled soil around fire sites and picnic tables; in those plots, almost all sporocarps were from less disturbed microhabitats within them. The authors conclude “intensive recreational use did not adversely impact the quantities of sporocarps collected or the diversity of mycorrhizal fungi at the macrosite scale”. It would therefore appear that fungal conservation of ectomycorrhizal species is not incompatible with recreational usage except at a microsite level in the coniferous forests of the Pacific Northwest, and it would now be of interest to have data to determine if after conclusion could be extrapolated to species in deciduous woodlands.

Trappe MJ, Cromack K jr, Trappe JM, Wilson J, Rasmussen MC, Castellano MA, Miller SL, 2009. Relationships of current and past anthropogenic disturbance to mycorrhizal sporocarp fruiting patterns at Crater Lake National Park, Oregon. *Canadian Journal of Forest Research* **39**: 1662–1676.

New scientific names in this issue

Cortinarius casimiri var. *hoffmannii* comb. nov. (syn. *C. decipiens* var. *hoffmannii*)

C. subturibolus var. *bomybycinus* comb. nov. (syn. *C. bombycinus*)

C. vernus var. *nevadavernus* var. nov.

Eonema gen. nov.

E. pyriforme comb. nov. (syn. *Xenasma pyriforme*)

Muscinupta gen. nov.

M. laevis comb. nov. (syn. *Cantharellus laevis*)

Sphaerodes mycoparasitica sp. nov.

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