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Mycological Research News[1]

This issue of *Mycological Research News* features: In this issue; and Changing the biological clock in *Neurospora crassa*.

Original papers in this number include morphological and molecular investigations on: *Endophyllum* species on asteraceous plants; *Melampsora* rusts on *Salicaceae*; myxotoxin producing *Fusarium* chemotypes; host specificity and nutrient uptake in *Eudarluca caricis*; *Ampelomyces* populations on powdery mildews; salt marsh populations of *Claviceps purpurea*; the classification of *Omphalina foliacea*; and endophytes in different genera of native Australian orchids.

A gene encoding a malic enzyme involved in the anaerobic growth of *Mucor circinelloides* is characterized. In the ericoid mycorrhizal *Hymenoscyphus ericae*, one paper shows how carbon availability affects nitrogen source utilisation, and another the effects of copper toxicity in relation to phosphatase activity.

The colonization of wood by airborne spores has been studied in experimental forest plots, and the climatic and altitudinal factors correlated with spore catches of *Alternaria* and *Cladosporium* determined.

Early development of *Morchella* fruit bodies is described and documented by scanning electron microscopy.

The following new scientific names are introduced in this issue: *Endophyllum dimorphothecae* sp. nov.; *E. elytropappi* (syn. *Aecidium elytropappi*) comb. nov.

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IN THIS ISSUE

The March number of *Mycologial Research* included ten papers on the theme of insect-fungal interactions and their use in biocontrol (*Mycological Research* **109** (3): 261–354, March 2005). The lead paper in this issue is concerned with a rust fungus, *Endophyllum osteospermi*, endemic to South Africa being considered for release in Australia for the control of the woody shrub *Chrysanthemoides monilifera*. The occurrence and host range in South Africa have been examined in depth and the species was found to be restricted to a small group of related plants in the *Calenduleae*; in the process two additional species of *Endophyllum* were discovered on different hosts (pp. 387–400). *Melampsora* rusts occurring on *Populus* and *Salix* species will be familiar to most field mycologists and tree pathologists; numerous species and special forms have been recognized, and here the LSU and ITS sequences of the rDNA of 14 taxa are compared, and in general support existing species concepts and shed new light on relationships (pp. 401–409). The *Fusarium graminearum* complex is now recognized as containing nine species as a result of molecular phylogenetic and micromorphological investigations (see Mycological Research News, *Mycological Research* **108** (10): 1110, October 2004). Here we report additional molecular studies on New Zealand isolates which show three species occur in the country and that mycotoxin production is not species-specific (pp. 410–420).

Two papers concern mycoparasites of plant pathogens. *Eudarluca caricis* is proved to be a mycoparasite by experiments with stable ^{15}N isotopes which become concentrated in the *Eudarluca* compared with the host rusts; the fungus had been assumed to be nonspecific, but both inoculation experiments and ITS sequence data indicate that may not be the case and that the genus shares a common ancestor with the powdery mildew mycoparasites belonging to *Ampelomyces* (pp. 421–428). A major study of *Ampelomyces* material attacking *Podosphaera leucotricha* using ITS-SSCP patterns and sequences showed the populations on that fungus to be homogenous, but material from other host fungi included for comparison belonged to seven other groups; two growth rate categories were also distinguished, the faster perhaps not even belonging to the genus (pp. 429–438).

A genotype of *Claviceps purpurea* occurring in marshes first recognized in the USA and UK, is reported from new sites in Europe, South and North America; ALFP and RAPD analyses show structure within the populations which suggests that Pacific coast ones are recently introduced; the occurrence of three discrete groups in the species is also confirmed (pp. 439–446). Studies on the ITS and LSU rDNA regions of the

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sterile lichen *Omphalina foliacea* show this to be a basidiomycete lichen belonging to the hymenochaetoid clade, but one lacking close relatives (pp. 447–451). ITS-RFLP and sequence analysis of endophytes in six Queensland orchids revealed specificity for fungal partners at the generic level (pp. 452–460).

Mucor circinelloides has been discovered to have more isoforms of malic enzyme than any fungus or microorganism so far studied; one gene was cloned and sequenced and appeared to be an anaerobic isoform, but this is evidently one of at least two structural genes for malic enzyme in this fungus (pp. 461–468).

Two papers concern the ericoid mycorrhizal fungus *Hymenoscyphus ericae*. Under carbon-limiting conditions, strain differences are linked with nitrogen-use efficiency, and there is evidence for intraspecific variation in other physiological parameters such as glutamine shifts suggestive of variations in glutamine metabolic pathways (pp. 469–477). A comparison of strains from *Calluna vulgaris* growing on copper-contaminated mine-spoil and unpolluted heathland showed those from the contaminated site to be more tolerant of elevated copper concentrations in culture experiments; phosphomonesterases and phosphodiesterase activities were also monitored (pp. 478–486).

Just how effective fungi are at colonizing woody debris and its importance in maintaining fungal diversity in a site is demonstrated by a field experiment in Sweden in which 120 freshly cut *Picea abies* logs were exposed in two forests for seven weeks in both the summer and autumn; 943 strains representing 97 species were recovered, 64 (66 %) species being found only in one plot (pp. 487–496). Fungal spores have been trapped for one year in sites with different weather patterns and at various altitudes in north-west Spain; *Cladosporium* species spores increased with increasing height and continentality, whereas those of *Alternaria* species declined, weather giving the strongest correlations with the results (pp. 497–507).

The early stages of fruit body initiation and development have been followed in a *Morchella* sp. grown under controlled conditions by scanning electron microscopy, which enabled four stages of primordial development to be distinguished (pp. 508–512).

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CHANGING THE BIOLOGICAL CLOCK IN *NEUROSPORA CRASSA*

Rhythmic responses of changes in light regimes involve 'clock genes' that form a self-regulating transcription/translation negative feedback mechanism in most organisms studied in detail. In the case of *Neurospora*, a dramatic increase in clock gene *frq* RNA levels occurs after the introduction of light (Crossthwaite, Loros & Dunlap 1995). The *frq* gene has been found to be essential for adaptation to different light regimes in *N. crassa* (Merrow, Brunner & Roenneberg 1999). The *frq* gene and the FRQ protein produced can be monitored, and now Tan *et al.* (2004) have studied molecular light regulation in this fungus in four different photoperiods designed to mimic seasonal changes. They discovered that *frq* RNA increased aproximately ten-fold with the onset of light, but then dropped to about half the peak value for the rest of the light period. On becoming dark, *frq* rapidly decreased, but in nights of 10 h or longer the *frq* levels started to rise about 8 h after the lights were turned out. However, the FRQ protein levels followed neither the RNA levels nor the changes in light, with differences in responses of as much as 6 h. FRQ abundance does, however, seem to regulate the production of conidia, which are formed 7 h after lights are put out in 50 % light:dark cycles and mainly around midnight when the FRQ protein was at about half its peak level.

A dissociation of transcription, translation and protein stability is evidently fundamental to the circadian mechanism in *N. crassa*. A simple feed-back mechanism was insufficient to explain the results obtained, and the process is evidently more complex than was previously thought. It appears that light is not the only factor driving the circadian response, and that clock control of light input pathways involves post-transcriptional regulation. However, the regulators controlling the dissociation between the *frq* RNA and FRQ protein levels are yet to be identified. Discovering just what these regulators are is likely to be the key to understanding circadian timing in at least this model fungus at the molecular level.

Crossthwaite, S. K., Loros, J. J. & Dunlap, J. C. (1995) Light-induced resetting of a circadian clock is mediated by a rapid increase in *frequency* transcript. *Cell* **81**: 1003–1012.

Merrow, M., Brunner, N. & Roenneberg, T. (1999) Assignment of circadian function for the *Neurospora* clock gene *frequency*. *Nature* **399**: 584–586.

Tan, Y., Dragovic, Z., Roenneberg, T. & Merrow, M. (2004) Entrainment dissociates transcription and translation of a circadian clock gene in *Neurospora*. *Current Biology* **14**: 433–438.