

**A multigene phylogeny for *Cordyceps* and the Clavicipitaceae.** G.-H. SUNG (1), K. T. Hodge (2), and J. W. Spatafora (1). (1) Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR, USA; (2) Depts. of Plant Biology & Plant Pathology, Cornell University, Ithaca, N.Y., USA. *Phytopathology* 91:S125. Publication no. P-2001-0161-MSA.

*Cordyceps* is a morphologically and ecologically diverse genus of entomopathogenic and fungicolous fungi classified in the Clavicipitaceae. The family includes pathogens of nine orders of arthropods, the grass family Poaceae, and the truffle genus *Elaphomyces*. This disparate host range is the major basis for the current subfamilial classification of the family. To test familial, subfamilial, and generic classifications and to develop phylogenetic hypotheses for the evolution of host affiliation, we have initiated a multigene phylogenetic study of *Cordyceps* and the Clavicipitaceae. Nucleotide sequence data was determined for the small and large subunit rDNA, beta-tubulin, and elongation factor 1-alpha. In addition to species of *Cordyceps*, we also sampled species of other entomopathogenic (e.g., *Torrubiella*) and plant-associated (e.g., *Epichloe*) teleomorphs and numerous entomopathogenic, nematophagous, and fungicolous anamorphs (e.g., *Verticillium*). Phylogenetic analyses of separate and combined data sets do not support the monophyly of *Cordyceps*, which is represented in at least three separate clades. In addition, these results reject the ecologically based subfamilial classification of the Clavicipitaceae. The use of multigene phylogeny to infer ancestral ecologies will be discussed.

**Examination of genet size of two ectomycorrhizal fungi from the southern Sierra Nevada: *Gautieria monticola* and *Suillus (Gastrosporella) suilloides* using AFLP markers.** J. TAN, L. C. Grubisha, F. J. Camacho, and T. D. Bruns. Dept. of Plant and Microbial Biology, University of California, Berkeley, 94720 USA. *Phytopathology* 91:S125. Publication no. P-2001-0162-MSA.

We are investigating the genet sizes of *Gautieria monticola* and *Suillus (Gastrosporella) suilloides*, two species of ectomycorrhizal fungi found in mixed conifer stands from the southern Sierra National Forest. The study of the genet sizes of these two species will help us gain a better understanding of their population biology. Basidiocarps from three sites for each species were mapped, collected, and analyzed with AFLPs to generate genetic fingerprints for the fruitbodies. We screened multiple primer pairs and chose two primer combinations for each species. Preliminary analyses suggest that the two species have different population structures. Within a single population, *Gautieria monticola* forms several small genets often with several clustered fruitbodies, whereas *Suillus suilloides* has fewer but occasionally larger genets, the largest spanning 10 meters between fruitbodies. Within the space of the large genet are smaller genets. The small size of *Gautieria* genets corresponds to previous reports of small *Gautieria* mats found in young Douglas-fir stands, while the size of *Suillus suilloides* genets are within the range seen in other *Suillus* species. *Suillus suilloides* has low AFLP similarity between populations, relative to within populations. This suggests low gene flow between sites, which is similar to what has been reported in its sister taxon *Suillus tomentosus*.

**Extreme morphological variability among sympatric neotropical species of *Clavulina* and *Craterellus*.** J. THACKER, T. W. Henkel, and R. Vilgalys. Department of Biology, Duke University, Durham, NC 27708. *Phytopathology* 91:S125. Publication no. P-2001-0163-MSA.

Recent systematic studies have revealed that the homobasidiomycete genera *Clavulina* J. Schrt. and *Craterellus* Pers., although morphologically dissimilar, are closely related. Nutritional habit of both of these genera is thought to be exclusively ectomycorrhizal (EM). The majority of species in both genera have been described from temperate regions, though recent studies have uncovered a wealth of new and unusual taxa from neotropical forests of Guyana. *Clavulina* and *Craterellus* are species-rich in the Pakaraima Mountains of Guyana and basidiomes of each are some of the most abundant and frequent in forests dominated by EM Dicycbe spp. (Caesalpinaceae). *Clavulina* is especially speciose at this site, with 10+ species, most of which are undescribed, recorded from a small collecting area. Basidiomes among sympatric Guyanese *Clavulina* species exhibit extreme macromorphological variability, including monopodial, highly branched corals, and funnel-shaped, *Craterellus*-like forms. *Craterellus* basidiomes range from typically infundibuliform to astipitate, pleurotooid forms fruiting on standing deadwood. Molecular systematic studies investigated the phylogenetic relationships of neotropical and temperate *Clavulina* and *Craterellus*, examined the mycorrhizal status of certain taxa, and assessed their macro- and micromorphological plasticity.

**Nitrogen stable isotope ratios in sporocarps of ectomycorrhizal fungi: Influence of phylogenetic and environmental factors.** S. A. TRUDELL (1), P. T. Rygielwicz (2), and R. L. Edmonds (1). (1) Ecosystem Science Division,

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It has been suggested that nitrogen stable isotope ratios (expressed as delta 15-N) of fungus sporocarps, in conjunction with delta 15-N data from other ecosystem compartments, can be used to elucidate key processes in forest N-cycling. Although results of previous studies generally support this idea, they also show that the large number of factors that influence delta 15-N can complicate interpretation of the data. To date, there has been no integrated study of the relative degree to which the different sources of variation contribute to the observed delta 15-N of fungus sporocarp samples. Here, we report initial delta 15-N measurements on a large number of sporocarp collections from two conifer forests located in contrasting environmental zones on the Olympic Peninsula, Washington. Based on these data, we provide estimates of variance in delta 15-N for individual species and genera of ectomycorrhizal fungi and assess the degree to which phylogenetic and environmental factors appear to influence delta 15-N values. The results of our overall study, of which this work is one component, will increase the usefulness of stable isotope ratios in understanding N-cycling and, hopefully, help draw greater attention to the critical ecosystem roles played by fungi.

**Longitudinal and temporal distribution of freshwater ascomycetes and dematiaceous hyphomycetes in the Lam Tsuen River, Hong Kong.** C. K. M. TSUI, K. D. Hyde, and I. J. Hodgkiss. Center for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Pokfulam Road, Hong Kong, China. *Phytopathology* 91:S125. Publication no. P-2001-0165-MSA.

Longitudinal and temporal distribution patterns of freshwater ascomycetes and dematiaceous hyphomycetes on submerged wood were investigated along the Lam Tsuen River in Hong Kong. Two hundred and six species were recorded. Ascomycete genera were dominated by Annulatascaceae, Halosphaeriaceae, Lasiosphaeriaceae, Lophiostomataceae and Magnaportheaceae; the most common taxa were *Aniptodera chesapeakeensis*, *Aquaticola rhomboidea*, *Massarina purpurascens*, *M. thalassioidea*, *Ophioceras commune* and *Sporoschisma uniseptatum*. There were no significant differences ( $p > 0.05$ ) in total number of species among sites, but the number of species in Halosphaeriaceae ( $p < 0.01$ ) and Lasiosphaeriaceae ( $p < 0.05$ ) was significantly higher at downstream sites, whereas Annulatascaceae was dominant at upper sites. The downstream changes in species composition were strongly correlated with elevated concentrations of nitrate, ammonia and phosphorus due to human disturbances. The variation in species composition was also weakly affected by other physicochemical characteristics. Species diversity fluctuated temporally but did not change ( $p > 0.05$ ) between dry and wet seasons. Frequency of occurrence for certain dominant taxa appeared to decline after heavy rainfall associated with El Nino, possibly due to the effects of heavy rainfall on river discharge, which washed away well-colonized woody substrates.

**Biodiversity of nematophagous fungi in Hong Kong.** C. K. M. TSUI (1), K. D. Hyde (2), and S. F. Chen (1). (1) Department of Botany, The University of Hong Kong, Pokfulam Road, Hong Kong, China; (2) Centre for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Pokfulam Road, Hong Kong. *Phytopathology* 91:S125. Publication no. P-2001-0166-MSA.

Nematodes cause serious problems in agriculture and forestry. Yields of banana and tobacco are seriously reduced due to infection by root nematodes in China, whereas in Hong Kong pine wood nematodes virtually eliminated local *Pinus massoniana*. In collaboration with the Yunnan University we are investigating the diversity of nematode-trapping fungi and trying to identify new chemicals that can be used as nematicides from Hong Kong macrofungi. To date, ten nematode-trapping fungi have been identified, e.g., *Arthrobotrys japonica*, *A. oligospora*, *Monacrosporium eudermatum*. By screening fungi we have isolated several *Pleurotus* spp. that are good producers of nematotoxin and expect to discover novel bioactive compounds against nematodes. By carrying out these investigations, it should be possible to develop an environmental friendly chemical to control nematode problems.

***Cryphonectria cubensis* represents a new genus comprised of three species.** M. VENTER (1), H. Myburg (2), M. J. Wingfield (1), and B. D. Wingfield (2). (1) Tree Pathology Co-operative Programme (TPCP), Forestry and Agricultural Biotechnology Institute (FABI), Department of Microbiology and Plant Pathology, Department of Genetics (2) University of Pretoria, Pretoria, 0002 South Africa. *Phytopathology* 91:S125. Publication no. P-2001-0167-MSA.