the major species associated with *T. fuscum* in Canada. A single earlier report of this fungus exists for Canada, and it was compared to the isolates from Atlantic Canada.

***Gliocephalis hyalina*: An obligate parasite of *Fusarium* species.** K. JACOBS, K. M. Holzman, and K. A. Seifert. Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Ottawa, Canada, K1A 0C6. Phytopathology 91:S114. Publication no. P-2001-0085-MSA.

Gliocephalis hyalina Matruchot 1899 is the single species of the hyphomycete genus, *Gliocephalis*, characterized by the production of *Aspergillus*-like conidiophore with conidia produced in slime. This species is morphologically similar to *Goidanichiella barronii*, from which it is distinguished primarily by the absence of septa and pigmentation in the stipe. *Gliocephalis hyalina* has been reported only three times, each time in association with other fungi and bacteria. Attempts to purify the fungus led to the loss of the cultures. Recently, an isolate of *G. hyalina* was obtained from soybean roots on the Central Experimental Farm in Ottawa. The fungus would not grow alone, and could only be maintained in mixed culture with *Fusarium*, leading to the hypothesis that it is an obligate parasite. SEM and TEM were used to determine the mode of infection. *Fusarium* strains grown in the presence of *G. hyalina* showed no change in growth rate or colony morphology. Several other soil-borne fungi were tested as possible hosts, but *G. hyalina* appears to be specific to *Fusarium* species. We also attempted to clarify its phylogenetic position in the fungal kingdom and compared it to other Aspergilloid genera such as *Goidanichiella, Aspergillus, Escovopsis, Knoxdaviesia, Gliocephalotrichum* and *Gibellula* based on the ITS and 18S ribosomal gene sequences.

***Neurospora* in western North America: A model system in the backyard.** D. L. JACOBSON (1,2), M. M. Barton (2), J. R. Dettmena (2), A. J. Powell (3), G. S. Saenx (3), J. C. Hirsch (3), J. W. Taylor (2), N. L. Glass (2), and D. O. Natvig (3). (1) Dept. of Biological Sciences, Stanford University, Stanford, CA 94305 USA; (2) Dept. of Plant and Microbial Biology, University of California, Berkeley, CA 94720 USA; (3) Dept. of Biology, University of New Mexico, Albuquerque, NM 87131 USA. Phytopathology 91:S114. Publication no. P-2001-0086-MSA.

Species of *Neurospora* have been found mostly in the moist tropics and subtropics. During 2000, we observed *Neurospora* in the arid western United States as a primary colonizer of trees and shrubs killed by wildfires, significantly expanding the known geographic range and habitats of the genus. *Neurospora* colonies were observed in 23 forest fire sites in habitats ranging from cottonwood stands along the Rio Grande to mountain forests in New Mexico, California, Nevada, Idaho, and Montana to the Canadian border. Colonization occurred beneath the bark of diverse deciduous and conifer hosts. The combined 2000 collection includes 314 isolates from 35 to near 49° north latitude and from 750 m to 2400 m altitude. To date, 134 isolates have been identified to species; 130 (97%) are *N. discreta*. Within a site, mating type among individuals is often significantly skewed from a 1:1 ratio. The occurrence of *Neurospora* under these circumstances raises fundamental questions with respect to ecology and population biology: How does *Neurospora* gain access beneath apparently intact tree bark? How is it dispersed or vectored? How and where does it survive for decades between forest fires? What are the reproductive or genetic factors that cause the skewed mating type distribution? The 2000 collection provides a resource to begin addressing these questions.

***mip* as a tool for cloning hymenomycete mating-type genes.** T. Y. JAMES (1), U. Kues (2), and R. Vilglays (1). (1) Dept. of Biology, Duke University, Durham, NC 27708 USA; (2) Institute of Microbiology, Swiss Federal Institute of Technology, CH-8092 Zurich, Switzerland. Phytopathology 91:S114. Publication no. P-2001-0087-MSA.

The mitochondrial intermediate peptidase (*mip*) gene was isolated in the mushroom *Schizophyllum commune* as a metalloproteinase physically adjacent to the A-alpha mating-type locus (Stankis et al. 1992, PNAS 89:7169). While the linkage of *mip* to the A-alpha locus is extremely tight (<1kbp), transformation experiments have shown that *mip* does not function in mating or sexual differentiation processes. Hymenomycete mating-type genes are at present difficult to clone because of the extreme level of sequence divergence between alleles both among as well as within species. The positional cloning of mating-type genes has been accomplished by using the more conserved neighboring genes, such as *mip*, to isolate the chromosomal region containing the A-alpha mating locus of *Coprinus* spp. In this study we discuss the potential for this strategy to be applied to a wider group of hymenomycete taxa by exploring linkage relationships of *mip* to the *A* mating-type locus in other hymenomycetes. In addition, we suggest the gene might be useful as a marker for understanding mating systems of less genetically tractable mushroom species.

Morphogenesis and apical surface gradients in saprolegniaceous hyphae. D.-U. JAVIER (1), G. Gerhard (2), and B.-G. Salomon (3). Depts. of (1) Plant Pathology and (2) Mathematics, University of California, Riverside, CA 92521. USA; (3) CICESE, Centro de Investigaciones Cientificas y Estudios Superiores de Ensenada, 22830 B.C. MEXICO. Phytopathology 91:S114. Publication no. P-2001-0088-MSA.

Because of their wide range of apical morphology, saprolegniaceous fungi were chosen to analyze gradients of surface extension during tip growth. As we showed previously, hyphae are generated by a sharp gradient of wall construction centered at the apical pole. The hyphoid equation $y \; x \; cot \; (xV/N)$ describes both the gradient of exocytosis and cell shape. All hyphal tips of *Saprolegnia parasitica* analyzed conformed closely to the hyphoid equation. Concordance extended for hyphal lengths up to 230 um. By contrast, most hyphal tips of *Achlya* spp. matched the hyphoid equation only in the apical region (ca 6 um); beyond the apex, most hyphae adopted a conoid shape. Hyphae of *Aphanomyces astaci* and *Leptolegnia* approximated the hyphoid shape but their tips tended to be more rounded. Since all 4 species were capable of growing hyphoid shapes, we conclude that the tip growth mechanism in oomycetous fungi must be basically the same as that predicted for higher fungi, i.e. controlled by a VSC (vesicle supply center). The departure from the hyphoid shape in *Achlya* denotes an exocytosis gradient that is not tightly centered around a discrete VSC but tapers more gradually into the subapex. A mathematical model was developed that stretched part of the VSC to generate a more gradual gradient of surface growth; the model duplicated well the conoid shape of *Achlya* hyphae.

Phylogenetic relationships of *Pestalotiopsis* and allied genera inferred from ribosomal DNA sequences. R. V. JEEWON, E. C. Y. Liew, G. J. Smith, I. J. Hodgkiss, and K. D. Hyde. Centre for Research in Fungal Diversity, Dept of Ecology & Biodiversity, The University of Hong Kong, Pokfulam Rd, Hong Kong. Phytopathology 91:S114. Publication no. P-2001-0089-MSA.

The phylogenetic relationships of *Pestalotiopsis* and allied genera *Bartalinia, Discosia, Monochaetia, Pestalotia, Seimatosporium, Seiridium* and *Truncatella* were investigated. A data set of 888 aligned sites from the 5' end of the 28S rDNA gene for 31 ingroup taxa and 6 outgroup taxa from different orders was employed to infer phylogenies at the intergeneric level. In addition a data set of 600 aligned sites from the faster evolving ITS regions were used to assess infrageneric relationships among 35 strains of *Pestalotiopsis*. Phylogenetic analyses were conducted using different optimality criteria, including parsimony and maximum likelihood. Results of the 28S phylogenetic scheme showed that *Bartalinia, Pestalotiopsis, Seimatosporium, Seiridium* and *Truncatella* represent distinct monophyletic clades with high bootstrap values. Well-supported clades corresponding to groupings based on conidial morphology were resolved and results verify that these genera should be recognized as distinct genera except for *Monocheatia* and *Discosia* where further taxon sampling is required. Further discussion includes the taxonomic implication of the analyses based on the ITS regions to resolve infrageneric relationships within *Pestalotiopsis*.

Optimizing polygalacturonic acid in NP-10 medium to improve *Verticillium dahliae* recovery from soil. Z. KABIR, R. G. Bhat, and K. V. Subbarao. UC Davis, 1636 E. Alisal St. Salinas, CA 93906. Phytopathology 91:S114. Publication no. P-2001-0090-MSA.

Polygalacturonic acid (PGA) is an important constituent of Sorensen's NP-10 medium used to estimate population density of *V. dahliae*. Different types of PGA are available, but not all of them favor the growth of *V. dahliae*. Unavailability of PGA sodium salt from orange (P-1879, Sigma Chemical Co.) has created an unprecedented problem for the quantification of microsclerotia (MS) of *V. dahliae* in the soil. The PGA from orange (P-3889) that is now available does not support the growth of *V. dahliae*. Therefore, P-3889 was added to NP-10 medium amended with different concentrations of NaOH. The pH of the medium increased from 2.63 to 8.41 as the concentration of NaOH increased from 0 to 0.055N. Seven soils were assayed for MS, and 8 isolates of *V. dahliae* were evaluated for growth on these media and the original NP-10 medium. P-3889 in NP-10 medium with NaOH @ 0.035N reduced mycelial growth and MS production, but did not reduce recovery of MS from soils. P-3889 in NP-10 medium with 0.025N NaOH consistently yielded similar colony numbers of *V. dahliae* from test soils and supported similar colony growth compared with the original NP-10 medium.