FUNGAL DIVERSITY IN WOODY ROOTS OF EAST-SLOPE CASCADE PONDEROSA PINE (*PINUS PONDEROSA*) AND DOUGLAS-FIR (*PSEUDOTSUGA MENZIESII*)

By

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The members of the Committee appointed to examine the thesis of JILL ANNE HOFF find it satisfactory and recommend that it be accepted.

Chair

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Abstract

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Because the fungal community of large woody roots of conifers is not well documented, a mycodiversity study was conducted using increment cores from the woody roots of Douglas-fir (*Pseudotsuga menziesii*) and ponderosa pine (*Pinus ponderosa*) in the dry forests of the east-slope Cascades. Fungal isolates were identified using molecular techniques in combination with morphological characterization. Fungal species identified in this study will serve as a baseline for fungal diversity. Examination of rDNA internal transcribed spacer sequences and morphology of the cultured fungi delineated 27 fungal genera. Two groups predominated: *Byssochlamys* species (39 % of isolations) and *Umbelopsis/Micromucor* species (27 % of isolations). This is the first report of these fungi present on the large woody roots of conifers. These two species, as well as other species isolated in this study (e.g. *Epicoccum* sp., *Phialophora* sp., and *Phlebiopsis gigantea*) have potential as biological control agents. *Byssochlamys* species are heat-resistant fungi in which the ascospores can withstand heat up to 99 C. The occurrence of this fungus is potentially related to fire regimes. In the confines of this

study, the distribution of these genera was not affected by host or habitat type. More information is needed regarding the ecological role of these fungi, their relationship with fire, and their potential for biological control of forest pathogens.

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CHAPTER ONE

LITERATURE REVIEW

Fungal Diversity

In recent years, ecologists have increased efforts to understand critical below-ground interactions in forest ecosystems. Dynamic interactions that occur among plant roots, animals, and microorganisms are determining factors for ecosystem processes. Ecologists have barely begun to study the biodiversity that underpins these interactions (Copely 2000).

Fungi of forest ecosystems are tremendously diverse and play wide-ranging roles in forest ecosystem processes (Rossman 1998). Their capacity for growth on various substrates depends on a complex set of metabolic enzymes and the ability to absorb essential nutrients. Because they obtain their nutrients through absorption, many fungi can successfully exploit organic matter of diverse origin. Fungi play a number of key roles within the world's ecosystems; the most important of which may be the cycling of nutrients derived from the breakdown of plant and animal matter, allowing the re-use of limited biotic and abiotic resources (Rossman et al. 1998).

Studies of fungal biodiversity in forest ecosystems could provide baseline information for determining interrelationships among organisms and indicate potential roles of fungi in forest ecosystem dynamics. Understanding the role of fungi in forest ecosystem processes is key to successful characterization of biological resources. In addition, fungal biodiversity studies will contribute to the discovery and characterization of fungal resources, provide insight into their sustainability, and help slow the loss of these biological resources (Rossman et al. 1998)

Due to their widespread distribution and association with diverse organic and inorganic substrates, the actual number of fungal species in existence is difficult to assess (Rossman et al. 1998). A wide range of fungi have been found to occur in wood including certain Mucoraceous species, Ascomycetes, Basidiomycetes, and Fungi Imperfecti (Rayner and Todd 1979).

Wood decay fungi

Species composition estimates of wood decay fungi in coniferous forests are usually based on the distribution of fruiting bodies. Since fruiting bodies are formed in response to specific environmental conditions, such inventories can span several years and still not guarantee accurate reflections of the fungal species present (Johannesson and Stenlid 1999). Decaying wood presents unique opportunities to investigate fungal growth and interactions within populations and communities of the substrata. The primary biotic decomposers of wood are basidiomycetous decay fungi, which can attack and degrade both wood in the forest and wood in commercial service. In the forest ecosystem, wood decay fungi play an important role in carbon and nitrogen cycling and help convert organic debris into the humus layer of the soil. Some fungi attack living trees; others invade down timber and slash on the forest floor, and lumber. Wood decay basidiomycetes colonize and degrade wood using enzymatic and nonenzymatic processes. Brown-rot fungi preferentially attack and rapidly depolymerize the structural carbohydrates (cellulose and hemicellulose) in the cell wall leaving the modified lignin behind. White-rot fungi can progressively utilize all major cell wall components, including both the carbohydrates and the lignin (Jasalavich et al. 2000).

Pathogenic fungi

Species of fungi in the families Polyporaceae, Hymenochaetaceae, Stereaceae, and Hericiaceae, which reside in the Aphyllophorales, are specialized to enter wounds in living trees and penetrate to the heartwood. Some heart-, butt-, and root-rot fungi are pathogenic and can kill living trees by attacking functional vascular tissues (Alexopoulos et al. 1996). Laminated root rot, caused by *Phellinus pini* (Murrill.) R.L. Gilbertson, kills trees in slowly expanding mortality centers, creating gaps in the forest canopy. *P. pini* is widespread, locally abundant, and very long-lived. It is among the most important disturbance agents in the long intervals between stand-replacing events, such as wildfire or harvest, in these ecosystems and shapes the structure and composition of both wild and managed forests (Hanson and Goheen 2000).

Annosus root disease, caused by the basidiomycete *Heterobasidion annosum* Fr. (Bref.), is a root pathogen present in coniferous forests of the Northern Hemisphere. This species complex includes at least three biological species which display a marked host preference. Stumps and wounds can act as infection courts for this fungus, and roots are common routes of secondary spread from tree to tree. Once the pathogen has established itself in a stand, it will often spread progressively to neighboring trees creating mortality centers (Garbelotto et al. 1997.)

Endophytic fungi

Fungal endophytes can live internally, intercellulary or intracellularly, and asymptomatically. They usually occur in above-ground plant tissues, but also occur

occasionally in roots, and are distinguished from mycorrhizal fungi by lacking extra radical hyphae or mantles. The definition of endophyte has been modified over the last decade and disagreement continues as to the definition of endophyte. For our purposes, endophytes are fungi that live for all, or at least a significant part, of their life cycle internally and asymptomatically in plant parts (Saikkonen et al. 1998.)

While a large body of information is available on pathogens and mycorrhizal fungi, little is known about other symptomless – possibly neutral or mutualistic - endophytic symbionts of aerial plant organs or root associates. Symptomless endophytes can be assembled into two distinct ecological groups: the clavicipitaceous system endophytes, and the endophytes of trees and shrubs including the non-clavicipitaceous grass endophytes (Petrini 1997). Fungal endophytes have been found in all woody plants studied, and numerous species of fungal endophytes have been found in individual plant species and even in individual plants. Trees and shrubs usually contain numerous fungal species. However, there has been little attempt to integrate ecological and evolutionary aspects of fungal endophytes of grasses and woody plants (Saikkonen et al. 1998).

Epiphytic fungi

The external plant provides a suitable environment for diverse microbial flora that vary in kinds, numbers, properties, and local distribution patterns. Surface growth has several implications for microbial structure and function. The plant surface is living and thus establishes several specialized implications depending on the plant species, plant organ, and surrounding biotic and abiotic environment. New areas become progressively

available for colonization as the plant grows (Andrews and Harris 2000). Many researchers have noted the existence of seasonal patterns in the composition of phyllosphere microbial communities. Lindsey and Pugh (1976) reported ascomycetes to be the major group of epiphytic fungi inhabiting leaves. These genera include: *Phoma* spp., *Epicoccum* spp., *Penicillum* spp., and *Cladosporium* spp. Epiphytic fungi of woody roots are not well documented and warrant further study.

Ectomycorrhizal fungi

Ectomycorrhizal (EM) symbioses are important on a global scale because most trees are ectomycorrhizal throughout the world's boreal, temperate, subtropical, and tropical forests. For host trees, these fungi serve as the primary nutrient gathering interface, scavenging nitrogen, phosphorus, and trace elements from both inorganic and organic pools in the soil; this is done in exchange for fixed carbon from the tree (Horton and Bruns 2001). These mutualistic symbioses also provide plants with increased access to other resources, such as water. They also protect plants from pathogens, chemical extremes (e.g., high pH), and heavy-metal contamination (Cullings et al. 2000). Until the middle 1990s, knowledge of EM fungal community structure, and the degree to which species assemblages show predictable colonization patterns in space and time, was almost exclusively based on sporocarp surveys (Dahlberg 2001). EM fungi are generally basidiomycetous fungi (e.g., species of *Russula*, *Cortinarius*, *Chroogomphus*, *Lactarius*, *Suillus*, *Paxillus*) (Cullings et al. 2000; Horton and Bruns 2001).

Mycoparasitic fungi

Interactions between biocontrol fungi and their pathogens are the focus of many continuing research efforts. Some recent examples of fungal-fungal interactions in the rhizosphere and spermosphere include *Trichoderma hamatum* (Bonorden) Bainier with *Rhizoctonia solani* Kuhn, *Phialophora* sp. with *Gaeumannomyces gramminis* var. *tritici* (Ggt). Haver, and *Cladorrhinum foecundissimum* Saccardo & Marchal with *Pythium ultimum* Trow (Whipps 2001).

Mycoparasites are extremely common in soil, where they can act as natural regulators of fungal populations (Mulligan and Deacon 1992). The relationships may be biotrophic, with the host showing few symptoms other than reduced growth rate, or necrotrophic, with the host tissue being killed under some conditions. Researchers are actively pursuing the use of mycoparasitic fungi (e.g., *Trichoderma* spp.) as agents of biological control, and several formulations are available for use against certain plant pathogens including *Pythium* spp. and *Heterobasidion annosum* (Alexopolous et al. 1996).

Species concepts and identification

The species concept is central to biology and has caused considerable debate, yet a universal definition of species has not been found. Much of the discussion has centered on animals and plants, while fungi have received less attention. Species definitions have been based on phenotypic similarity, ecological parameters, reproductive isolation or cohesion, evolutionary principles, and various combinations of the above. Fungal species concepts, in practice, have evolved from strictly morphological descriptions, to a

biological species concept, to phylogenetically based species concepts (Harrington and Rizzo 1999).

In some cases, ecological species have been based on adaptation to a particular niche, or in plant pathology some fungal pathogens have been defined mainly on the basis of disease symptoms or host association. Morphological, ecological, and pathological species are all, therefore, defined from phenetic characters, most of which relate directly to functional and structural attributes. PCR amplification provides information on deoxyribonucleic acid (DNA) sequences, and thereby allows the testing of hypotheses about relationships within and among phenetically defined species (Bridge et al. 1998).

Information on DNA sequences may reinforce existing phenetic species groupings, and in these cases the species can be described as polythetic. But, DNA sequence information can also provide valuable insights into the evolutionary history of phenetic species. This can be especially important in species where the major functional characters available relate to an aspect of their environmental niche, such as in ecological species (Bridge et al. 1998).

Genetic similarities and differences at the molecular level provide a reliable means for assessing phylogenetic relationships. Redecker et al. (1999) reported that single spores of the Glomales contain divergent ribosomal DNA (rDNA) sequences due to the fact these spores contain several thousand nuclei. They examined sequences of *Acaulospora gerdemannii* Schenk & Nicolson and *Glomus leptotichum* Schenck and Smith which possess dimorphic spore types that are divergent to the extent expected for two different genera. The level of sequence divergence found [due to considerable

degree of variation detected among copies of rDNA within single spores of the Glomales (Redecker et al. 1999)] is within the range expected for intraspecific variability. Their phylogenetic analyses indicate that evolutionary patterns in the Glomales are much more complex than previously thought, which makes it difficult to distinguish closely related arbuscular mycorrhizal (AM) fungi by sequence comparisons.

Morphological identification of fungi isolated from wood is difficult and tedious, and many fungal species that grow in wood may not be culturable (Johannesson and Stenlid 1999). Moreover, an additional problem occurs with the identification of cultures of wood-rotting fungi. Even though fungal isolates belong to species that have already been described on the basis of sporocarp morphology, the cultures do not exhibit the characters by which they may be assigned to genera or families (Nobles 1948). Molecular techniques have proven valuable in the identification of fungi from plants and in many disciplines in the biological sciences, including systematics soil (e.g., Vandenkoornhuyse et al. 2002; Horton and Bruns 2001; Johannesson and Stenlid 1999; LanFranco et al. 1998; Liesack et al. 1997), and the elucidation of evolutionary relationships among major groups of fungi (Klich and Mullaney 1992).

Sequences of conserved DNA regions have successfully resolved broad evolutionary relationships among fungi at the family, order, and class levels, but species-level relationships require more variable DNA regions. Ribosomal repeats in rDNA have been regions of choice in identification and phylogenetics for various reasons. Fungal nuclear ribosomal gene clusters are arranged in roughly 200 tandem repeats (Berbee and Taylor 2001). Because each nucleus contains approximately 200 copies of the region, at least one intact copy for molecular analysis can usually be recovered, even from low-

quality DNA preparations (Berbee and Taylor 2001). The transcribed spacer regions in the rDNA operon (internal transcribed spacer regions, ITS1 and ITS2) and the non-transcribed spacer regions between the tandem repeats of the rDNA operon (the intergenic spacer region, IGS) have been successfully used to identify distinct lineages of fungal species and resolve relationships between closely related species (Harrington and Rizzo 1999).

Most of the molecular ecology on EM fungi has involved the restriction analyses of the ITS region. This nuclear region lies between the small subunit (SSU, 17S) and the large subunit (LSU, 25S) rDNA genes and contains two noncoding spacer regions (ITS1 and ITS2) separated by the 5.8S rRNA gene (Horton and Bruns 2001).

In the past, the different methods for identifying fungi used by various authors made it difficult to translate the data supplied by different authors (Nobles 1948). Presently, sequences are published and/or deposited in electronic databases (eg., GenBank, EMBL, and DDBJ), so results from different laboratories can be compared directly. Results can be confirmed or applied to other taxa without obtaining biological strains or clones. However, a limitation to this approach is that there may not be a way to confirm the accuracy of the identification on the sequences deposited. DNA information (e.g., nuclear and mitochondrial DNA sequences), PCR-RFLP, random amplified polymorphic DNA (RAPD), and amplified polymorphic PCR (AP-PCR) have also proved useful for phylogenetic analysis (Takamatsu 1998).

The ITS regions are ideal for identification because they typically have the resolving power to place unknown organisms to the species level or at least within a genus. A fast way to take advantage of the ITS data currently deposited is to search

GenBank or EMBL using only the ITS sequences from unknown samples; sequence variation within spacers is so high that only very closely related taxa are retrieved (Horton and Bruns 2001). For the purposes of the diversity study, we chose to amplify the ITS region of the rDNA to assess species diversity of fungi present in woody roots of Douglas-fir and ponderosa pine. The application of molecular techniques contributes to a more comprehensive assessment of fungal diversity than a diversity study that is based solely on morphology. It allows us to identify fungal species that are non-sporulating and non-sporocarp forming. As the role of fungal diversity in ecosystem processes becomes better understood, information can be used to develop sustainable forest practices (e.g., using prescribed burning to favor fungi that are more heat resistant, with biological control capabilities, and could potentially displace fungal pathogens which are less heat tolerant).

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CHAPTER TWO

FUNGAL BIODIVERSITY OF DOUGLAS-FIR (*PSEUDOTSUGA MENZIESII*) AND PONDEROSA PINE (*PINUS PONDEROSA*) WOODY ROOTS

Introduction

Evolutionary history of organisms comprising a forest ecosystem is characterized by mortality-causing natural disturbance regimes (e.g., fires, predation, disease, insect attack) that have varied in kind, frequency, intensity, and extent. Transitory phenomena dominate evolutionary history of organisms to the extent that a constant state of instability is considered characteristic of natural systems (Covington and Moore 1994). Abiotic disturbances, such as fire, wind, landslides, and mudflows, have long been recognized for their critical influences on vegetation patterns within a forest ecosystem. In addition, pathogens, mutualists, and saprophytes are starting to be recognized for their key roles in structuring natural forest ecosystems.

Application of molecular techniques can provide a more comprehensive assessment of fungal diversity. They allow us to explore unique niches of fungal diversity that are occupied by non-sporulating fungi. For example, a study conducted by Vandenkoornhuyse et al. (2002) found 49 phylotypes in the roots of the grass *Arrhenatherum elatius* using newly designed fungal-specific polymerase chain reaction (PCR) primers for small subunit ribosomal DNA. The phylotypes represented the four recognized fungal taxa: Ascomycota, Basidiomycota, Chytridiomycota, and Zygomycota. Their study also suggested the existence of previously unknown groups of fungi, with two of these groups containing two deeply branching lineages in the phylogenetic tree

that may represent new phyla. In contrast, the authors noted that similar culture-based studies have yielded primarily ascomycetes (Vandenkoornhuyse et al. 2002).

Our overall objective was to establish baseline information on fungal diversity associated with woody roots of Douglas-fir and ponderosa pine (in relation to host species and habitat type) within a relatively dry forest ecosystem in the Wenatchee National Forest, east of the Washington Cascades. In 5 years, a subsequent diversity survey will follow fire treatments to determine the effects of fire regimes on fungal diversity. As the role of fungal diversity in ecosystem processes becomes better understood, such information can be used to develop sustainable forest practices.

Materials and Methods

Study Design

Our study was conducted on south, west, and east aspects in the Mission Creek watershed, Wenatchee National Forest, Wenatchee, WA. On these aspects, a mixed-conifer forest is dominated by ponderosa pine (*P. ponderosa*) and Douglas-fir (*P. menziesii*). Generally, this type of dry forest dominates the eastern edge of the Wenatchee National Forest. A fire-return interval of 10-20 years occurs over the 890,308 ha in the Wenatchee National Forest (http://www.fs.fed.us/pnw/weblab). The Wentachee National Forest receives less than 762 mm of annual precipitation.

The study consisted of 12 experimental units (10-20 ha in size) that will undergo different fire treatments (Fig. 1) (Hessburg and Edmonds, unpublished). When the fire treatments are applied, three units will serve as controls, three as burn-only [prescribed fire only, with periodic burns (Agee et al. 2001)], three as thin-only [periodic cutting,

followed by mechanical fuel treatment and/or physical removal of residue; no use of prescribed fire (Agee et al. 2001)], and three as thin-and-burn [initial and periodic cutting, followed by prescribed fire; fire alone could be used one or more times between cutting intervals (Agee et al. 2001)] (Hessburg and Edmonds, unpublished). Units were placed on all aspects except north, on slopes < 40 %, with no more than 10 % rock cover. Areas that included rare plant species were avoided. Units were placed in a narrow range of dry forest environments, and were indicated by dry Douglas-fir potential vegetation types including the PSME-SPBEL (*Pseudotsuga menziesii/ Spiraea betulifolia* Pall.), PSME-PUTR (*P. menziesii/Purshia tridentata* (Pursh) DC.), PSME-CARU (*P. menziesii/Calamagrostis rubescens* Buckley), and PSME-SYAL (*P. menziesii/Symphoricarpos albus* (L.) S.F. Blake) plant associations (Williams and Smith 1991).

Pretreatment surveys of existing disease symptoms or mortality associated with root pathogens and fungi associated with woody roots of ponderosa pine and Douglas-fir occurred during the 2000 field season (May-September); thinned units were harvested in 2001 after sample collections, and burn treatment units will be ignited in 2002. Post-treatment surveys (identification and mapping of new symptoms or mortality associated with a root disease pathogen) will occur during the 2003 and 2004 field seasons.

Area and Treatment Units

The experimental area and units are shown in Fig. 1. During pre- and post-treatment surveys, trees showing new symptoms or mortality associated with a root pathogen were identified. Root pathogens of original interest were 1) *Phellinus weirii*

(Murrill.) (PHWE), the cause of laminated root rot, 2) *Heterobasidion annosum.* (HEAN; both S- and P-groups), the cause of Annosum root disease, 3) *Armillaria* spp., especially *A. ostoyae* (Romagnesi) Herink (AROS), the cause of Armillaria root disease, and 4) *Leptographium wageneri* (Kendrick) M.J. Wingfeld (LEWA), the cause of black stain root disease (Hessburg and Edmonds, unpublished).

Trees with symptoms (e.g., thinning crown, topkill, resinosus) were identified. An increment borer, which was surfaced sterilized with ethanol after each use, was used to extract increment cores (ca. 5 mm diameter) from the tree roots. Then, the root core was placed in a plastic soda straw with both ends of the straw sealed with masking tape, stored at 4 C, and shipped to the Forestry Sciences Laboratory (USDA Forest Service, RMRS, Moscow, ID) for fungal isolation and identification.

In addition to collecting root cores from all visibly symptomatic trees, trees without visible symptoms of root disease or other damaging agents were surveyed. When an apparently healthy appearing tree was randomly sampled, the tree was mapped, site and tree attribute data were recorded, and one major lateral root was examined in the same manner as previously described (Hessburg and Edmonds, unpublished).

Laboratory Processing of Samples

The samples were stored on ice or at 4 C in a styrofoam cooler for 10 days to 4 weeks after collection in the field. Samples were processed within hours after arrival at the Forestry Sciences Laboratory, Moscow, ID. Depending on the length of the lateral root increment core, it was split into several pieces (ca. 2.5 cm). Each core piece was submerged into 70 % ethanol, flame-sterilized, and placed onto a 60 x 15 mm petri dish

containing a medium selective for basidiomycetous fungi, then placed into an incubator at 21 C in the dark. The selective medium was a benomyl dichloran streptomycin (BDS) agar containing 15 g malt extract, 15 g agar, 40 mg benomyl, 20 mg dichloran (2,6-dichloro-4-nitroaniline), and 100 mg streptomycin per L (Worrall and Harrington 1993).

After 2 months of incubation, the cores were examined for mycelial growth. Subcultures were made on BDS, a nutrient-rich medium (3 % dextrose, 1 % peptone, 1.5 % agarose, and 3 % malt extract), and 2 % malt extract agar (MEA) medium. Cores that supported mycelial growth limited to wood were placed on a non-selective medium (MEA and/or nutrient rich medium) to facilitate growth.

Morphological characterization

To morphologically characterize fungal isolates, specimens were examined with bright-field and phase-contrast optics using an Olympus BX 60 microscope after staining with Melzer's Reagent (Melzer 1924). Depending on the isolate, general morphological characters, such as hyphae, basidia, basidiospores, asci, ascospores, sporangiophores, sporangiospores, zygospores, and chlamydospores, were observed and measured. Taxonomic keys such as: Barron 1971; Kendrick 1971; O'Donnell 1979; Von Arx 1981; Gilbertson 1986; Ellis 1993; Hanlin 1997, etc. were used to aid in identification of fungal cultures. Photographic images were taken with a Nikon Cool Pix 990 ® digital camera (Melville, NY). Permanent slides were prepared using Shurmount® aqueous mounting medium (Triangle Biomedical Sciences, Durham, NC).

Use of Polymerase Chain Reaction (PCR) as a Diagnostic Tool

A mycelial scrape was placed in a 50-µl PCR amplification mixture. When direct mycelial scraping did not provide a suitable DNA template for PCR, mycelial samples were treated with Lyse-N-Go ™ PCR reagent (Pierce, Rockford, IL) following the protocol of the manufacturer. Each 50-µl PCR amplification mixture contained 1.2 U AmpliTaq® (Applied Biosystems, Foster City, CA), 5 µl 10X PCR buffer (Applied Biosystems), 200 µM dNTPs, 4.0 µM $MgCl_2$, 0.5 µM ITS-1 primer, and 0.5 µM ITS-4 primer (White et al. 1990). The cycling parameters were modified from Pimentel et al. (1998): DNA was denatured for 5 min at 94 C, followed by 30 cycles of denaturation at 94 C for 90 s, annealing at 50 C for 1 min 30 s, and extension at 72 C for 2 min 30 s. A final extension was performed at 72 C for 5 min. Amplified products (4 µl) were subjected to agarose-gel electrophoresis at 9V/cm for 2 hr, then viewed with UV light after staining in ethidium bromide.

DNA products were prepared using Exosap-IT (USB, Cleveland, OH) PCR product clean up, following the protocol of the manufacturer. The reaction conditions were 37 C for 15 min followed by 80 C for 15 min. The DNA products were sent to Amplicon Express (Pullman, WA) for sequencing.

Single-stranded sequences were trimmed on both ends, then used to generate double-stranded contigs using BioEdit (Hall 2001). The contigs were then entered into the National Center for Biotechnology Information's GenBank nucleotide BLAST search to facilitate species identification.

Statistical Analyses

Chi-square tests for independence were conducted using Web Chi Square Calculator (http://www.georgetown.edu/cball/webtools/web_chi.html) to determine host and habitat influence on fungal occurrence in the study sites and the relationship of fungal occurrence with symptom expression.

Results

Significance of plant association and host on fungal species occurrence

Approximately 402 cores were processed, of which 28 cores yielded growth of more than one fungal species, 160 yielded growth of one fungal species, and 214 cores did not yield any fungal growth. Of the 402 increment cores obtained within the two types of plant series (PSME and PIPO), 47 % of the samples yielded growth on the increment cores (see Table 1 for summary of isolated fungal genera). However, plant associations had no significant influence on fungal occurrence ($P = 0.66 < 1.0$; Table 2). Of the tree hosts across all of the units, 52 % yielded fungal isolates. However, host species did not significantly influence fungal occurrence ($P = 0.18 < 0.10$; Table 3).

Predominant fungal species occurring in the study sites

Two different fungal genera predominated across all of the units (Table 1). *Byssochlamys* and a species resembling *Umbelopsis* sp. *or Micromucor* sp. (a definitive identification of these isolates could not be made, thus these fungi will be referred to as Group 1), occurred in all of the plant association and host species. *Byssochlamys* spp. comprised 39 % (74 isolates) of the total fungal isolates cultured (188), [18 % of the total

root cores collected (402)] (Tables 4 and 5), and fungal isolates from Group 1 consisted of 27 % (50 isolates) of the fungal isolates cultured [12 % of the total root cores collected (402)] (Tables 6 and 7). However, no significant interactions were observed among the occurrence of the two genera by plant association (*Byssochlamys* spp.: $P = 0.08 < 0.10$; Table 4); (Group 1: $P = 0.43 < 1.0$; Table 6), or by tree host (*Byssochlamys* spp.: $P = 0.18 < 1.0$; Table 5); (Group 1: $P = 0.07 < 0.10$; Table 7), The increment cores from which fungi were isolated came from apparently healthy wood.

ITS sequences of *Byssochlamys* spp. isolates revealed a 93-95 % sequence identity with *B. nivea* (U18361, GenBank). However, *B. nivea* was the only *Byssochlamys* species with ITS sequence information entered into GenBank.

Morphologically, the asci and ascospores of *Byssochlamys* spp. isolates resembled *Byssochlamys nivea* (Westling), and ascogonial initials were observed twice in culture. Chlamydospores (5-7 µm diam) and conidia [(3.0)-4.0 µm x (1.5)-2.5 µm] were frequently observed (Fig. 2), and phialides occasionally observed. They resembled a *Penicillium*-type conidiophore, with long, tapering phialides. The conidia were borne in chains. The ascospores of *B. nivea* are approximately 3 µm in diameter at maturity (Hanlin 1998), the ascospores of our *Byssochlamys* sp. isolated were approximately 3-4 µm in diameter; the asci were approximately 11 µm in diameter. The hyphae were irregularly branched and septate. The color of the mycelia in culture (2 % MEA) ranged from olive to brown with areas of white mycelia interspersed throughout in most cultures (Fig. 2).

Group 1 fungal isolates were isolated from the roots of the conifer species and this group showed morphological relationship to zygomycetous fungi. Surprisingly, ITS

sequences of Group 1 had a sequence identity (90-98 %) to sequences attributed to *Acaulospora colossica* Schultz, Bever Morton (AF133780 and AF133780, GenBank) (Pringle et al. 2000), an arbuscular mycorrhizal fungus that cannot be cultured. Consequently, a subset of our Group 1 fungal isolates were sent to A. Schüßler (Institute of Botany, U. of Darmstadt, Germany) for small subunit (SSU) rDNA sequence analyses, which revealed a high sequence identity with *Umbelopsis* spp. and/or *Micromucor* spp. Additional analyses utilized ITS sequences from other Group 1-like fungal isolates provided by R. Vilgalys (Duke University), E. Vandegrift (Oregon State University), and K.L. O' Donnell (USDA ARS, Peoria, IL) (refer to Chapter 3). These ITS analyses corroborated the identification of our isolates as either *Umbelopsis* sp. or *Micromucor* sp. Further morphological characterization of these fungi is found in Chapter 3.

The occurrence of *Byssochlamys* spp. was not significantly associated with symptomatic nor nonsymptomatic trees (*Byssochlamys* spp: $P = 0.81 < 0.10$; Table 9); However, the occurrence of Group 1 was associated with symptomatic trees (Group 1: $P = 0.03 < 0.05$; Table 8).

Fungal taxa present in study units

The Crow 1 unit, located in the Crow and Pendleton area, consisted of *P. ponderosa/Purshia tridentata*, *P. menziesii/P. tridentata/Agropyron spicatum*, and *P. menziesii/Symphoricarpos albus* plant associations. Sixty-eight percent (32 cores) of the increment cores in this unit yielded fungal growth, while 32 % (15 cores) yielded no fungal growth. Five different genera were found, with Group 1 fungal isolates

(69 %) and *Byssochlamys* spp. (28 %) predominating. One *Mucor* sp., one *Cladosporium* sp., one *Mycena* sp., and three unidentified fungal isolates constituted the remaining 19 % of fungal isolates.

The Crow 3 unit is also located in the Crow and Pendleton area. Sixty-two percent of the increment cores in this unit (18 cores) yielded growth, while 38 % (11 cores) of the increment cores did not yield any growth. Five different genera were found, with *Byssochlamys* spp. (55 %) and Group 1 fungal isolates (38 %) predominating. Two *Epicoccum* species, two *Cladosporium* spp., one *Mucor* spp., and one unidentified fungal isolate constituted the remaining 33 % of fungal isolates.

The Crow 6 unit is also located in the Crow and Pendleton area. Fifty-three percent of the increment cores in this unit (28 cores) yielded growth, while 47 % (25 cores) did not yield any fungal growth. Eight different genera were found, with Group 1 fungal isolates (36 %) and *Byssochlamys* spp. (18 %) predominating. Two *Penicillium* spp., one *Alternaria* sp., one *Phialophora* sp., one *Ulocladium* sp., one *Rhinocladella* sp., one unknown zygomycete and nine unidentified isolates constituted the remaining 57 % of fungal isolates.

Pendleton 30 is found in the Crow and Pendleton area. Forty-nine percent (17 cores) of the increment cores yielded fungal growth, while 51 % (18 cores) of the increment cores did not yield any fungal growth. Five different fungal genera were found with *Byssochlamys* spp. (41 %) predominating. Two *Tremella* sp., one *Tyromyces* sp., one *Heterobasidion* sp., one *Verticillium* sp. and four unidentified fungal isolates constituted the remaining 53 % of fungal isolations. Group 1 fungal isolates did not occur in this unit.

The Unit Ruby is located in the Deer Park Springs area, which also included units Little Camas #11 and Spromberg #4. The plant associations in this area are *P. ponderosa/Rosa woodsii*, *P. ponderosa/S. albus*, and *P. ponderosa/S. albus/C. rubescens*. Sixty-five percent (20 cores) of the increment cores in this unit yielded fungal growth, while 35 % (11 cores) of the increment cores did not yield any growth. Eight different genera were found with *Mucor* spp. (30%) and *Byssochlamys* spp. (20 %) predominating. Two *Mortierella* sp., two *Penicillium* spp., one *Ganoderma* sp., one *Pesotum* sp., one *Verticillium* sp., one ericoid mycorrhizal fungus, and four unidentified fungal isolates constituted the remaining (55 %) fungal isolates. Group 1 fungal isolates did not occur in this unit.

The unit Spromberg #4 is found in the Deer Park area. Fifty percent (18 cores) of the increment cores yielded fungal growth, while 50 % (18 cores) of the increment cores did not yield any growth. Three different fungal genera were found with *Mucor* spp. (44 %), Group 1 fungal isolates (28 %), and *Byssochlamys* spp. (28%) predominating. Six unidentified fungal isolates constituted the remaining 33 % of fungal isolates.

The unit Little Camus # 11 is found in the Deer Park area. Thirty percent (7 cores) of the increment cores yielded fungal growth, while 70 % (16 cores) did not yield any growth. Three different genera were found in this unit with *Byssochlamys* spp. (29%) predominating, and Group 1 constituted 14 % of fungal isolates. One *Phlebiopsis* sp. and three unidentified fungal isolates constituted 57 % of the remaining fungal isolates.

The Unit Slawson 8b is located in the Poison, Slawson, and Tripp Canyon area. The plant associations with this unit are *P. menziesii/Holodiscus discolor*, *P.*

menziesii/Holodiscus discolor/C. *rubescens*, and *P. menziesii/Spiraea betulifolia*. Fifty-one percent (18 cores) of the increment cores yielded fungal growth, while 49 % (17 cores) did not yield any fungal growth. Ten different genera were found with *Byssochlamys* spp. predominating (28 %). Two Group 1 fungal isolates, two *Tremella* sp., two *Mucor* spp., two *Penicillium* spp., one *Merimbla* sp., one *Cladosporium* sp., one *Pycnoporus* sp., one *Clavulina* sp., one *Hypocrea* sp., and two unidentified fungal isolates constituted the remaining 83 % of the fungal isolates.

The unit Tripp is located in the Poison, Slawson, and Tripp Canyon area. Thirty-nine percent (13 cores) of the increment cores yielded fungal growth, while 61 % (20 cores) did not yield any fungal growth. Two different genera were found with *Byssochlamys* spp. (77 %) predominating. One *Mucor* sp. and two unidentified fungal isolates constituted the remaining 23 % of the fungal isolates.

The unit Poison is located in the Poison, Slawson, and Tripp Canyon area. Thirty-four percent (10 cores) of the increment cores yielded fungal growth, while 66 % (19 cores) did not yield any fungal growth. Six different genera were found on this site with *Byssochlamys* spp. (30 %) and *Verticillium* sp. (20 %) predominating. One *Eupenicillium* sp., one *Mucor* sp., one *Penicillium* sp., and one unidentified fungal isolate constituted the remaining 60 % of the fungal isolates.

Units Sand 2 and Sand 19 are located in the Sand Creek area. Forty-three percent (13 cores) of the increment cores yielded fungal growth, while 57 % (17 cores) did not yield any fungal growth. Four different genera were found with *Byssochlamys* spp. (77 %) predominating. Two *Penicillium* sp., one *Hormonema* sp., one Group 1 fungal

isolate, and one unidentified fungal isolate constituted the remaining 39 % of the fungal isolates.

In the Sand 19 unit, only 18 % (6 cores) of the increment cores yield fungal growth, while 82 % (27 cores) did not yield any fungal growth. Two different genera were found in this unit, with *Byssochlamys* spp. (67 %) predominating. Two *Penicillium* sp. and one unidentified fungal isolate constituted the remaining 50 % of the fungal isolates.

Discussion

Results revealed woody roots of Douglas-fir and ponderosa pine were colonized by a range of fungi including *Byssochlamys* spp., Group 1 fungal isolates, *Mucor* spp., *Tremella* sp., *Penicillium* spp., *Verticillium* sp., *Ganoderma* sp., and other species. If these fungi are actively growing in woody roots, their ecological role is unknown and warrants further investigation.

Originally, this study was designed to survey for *Heterobasidion annosum,* which is a basidiomycete affecting a wide array of coniferous tree species worldwide. Only one isolate (Pendleton G10-1-1) was found across the units in this study. Studies on the etiology of this pathogen in *Pinus* spp. and *Picea* spp. have indicated that stumps are important sites for fungal primary infections, presumably by basidiospores (Garbelotto et al. 1999). The creation of stumps, by extensive logging of conifer forests, have favored the establishment of this pathogen in stands where originally it may have been rare (Garbelotto et al. 1999).

Phlebiopsis gigantea was another species isolated from woody roots, and is a common colonizer of fresh conifer wood in boreal and temperate forests throughout the world. This fungus typically causes a white rot of coniferous timber and is a primary colonizer of wood, requiring high moisture content for its growth (Holdenreider and Greig 1998). It is a primary colonizer of conifer logs, and, over time, can cause significant deterioration in the forest. Basidiomata of *P. gigantea* frequently form on stumps, fallen trunks, and log piles (Holdenrieder and Greig 1998). Fructification occurs normally within 1 yr after infection and continues for up to 3 or 4 yrs.

In studies on *H. annosum*, Rishbeth (1963) found that *P. gigantea* colonized stumps and showed some ability to replace *H. annosum* in roots. The level of natural colonization of pine stumps by *P. gigantea* can be high. The strong ability of *P. gigantea* to colonize pine stumps indicates that natural infection alone could potentially protect stumps against invasions by *H. annosum* (Holdenrieder and Greig 1998). Treating stumps with *P. gigantea* to control *H. annosum* is an example of successful biological control of a fungal disease in forestry.

The isolation of *P. gigantea* from the woody roots of conifers raises questions about its ecological relationship with the roots. Perhaps its mycelium can colonize the woody root system in addition to stumps of pine. Woody roots may represent the initial colonization site for mycelium that eventually grows to the stump surface following tree cutting. Because only one isolate of *P. gigantea* was isolated, the role that *P. gigantea* played in limiting the occurrence of *H. annosum* cannot be determined.

Verticillium species are commonly found in soil or in decaying plant matter (Gams 1971). *Verticillium* spp. invade plant roots as they grow through the soil.

(Gleason and Flynn 1998). However, the occurrence of *Verticillium* spp. in roots of conifers is not well-documented, and thus the occurrence of *Verticillium* sp. needs to be examined further.

Species of Mortierellaceae (Zygomycota) commonly are isolated from soil, but can also be found in wood, leaves, fungi, and other organic material (Alexopoulos et al. 1996). Members of the genus *Mortierella* are typically found in soil and are thought to play significant roles in the ecology of forest soils (Carreiro and Koske 1992). Reports of the occurrence of *Mortierella* spp. with woody roots were not found in existing literature, and the nature of the association between the fungus on conifer roots remains unknown.

Epicoccum species are widely distributed and commonly isolated from air, soil, and foodstuff (Domsch et al. 1980). This genus occurs in association with some animals and textiles, although it is not known to cause symptoms of infection in animals. *Epiccocum nigrum* Link. is the common causative agent of leaf spots of various plants (Pritchard and Muir 1987), and is common on dead or dying plants (Domsch 1980). *Epicoccum* spp. can also serve as a biocontrol agent to control *Sclerotium sclerotiorum* (Lib.) de Bary (Huang et al. 2000). Piirto et al. (1998) reported the occurrence of *Epicoccum nigrum* on giant sequoias [*Sequoiadendron giganteum* (Lindl.) Buchholz] and it is also known as a soft rotter of wood (Piirto et al. 1998).

Byssochlamys species and Group 1 fungal isolates were the predominant fungi occupying the study sites (Tables 4, 5, 6, and 7) (see Chapter 3 for further discussion on Group 1 fungal isolates). *Byssochlamys* spp. is an ascomycete genus characterized by rudimentary cleistothecia, which envelop asci during development in most ascomycetes.

Asci in *Byssochlamys* spp. are associated with unstructured wefts of white fine hyphae (Beuchat and Pitt 2002).

Piirto et al. (1998) reported a high incidence (38 %; 34 out of 90 fire scars) of *Byssochlamys fulva* isolated from fire scars of giant sequoia. *B. fulva* was found most commonly in fire scars in the 5-year burn group (85 %) versus unburned group (29 %) and 1-year burned (8 %). *Byssochlamys* spp. may have a great potential to serve as biological control agents for forest pathogens such as *Heterobasidion annosum* and *Armillaria* spp. Further study is required to determine what interactions occur between *Byssochlamys* spp. and *H. annosum*, *Armillaria* spp, or other forest pests. At this point, it remains unknown if *Byssochlamys fulva* was isolated from the roots of Douglas-fir and ponderosa pine in our study, ITS sequence information for *B. fulva* is unavailable in either GenBank or EMBL to allow more definitive comparisons.

Both *B. fulva* and *B. nivea* are heat-resistant fungi; ascospores can survive heat exposure up to 99 C (Beauchat and Pitt 2002). *B. nivea* has been shown to be a potential biocontrol species. It is known to inhibit *in vitro* growth of plant pathogenic fungi *Fusarium oxysporum* Schlecht, *Gaeumannomyces graminis* (Sacc.) von Arx and Olivier var. tritici J. Walker, *Phytophthora cinnamoni* Rands, *Pythium irregulare* Buisman, and *Rhizoctonia solani* Kuhn (Park et al. 2001). In this study, *Byssochlamys* spp. were not associated with obvious signs of pathogenicity ($P = 0.8138$; Table 8), but a pathogenic role of this fungus cannot be ruled out. *Byssochlamys nivea* also has been found to cause cuticular disruption, inhibit hatching of eggs, and cause death in nematodes (Park et al. 2001).

Because of its heat resistant nature, fire could potentially be used to favor *Byssochlamys* spp., and could displace root pathogens such as *H. annosum* and *Armillaria ostoyae*. After determining the heat tolerance of root pathogens, a prescribed burn of particular heat intensity above the tolerance level of the pathogen could be used to destroy pathogenic inoculum and favor *Byssochlamys* spp., as long as the heat threshold remains under the tolerance range of *Byssochlamys* spp.

The presence of *Byssochlamys* spp. may remain relatively the same after the 2002 burn. Alternatively, the occurrence of *Byssochlamys* spp. may increase in years following the fire. Other fungal species, which are not heat-resistant, should decline in number or be completely eliminated. This process could allow *Byssochlamys* spp. to establish itself in a manner that could prevent or suppress the establishment of root pathogens and insect pathogens. Such interactions would be especially beneficial in dry forests since they are more prone to pest damage (Wenatchee National Forest 2000). These fungi could also aid in recycling nutrients into the soil, and also could also act as a catalyst for fungal succession after a burn.

Further research (e.g., *in vitro* tests studying interactions between *Byssochlamys* spp. and pathogenic fungi such as *Armillaria* spp. and *H. annosum*; inoculating insect larvae such as pine sawflies, western pine beetle, Douglas-fir tussock moth, Douglas-fir beetle, spruce budworm, and inoculating various conifer species to screen for pathogenic tendencies of *Byssochlamys* spp.) is needed to fully understand potential biological control capabilities of *Byssochlamys* spp., and how to manipulate its presence in a forest ecosystem on the basis of its thermophilic nature. The diversity of the fungal community in large woody roots after the burn treatment should reveal a composition of fungi that

have ruderal characteristics, including effective dispersal, rapid uptake in nutrients, rapid extension for resource capture, and stress tolerance. These characteristics are representative of fungi that favor disturbance (Pugh and Boddy 1988). Because surveys on fungi inhabiting older sections of woody roots have not been previously reported, it cannot be determined if the fungi found in this study are representative of fungi that favor non-stressed environments.

Neither host nor habitat type had any apparent influence on any of the fungal species isolated (Table 2). This may be due to closely related habitat types found across all of the study units. Although plant association did not significantly influence *Byssochlamys* spp. occurrence statistically, *Byssochlamys* spp. occurred in a higher percentage in the PSME series. This trend could be due to the fact that the PSME association is in a more moist environment versus the PIPO association, where the environment is drier.

The overall lack of association between host, plant series, and fungal occurrence could be due to relative similarity in the environmental conditions of Douglas-fir and ponderosa pine associations, or that these fungi are nonspecific. Another possibility is that the fungi found in this study inhabit a micro-environment that is more protected from disturbances, than many ectomycorrhizal fungi. Fungi that colonize fine woody roots are more exposed to the surrounding environment and are easily influenced by varying disturbance regimes (moisture, temperature, logging, fire, etc.). Stendall et al. (1999), found significantly less ectomycorrhizal biomass in soil cores from the top layer (litter and organic horizons) after fire; no significant differences were detected for the middle

and bottom layers of the fire plot cores. In the unburned, control plots, no significant change in ectomycorrhizal biomass was observed between years for any core layer.

The fungal community occupying older sections of woody roots may be less prone to dynamic change after a disturbance such as fire. Further investigations are needed to identify and determine the ecological roles of fungal species that occupy specialized niches that have not been previously known to be inhabited by fungi.

A more extreme variation in environmental conditions, such as moist habitats versus dry habitats, would more likely exhibit a significant influence on the types and number of fungal species isolated. This study was originally designed to determine the amount of *Armillaria* spp. and *Heterobasidion annosum* occupying the study sites before a scheduled 2002 burn. Because of the dry habitats, *Armillaria* spp. (McDonald et al. 1999) and *H. annosum* (P. Hessburg, per. comm.) were not expected to predominate. In 5 yrs, another survey is planned to examine the presence of these pathogens and other fungi to determine how fire treatments impacted the fungal communities inhabiting these sites, and determine if fungal diversity increased or decreased after fire treatments. It would be of further interest to study how fungi occupying these recently discovered niches influence the community dynamics of other fungi in the rhizosphere of forest trees.

Considerations for future diversity studies

To fully encompass the diversity of fungal communities within a geographic region, diverse sites are required that vary in moisture, elevation and aspect. To fully understand diversity of fungal flora in forest ecosystems, other parts of the host must be

examined, such as its bole, branches (upper and lower crown), leaves (upper and lower crown), fine roots, and rhizosphere. Such studies should span time and seasons. Also, a selective medium should be used for each class of fungi (e.g., basidiomycetes, ascomycetes, zygomycetes, etc.). Different methods of sterilization may be necessary and sample processing needs to be done as quickly as possible to avoid loss of fungal isolates. When using an increment borer, effective sterilization must be employed after each use. Ethanol may not be the most effective decontaminating agent since some fungi could be resistant to alcohol, e.g., *Byssochlamys* spp. (Brown and Smith 1957). The numerous fungal isolates that were obtained from such dry locations is indicative of the potential diversity of fungi that could be obtained from other environments that have not been well studied previously. The use of molecular tools can aid in faster identification in a culture-based study. These tools should save time in keying out species versus using morphology alone, tentative identification can be facilitated through GenBank, followed by morphological verification. Using molecular techniques to identify fungi directly from the substrate (which is beneficial for fungal species that cannot be cultured or are non-sporulating) can yield in a higher percentage of diversity, but the disadvantage is that there is no culture available for further identification of taxonomic status. We have not yet reached the point where identifications can be based solely on molecular data available in databanks, but the utility of molecular data is continually increasing.

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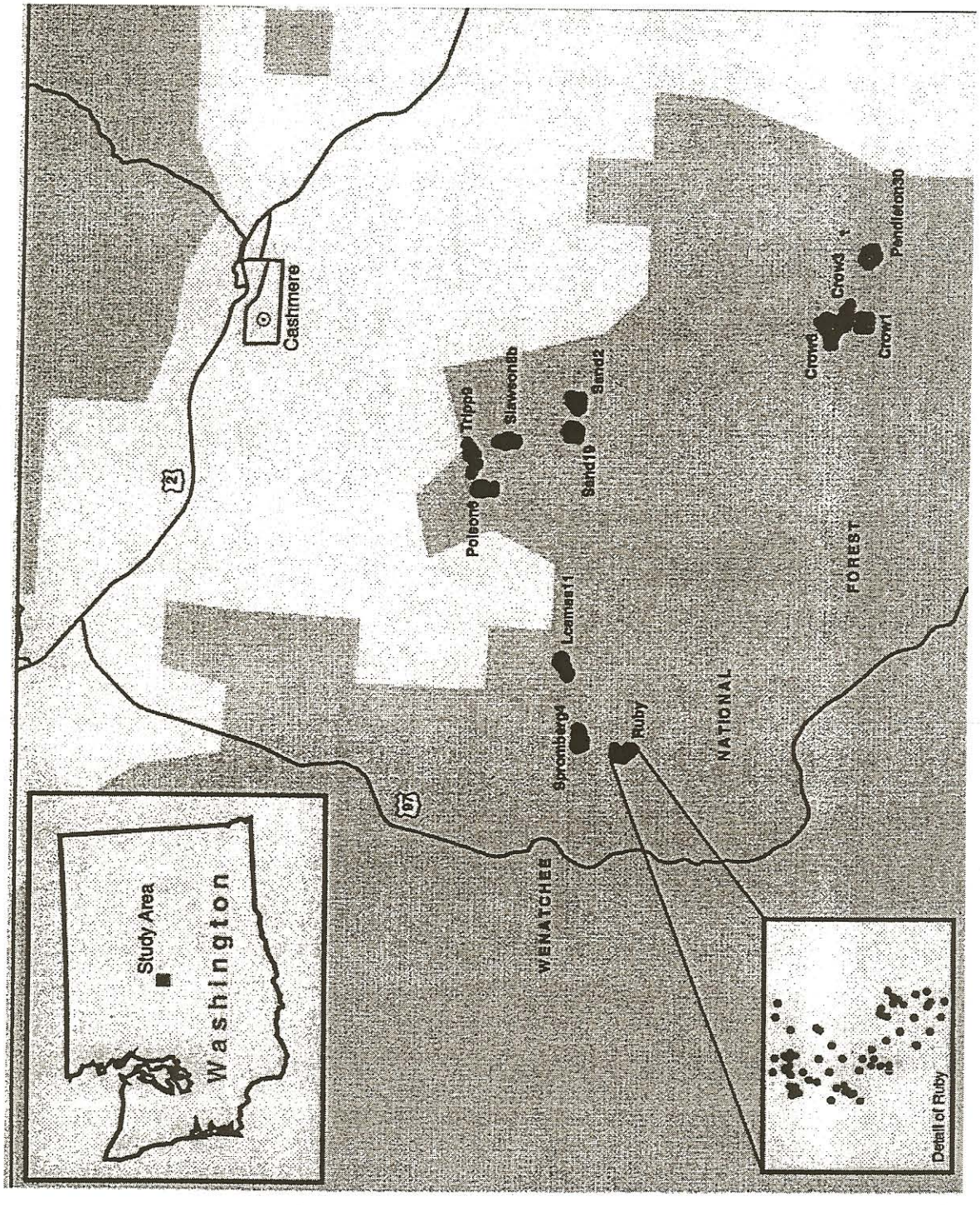

Fig. 1. Experimental plot locations in Wenatchee National Forest. Inset: individual trees sampled within unit Ruby.

Table 1: Fungal genera isolated from woody roots of ponderosa pine and Douglas-fir in decreasing order of frequency.

Taxon	# Isolations	% of Total	% Sequence identity with taxa from GenBank
Byssochlamys spp.	74	39	93-95 % U18361
Group 1	50	27	90-98 % AF133780, AF133782
Mucor sp. 1	11	5.9	Morphologically identified only
Mucor sp. 2	5	2.7	97-98 % AF412291
Verticillium sp.	4	2.1	99-100 % AF033410
Tremella sp.	4	2.1	96 % AF042453
Penicillium sp. 1	3	1.6	100 % AF034448
Cladosporium sp.1	2	1.1	98 % AF393714
Epicoccum sp.	2	1.1	100 % AF279486
Mortierella sp.	2	1.1	100 % AJ 271360
Penicillium sp. 2	2	1.1	99 % AJ279476
unknown zygomycete (oat-root assoc. fungus))	2	1.1	97 % AJ246162
Cladosporium sp. 2	1	1.1	100 % AF393712
Penicillium sp. 3	1	.005	99 % AF033410
Penicillium sp. 4	1	.005	99 % AF034450
Penicillium sp. 5	1	.005	100 % AF033493
Penicillium sp. 6	1	.005	99 % AF033459

Penicillium sp. 7	1	.005	97 % AF033445
Penicillium sp. 8	1	.005	99 %AF033489
Eupenicillium sp.	1	.005	94 % U18358
Rhinocladiella sp.	1	.005	98 % AF229487
Phlebiopsis sp.	1	.005	99 % AF087488
Ganoderma sp.	1	.005	95 % AF255097
Heterobasidion sp.	1	.005	99 % X70023
Phialophora sp.	1	.005	94 % AF083200
Hormonema sp.	1	.005	98 % AF013228
Merimbla sp.	1	.005	93 % AF368298
Pycnoporus sp.	1	.005	94 % AF363772
Alternaria sp.	1	.005	98 % AF314587
Hypocrea sp.	1	.005	97 % AF275330
Clavulina spp.	1	.005	99 % AF335456
Mycena sp.	1	.005	92 % AF335444
Pesotum sp	1	.005	95 % AF198248
Mucor sp. 3	1	.005	93 % AF474242
Chrysosporium sp.	1	.005	99 % AJ131680
Ulocladium sp.	1	.005	98 % AF229487
unidentified white mycelium	1	.005	93 % AB041994
unknown genus (Ericoid mycorrhizal)	1	.005	94 % AF072297

Table 2. Chi-square results for significance of plant association on fungal occurrence.

HOST	FUNGAL GROWTH # cores	%	NO FUNGAL GROWTH # cores	%	TOTAL (cores/series) # cores	%	CHI-SQUARE
PSME	32	49	33	50	65	100	0.189
PIPO	156	46	181	54	337	100	
TOTAL	188	47	214	53	402	100	

df = 1, $\alpha = 0.05$, P = 0.66 < 1.0.

PIPO = ponderosa pine
PSME = Douglas-fir

Table 3. Chi-square results for significance of host/plant association on fungal occurrence.

HOST/PLANT ASSOCIATION	FUNGAL GROWTH # cores	%	NO FUNGAL GROWTH # cores	%	TOTAL TREES (cores/host) # cores	%	CHI-SQUARE
PIPO/PIPO	32	49	33	50	65	100	0.734
PIPO/PSME	83	48	89	51	172	100	
PSME/PSME	73	44	92	56	165	100	
TOTAL	188	47	214	53	402	100	

df = 2, $\alpha = 0.05$, P = 0.18 < 1.0.

PIPO = ponderosa pine
PSME = Douglas-fir

Table 4. Chi-square results for occurrence of *Byssochlamys* spp. within a plant association.

HOST	*Byssochlamys* spp.		No *Byssochlamys* spp.		TOTAL (cores/series)		CHI-SQUARE
	# cores	%	# cores	%	# cores	%	
PSME	7	11	58	89	65	100	3.012
PIPO	67	20	270	80	337	100	
TOTAL	74	18	328	82	402	100	

df = 1, $\alpha = 0.05$, P = 0.08

PIPO = ponderosa pine
PSME = Douglas-fir

Table 5. Chi-square results for occurrence of *Byssochlamys* spp. on host.

HOST/PLANT ASSOCIATION	*Byssochlamys* spp.		No *Byssochlamys* spp.		TOTAL (cores/host)		CHI-SQUARE
	# cores	%	# cores	%	# cores	%	
PIPO/PIPO	7	11	58	89	65	100	3.394
PIPO/PSME	32	19	140	81	172	100	
PSME/PSME	35	21	130	79	165	100	
TOTAL	74	18	328	82	402	100	

df = 2, $\alpha = 0.05$, P = 0.18 < .20.

PIPO = ponderosa pine
PSME = Douglas-fir

Table 6. Chi-square results for occurrence of Group 1 within plant association.

HOST/PLANT ASSOCIATION	Group 1		No Group 1		TOTAL (cores/series)		CHI-SQUARE
	# cores	%	# cores	%	# cores	%	
PSME	10	15	55	85	65	100	0.618
PIPO	40	12	297	88	337	100	
TOTAL	50	12	352	88	402	100	

df = 1, $\alpha = 0.05$, P = 0.43 < 1.0.

PIPO = ponderosa pine
PSME = Douglas-fir

Table 7. Chi-square results for occurrence of Group 1 on host.

HOST	Group 1		No Group 1		TOTAL (cores/series)		CHI-SQUARE
	# cores	%	# cores	%	# cores	%	
PIPO/PIPO	10	15	55	85	65	100	5.346
PIPO/PSME	27	16	145	84	172	100	
PSME/PSME	13	8	152	92	165	100	
TOTAL	50	12	352	88	402	100	

df = 2, $\alpha = 0.05$, P = 0.07 < 0.10.
PIPO = ponderosa pine
PSME = Douglas-fir

Table 8. Chi-square results: Group 1 in symptomatic versus nonsymptomatic trees.

	Group 1 +		Group 1 -		TOTAL		CHI-SQUARE
	#	%	#	%	#	%	
NONSYMP	26	9	268	91	294	100	*4.568
SYMP	14	17	68	83	82	100	
TOTAL	50	13	336	89	376	100	

df = 1, $\alpha = 0.05$, P = 0.03 < 0.05.

Table 9. Chi-square results: *Byssochlamys* spp. in symptomatic versus nonsymptomatic trees.

	Byssochlamys spp. +		*Byssochlamys* spp. -		TOTAL		CHI-SQUARE
	#	%	#	%	#	%	
NONSYMP	54	18	240	82	294	100	0.0555
SYMP	16	20	66	80	82	100	
TOTAL	70	19	306	81	376	100	

df = 1, $\alpha = 0.05$, P = 0.81 < 1.0

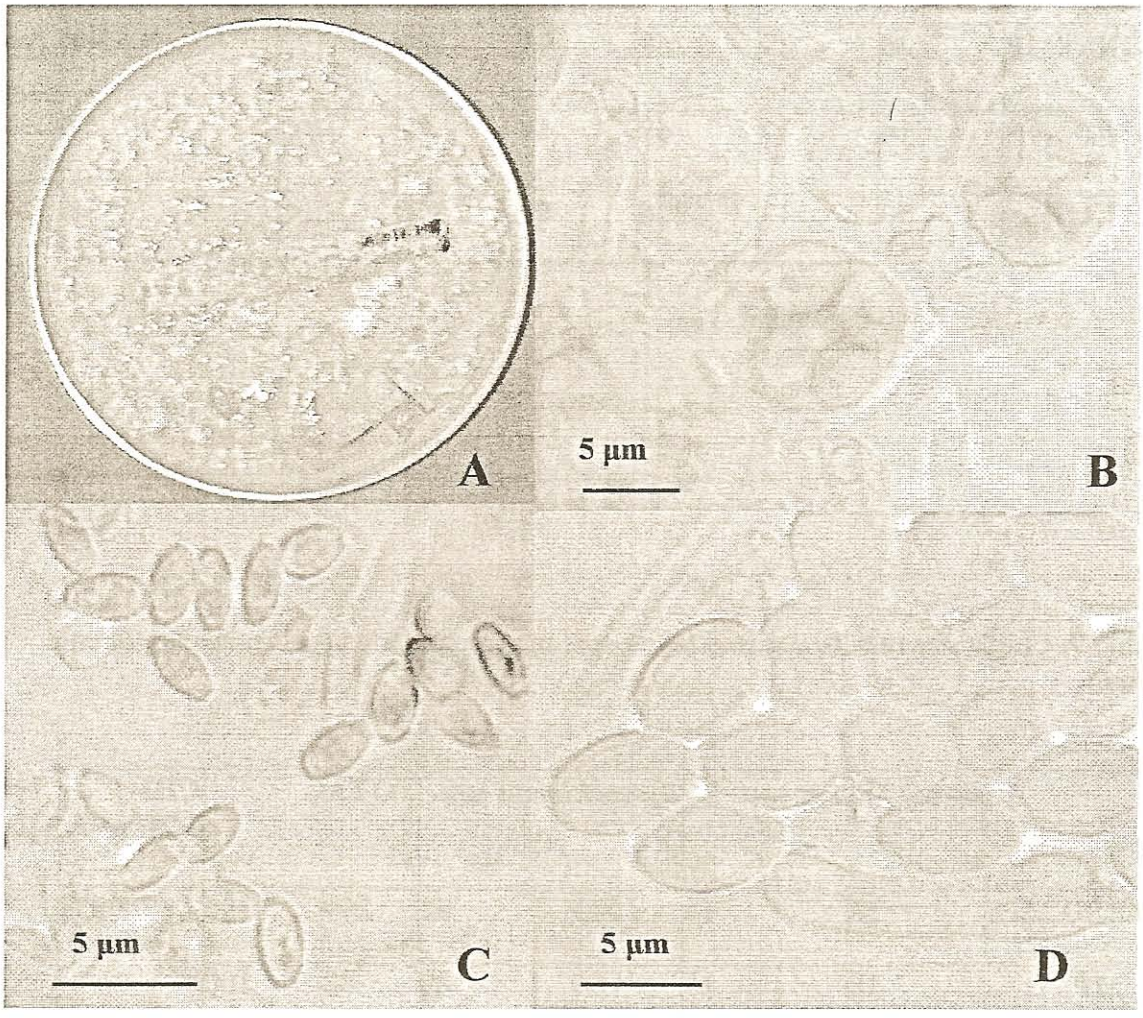

Fig. 2 A. culture of *Byssochlamys* sp.; B. asci containing ascospores; C. conidia; D. chlamydospores

CHAPTER THREE

DESCRIPTION AND POSSIBLE ECOLOGICAL SIGNIFICANCE OF GROUP 1 FUNGAL ISOLATES

Introduction

Ecologists are becoming increasingly aware that many critical interactions with plants occur below ground. In the soil, dynamic interactions among plant roots, animals, and microbes help determine composition of plant communities. The biodiversity that drives these interactions is poorly understood. As ecologists attempt to understand these interactions, a primary hindrance is that soil and roots can contain thousands of unidentified and potentially unculturable species of microorganisms and invertebrates (Copely 2000).

In this study, 50 isolates of a predominantly nonsporulating fungus were isolated from the woody roots of Douglas-fir [*Pseudotsuga menziesii* (Mirb.) Franco] and ponderosa pine (*Pinus ponderosa* Douglas *ex* Lawson & C. Lawson). Twenty-seven different genera were isolated out of 188 total increment cores yielding fungal isolates (402 total increment cores processed), with the unknown group encompassing approximately 27 % of the fungal isolates collected. Sequence data of the small subunit (SSU) indicate this group of fungi belong to *Umbelopsis* or *Micromucor* (A. Scheüßler, per. com.). Morphological features were insufficient for identification thus we will refer to these fungal isolates as Group 1 for the purposes of this study. *Umbelopsis* might be common in forest ecosystems: they been found in soil (K.L. O'Donnell per. comm.; R. Vilgalys, per. comm.), in large woody roots and boles of various conifer species (E.Vandegrift, per. comm.; J.W. Hanna, per. comm.; J.A. Hoff, unpublished), in the roots

of deciduous trees (Amos and Barnett 1966), in association with other fungi [e.g., *Peziza* sp.; (Kendrick et al. 1994)], and in association with tree diseases [e.g., blister rust canker, oak wilt; (B.A. Richardson, per. comm.; Amos and Barnett 1966)].

Objectives

The specific objectives of this study were to:

1) Demonstrate the limitations of morphology and sequence data from the internal transcribed spacer region (ITS) of ribosomal DNA (rDNA) for identification of certain groups of fungi.
2) Determine effects of habitat type, host tree, and geographic location of Group 1 and distribution.

Materials and Methods

Study Design

Our study was conducted on south, west, and east aspects in the Mission Creek watershed, Wenatchee National Forest, Wenatchee, WA. On these aspects, a mixed-conifer forest is dominated by ponderosa pine and Douglas-fir. Generally, this type of dry forest dominates the eastern edge of the Wenatchee National Forest. A fire return interval of 10-20 years occurs over the 890,308 ha in the Wenatchee National Forest (http://www.fs.fed.us/pnw/weblab). Wentachee National Forest receives less than 762 mm of annual precipitation.

The study consisted of 12 experimental treatment units ranging in size from 10-20 ha (Fig. 1) (Hessburg and Edmonds, unpublished). When the fire treatments are applied,

three units will serve as controls, three as burn-only [prescribed fire only, with periodic burns (Agee et al. 2001)], three as thin-only [periodic cutting, followed by mechanical fuel treatment and/or physical removal of residue; no use of prescribed fire (Agee et al. 2001)], and three as thin-and-burn [initial and periodic cutting, followed by prescribed fire; fire alone could be used one or more times between cutting intervals (Agee et al. 2001)] (Hessburg and Edmonds, unpublished). Units were placed on all aspects except north, on slopes < 40 %, with no more than 10 % rock cover. Areas that included rare plant species were avoided. Units were placed in a narrow range of dry forest environments, and were indicated by dry Douglas-fir potential vegetation types including the PSME-SPBEL (*Pseudotsuga menziesii/ Spiraea betulifolia* Pall.), PSME-PUTR (*P. menziesii/Purshia tridentata* (Pursh) DC.), PSME-CARU (*P. menziesii/Calamagrostis rubescens* Buckley), and PSME-SYAL (*P. menziesii/Symphoricarpos albus* (L.) S.F. Blake) plant associations (Williams and Smith 1991).

Pretreatment surveys of existing disease symptoms or mortality associated with root pathogens and fungi associated with woody roots of ponderosa pine and Douglas-fir occurred during the 2000 field season (May-September); thinned units were harvested in 2001 after sample collections, and burn treatment units will be ignited in 2002. Post-treatment surveys (identification and mapping of new symptoms or mortality associated with a root disease pathogen) will occur during the 2003 and 2004 field seasons.

Area and Treatment Units

The experimental area and treatment units are shown in Fig. 1. During pre- and post-treatment surveys, trees showing new symptoms or mortality associated with a root

pathogen were identified. Root pathogens of original interest were 1) *Phellinus weirii* (PHWE), the cause of laminated root rot, 2) *Heterobasidion annosum* (Fr.) Bref. (HEAN; both S- and P-groups), the cause of Annosum root disease, 3) *Armillaria* spp., especially *A. ostoyae* (Romagnesi) Herink (AROS), the cause of Armillaria root disease, and 4) *Leptographium wageneri* (Kendrick) M.J. Wingfeld (LEWA), the cause of black stain root disease (Hessburg and Edmonds, unpublished).

Trees with symptoms (e.g., thinning crown, topkill, resinosus) were identified. An increment borer, which was surfaced sterilized with ethanol after each use, was used to extract increment cores (ca. 5 mm in diameter) from the tree roots. Then, the root core was placed in a plastic soda straw with both ends of the straw sealed with masking tape, stored at 4 C, and shipped to the Forestry Sciences Laboratory (USDA Forest Service, RMRS, Moscow, ID) for fungal isolation and identification.

In addition to collecting root cores from all visibly symptomatic trees, trees without visible symptoms of root disease or other damaging agents were surveyed. When a healthy appearing tree was randomly sampled, the tree was mapped, site and tree attribute data were recorded, and one major lateral root was examined in the same manner as previously described (Hessburg and Edmonds, unpublished).

Laboratory Processing of Samples

The samples were stored on ice or at 4 C in a styrofoam cooler for 10 days to 4 weeks after collection in the field. Samples were processed within hours after arrival at the Forestry Sciences Laboratory, Moscow, ID. Depending on the length of the lateral root increment core, it was split into several pieces (ca. 2.5 cm). Each core piece was

submerged into 70 % ethanol, flame sterilized, and placed onto a 60 x 15 mm petri dish containing a medium selective for basidiomyetous fungi, then placed into an incubator at 21 C in the dark. The selective medium was a benomyl dichloran streptomycin (BDS) agar containing 15 g malt extract, 15 g agar, 40 mg benomyl, 20 mg dichloran (2,6-dichloro-4-nitroaniline), and 100 mg streptomycin per L (Worrall and Harrington 1993).

After 2 months of incubation, the cores were examined for mycelial growth. Subcultures were made on BDS, a nutrient-rich medium (3 % dextrose, 1 % peptone, 1.5 % agarose, and 3 % malt extract), and 2 % malt extract agar (MEA) medium. Cores that supported mycelial growth limited to wood were placed on a non-selective medium (MEA and/or nutrient rich medium) to facilitate growth.

Morphological characterization

To morphologically characterize fungal isolates, specimens were stained with Melzer's Reagent (Melzer 1924), and examined with bright-field and phase-contrast optics using an Olympus BX 60 microscope. Each isolate was examined for morphological characters, such as hyphae, sporangiophores, sporangiospores, and chlamydospores. Also, variations in colony color were noted. Photos were taken with a Nikon Cool Pix® digital camera (Melville, NY). Permanent slides were prepared using Shurmount® aqueous mounting medium (Triangle Biomedical Sciences, Durham, NC). Representative cultures will be deposited into American Type Culture Collections (ATCC) (Manassas, VA), and representative cultures will also be archived at the USDA Forest Service, Forestry Sciences Laboratory (Moscow, ID).

Use of Polymerase Chain Reaction (PCR) as a Diagnostic Tool

A mycelial scrape was placed in a 50-µl PCR amplification mixture. When direct mycelial scraping did not provide a suitable DNA template for PCR, mycelial samples were treated with Lyse-N-Go ™ PCR reagent (Pierce, Rockford, IL) following the protocol of the manufacturer. Each 50-µl PCR amplification mixture contained 1.2 U AmpliTaq® (Applied Biosystems, Foster City, CA), 5 µl 10X PCR buffer (Applied Biosystems), 200 µM dNTPs, 4.0 µM $MgCl_2$, 0.5 µM ITS-1 primer, and 0.5 µM ITS-4 primer (White et al. 1990). The cycling parameters were modified from Pimentel et al. (1998): DNA was denatured for 5 min at 94 C, followed by 30 cycles of denaturation at 94 C for 90 s, annealing at 50 C for 1 min 30 s, and extension at 72 C for 2 min 30 s. A final extension was performed at 72 C for 5 min. Amplified products (4 µl) were subjected to agarose-gel electrophoresis at 120 V for 2 hr, then viewed with UV light after staining in ethidium bromide.

DNA products were prepared using Exosap-IT (USB, Cleveland, OH) PCR product clean up, following the protocol of the manufacturer. The reaction conditions were 37 C for 15 min followed by 80 C for 15 min. The DNA products were sent to Amplicon Express (Pullman, WA) for sequencing on an ABI 377 sequencer (Applied Biosystems, Foster City, CA).

Single-stranded sequences were trimmed on both ends, then used to generate double-stranded contigs using BioEdit (Hall 2001). Multiple sequences were aligned in ClustalX (Higgins et al. 1996) using default settings and checked visually. Cluster analysis was then performed to demonstrate the diversity of phylogenetic clades where these fungi are found. Phylogenetic analysis was performed using MEGA2: Molecular

Evolutionary Genetics Analysis software (Sudhir et al. 2001). Representative of rDNA (ITS-1, 5.8S, ITS-2) sequences will be deposited at GenBank.

Results

A total of 402 increment cores were processed. Of the 402 cores processed, 188 of the cores yielded fungal growth, and Group I constituted 27 % of those isolates (Refer to Chapter 2).

Host and Habitat Influence on Group 1 Occurrence

Group 1 was not significantly associated with plant association ($P = 0.43 < 1.0$) or host species ($P = 0.07 < 0.10$), and were found across all of the sites (Tables 6 and 7, Chapter 2). They were isolated from 37 ponderosa pines out of a total of 144, in PIPO and PSME series, and isolated from 13 Douglas-fir (in PSME series) out of a total 165 (Table 6, Chapter 2). In addition, Group 1 isolates showed a significant association with symptomatic trees ($P = 0.0326 < 0.05$) (Table 8, Chapter 2).

Sequence analysis

The ITS-1, 5.8S, ITS-2 rDNA sequences of Group 1 fungal isolates were entered into GenBank for species identification. BLAST results showed that sequences from several of Group 1 isolates had high sequence identity with *Acaulospora colossica* Schultz, Bever and Morton rDNA sequences deposited into GenBank by Pringle et al. (2000), specifically, the Type 2 cluster they acquired from spore types IVB.10 and IVB.12 collected from a site in Durham, NC. These results were unexpected because, unlike arbuscular mycorrhizal (AM) fungi, our Group 1 isolates were derived from

woody roots of conifers, and the fungi were able to grow independently in culture, without the aid of plant material. An isolate subset (CROW1 G 8-2-2, Sl.8b A3-3-6, CROW1 F5-3-3, CROW3 C7-2-4) was sent to A. Schüßler (Institute of Botany TU Darmstadt, Germany) for rDNA small subunit (SSU; 17S) sequencing.

Due to high variability within the ITS regions of zygomycetes, we compared the 5.8S rDNA sequence with the database of Redecker et al. (1999). Cluster analysis with the 5.8S rDNA sequences of Glomalean fungi, basidiomycetes, and ascomycetes (Redecker et al. 1999) defined one group of our fungal isolates (Group 1) (Fig. 2). They separated into a distinct cluster in comparison with the other groups of fungi, but also included in this cluster were *A. colossica* spore types IVB.10 and IVB.12 (Pringle et al. 2000), which also displayed the highest ITS sequence identity (95-98 %) to Group 1. ITS sequences of *Umbelopsis* spp. and *Micromucor* spp. were not available in GenBank or EMBL for comparison with Group 1. However, culture isolates or ITS sequences of *Umbelopsis* spp. and *Micromucor* spp. were provided by E. Vandegrift, (Oregon State University), R. Vilgalys (Duke University), and K.L. O'Donnell (USDA-ARS) for incorporation and comparison with the 5.8S sequence dataset of Redecker et al. (1999). These sequence data were compared with our Group 1 isolates and other fungal groups. Bootstrap values (65 %) do not support the distinction between *Umbelopsis* spp. or *Micromucor* spp (Fig. 2).

ITS phylogenetic analysis indicates that there is sequence variability among Group 1 fungal isolates (Fig. 3). Within the clade that constitutes Group 1 (100 % bootstrap support), 2 distinct clusters formed, with three of the ITS sequences from Group 1 clustering closely with *Umbelopsis isabellina*, while the other sequences are not

associated directly with either *Umbelopsis isabellina* or *Micromucor rammanianus* Möller. Thus, it is difficult to conclusively determine the taxonomic identity of Group 1.

Morphology

Group 1 isolates produced abundant growth on BDS, a nutrient-rich medium, and 2% (MEA). Culture colonies ranged from cream to tan in color, and some exhibited a grayish color. Three isolates had colonies which were pink (Fig. 3). The mycelia and chlamydospores were filled with lipid droplets, that were visible microscopically (Fig. 3). Hyphae were coencocytic, with an apparently random branching pattern. Intercalary and terminal chlamydospores were formed that were 20-(49) x 22-(49) µm in diameter (Fig. 3). Sporangia, with sporangiospores were occasionally observed in some of the isolates (Fig. 3).

Discussion

Morphologically, it is difficult to conclusively determine whether our Group 1 fungal isolates are identical to *Umbelopsis* or *Micromucor*. These isolates tend to demonstrate morphological variability among chlamydospores within isolates (Fig. 4). Sporangiospores have been reported that were seemingly abundant and highly variable in *Umbelopsis versiformis* (Amos and Barnett 1966; Kendrick et al. 1994). Our Group 1 fungal isolates and *Umbelopsis versiformis* have both been isolated from woody roots of trees. However, Group 1 was isolated from conifers, whereas *Umbelopsis* species were previously isolated from deciduous trees and from a *Peziza* species (Amos and Barnett 1966; Kendrick et al. 1994).

Variability of the ITS sequences within Group 1 fungal isolates may indicate that ITS sequences alone may be insufficient for taxonomic classification of this particular fungal group. Perhaps a more in depth sequence analysis of other regions of the genome (i.e., SSU or LSU) may give more definitive insights into the taxonomic classification of these isolates.

Morphologically, Group 1 isolates are of zygomycetous nature based on the morphology of the sporangia and chlamydospores (Fig. 4). However, phylogenetically, it is difficult to assess exactly where Group 1 fits (Figs. 2 and 3) within the Zygomycota, and separation of *Micromucor* and *Umbelopsis* is not well-supported by bootstrap values in the phylogenetic analysis of 5.8S sequences (65 %, Fig. 2). However, phylogenetic analysis of ITS, 5.8S, and ITS 2 sequences indicates a separation of these two species (83 %, Fig. 3). Neither morphological data, 5.8S sequence data, nor ITS sequence data were sufficient for definitive classification of Group 1 within the zygomycetes, although SSU data reveal a similarity to *Umbelospis isabellina* (A. Schüßler, per. com.). This ambiguity is partially due to the current state of uncertainty regarding zygomycete taxonomy. Voigt and Wöstemeyer (2001) examined the taxonomic placement of *Umbelopsis* spp. and *Micromucor* spp. using sequence data from the actin and translation elongation factor (EF-1α) genes, and considered these genera as members of the Mucorales rather than the Mortierellales where they have been placed. Based on 18S and 28S rDNA, Voigt et al. (1999) stated that *Micromucor ramannianus* represents one of the basal divergences within the Mucorales. O'Donnell et al. (2001) using 18S rDNA, 28S rDNA, and EF-1α gene exons showed that a *Micromucor-Umbelopsis* clade, traditionally included in the Mortierellaceae, was the basal sister-group to all other Mucorales. Their

report showed that traditional family-level classification schemes for this order appear to be highly ambiguous as evidenced by polyphyly of four of the seven families containing two or more genera.

The fungal kingdom has been delineated by the use of morphological, biochemical, and molecular studies. However, phylogenetic groupings at the more 'primitive' end of the clade, including Zygomycota, have yet to be defined. Ascomycetes and basidiomycetes are monophyletic (Schüßler et al. 2001), but according to Voigt and Wöstemeyer (2001), a complete revision of the classification of zygomycetes is needed.

Considerations of using ITS for determining fungal phylogenies and identification

The results in this study indicate limitations of internal transcribed spacer region (ITS) and 5.8S rDNA for phylogeny and identification, related to high variability of ITS in some fungal taxa (Schüßler 1999). Apparent similarity of ITS sequences may indicate a potential affiliation of this fungal group with Glomalean fungi. Alternatively, relationships among ITS sequences may reflect high ITS sequence divergence found within Glomales and Group 1. Sequence data from other regions of the genome could provide more information for discerning species and evaluating phylogenetic relationships. Commonly, the SSU region of rDNA is used in Glomalean fungal diversity and phylogeny (Simon et al. 1992; Clapp et al. 1995; Sanders et al. 1996; Bago et al. 1998; Sawaki et al. 1999; Schüßler 1999; Redecker et al. 1999; O'Donnell et al. 2001).

This and other studies are hampered by uncertainty in the reliability of taxonomic identification of sequences entered into databases. This issue is particularly relevant for fungi that cannot be cultured, have non-sporulating strains, or fungi for which taxonomic

status is tenuous. Glomalean fungi are obligate symbionts and must be cultured in association with a host plant. As a consequence, these fungi are difficult to maintain free from contaminating organisms. In a recent study on a number of Glomalean fungi, about 30 % of the cleaned single spores investigated gave rise to sequences from plant, animal, or ascomycetous contaminates (Schüßler 1999). The questionable validity of Glomalean sequences was further emphasized by Redecker et al. (1999) who reported that a published SSU r RNA sequence for *Scutellospora castanea* did not cluster within the Glomaceae, but within the Ascomycetes, with very high bootstrap support. The published sequence was probably derived from an ascomycetous contaminant. Another possibility they proposed was that *S. castanea* contains Ascomycete-related SSU rRNA genes, but that hypothesis is much less probable when compared with the assumption that the DNA isolated from some of the spores investigated was simply contaminated.

This study supports that molecular, morphological, and physiological characters are necessary to assess the taxonomic relatedness and ecology of fungal organisms.

Ecological significance of Group 1

Group 1 isolates are fungi that can inhabit living roots of woody plants or function as hyperparasites of other fungi that are inhabiting woody roots; however, their exact ecological function remains unknown. Group 1 isolates were found on both ponderosa pine and Douglas-fir on dry sites. Thus, neither habitat type nor host species have an apparent strong influence on the presence of this group of fungi (Tables 6 and 7, Chapter 2). In this study, Group 1 isolates were correlated with damage symptoms (Table 8, Chapter 2). At this point it is difficult to assess what factors are driving this relationship.

One possibility is that Group 1 is carried in with insects and establishes itself in trees that are already stressed. This fungus could be occurring in association with pathogens that are actually responsible for pathogenicity. Further research, including a test of Koch's postulates, is warranted to arrive at a more definitive conclusion on the role of pathogenicity, if any, of this fungus.

Other occurrences indicate that these fungi may commonly occur in forest ecosystems. A similar fungus was isolated from wood of Douglas-fir located in a mortality center near Chewelah, WA (J.W. Hanna, USDA Forest Service, Moscow, ID, per. comm.) and from a white pine blister rust (*Cronartium ribicola* Fischer) canker on white pine (*Pinus monticola* Douglas ex D. Don) near Bovill, ID (B.A. Richardson, USDA Forest Service, Moscow, ID, per. comm.). Amos and Barnett (1966) isolated an *Umbelopsis* species while isolating *Ceratocystis fagacearum* (Bretz) Hunt in the roots of naturally infected oak trees.

Recently, E. Vandegrift (Oregon State University, per. comm.) isolated a similar fungus from woody roots of Douglas-fir, western hemlock [(*Tsuga heterophylla* (Raf.) Sarg.], Sitka spruce [(*Picea sitchensis* (Bong.) Carriére], ponderosa pine, and lodgepole pine (*Pinus contorta* Louden). Her study area covers three geographic regions: Oregon coast, Washington Cascades, and high desert in Oregon. She also observed a high ITS sequence similarity with *Acaulospora colossica* (Pringle et al. 2000) (E. Vandegrift, per. comm.) An ITS sequence obtained from Vandegrift clustered with Group 1 (Figs. 2 and 3). Additionally, the SSU and LSU sequence data of her isolates demonstrated high sequence similarity with *Umbelopsis isabellina* (E. Vandegrift, per. comm.).

Alternatively, Group 1 fungi may function as mycorrhizal symbionts, endophytes, or possible agents of biological control. One goal of this study was to survey for *Heterobasidion* spp. and *Armillaria* spp. However, the occurrence of these two pathogens and other pathogenic fungi was limited in the study sites. Because Group 1 fungi were among one of the predominant fungi isolated, further studies are needed to determine if interactions are occurring among Group 1, *Heterobasidion* spp., *Armillaria* spp., and other root pathogens, and bole pathogens.

Group 1 fungi may impact ecosystem processes in an indirect manner. For example, these fungi may alter the rhizosphere to allow colonization of other fungi that can compete with pathogenic fungi. A number of questions remain to be answered: How do these fungi enter woody roots? What sort of symbioses (e.g., competitive, mutualistic, commensalistic, or parasitic) are occurring with this group and other fungi in the rhizosphere? Is competition occurring among them, or is mutualistic symbiosis occurring? And, how do these biological interactions affect the surrounding plant community? Thus, ecological interactions must be considered at multiple levels to determine potential ecological roles of Group 1 fungi.

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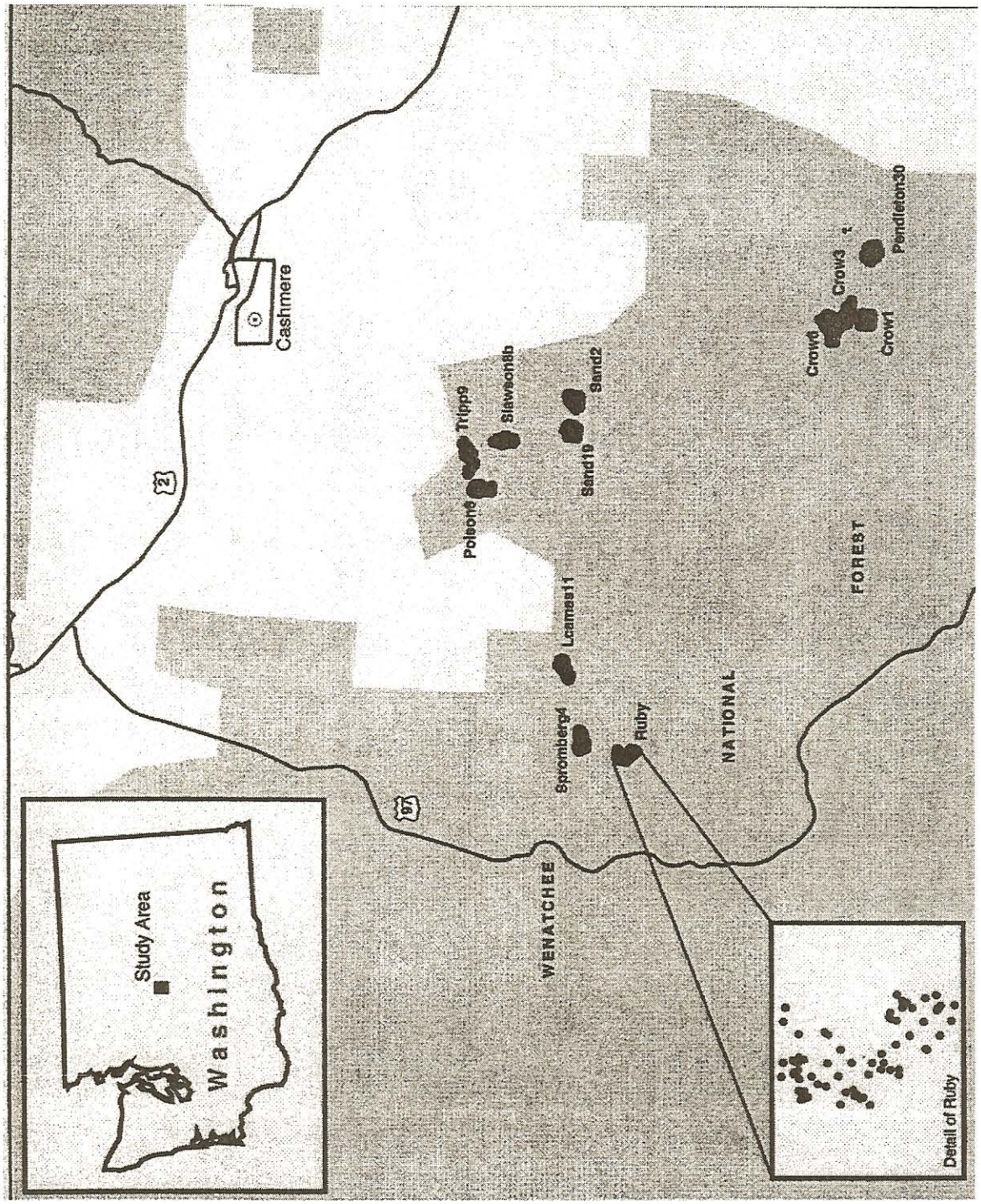
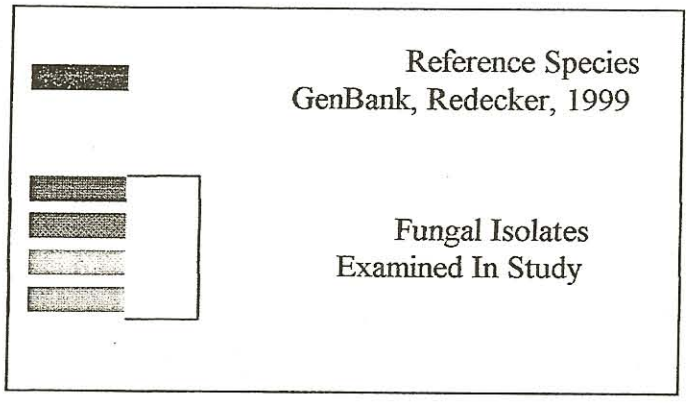


Fig. 1. Experimental plot locations in Wenatchee National Forest. Inset: individual trees sampled within unit Ruby.



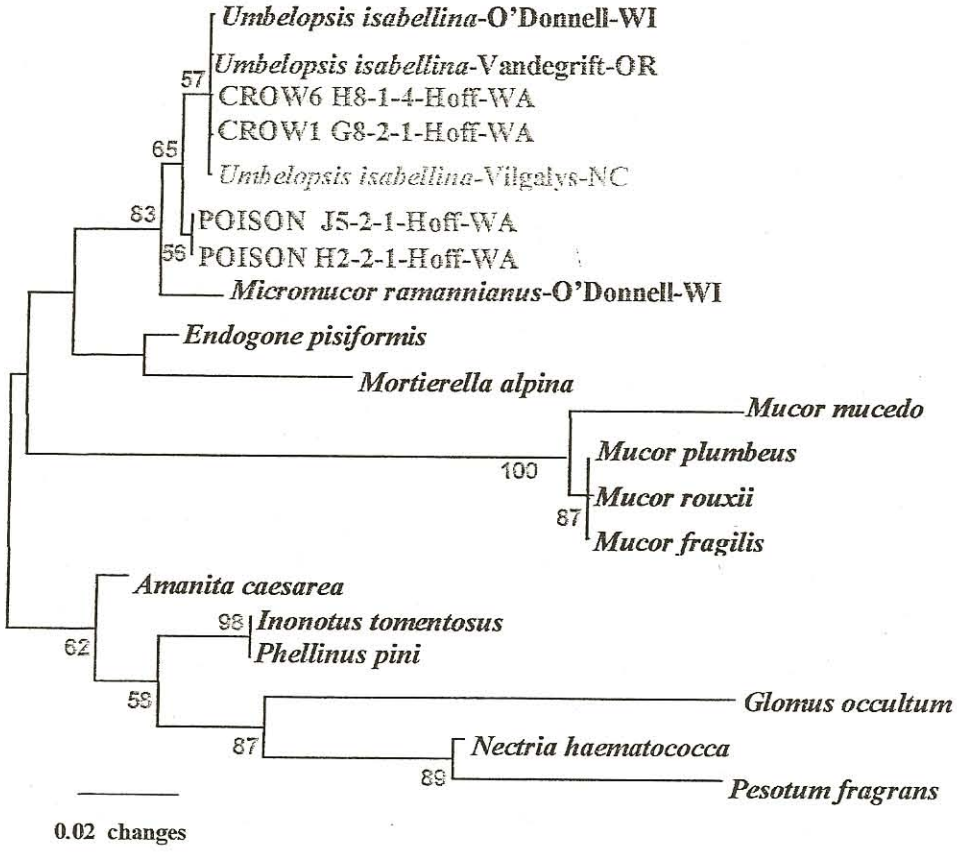


Fig.2. Neighbor-joining tree (1000 bootstraps) of fungal isolates and reference species based on 5.8 S rDNA. Bootstrap values under 50 % were not included in the tree.

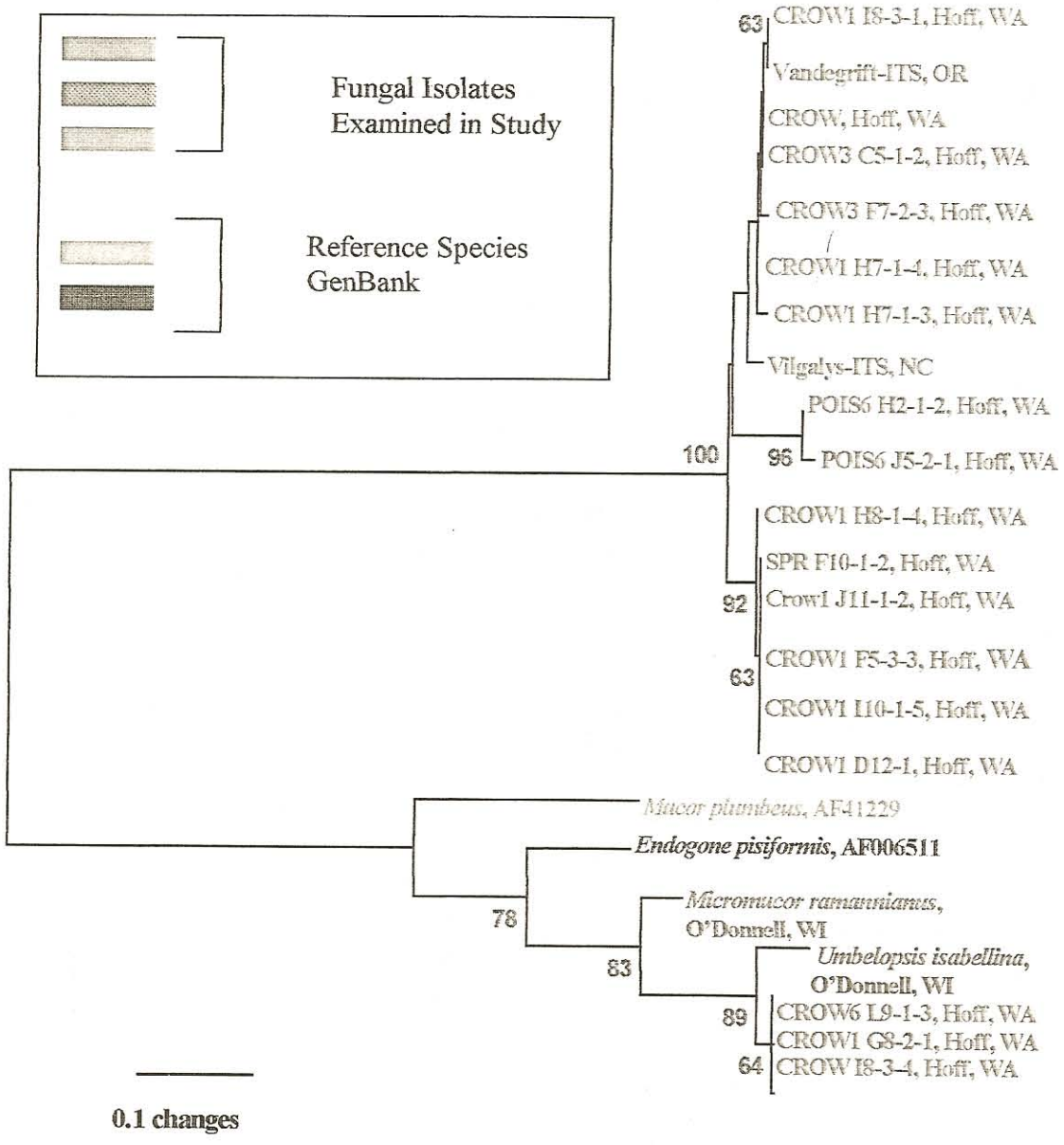


Fig. 3. Neighbor-joining tree (1000 bootstraps) of ITS-1 and ITS-4 rDNA fungal sequences examined and reference sequences from genBank. Bootstrap values under 50 % were not included in tree.

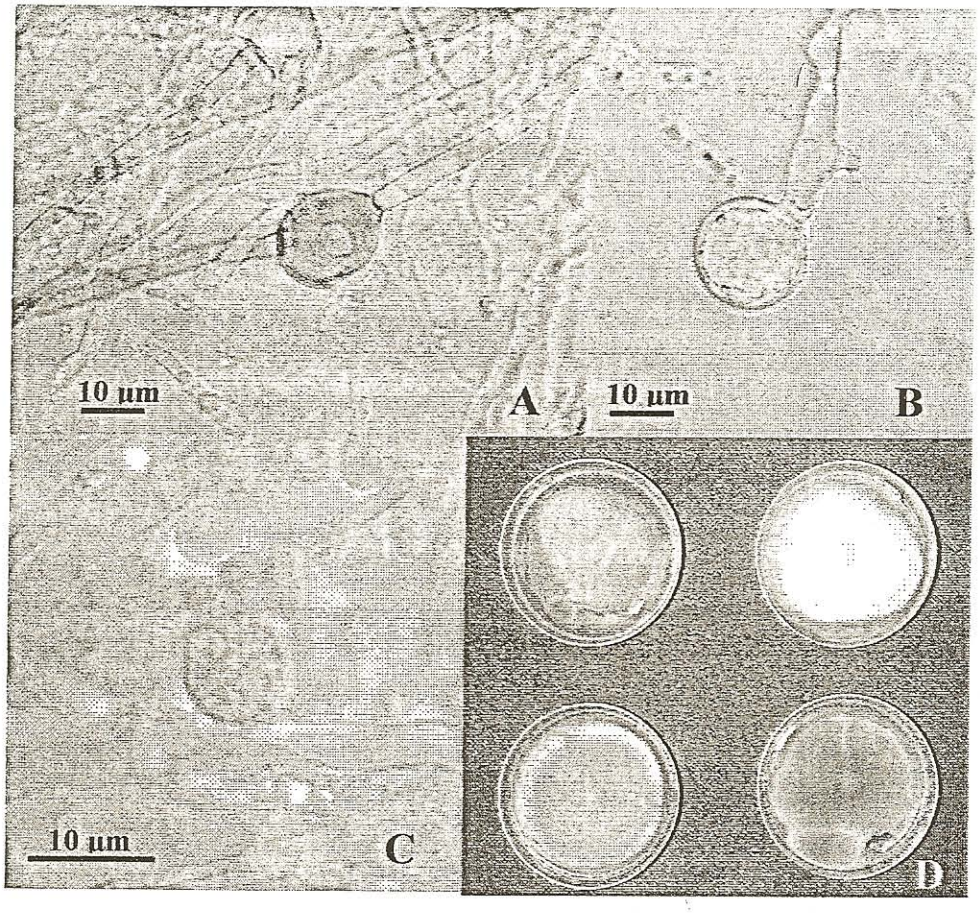


Fig. 3. Morphology of Group 1 fungal isolates A: Intercalary chlamydospores; B: Terminal chlamydospores; C: Sporangia; D. Color variations in colonies

APPENDIX

B. Summary Table of Fungal Taxa Found Within Each Study Unit.

UNITS	NO GROWTH	*BYSSOCHLAMYS* SPP.	GROUP 1	*ALTERNARIA* SP.	*CHRYSOSPORIUM* SP.	*CLADOSPORIUM* SPP.	*CLAVULINA* SP.	*EPICOCCUM* SPP.	*EUPENICILLIUM* SP.	*GANODERMA* SP.	*HETEROBASIDION* SP.	*HORMONEMA* SP.	*HYPOCREA* SP.	*MERIMBLA* SP.	*MUCOR* SPP.	*MORTIERELLA* SP.	*MYCENA* SP.	*PENICILLIUM* SPP.	*PESOTUM* SP.	*PHLEBIOPSIS* SP.	*PHIALOPHORA* SP.	*PYCNOPORUS* SP.	*RHINOCLADIELLA* SP.	*TREMELLA* SP.	*TYROMYCES* SP.	*ULOCLADIUM* SP.	*VERTICILLIUM* SP.	ERICOID MYCORRHIZAL	UNIDENTIFIED WHITE MYCELIUM	UNKNOWN ZYGOMYCETE	UNIDENTIFIED
CROW 1	15	9	22	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3
CROW 3	11	10	7	0	0	2	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CROW 6	25	5	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	1	0	0	1	0	0	0	1	9
L. CAMUS	16	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	3
PENDLETON 30	18	7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	1	0	0	0	4
POISON 6	19	3	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	1
RUBY	11	4	0	0	0	0	0	0	0	1	0	0	0	0	6	1	0	2	1	0	0	0	0	0	0	0	1	1	0	0	4
SAND 19	27	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1
SAND 2	17	10	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0
SLAWSON	17	5	2	0	0	1	1	0	0	0	0	0	1	1	2	0	0	2	0	0	0	1	0	2	0	0	0	0	0	0	2
SPROMBERG 4	18	5	5	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6
TRIPP 9	20	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2

A. Table of Fungal Isolates Containing Host and Habitat Information.

SITE	UTM cell	TREE NUMBER	UNIT ID	PLANT ASSOCIATION	UNDERSTORY	PHASE	TREE SPECIES	STATUS	DBH	HEIGHT	Radial Growth	LCR	ELEVATION	ASPECT	ITS ID	ITS % IDENTITY/ACCESSION NUMBERS	MORPHOLOGICAL IDENTIFICATION
CROW1	C8	1	C8-1	PSME	SYAL	AGSP	PIPO	NONS	17.1	74	8	50	2860	30			*Mucor* sp., *Byssochlamys* sp.
CROW1	D10	1	D10-1	PSME	SYAL	AGSP	PIPO	TPKL	16.7	67	7	20	2920	277	*Umbelopsis/Micromucor* and *Mycena aff. Murina*	*Mycena* -92 % AF335444	
CROW1	D12	1	D12-1	PSME	PUTR	AGSP	PIPO	NONS	14.5	53	10	70	2930	125	*Umbelopsis/Micromucor*	98 %-AF133780	*Umbelopsis/Micromucor*
CROW1	D5	1	D5-1	PSME	SYAL	AGSP	PSME	NONS	19.4	91	11	80	2600	152	NO GROWTH		NO GROWTH
CROW1	D7	1	D7-1	PSME	SYAL	AGSP	PIPO	NONS	14.4	74	8	40	2850	174	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	D9	1	D9-1	PIPO	PUTR	AGSP	PIPO	NONS	27.6	71	9	75	2860	226	NO GROWTH		NO GROWTH
CROW1	E10	1	E10-1	PSME	SYAL	AGSP	PIPO	NONS	11.8	34	9	50	2850	245	yellow fungus-UNIDENTIFIED		
CROW1	E11	1	E11-1	PSME	PUTR	AGSP	PIPO	TPKL	17.5	76	5	25	2900	194	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	E12	1	E12-1	PSME	SYAL	AGSP	PIPO	NONS	11.6	62	8	20	2910	130	uniden white mycellium		
CROW1	E6	1	E6-1	PSME	SYAL	CARU	PIPO	NONS	10.8	61	6	40	2530	146	NO GROWTH		NO GROWTH
CROW1	E8	1	E8-1	PSME	SYAL	AGSP	PIPO	DEAD	22.1	9	NA	NA	2830	188	NO GROWTH		NO GROWTH
CROW1	E8	11	E8-11	PSME	SYAL	AGSP	PIPO	NONS	11.9	71	10	50	2810	190	NO GROWTH		NO GROWTH
CROW1	E8	12	E8-12	PSME	SYAL	AGSP	PIPO	SYMP	11.4	64	9	50	2810	250	*Umbelopsis/Micromucor*	97 %-AF133780	*Umbelopsis/Micromucor*
CROW1	F11	2	F11-2	PSME	SYAL	AGSP	PIPO	NONS	11.8	71	8	45	2880	204	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	F5	3	F5-3	PSME	PUTR	CARU	PSME	NONS	19.7	92	19	70	2540	148	*Umbelopsis/Micromucor*	97 % AF133780	*Byssochlamys* sp.
CROW1	F6	5	F6-5	PSME	SYAL		PIPO	TPKL	21.9	86	5	15	2590	150	*Umbelopsis/Micromucor*	91 % AF133780	*Byssochlamys* sp.
CROW1	F6	6	F6-6	PIPO	SYAL		PIPO	DEAD	10.7	69	4	0	2540	146	*Umbelopsis/Micromucor*		*Byssochlamys* sp.
CROW1	F7	1	F7-1	PSME	SYAL	CARU	PIPO	NONS	19.7	89	14	55	2820	167	UNIDENTIFIED		UNIDENTIFIED
CROW1	F9	1	F9-1	PSME	SYAL	AGSP	PIPO	NONS	9.6	60	10	25	2810	195	NO GROWTH		NO GROWTH
CROW1	G10	1	G10-1	PSME	SYAL	AGSP	PIPO	NONS	11.8	42	16	60	2780	167			*Byssochlamys* sp.
CROW1	G12	1	G12-1	PIPO	SYAL		PIPO	NONS	10.2	55	11	35	2490	168			*Umbelopsis/Micromucor*, *Byssochlamys* sp.
CROW1	G6	1	G6-1	PSME	SYAL		PIPO	NONS	11.3	75	15	65	2510	150	NO GROWTH		NO GROWTH
CROW1	G8	1	G8-1	PSME	SYAL	CARU	PIPO	TPKL	14.0	66	4	20	2810	224	NO GROWTH		NO GROWTH
CROW1	G8	2	G8-2	PSME	SYAL	AGSP	PIPO	NONS	20.1	91	11	55	2800	218	*Umbelopsis/Micromucor*	97 %-AF133782	*Umbelopsis/Micromucor*
CROW1	H11	1	H11-1	PIPO	SYAL	CARU	PIPO	NONS	16.1	58	17	55	2470	274	*Cladosporium magnesianum*	100 % AF393712	
CROW1	H5	4	H5-4	PSME	SYAL		PSME	NONS	19.0	98	13	45	2530	60			
CROW1	H7	1	H7-1	PSME	SYAL	CARU	PIPO	TPKL	21.5	77	4	20	2790	167	*Umbelopsis/Micromucor*	98 % AF133782	*Byssochlamys* sp.
CROW1	H7	2	H7-2	PSME	SYAL	CARU	PIPO	NONS	8.1	39	5	30	2790	150	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	H8	1	H8-1	PIPO	PUTR	AGSP	PIPO	DEAD	9.1	42	NA	NA	2800	234	*Umbelopsis/Micromucor*	97 %-AF133782	*Umbelopsis/Micromucor*
CROW1	H9	1	H9-1	PSME	SYAL	AGSP	PIPO	NONS	8.3	50	3	10	2750	223	NO GROWTH		NO GROWTH
CROW1	I10	1	I10	PSME	SYAL	AGSP	PIPO	NONS	10.4	63	10	50	2720	244	*Umbelopsis/Micromucor*	98 %-133782	*Byssochlamys* sp. and *Umbelopsis/Micromucor*
CROW1	I12	1	I12-1	PIPO	SYAL	AGSP	PIPO	NONS	12.9	50	10	50	2420	155	UNIDENTIFIED		UNIDENTIFIED
CROW1	I8	1	I8-1	PSME	SYAL	CARU	PIPO	NONS	10.6	69	7	30	2780	110	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	I8	2	I8-2	PSME	SYAL	CARU	PIPO	SYMP	16.0	66	4	10	2780	192	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor* and *Byssochlamys* sp.
CROW1	I8	3	I8-3	PSME	SYAL	CARU	PIPO	SYMP	19.5	67	3	35	2800	247	*Umbelopsis/Micromucor*	97 %-AF133780	*Umbelopsis/Micromucor*
CROW1	I9	1	I9-1	PSME	SYAL	AGSP	PIPO	SYMP	19.0	80	10	20	2720	200	NO GROWTH		NO GROWTH
CROW1	J11	1	J11-1	PIPO	SYAL	PUTR	PIPO	NONS	18.1	73	10	70	2430	158	*Umbelopsis/Micromucor*	98 %-AF133780	? *Umbelopsis/Micromucor*
CROW1	J7	2	J7-2	PSME	SYAL		PIPO	NONS	8.8	62	2	NA	NA	95	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	J9	1	J9-1	PSME	SYAL	CARU	PIPO	NONS	11.2	69	6	25	2770	161	NO GROWTH		NO GROWTH
CROW1	K10	1	K10-1	PSME	SYAL	CARU	PIPO	NONS	12.5	44	4	45	2740	184	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	K12	1	K12-1	PSME	SYAL	CARU	PIPO	SYMP	8.9	46	5	10	2430	316	UNIDENTIFIED		*Mucor* sp. ?
CROW1	K12	2	K12-2	PSME	SYAL	CARU	PIPO	NONS	10.0	50	6	35	2430	316	NO GROWTH		NO GROWTH
CROW1	K5	2	K5-2	PIPO	PUTR	AGSP	PIPO	SYMP	23.4	95	4	40	2570	110	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW1	K6	1	K6-1	PSME	SYAL		PIPO	NONS	20.3	67	5	60	2540	120	NO GROWTH		NO GROWTH
CROW1	K8	6	K8-6	PIPO	SYAL		PIPO	NONS	12.2	63	NA	NA	2500	124	NO GROWTH		NO GROWTH

SITE	UTM cell	TREE NUMBER	UNIT ID	PLANT ASSOCIATION	UNDERSTORY	PHASE	TREE SPECIES	STATUS	DBH	HEIGHT	Radial Growth	LCR	ELEVATION	ASPECT	ITS ID	ITS % IDENTITY/ACCESSION NUMBERS	MORPHOLOGICAL IDENTIFICATION
CROW1	K9	12	K9-12	PSME	SYAL	CARU	PIPO	DEAD	10.5	25	3	0	2750	187			
CROW1	K9	2	K9-2	PSME	SYAL		PIPO	DEAD	12.4	59	NA	NA	2460	85	NO GROWTH		*Umbelopsis/Micromucor* ???
																	NO GROWTH
CROW3	B8	1	B8-1	PSME	SPBEL	AGSP	PSME	NONS	15.5	86	11	45	2430	241			
CROW3	C10	1	C10-1	PSME	PUTR	AGSP	PIPO	DEAD	10.3	38	NA	NA	2550	240	NO GROWTH		*Byssochlamys sp.*
CROW3	C3	1	C3-1	PSME	SYAL		PSME	NONS	11.7	60	18	50	2260	340			NO GROWTH
CROW3	C5	1	C5-1	PSME	SYAL		PSME	NONS	13.9	83	21	50	2290	360	*Umbelopsis/Micromucor*		*Byssochlamys sp.*
CROW3	C7	1	C7-1	PSME	CARU	AGSP	PIPO	TPKL	20.9	76	2	30	2430	339	*Epicoccum sp.*		*Umbelopsis/Micromucor*
CROW3	C7	2	C7-2	PSME	PUTR	AGSP	PSME	NONS	8.3	42	18	80	2430	355	*Umbelopsis/Micromucor*	98 % AF133782	*Epicoccum sp.* and *Byssochlamys sp.*
CROW3	D10	2	D10-2	PSME	PUTR	AGSP	PIPO	NONS	17.0	58	7	65	2570	207	*Umbelopsis/Micromucor*		*Byssochlamys sp.*
CROW3	D13	1	D13-1	PIPO	PUTR	AGSP	PIPO	NONS	20.5	82	12	60	2610	247	NO GROWTH		*Byssochlamys sp.*
CROW3	D2	1	D2-1	PSME	SPBEL		PIPO	NONS	22.9	72	4	55	2270	342	NO GROWTH		NO GROWTH
CROW3	D4	3	D4-3	PSME	PUTR		PSME	TPKL	27.0	110	2	55	2370	360	NO GROWTH		NO GROWTH
CROW3	D7	1	D7-1	PSME	AGSP		PIPO	NONS	10.9	53	12	60	2480	307	*Umbelopsis/Micromucor*	95 %-AF133780	NO GROWTH
CROW3	E11	1	E11-1	PSME	PUTR	AGSP	PIPO	TPKL	10.8	42	2	25	2540	208	UNIDENTIFIED		*Byssochlamys sp.*
CROW3	E11	2	E11-2	PSME	SYAL		PSME	NONS	19.9	89	21	80	2510	210	*Umbelopsis/Micromucor*	98 %-AF 133780	UNIDENTIFIED
CROW3	E3	1	E3-1	PSME	CARU	CARU	PIPO	DEAD	8.9	42	NA	NA	2330	265	NO GROWTH		*Umbelopsis/Micromucor*
CROW3	E5	1	E5-1	PSME	SYAL		PIPO	CURA	11.1	70	12	5	2350	220	NO GROWTH		NO GROWTH
CROW3	E7	1	E7-1	PIPO	PUTR		PIPO	NONS	18.7	82	12	50	2470	239	*Epicoccum sp.*	100 %-AF279486	NO GROWTH
CROW3	E8	1	E8-1	PSME	PUTR	AGSP	PIPO	TPKL	12.9	57	2	10	2530	253	*Mucor* sp. and *Byssochlamys* sp.		
CROW3	F10	3	F10-3	PSME	PUTR	AGSP	PIPO	NONS	14.0	56	12	80	2480	274			*Mucor* sp. and *Byssochlamys* sp.
CROW3	F12	1	F12-1	PSME	SYAL	AGSP	PIPO	NONS	25.6	95	6	60	2520	240			*Byssochlamys sp.*
CROW3	F16	1	F16-1	PSME	PUTR	AGSP	PIPO	NONS	11.5	38	12	75	2650	234			*Umbelopsis/Micromucor*
CROW3	F4	2	F4-2	PSME	SYAL		PIPO	NONS	20.1	105	12	45	2280	230	NO GROWTH		*Byssochlamys sp.*
CROW3	F7	2	F7-2	PIPO	PUTR		PIPO	DEAD	19.1	58	NA	NA	2440	109	*Umbelopsis/Micromucor*	95 % AFO133782	NO GROWTH
CROW3	G10	1	G10-1	PSME	SYAL	CARU	PIPO	NONS	19.4	78	10	50	2440	234			*Umbelopsis/Micromucor*
CROW3	G11	1	G11-1	PSME	SYAL	CARU	PSME	NONS	16.9	82	17	50	2460	252	*Cladosporium malorum*		*Byssochlamys sp.*
CROW3	G13	1	G13-1	PSME	SYAL	AGSP	PIPO	NONS	16.6	77	7	35	2550	239	NO GROWTH		
CROW3	G15	4	G14-4	PSME	PUTR	CARU	PIPO	CURA	11.8	66	12	30	2630	280	NO GROWTH		NO GROWTH
CROW3	G15	3	G15-3	PSME	PUTR	CARU	PIPO	NONS	8.0	54	4	60	2620	283	NO GROWTH		NO GROWTH
CROW3	G15	5	G15-5	PSME	PUTR	AGSP	PIPO	SYMP	16.4	61	5	45	2650	280	*Cladosporium malorum*	98 % AF393714	NO GROWTH
CROW3	H15	1	H15-1	PSME	PUTR	AGSP	PIPO	SYMP	10.7	60	7	25	2650	280	NO GROWTH		
																	NO GROWTH
CROW6	A16	1	A16	PIPO	PUTR	CARU	PIPO	NONS	20.1	92	7	50	2530	79	oat root assoc. fungus	97 %-AJ246162	
CROW6	B15	1	B15-1	PIPO	PUTR	CARU	PIPO	NONS	15.0	42	14	70	2550	240	NO GROWTH		*Umbelopsis/Micromucor?*
CROW6	C14	1	C14-1	PSME	PUTR	AGSP	PIPO	NONS	12.8	50	11	60	2530	116	*Umbelopsis/Micromucor*	92 %-AFO133782	NO GROWTH
CROW6	D12	1	D12-1	PIPO	PUTR	AGSP	PIPO	NONS	15.7	48	9	80	2480	240	UNIDENTIFIED		*Umbelopsis/Micromucor*
CROW6	D17	5	D17-5	PIPO	SPBEL	CARU	PIPO	TPKL	10.4	55	2	5	2480	54	NO GROWTH		UNIDENTIFIED
CROW6	D17	6	D17-6	PIPO	SPBEL	CARU	PIPO	NONS	9.4	42	6	35	2480	82	NO GROWTH		NO GROWTH
CROW6	E11	1	E11-1	PSME	PUTR	CARU	PIPO	NONS	10.0	48	7	75	2480	184	NO GROWTH		NO GROWTH
CROW6	E13	1	E13-1	PSME	SYAL	AGSP	PIPO	NONS	14.7	49	8	55	2420	230	*Umbelopsis/Micromucor*		NO GROWTH
CROW6	E14	3	E14-3	PIPO			PIPO	NONS	10.0	50	10	55	2490	192	NO GROWTH		*Umbelopsis/Micromucor*
CROW6	E15	4	E15-4	PIPO		CARU	PIPO	CURA	22.9	57	5	20	2470	128	NO GROWTH		NO GROWTH
CROW6	E16	1	E16-1	PIPO	PUTR	CARU	PIPO	TPKL	24.9	72	5	40	2470	230	*Umbelopsis/Micromucor*		NO GROWTH
CROW6	E18	4	E18-4	PIPO	CARU		PIPO	NONS	9.6	57	5	25	2490	102	*Phialophora sp.*	94 %-AF083200	*Umbelopsis/Micromucor*

SITE	UTM cell	TREE NUMBER	UNIT ID	PLANT ASSOCIATION	UNDERSTORY	PHASE	TREE SPECIES	STATUS	DBH	HEIGHT	Radial Growth	LCR	ELEVATION	ASPECT	ITS ID	ITS % IDENTITY/ACCESSION NUMBERS	MORPHOLOGICAL IDENTIFICATION
CROW 6	F10	1	F10-1	PSME	PUTR	CARU	PIPO	NONS	13.0	44	15	75	2440	138	*Alternaria longipipes*	98 % AF314587	
CROW 6	F10	2	F10-2	PSME	PUTR	CARU	PIPO	DEAD	12.8	48	NA	NA	2440	172	UNIDENTIFIED		UNIDENTIFIED
CROW 6	F12	1	F12-1	PSME	PUTR	CARU	PIPO	DEAD	19.3	53	NA	NA	2390	254	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor , Byssochlamys sp.*
CROW 6	F14	1	F14-1	PIPO	PUTR	AGSP	PIPO	SYMP	17.0	52	5	50	2490	183			*Byssochlamys sp.*
CROW 6	F14	2	F14-2	PIPO	PUTR	AGSP	PIPO	SYMP	24.0	62	4	15	2480	206	NO GROWTH		NO GROWTH
CROW 6	F17	1	F17-1	PIPO	SYAL	CARU	PIPO	NONS	17.3	62	12	70	2470	196	NO GROWTH		NO GROWTH
CROW 6	G13	2	G13-2	PIPO	PUTR	AGSP	PIPO	NONS	19.6	75	12	55	2370	230	NO GROWTH		NO GROWTH
CROW 6	G14	2	G14-2	PSME	CARU		PIPO	NONS	14.2	66	7	65	2470	180	NO GROWTH		NO GROWTH
CROW 6	G16	1	G16-1	PIPO	PUTR	CARU	PIPO	NONS	13.0	43	8	55	2470	307	UNIDENTIFIED		UNIDENTIFIED
CROW 6	G16	1	G16-1	PIPO	PUTR	CARU	PIPO	NONS	13.0	43	8	55	2470	307	NO GROWTH		NO GROWTH
CROW 6	G9	1	G9-1	PIPO	PUTR		PIPO	NONS	16.9	56	7	80	2420	196	NO GROWTH		NO GROWTH
CROW 6	H10	9	H10	PIPO	AGSP		PIPO	NONS	10.3	46	9	70	2360	160	UNIDENTIFIED		UNIDENTIFIED
CROW 6	H13	1	H13-1	PIPO	PUTR	AGSP	PIPO	NONS	25.0	80	6	50	2320	220	NO GROWTH		NO GROWTH
CROW 6	H15	2	H15-2	PSME	PUTR	CARU	PIPO	NONS	10.1	42	13	35	2560	226	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
CROW 6	H17	1	H17-1	PIPO	PUTR	AGSP	PIPO	NONS	14.8	56	NA	NA	2450	108	*Ulocladium botrytis*	98 % AF229487	
CROW 6	H6	1	H6-1	PSME	SYAL	CARU	PIPO	NONS	13.3	63	9	45	2340	178	*Rhinocladiella atrovirens*	98 % AF423122	
CROW 6	H8	1	H8-1	PIPO	PUTR		PIPO	NONS	20.1	61	16	75	2380	234	UNIDENTIFIED		UNIDENTIFIED
CROW 6	H8	2	H8-2	PIPO	PUTR		PIPO	SYMP	15.5	55	5	55	2390	150			*Umbelopsis/Micromucor*
CROW 6	I11	3	I11-3	PSME	CARU		PIPO	DEAD	11.2	52	NA	NA	2320	100	NO GROWTH		NO GROWTH
CROW 6	I11	4	I11-4	PSME	CARU		PIPO	DEAD	9.8	25	NA	NA	2320	160	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor and Byssochlamys sp.*
CROW 6	I12	1	I12-1	PSME	PUTR	CARU	PIPO	NONS	8.8	52	13	35	2280	149	NO GROWTH		NO GROWTH
CROW 6	I16	1	I16-1	PIPO	PUTR	CARU	PIPO	NONS	14.5	51	13	70	2450	201	NO GROWTH		NO GROWTH
CROW 6	I17	1	I17-1	PIPO	PUTR	CARU	PIPO	TPKL	8.7	47	7	15	2410	130	NO GROWTH		NO GROWTH
CROW 6	I17	5	I17-5	PSME	PUTR		PIPO	TPKL	11.5	64	6	20	2410	97	UNIDENTIFIED		UNIDENTIFIED
CROW 6	I5	1	I5-1	PSME	SYAL	CARU	PIPO	NONS	13.0	42	9	55	2320	156	UNIDENTIFIED		UNIDENTIFIED
CROW 6	I6	1	I6-1	PSME	PUTR	CARU	PIPO	SYMP	8.3	50	8	25	2310	213			*Umbelopsis/Micromucor and Byssochlamys sp.*
CROW 6	I6	2	I6-2	PSME	PUTR		PIPO	DEAD	11.6	42	NA	NA	2300	204	NO GROWTH		NO GROWTH
CROW 6	I9	1	I9-1	PSME	PUTR		PIPO	NONS	13.2	75	6	30	2360	185	NO GROWTH		NO GROWTH
CROW 6	J12	1	J12-1	PSME	PUTR	CARU	PIPO	NONS	15.1	58	16	60	2240	162	*Penicillium thomii*	100 % AF034448	
CROW 6	J14	3	J14-3	PIPO	SYAL	CARU	PIPO	SYMP	12.6	53	5	20	2400	240	NO GROWTH		NO GROWTH
CROW 6	J15	2	J15-2	PIPO	PUTR	AGSP	PIPO	NONS	11.5	53	5	15	2490	210	NO GROWTH		NO GROWTH
CROW 6	J17	1	J17-1	PSME	SYAL	CARU	PIPO	NONS	8.5	48	12	70	2410	145			*Penicillium sp.?*
CROW 6	J4	1	J4-1	PSME	PUTR	AGSP	PIPO	NONS	9.7	37	6	45	2370	210	NO GROWTH		NO GROWTH
CROW 6	J8	2	J8-2	PSME	PUTR	CARU	PIPO	NONS	14.8	78	6	35	2270	166	NO GROWTH		NO GROWTH
CROW 6	K10	5	K10-5	PSME	CARU		PIPO	DEAD	11.3	50	NA	NA	2290	246	NO GROWTH		NO GROWTH
CROW 6	K14	2	K14-2	PIPO	SYAL		PIPO	TPKL	22.3	86	5	24	2390	224	UNIDENTIFIED		NO GROWTH
CROW 6	K7	7	K7-7	PSME	PUTR	CARU	PIPO	NONS	17.1	54	9	75	2280	142			UNIDENTIFIED
CROW 6	K9	2	K9-2	PSME	PUTR		PIPO	NONS	19.8	80	6	65	2270	180	NO GROWTH		*Byssochlamys sp.*
CROW 6	L8	1	L8-1	PIPO	PUTR	CARU	PIPO	NONS	12.8	55	9	25	2240	220	UNIDENTIFIED		NO GROWTH
CROW 6	L9	1	L9-1	PSME	CARU		PIPO	TPKL	22.9	82	2	10	2230	168	*Umbelopsis/Micromucor*	98 %-AF133780	UNIDENTIFIED
CROW 6	M11	2	M11-2	PSME	SYAL	CARU	PSME	NONS	14.2	60	14	85	2290	323	*Penicillium thomii*	100 % AF034448	*Umbelopsis/Micromucor*
L. CAMUS	B10	1	B10-1	ABGR	SPBEL	CARU	ABGR	TPKL	11.3	58	7	10	4170	78	NO GROWTH		
L. CAMUS	E10	1	E10-1	ABGR	HODI	CARU	ABGR	NONS	12.0	41	6	75	3800	65	NO GROWTH		NO GROWTH
L. CAMUS	F7	1	F7-1	PSME	SPBEL	CARU	PSME	NONS	8.2	51	10	60	3770	198	UNIDENTIFIED		NO GROWTH
L. CAMUS	F9	1	F9-1	ABGR	ACCI		PIPO	DEAD	13.8	84	NA	NA	3710	170	NO GROWTH		UNIDENTIFIED
L. CAMUS	F9	3	F9-3	ABGR	ACCI		PIPO	CURK	12.0	78	NA	NA	3700	125	*Phlebiopsis gigantea*		NO GROWTH
L. CAMUS	G6	1	G6-1	PSME	SPBEL	CARU	PSME	NONS	10.6	98	19	70	33740	168	UNIDENTIFIED		*Phlebiopsis gigantea*
L. CAMUS	G8	1	G8-1	ABGR	ACCI		PSME	NONS	17.0	102	15	55	3710	173	NO GROWTH		UNIDENTIFIED
L. CAMUS	H5	1	H5-1	PSME	SPBEL	CARU	PSME	NONS	9.9	56	8	75	3780	90	NO GROWTH		NO GROWTH

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L. CAMUS	H5	2	H5-2	PSME	SPBEL	CARU	PSME	DEAD	14.8	67	NA	NA	3740	75	*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
L. CAMUS	H5	3	H5-3	PSME	SPBEL	CARU	PSME	DEAD	23.0	81	NA	NA	3740	75	NO GROWTH		NO GROWTH
L. CAMUS	H6	2	H6-2	PSME	SPBEL	CARU	PSME	NONS	11.8	52	11	65	3730	92			*Byssochlamys sp.*
L. CAMUS	H9	1	H9-1	ABGR	SPBEL	CARU	PSME	NONS	14.8	102	6	45	3650	105	NO GROWTH		NO GROWTH
L. CAMUS	I5	1	I5-1	PSME	SPEL	CARU	PIPO	NONS	8.8	42	3	60	3740	120	NO GROWTH		NO GROWTH
L. CAMUS	I6	1	I6-1	PSME	SPBEL	CARU	PSME	NONS	12.3	58	12	35	3720	79			*Byssochlamys sp.*
L. CAMUS	I8	2	I8-2	PSME	PUTR	CARU	PIPO	NONS	11.7	35	11	60	3680	111	UNIDENTIFIED		UNIDENTIFIED
L. CAMUS	J3	1	J3-1	ABGR	HODI	CARU	ABGR	TPKL	13.9	82	2	15	3600	79	NO GROWTH		NO GROWTH
L. CAMUS	J7	1	J7-1	PSME	SPBEL	CARU	ABGR	DEAD	12.7	48	NA	NA	3580	79	NO GROWTH		NO GROWTH
L. CAMUS	L3	1	L3-1	PSME	SPBEL	CARU	PIPO	NONS	22.2	82	6	75	3600	165	NO GROWTH		NO GROWTH
L. CAMUS	L5	1	L5-1	PSME	SPBEL	CARU	PSME	SYMP	12.0	63	2	15	3550	90	NO GROWTH		NO GROWTH
L. CAMUS	L7	2	L7-2	ABGR	HODI	CARU	PIPO	NONS	17.4	89	6	70	3560	90	NO GROWTH		NO GROWTH
L. CAMUS	M6	1	M6-1	PSME	SPBEL	CARU	PSME	NONS	20.3	89	8	65	3560	75	NO GROWTH		NO GROWTH
L. CAMUS	N3	2	N3-2	PIPO	AGSP	CARU	PSME	NONS	13.4	66	19	90	3540	112	NO GROWTH		NO GROWTH
L. CAMUS	O4	1	O4-1	ABGR	HODI	CARU	ABGR	NONS	9.3	87	28	95	3460	116	NO GROWTH		NO GROWTH
PEND 30	B5	2	B5-2	PIPO	PUTR	CARU	PIPO	NONS	16.0	64	7	40			UNIDENTIFIED		UNIDENTIFIED
PEND 30	B6	3	B6-3	PSME	PUTR	AGSP	PIPO	NONS	21.1	79	6	60			NO GROWTH		NO GROWTH
PEND 30	B7	1	B7-1	PSME	SYAL	CARU	PIPO	NONS	10.8	33	4	60			NO GROWTH		NO GROWTH
PEND 30	C4	1	C4-1	PSME	SYAL	CARU	PIPO	NONS	16.7	80	9	30			NO GROWTH		NO GROWTH
PEND 30	D3	1	D3-1	PSME	PUTR		PIPO	NONS	17.7	70	8	40					*Byssochlamys sp.*
PEND 30	D5	1	D5-1	PSME	PUTR	CARU	PIPO	NONS	24.0	105	7	50					*Byssochlamys sp.*
PEND 30	D7	1	D7-1	PSME	PUTR		PIPO	NONS	26.0	93	3	50			UNIDENTIFIED		*Byssochlamys sp.* ?
PEND 30	E10	1	E10-1	PIPO	PUTR	AGSP	PIPO	NONS	11.6	206	NA	NA			*Tremella giraffa*	96 %AF042453	UNIDENTIFIED
PEND 30	E4	3	E4-3	PIPO	PUTR	CARU	PIPO	NONS	8.8	60	10	15					*Byssochlamys sp.*
PEND 30	E6	1	E6-1	PIPO	CARU		PIPO	NONS	11.4	63	8	25			NO GROWTH		*Verticillium sp.*
PEND 30	E8	3	E8-3	PSME	SYAL		PIPO	NONS	13.0	65	3	50			UNIDENTIFIED		NO GROWTH
PEND 30	F3	6	F3-6	PIPO	PUTR	CARU	PIPO	NONS	9.4	65	9	30			NO GROWTH		UNIDENTIFIED
PEND 30	F5	1	F5-1	PIPO		CARU	PIPO	NONS	12.3	80	9	30			NO GROWTH		NO GROWTH
PEND 30	F7	1	F7-1	PSME	SYAL	AGSP	PIPO	NONS	10.3	62	8	45			NO GROWTH		NO GROWTH
PEND 30	F9	3	F9-3	PSME	SYAL		PIPO	DEAD	13.6	62	NA	NA			NO GROWTH		NO GROWTH
PEND 30	F9	4	F9-4	PSME	SYAL		PIPO	NONS	13.3	75	5	45					NO GROWTH
PEND 30	G10	1	G10-1	PSME	PUTR	CARU	PIPO	NONS	13.4	174	NA	NA					*Byssochlamys sp.*
PEND 30	G6	1	G6-1	PIPO	PUTR	CARU	PIPO	NONS	12.0	48	12	55			*Heterobasidion annosum*	99 % X70023	*Heterobasidion annosum*
PEND 30	G8	1	G8-1	PSME	PUTR	AGSP	PIPO	NONS	12.8	45	5	55			NO GROWTH		NO GROWTH
PEND 30	H11	2	H11-2	PSME	SYAL	CARU	PIPO	NONS	10.9	70	8	30					*Byssochlamys sp.*
PEND 30	H5	1	H5-1	PIPO	PUTR	CARU	PIPO	NONS	8.9	36	7	50			NO GROWTH		NO GROWTH
PEND 30	H7	1	H7-1	PSME	PUTR	AGSP	PIPO	NONS	11.8	64	6	45			NO GROWTH		NO GROWTH
PEND 30	H9	1	H9-1	PSME	SYAL		PIPO	NONS	16.1	62	16	70			NO GROWTH		NO GROWTH
PEND 30	I10	2	I10-2	PSME	SYAL	CARU	PIPO	TPKL	13.7	212	NA	NA			NO GROWTH		NO GROWTH
PEND 30	I10	4	I10-4	PSME	SYAL	CARU	PIPO	SYMP	10.1	228	NA	NA			*Byssochlamys sp.*	95 % U18361	*Byssochlamys sp.*
PEND 30	I11	1	I11-1	PSME	SYAL	CARU	PIPO	NONS	12.3	78	16	40			*Tyromyces chioneus*	95 % AF335447	*Tyromyces chioneus*
PEND 30	I6	10	I6-10	PIPO	PUTR	CARU	PIPO	NONS	14.0	60	9	40			NO GROWTH		NO GROWTH
PEND 30	I8	1	I8-1	PIPO	PUTR	AGSP	PIPO	NONS	8.8	188	NA	NA			NO GROWTH		NO GROWTH
PEND 30	J6	2	J6-2	PSME	PUTR		PIPO	DEAD	18.3	79	NA	NA					*Byssochlamys sp.*
PEND 30	J7	3	J7-3	PSME	SYAL		PIPO	NONS	12.2	64	6	55					*Penicillium sp.*???
PEND 30	J8	1	J8-1	PSME	SYAL		PIPO	SYMP	15.0	84	3	35			NO GROWTH		NO GROWTH
PEND 30	J8	2	J8-2	PSME	SYAL		PIPO	SYMP	17.9	92	6	50			NO GROWTH		NO GROWTH
PEND 30	K10	1	K10-1	PSME	SYAL	CARU	PIPO	NONS	12.5	75	8	25			NO GROWTH		NO GROWTH
PEND 30	K6	5	K6-5	PSME	PUTR		PIPO	NONS	15.5	73	16	30			*Tremella giraffa*	96 % AF042453	*Tremella giraffa*
																	Byssochlamys sp.

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PEND 30	L10	1	L10-1	PSME	PUTR	CARU	PIPO	DEAD	10.2	21	NA	NA					UNIDENTIFIED
POISON 6	F3	1	F3-1	PSME	SYAL		PSME	NONS	17.2	97	17	45			NO GROWTH		NO GROWTH
POISON 6	F7	1	F7-1	PIPO	SYAL	CARU	PIPO	NONS	25.1	111	8	20			UNIDENTIFIED		*Penicillium* spp.?
POISON 6	G11	1	G11-1	PSME	CARU	AGSP	PSME	NONS	9.5	75	7	40			*Verticillium coccosporum*	99 % AF110531	
POISON 6	G14	1	G14-1	PIPO	PUTR	AGSP	PIPO	NONS	26.7	105	7	55					*Mucor* sp.
POISON 6	G2	1	G2-1	PSME	SYAL	CARU	PSME	NONS	13.9	80	18	70			NO GROWTH		NO GROWTH
POISON 6	G4	2	G4-2	PIPO	ROWO		PIPO	SYMP	10.0	68	10	50					*Verticillium coccosporum* ??
POISON 6	G4	3	G4-3	PIPO	ROWO		PIPO	NONS	12.5	86	11	40			*Verticillium coccosporum*	99 % AF110531	*Verticillium coccosporum* and *Byssochlamys* sp.
POISON 6	G6	1	G6-1	PIPO	SYAL	AGSP	PIPO	NONS	28.7	117	7	55			*Eupenicillium javanicum*	94 % U18358	*Byssochlamys sp.*
POISON 6	G6	2	G6-2	PIPO	SYAL		PIPO	TPKL	35.8	103	2	40			NO GROWTH		NO GROWTH
POISON 6	G8	1	G8-1	PSME	SYAL	CARU	PSME	NONS	10.6	88	10	15			NO GROWTH		NO GROWTH
POISON 6	G9	1	G9-1	PSME	SYAL	CARU	PIPO	TPKL	32.2	115	7	35			*Penicillium spinulosum*	99 %-AF033410	
POISON 6	H10	1	H10-1	PIPO	PUTR	AGSP	PIPO	NONS	17.9	85	18	75			NO GROWTH		NO GROWTH
POISON 6	H2	1	H2-1	PIPO	PUTR	AGSP	PIPO	NONS	15.3	69	11	70			NO GROWTH		NO GROWTH
POISON 6	H5	1	H5-1	PIPO	SYAL		PIPO	NONS	10.0	62	12	50			NO GROWTH		NO GROWTH
POISON 6	H6	1	H6-1	PSME	SYAL	CARU	PIPO	NONS	11.1	78	14	50			NO GROWTH		NO GROWTH
POISON 6	H7	1	H7-1	PSME	SYAL	CARU	PSME	NONS	17.7	110	6	15			NO GROWTH		NO GROWTH
POISON 6	I11	1	I11-1	PIPO	PUTR		PIPO	NONS	32.1	150	6	65			NO GROWTH		NO GROWTH
POISON 6	I13	2	I13-2	PSME	SYAL	CARU	PIPO	CURA	14.5	65	17	25			NO GROWTH		NO GROWTH
POISON 6	J13	1	J13-1	PIPO	CARU	AGSP	PIPO	NONS	13.7	57	18	45			NO GROWTH		NO GROWTH
POISON 6	J5	1	J5-1	PIPO	SYAL		PIPO	TPKL	35.8	130	2	20			NO GROWTH		NO GROWTH
POISON 6	J5	2	J5-2	PIPO	SYAL		PIPO	NONS	13.0	67	13	40			*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor*
POISON 6	J7	1	J7-1	PSME	CARU		PSME	NONS	19.2	105	9	45			NO GROWTH		NO GROWTH
POISON 6	J8	1	J8-1	PSME	SYAL		PSME	TPKL	18.5	108	6	10			NO GROWTH		NO GROWTH
POISON 6	J9	1	J9-1	PSME	PUTR	CARU	PIPO	TPKL	29.4	78	7	45					*Byssochlamys sp.*
POISON 6	K14	1	K14-1	PSME	SYAL	AGSP	PSME	NONS	18.3	98	22	65			NO GROWTH		NO GROWTH
POISON 6	K3	1	K3-1	PSME	SYAL	AGSP	PIPO	NONS	8.6	51	5	50			*Mucor plumbeus*	98 %-AF412291	Mucor plumbeus
POISON 6	K4	2	K4-2	PSME	SYAL	AGSP	PSME	NONS	14.9	71	21	95			NO GROWTH		NO GROWTH
POISON 6	K5	1	K5-1	PSME	SYAL	AGSP	PSME	TPKL	16.2	63	14	50			NO GROWTH		NO GROWTH
POISON 6	K6	1	K6-1	PSME	SYAL	AGSP	PSME	NONS	18.0	94	21	85			NO GROWTH		NO GROWTH
RUBY	D10	6	D10-6	PSME	SYAL	CARU	PSME	NONS	12.6	108	9	70	2820	232	UNIDENTIFIED		UNIDENTIFIED
RUBY	D6	3	D6-3	PSME	SYAL	CARU	PSME	SYMP	18.7	88	5	45	3200	148	*Mucor* sp.		*Byssochlamys sp.*
RUBY	D6	4	D6-4	PSME	SYAL	CARU	PSME	SYMP	14.2	93	8	30	3190	170	*Mucor plumbeus* and *Penicillium* sp.	Mucor- 98 % af412291*Penicillium*-99 % AJ279476	*Mucor* sp. **
RUBY	D6	5	D6-5	PSME	SYAL	CARU	PSME	SYMP	25.1	126	6	90	3170	53	UNIDENTIFIED		UNIDENTIFIED
RUBY	E9	1	E9-1	PSME	SYAL	CARU	PSME	NONS	24.2	110	9	55	3000	238	NO GROWTH		NO GROWTH
RUBY	F10	1	F10-1	PSME	SPBEL		PSME	NONS	15.0	97	17	80	2950	147	*Verticillium coccosporum*	99 % AF110531	
RUBY	F12	3	F12-3	PSME	SPBEL	CARU	PSME	NONS	24.9	124	13	75	2890	228	NO GROWTH		NO GROWTH
RUBY	F4	1	F4-1	PSME	SYAL	CARU	PIPO	NONS	12.1	38	5	85	3290	209	*Mucor plumbeus*	98 %-AF412291	*Mucor* sp. **
RUBY	F5	4	F5-4	PSME	SYAL	CARU	PIPO	DEAD	9.9	60	NA	NA	3220	240			UNIDENTIFIED
RUBY	F8	1	F8-1	PSME	SYAL	CARU	PSME	NONS	10.8	63	13	80	3100	209	UNIDENTIFIED		*Penicillium* sp.?
RUBY	G11	3	G11-3	PSME	SPBEL	CARU	PSME	NONS	19.2	115	13	60	2960	263			*Mucor* sp.
RUBY	G4	1	G4-1	PSME	SYAL	CARU	PIPO	NONS	16.5	90	20	70	3310	232	UNIDENTIFIED		MUCORACEOUS SP.?
RUBY	G5	1	G5-1	PSME	SYAL	CARU	PSME	NONS	17.7	99	24	60	3270	229	NO GROWTH		*Byssochlamys sp.*
RUBY	G7	1	G7-1	PSME	SYAL	CARU	PSME	NONS	13.5	52	12	45	3180	146	NO GROWTH		NO GROWTH
RUBY	G9	1	G9-1	PSME	HODI	CARU	PSME	NONS	14.0	93	21	90	3050	175	*Pesotum fragrans*	95 %-AF198248	*Pesotum fragrans*
RUBY	H12	1	H12-1	PSME	SPBEL	CARU	PSME	NONS	8.2	57	16	85	3050	237	NO GROWTH		NO GROWTH
RUBY	H14	1	H14-1	PSME	SPBEL	CARU	PSME	NONS	16.9	85	26	55	3000	270	NO GROWTH		NO GROWTH
RUBY	H8	1	H8-1	PSME	SYAL	CARU	PSME	NONS	22.7	135	15	50	3110	192	NO GROWTH		NO GROWTH

SITE	UTM cell	TREE NUMBER	UNIT ID	PLANT ASSOCIATION	UNDERSTORY	PHASE	TREE SPECIES	STATUS	DBH	HEIGHT	Radial Growth	LCR	ELEVATION	ASPECT	ITS ID	ITS % IDENTITY/ACCESSION NUMBERS	MORPHOLOGICAL IDENTIFICATION
RUBY	I13	1	I13-1	PSME	SPBEL	CARU	PIPO	NONS	36.2	157	4	40	3050	221	NO GROWTH		NO GROWTH
RUBY	I15	1	I15-1	PSME	SPBEL	CARU	PIPO	NONS	16.9	79	9	40	2990	223			*Mucor* sp.
RUBY	I5	1	I5-1	PSME	SYAL	CARU	PIPO	NONS	17.4	81	16	75	3360	161			*Byssochlamys sp.*
RUBY	I7	1	I7-1	PSME	SYAL	CARU	PIPO	NONS	17.2	80	13	65	3200	195	*Byssochlamys sp.*	95 %-U18361	
RUBY	J12	3	J12-3	PSME	SYAL	CARU	PIPO	DEAD	11.0	46	NA	NA	3200	284	*Ganoderma sp.*, *Mortierella alpina*	*Ganoderma* -95 % AF255097	
RUBY	J14	1	J14-1	PSME	SPBEL	CARU	PIPO	NONS	24.8	112	6	40	3080	245	Ericoid mychorrhizal	94 $-AF072297	
RUBY	J15	1	J15-1	PSME	SPBEL	CARU	PSME	DEAD	14.6	85	NA	NA	3100	221	ANOTHER UNIDENTIFIED, *Mortierella alpina*		*Byssochlamys sp.?*
RUBY	J4	1	J4-1	PSME	SYAL	CARU	PIPO	NONS	11.3	82	8	75	3450	186	*Penicillium chrysigerum*	99 %-AF034450	
RUBY	K13	1	K13-1	PSME	SPBEL	CARU	PSME	NONS	27.1	150	8	65	3200	232	*Mucor* sp.		*Mucor* sp.
RUBY	K15	1	K15-1	PSME	SPBEL	CARU	PSME	NONS	15.5	92	8	70	3100	250	NO GROWTH		NO GROWTH
RUBY	K16	1	K16-1	PSME	SPBEL	CARU	PIPO	CURK	11.8	30	NA	NA	3050	174	UNIDENTIFIED		UNIDENTIFIED
RUBY	K4	1	K4-1	PSME	SYAL	CARU	PSME	NONS	15.0	82	21	65	3460	165	NO GROWTH		NO GROWTH
RUBY	L12	1	L12-1	PSME	SYAL	CARU	PSME	NONS	14.7	71	14	80	3300	234	NO GROWTH		NO GROWTH
SAND 19	D11	1	D11-1	PSME	SYAL	AGSP	PSME	NONS	9.5	67	9	50					
SAND 19	D13	1	D13-1	PSME	PUTR	AGSP	PSME	NONS	15.9	68	10	85			NO GROWTH		NO GROWTH
SAND 19	D7	1	D7-1	PSME	PUTR	AGSP	PSME	TPKL	30.4	74	6	15			NO GROWTH		NO GROWTH
SAND 19	D7	2	D7-2	PSME	SYAL		PSME	NONS	13.0	70	12	70			NO GROWTH		NO GROWTH
SAND 19	E8	1	E8-1	PSME	PUTR		PSME	NONS	13.8	74	9	80			NO GROWTH		NO GROWTH
SAND 19	E9	1	E9-1	PSME	SYAL	CARU	PSME	TPKL	26.3	66	1	10			*Penicillium* sp.	99 % AJ279476	
SAND 19	F11	1	F11-1	PSME	SYAL	CARU	PSME	NONS	25.6	130	10	60			NO GROWTH		NO GROWTH
SAND 19	F13	1	F13-1	PSME	SYAL	CARU	PIPO	NONS	11.8	87	8	25			NO GROWTH		NO GROWTH
SAND 19	F7	2	F7-2	PSME	PUTR	AGSP	PIPO	NONS	10.0	41	6	85			UNIDENTIFIED		UNIDENTIFIED
SAND 19	F9	1	F9-1	PSME	PUTR	AGSP	PIPO	NONS	20.2	68	13	55			NO GROWTH		NO GROWTH
SAND 19	G10	1	G10-1	PSME	SYAL		PSME	NONS	14.6	92	10	30			NO GROWTH		NO GROWTH
SAND 19	G12	1	G12-1	PSME	SYAL	CARU	PSME	NONS	11.5	80	10	75			NO GROWTH		NO GROWTH
SAND 19	H11	2	H11-2	PSME	PUTR	AGSP	PSME	NONS	17.1	99	12	85			NO GROWTH		NO GROWTH
SAND 19	H6	1	H6-1	PSME	PUTR	AGSP	PIPO	NONS	15.3	43	4	40			NO GROWTH		NO GROWTH
SAND 19	H7	1	H7-1	PSME	SYAL	AGSP	PIPO	NONS	10.8	35	3	40			NO GROWTH		NO GROWTH
SAND 19	H9	1	H9-1	PSME	AGSP		PSME	NONS	9.8	64	11	35			NO GROWTH		NO GROWTH
SAND 19	I10	1	I10-1	PSME	PUTR	AGSP	PSME	NONS	11.9	53	9	90			NO GROWTH		NO GROWTH
SAND 19	I10	2	I10-2	PSME	PUTR	AGSP	PSME	TPKL	50.6	105	5	70			NO GROWTH		NO GROWTH
SAND 19	I11	1	I11-1	PSME	PUTR	AGSP	PIPO	NONS	29.1	97	7	90			NO GROWTH		NO GROWTH
SAND 19	I12	1	I12-1	PSME	SYAL	AGSP	PSME	DEAD	57.5	84	NA	NA			NO GROWTH		NO GROWTH
SAND 19	I8	1	I8-1	PSME	SYAL		PSME	NONS	14.3	58	7	60			*Penicillium koligenum*		NO GROWTH
SAND 19	J11	1	J11-1	PSME	AGSP		PSME	NONS	14.8	71	9	70			NO GROWTH		*Byssochlamys sp.*
SAND 19	J13	2	J13-2	PSME	SYAL	CARU	PSME	NONS	21.2	92	10	60			NO GROWTH		NO GROWTH
SAND 19	J8	1	J8-1	PSME	PUTR		PIPO	NONS	18.6	56	6	80			NO GROWTH		NO GROWTH
SAND 19	J9	1	J9-1	PSME	SYAL	AGSP	PSME	NONS	49.0	104	5	55			NO GROWTH		NO GROWTH
SAND 19	K10	1	K10-1	PSME	AGSP		PSME	NONS	8.6	43	2	30			NO GROWTH		NO GROWTH
SAND 19	K11	2	K11-2	PSME	AGSP	CARU	PSME	NONS	20.9	98	12	50			NO GROWTH		NO GROWTH
SAND 19	K12	1	K12-1	PSME	CARU	AGSP	PSME	NONS	15.7	72	11	50			NO GROWTH		NO GROWTH
SAND 19	K6	1	K6-1	PSME	PUTR		PSME	NONS	15.3	73	14	90					NO GROWTH
SAND 19	K9	1	K9-1	PSME	SYAL		PSME	NONS	18.3	83	15	45	3570	174			*Byssochlamys sp.*
SAND 19	K9	3	K9-3	PSME	PUTR		PSME	TPKL	47.1	108	6	65					*Byssochlamys sp.*
SAND 19	L9	1	L19-1	PSME	PUTR	AGSP	PSME	NONS	18.7	88	7	75			NO GROWTH		*Byssochlamys sp.*
SAND 19	L9-1	1	L9-1	PSME	PUTR	AGSP	PSME	NONS	18.7	88	7	75			NO GROWTH		NO GROWTH
SAND 2	H18	1	H18-1	PSME	SYAL		PSME	NONS	18.0	120	19	45					NO GROWTH
SAND 2	H20	1	H20-1	PSME	SPBEL	CARU	PSME	NONS	11.7	63	10	50			UNIDENTIFIED		*Byssochlamys sp.*
SAND 2	H21	2	H21-2	PSME	SPBEL	CARU	PIPO	NONS	17.9	60	9	55			NO GROWTH		UNIDENTIFIED
																	NO GROWTH

SITE	UTM cell	TREE NUMBER	UNIT ID	PLANT ASSOCIATION	UNDERSTORY	PHASE	TREE SPECIES	STATUS	DBH	HEIGHT	Radial Growth	LCR	ELEVATION	ASPECT	ITS ID	ITS % IDENTITY/ACCESSION NUMBERS	MORPHOLOGICAL IDENTIFICATION
SAND 2	H22	1	H22-1	PSME	SPBEL	CARU	PIPO NONS		26.2	81	7	50			NO GROWTH		NO GROWTH
SAND 2	I17	1	I17-1	PSME	PUTR	AGSP	PIPO NONS		15.8	44	6	50					*Byssochlamys sp.*
SAND 2	I19	1	I19-1	PSME	SPBEL	CARU	PSME NONS		10.2	60	9	40			NO GROWTH		NO GROWTH
SAND 2	J17	1	J17-1	PSME	PUTR	AGSP	PSME NONS		12.4	65	11	90			*Hormonema dematoides*	98% AF013228	*Byssochlamys sp.*
SAND 2	J20	1	J20-1	PSME	SPBEL	CARU	PSME NONS		14.5	92	7	30					*Byssochlamys sp.*
SAND 2	J21	1	J21-1	PSME	SPBEL	CARU	PSME NONS		15.1	132	7	25			NO GROWTH		NO GROWTH
SAND 2	J22	1	J22-1	PSME	SPBEL	CARU	PSME NONS		16.4	108	6	20			UNIDENTIFIED		yellow fungus——
SAND 2	K15	3	K15-3	PSME	CARU	AGSP	PSME NONS		17.7	76	7	75			NO GROWTH		NO GROWTH
SAND 2	K19	1	K19-1	PSME	SYAL		PSME NONS		16.7	135	12	15			NO GROWTH		NO GROWTH
SAND 2	L16	1	L16-1	PSME	CARU		PSME NONS		15.8	92	10	40					*Byssochlamys sp.*
SAND 2	L17	1	L17-1	PSME	SPBEL	CARU	PSME NONS		14.5	119	10	20					*Byssochlamys sp.*
SAND 2	L18	1	L18-1	PSME	SPBEL	CARU	PSME NONS		15.4	99	7	20			*Penicillium donkii*	97 % AF033445	*Byssochlamys sp.*
SAND 2	L20	1	L20-1	PSME	SPBEL	CARU	PIPO SYMP		25.1	113	3	25					*Byssochlamys sp.*
SAND 2	L20	2	L20-2	PSME	CARU		PSME NONS		9.0	70	9	30			*Umbelopsis/Micromucor*		*Umbelopsis/Micromucor* and *Byssochlamys sp.*
SAND 2	L22	1	L22-1	PSME	SPBEL	CARU	PSME DEAD		30.2	109	NA	NA			NO GROWTH		NO GROWTH
SAND 2	L22	2	L22-2	PSME	CARU		PSME NONS		13.3	85	7	25			NO GROWTH		NO GROWTH
SAND 2	M17	4	M17-4	PSME	SPBEL	CARU	PSME NONS		11.0	81	7	40			NO GROWTH		NO GROWTH
SAND 2	M19	1	M19-1	PSME	SPBEL	CARU	PSME NONS		25.0	103	8	40			NO GROWTH		NO GROWTH
SAND 2	M22	1	M22-1	PSME	SPBEL	CARU	PIPO TPKL		22.9	78	2	10			*Penicillium thomii*	100 %-AF034448	
SAND 2	N14	1	N14-1	PSME	SYAL	CARU	PSME NONS		11.3	97	9	40			NO GROWTH		NO GROWTH
SAND 2	N16	1	N16-1	PSME	CARU		PSME DEAD		27.5	88	NA	NA			NO GROWTH		NO GROWTH
SAND 2	N21	1	N21-1	PSME	SPBEL	CARU	PSME NONS		14.5	119	1.5	75			NO GROWTH		NO GROWTH
SAND 2	N22	1	N22-1	PSME	SPBEL	CARU	PSME DEAD		20.2	86	NA	NA			NO GROWTH		NO GROWTH
SAND 2	O14	1	O14-1	PSME	SPBEL	CARU	PSME NONS		10.5	86	5	25			NO GROWTH		NO GROWTH
SAND 2	O15	1	O15-1	PSME	SYAL	CARU	PIPO NONS		24.0	84	6	30					*Byssochlamys sp.*
SAND 2	O16	2	O16-2	PSME	SPBEL	CARU	PIPO NONS		16.2	79	8	50			NO GROWTH		NO GROWTH
SAND 2	O17	1	O17-1	PSME	CARU		PSME NONS		25.6	116	4	40			NO GROWTH		NO GROWTH
SLAWSON	A8	1	A8-1	PSME	PUTR	AGSP	PSME DEAD		43.1	89	NA	NA			*Pycnoporous cinnabarinus*	94 %-AJ363772	
SLAWSON	B3	1	B3-1	PSME	SPBEL	CARU	PSME SYMP		26.1	106	3	20			*Umbelopsos/Micromucor*		*Umbelopsos/Micromucor* and *Byssochlalmys sp.*
SLAWSON	B4	1	B4-1	PSME	SPBEL	CARU	PIPO DEAD		19.0	65	NA	NA			NO GROWTH		NO GROWTH
SLAWSON	B6	2	B6-2	PSME	SPBEL		PIPO DEAD		26.0	92	NA	NA			*Clavulina cinerea* and *Hypocrea nigricans*	*Hypocrea* -97 %-AF275330	
SLAWSON	B7	1	B7-1	PSME	SYAL	CARU	PSME NONS		10.1	80	12	40			NO GROWTH		NO GROWTH
SLAWSON	B9	1	B9-1	PSME	SYAL	CARU	PSME NONS		9.3	70	11	20			UNIDENTIFIED		UNIDENTIFIED
SLAWSON	B9	2	B9-2	PSME	SYAL	CARU	PSME TPKL		19.6	90	3	10			NO GROWTH		NO GROWTH
SLAWSON	C10	1	C10-1	PSME	SYAL	CARU	PSME NONS		13.1	109	16	40			*Penicillium restrictum*	99 % AF033459	
SLAWSON	C12	1	C12-1	PSME	SYAL	CARU	PSME NONS		11.1	95	10	40			*Mucor plumbeus*	AF4 12291	
SLAWSON	C13	1	C13-1	PSME	SYAL	CARU	PSME TPKL		27.3	83	2	25			NO GROWTH		NO GROWTH
SLAWSON	C2	1	C2-1	PSME	SPBEL	CARU	PSME DEAD		33.3	165	NA	NA			NO GROWTH		NO GROWTH
SLAWSON	C4	1	C4-1	PSME	SPBEL	CARU	PIPO NONS		19.4	41	6	10			*Cladosporium filiform*	99 % AJ131680	
SLAWSON	C5	1	C5-1	PSME	SPBEL	CARU	PSME NONS		8.0	70	8	45			NO GROWTH		NO GROWTH
SLAWSON	C6	1	C6-1	PSME	SPBEL	CARU	PSME NONS		14.2	89	12	55			NO GROWTH		NO GROWTH
SLAWSON	C8	1	C8-1	PSME	SYAL	CARU	PSME NONS		11.2	71	6	30			NO GROWTH		NO GROWTH
SLAWSON	D11	1	D11-1	PSME	HODI	CARU	PSME NONS		14.0	82	13	50			*Mucor plumbeus*	97 %-AF412291	*Byssochlamys sp.?*
SLAWSON	D13	1	D13-1	PSME	SYAL	CARU	PSME NONS		9.8	82	16	55			NO GROWTH		NO GROWTH
SLAWSON	D15	1	D15-1	PSME	SYAL	CARU	PSME TPKL		45.7	105	3	45			*Penicillium canescens*	100 % AF033493	
SLAWSON	D15	2	D15-2	PSME	SYAL	CARU	PSME NONS		14.3	66	14	25			*Merimbla humicoleides*		
SLAWSON	D5	1	D5-1	PSME	SPBEL	CARU	PSME NONS		18.8	85	7	40					*Byssochlamys sp.*
SLAWSON	D5	2	D5-2	PSME	SPBEL	CARU	PSME SYMP		14.3	80	6	30			*Tremella giraffa*	*Tremella* -96 % AF042453	*Umbelopsos/Micromucor*
SLAWSON	D7	2	D7-2	PSME	SYAL	NONS	PSME NONS		12	70							*Byssochlamys sp.*

SITE	UTM cell	TREE NUMBER	UNIT ID	PLANT ASSOCIATION	UNDERSTORY	PHASE	TREE SPECIES	STATUS	DBH	HEIGHT	Radial Growth	LCR	ELEVATION	ASPECT	ITS ID	ITS % IDENTITY/ACCESSION NUMBERS	MORPHOLOGICAL IDENTIFICATION
SLAWSON	D9	1	D9-1	PSME	SYAL	CARU	PSME	NONS	13.5	73	7	50			NO GROWTH		NO GROWTH
SLAWSON	E10	1	E10-1	PSME	SYAL	CARU	PSME	NONS	19.8	87	5	50			NO GROWTH		NO GROWTH
SLAWSON	E13	1	E13-1	PSME	SYAL	CARU	PIPO	NONS	20.3	95	14	50			ost root assoc. fungus		
SLAWSON	E14	1	E14-1	PSME	SYAL	CARU	PSME	NONS	10.0	75	9	20			NO GROWTH		NO GROWTH
SLAWSON	E7	1	E7-1	PSME	HODI	CARU	PIPO	TPKL	33.3	142	4	25			*Tremella giraffa*	96 %-AF0424453	*Tremella giraffa*
SLAWSON	E8	1	E8-1	PSME	SYAL	CARU	PSME	NONS	13.0	70	6	50			*Byssochlamys sp.*	95 %-U18361	*Byssochlamys sp.*
SLAWSON	F11	1	F11-1	PIPO	HODI	AGSP	PIPO	NONS	26.9	96	5	50			NO GROWTH		NO GROWTH
SLAWSON	F14	1	F14-1	PIPO	SYAL	AGSP	PIPO	DEAD	18.3	95	NA	NA			UNIDENTIFIED		UNIDENTIFIED
SLAWSON	F8	2	F8-2	PSME	SYAL	CARU	PIPO	TPKL	32.9	102	3	10					*Byssochlamys sp.*
SLAWSON	F9	1	F9-1	PSME	SYAL	CARU	PIPO	NONS	13.4	61	3	45			NO GROWTH		NO GROWTH
SLAWSON	G10	1	G10-1	PSME	SYAL	CARU	PIPO	DEAD	14.6	51	NA	NA			NO GROWTH		NO GROWTH
SLAWSON	G10	2	G10-2	PSME	SYAL	CARU	PIPO	NONS	36.0	111	6	50			NO GROWTH		NO GROWTH
SLAWSON	G8	1	G8-1	PSME	SYAL	CARU	PSME	NONS	10.4	72	13	50			NO GROWTH		NO GROWTH
SPROM 4	C7	1	C7-1	PSME	SYAL	CARU	PSME	NONS	15.9	89	25	75	3670	190			
SPROM 4	C9	1	C9-1	PSME	SYAL	CARU	PSME	TPKL	11.2	47	2	25	3460	190	NO GROWTH		NO GROWTH
SPROM 4	C9	2	C9-2	PSME	SYAL	CARU	PSME	TPKL	9.7	45	2	15	3460	190	NO GROWTH		NO GROWTH
SPROM 4	C9	3	C9-3	PSME	SYAL	CARU	PSME	TPKL	17.0	19	3	70	3460	216	NO GROWTH		NO GROWTH
SPROM 4	D11	1	D11-1	PSME	HODI	CARU	PSME	NONS	14.0	82	13	50					NO GROWTH
SPROM 4	D8	1	D8-1	PSME	SYAL	CARU	PIPO	NONS	17.0	65	9	40	3550	210			*Byssochlamys sp.*
SPROM 4	D9	1	D9-1	PSME	HODI	CARU	PSME	TPKL	10.7	47	2	15	3450	208	NO GROWTH		NO GROWTH
SPROM 4	D9	2	D9-2	PSME	HODI	CARU	PSME	TPKL	11.2	64	3	55	3450	208	NO GROWTH		NO GROWTH
SPROM 4	E11	1	E11-1	PSME	SPBEL	CARU	PSME	NONS	11.7	57	13	35	3450	270	NO GROWTH		NO GROWTH
SPROM 4	E6	1	E6-1	PSME	SYAL	CARU	PIPO	TPKL	16.4	56	6	65	3790		UNIDENTIFIED		UNIDENTIFIED
SPROM 4	E9	1	E9-1	PSME	HODI	CARU	PSME	NONS	11.9	53	21	85	3480	256	UNIDENTIFIED		UNIDENTIFIED
SPROM 4	F10	1	F10-1	PSME	AGSP		PIPO	NONS	10.4	25	9	65	3540	280	*Umbelopsis/Micromucor* and *Mucor* sp.		*Umbelopsis/Micromucor* and *Mucor* sp.
SPROM 4	F6	2	F6-2	PSME	SPBEL	CARU	PIPO	NONS	25.4	99	10	50	3790	198	*Umbelopsis/Micromucor* and *Mucor* sp.		*Umbelopsis/Micromucor* and *Mucor* sp.
SPROM 4	F8	1	F8-1	PSME	SYAL	CARU	PIPO	NONS	23.6	80	6	75	3620	238	*Mucor fragilis*	93 % AF474242	*Byssochlamys sp.*
SPROM 4	G11	1	G11-1	PSME	SYAL	AGSP	PSME	NONS	12.1	42	10	45	3560	224	NO GROWTH		NO GROWTH
SPROM 4	G9	1	G9-1	PSME	SYAL	CARU	PSME	NONS	12.1	44	16	60	3620	265	UNIDENTIFIED		UNIDENTIFIED
SPROM 4	H10	1	H10-1	PSME	SYAL	AGSP	PSME	NONS	12.1	68	7	60	3570	175	NO GROWTH		NO GROWTH
SPROM 4	H6	1	H6-1	PSME	CARU		PSME	NONS	15.0	77	32	80	3840	287	*Umbelopsis/Micromucor* and *Mucor* sp.		*Umbelopsis/Micromucor* and *Mucor* sp.
SPROM 4	H8	1	H8-1	PSME	BASA	AGSP	PIPO	NONS	12.6	35	5	15	3770	140	*Umbelopsis/Micromucor* and *Mucor* sp.	97 % AF133782	*Umbelopsis/Micromucor* and *Byssochlamys sp.*
SPROM 4	I9	1	I9-1	PSME	SYAL	CARU	PSME	NONS	15.7	45	9	85	3640	176			*Byssochlamys sp.*
SPROM 4	J10	1	J10-1	PSME	SYAL	CARU	PSME	NONS	12.8	33	11	30	3560	150	*Mucor plumbeus*	97 % AF412291	
SPROM 4	J7	1	J7-1	PSME	CARU	BASA	PIPO	NONS	26.4	98	8	65	3780	180	NO GROWTH		NO GROWTH
SPROM 4	J8	1	J8-1	PSME	CARU	BASA	PIPO	NONS	8.9	54	12	65	3690	155	UNIDENTIFIED		UNIDENTIFIED
SPROM 4	K10	1	K10-1	PSME	SYAL	CARU	PSME	NONS	21.6	94	11	90	3470	194	NO GROWTH		NO GROWTH
SPROM 4	K6	1	K6-1	PIPO	CARU	AGSP	PIPO	NONS	9.2	32	6	30	3780	158			*Byssochlamys sp.*
SPROM 4	K8	1	K8-1	PSME	HODI	AGSP	PSME	TPKL	10.6	62	9	25	3680	192	NO GROWTH		NO GROWTH
SPROM 4	K8	2	K8-2	PSME	CARU	BASA	PSME	NONS	11.7	75	14	55	3650	180	UNIDENTIFIED		UNIDENTIFIED
SPROM 4	K9	1	K9-1	PSME	SYAL		PSME	NONS	18.3	83	15	45	3570	174	NO GROWTH		NO GROWTH
SPROM 4	L6	1	L6-1	PSME	SPBEL	CARU	PSME	NONS	24.0	92	29	90	3810	238			*Byssochlamys* sp. ? *Umbelopsis/Micromucor* ?
SPROM 4	M7	1	M7-1	PSME	BASA	CAGE	PIPO	NONS	14.7	68	14	75	3730	225	NO GROWTH		NO GROWTH
SPROM 4	M8	1	M8-1	PSME	BASA	CAGE	PSME	NONS	15.7	77	13	80	3700	165	NO GROWTH		NO GROWTH
SPROM 4	M9	1	M9-1	PSME	SYAL	CARU	PSME	NONS	14.1	37	20	90	3530	185	*Umbelopsis/Micromucor* and *Mucor* sp.		*Umbelopsis/Micromucor* and *Mucor* sp.
SPROM 4	N6	1	N6-1	PSME	SYAL	CARU	PSME	NONS	17.1	53	26	70	3840	178	NO GROWTH		NO GROWTH
SPROM 4	O6	1	O6-1	PSME	SYAL	CARU	PIPO	SYMP	8.9	52	8	25	3800	164	NO GROWTH		NO GROWTH
															UNIDENTIFIED		UNIDENTIFIED

SITE	UTM cell	TREE NUMBER	UNIT ID	PLANT ASSOCIATION	UNDERSTORY	PHASE	TREE SPECIES	STATUS	DBH	HEIGHT	Radial Growth	LCR	ELEVATION	ASPECT	ITS ID	ITS % IDENTITY/ACCESSION NUMBERS	MORPHOLOGICAL IDENTIFICATION
SPROM 4	O7	1	O7-1	PSME	SYAL	CARU	PIPO	NONS	8.5	44	7	40	3770	126	NO GROWTH		NO GROWTH
SPROM 4	P7	1	P7-1	PSME	SYAL		PIPO	NONS	15.9	70	23	75	3720	226			*Mucor* sp.
TRIPP 9	AA2	1	AA2-1	PSME	CARU		PIPO	NONS	11.5	59	4	20			NO GROWTH		NO GROWTH
TRIPP 9	AA4	1	AA4-1	PSME	CARU	AGSP	PIPO	NONS	20.0	91	10	45					*Byssochlamys sp.*
TRIPP 9	BB3	1	BB3-1	PSME	SYAL	AGSP	PIPO	DEAD	18.9	69	NA	NA			NO GROWTH		NO GROWTH
TRIPP 9	I7	1	I7-1	PSME	SPBEL	CARU	PSME	NONS	11.4	78	2	20			NO GROWTH		NO GROWTH
TRIPP 9	I8	2	I8-2	PSME	CARU	AGSP	PSME	TPKL	19.0	81	11	15			UNIDENTIFIED		UNIDENTIFIED
TRIPP 9	I8	3	I8-3	PSME	CARU	AGSP	PSME	DEAD	9.6	52	NA	NA					Mucor sp.
TRIPP 9	I8	4	I8-4	PSME	CARU	AGSP	PSME	TPKL	17.3	89	15	25					*Byssochlamys sp.* ?
TRIPP 9	L7	1	L7-1	PSME	CARU		PSME	NONS	22.5	125	14	30					*Byssochlamys sp.*
TRIPP 9	L8	1	L8-1	PSME	SYAL	CARU	PIPO	NONS	24.1	91	7	40			NO GROWTH		NO GROWTH
TRIPP 9	M10	1	M10-1	PSME	PUTR	CARU	PIPO	TPKL	31.3	133	3	25			NO GROWTH		NO GROWTH
TRIPP 9	M8	1	M8-1	PSME	CARU		PSME	TPKL	37.4	133	3	30					*Byssochlamys sp.*
TRIPP 9	M8	2	M8-2	PSME	SPBEL	CARU	PSME	NONS	12.4	92	12	60			NO GROWTH		NO GROWTH
TRIPP 9	M9	1	M9-1	PSME	CARU		PSME	NONS	16.1	76	7	30			NO GROWTH		NO GROWTH
TRIPP 9	M9	2	M9-2	PSME	CARU		PIPO	TPKL	29.8	122	6	30			NO GROWTH		NO GROWTH
TRIPP 9	N10	1	N10-1	PSME	PUTR	CARU	PIPO	NONS	21.2	87	12	45			NO GROWTH		NO GROWTH
TRIPP 9	N9	1	N9-1	PSME	SPBEL	CARU	PSME	NONS	17.6	94	11	45			NO GROWTH		NO GROWTH
TRIPP 9	P11	1	P11-1	PSME	SPBEL	CARU	PSME	TPKL	38.5	70	2	10			NO GROWTH		NO GROWTH
TRIPP 9	P9	2	P9-2	PSME	CARU		PSME	NONS	11.7	81	12	70			*Byssochlamys sp.*	93 % I18361	*Byssochlamys sp.*
TRIPP 9	Q10	1	Q10-1	PSME	CARU	AGSP	PSME	NONS	8.9	50	8	55					*Byssochlamys sp.*
TRIPP 9	Q10	2	Q10-2	PSME	SPBEL	CARU	PSME	TPKL	40.5	88	6	10			NO GROWTH		NO GROWTH
TRIPP 9	R8	1	R8-1	PSME	SPBEL	CARU	PIPO	TPKL	30.4	114	10	25			NO GROWTH		NO GROWTH
TRIPP 9	R9	1	R9-1	PSME	SYAL	AGSP	PSME	NONS	8.5	49	18	75			NO GROWTH		NO GROWTH
TRIPP 9	S7	2	S7-2	PSME	SPBEL	CARU	PSME	NONS	11.2	80	8	40					*Byssochlamys sp.*
TRIPP 9	S8	1	S8-1	PSME	SPBEL	CARU	PSME	NONS	10.9	82	15	35					*Byssochlamys sp.*
TRIPP 9	T4	1	T4-1	PSME	SYAL	CARU	PSME	NONS	11.5	54	7	60					*Byssochlamys sp.*
TRIPP 9	V7	1	V7-1	PSME	HODI	CARU	PSME	TPKL	26.6	87	2	10					*Byssochlamys sp.*
TRIPP 9	W5	1	W5-1	PSME	SPBEL	CARU	PIPO	TPKL	31.5	118	3	20			NO GROWTH		NO GROWTH
TRIPP 9	W6	1	W6-1	PSME	SYAL	CARU	PIPO	TPKL	32.2	63	4	10					*Byssochlamys sp.*
TRIPP 9	W8	1	W8-1	PSME	SYAL	AGSP	PIPO	NONS	34.2	67	3	60			NO GROWTH		NO GROWTH
TRIPP 9	X4	1	X4-1	PSME	SYAL	CARU	PIPO	TPKL	24.1	153	4	25			NO GROWTH		NO GROWTH
TRIPP 9	X7	1	X7-1	PSME	HODI	CARU	PIPO	NONS	23.8	108	2	40			NO GROWTH		NO GROWTH
TRIPP 9	Y4	1	Y4-1	PSME	SYAL	CARU	PSME	NONS	20.5	111	11	45			NO GROWTH		NO GROWTH
TRIPP 9	Z4	1	Z4-1	PSME	SYAL	CARU	PIPO	NONS	25.9	115	7	60			NO GROWTH		NO GROWTH