

AN ABSTRACT OF THE THESIS OF

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Abstract approved: _____

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The fungal ascomycete genus *Otidea* as represented in the Pacific Northwest of North America includes eight well known species and two poorly-known species. Cladistic analysis utilizing characters from ribosomal DNA and morphology allowed the development of a robust phylogenetic species concept for *Otidea*. The combination of characters from the ribosomal DNA internal transcribed spacer region and those characters coded from morphological descriptions proved both useful and robust towards the elucidation of a phylogenetic species concept. The resulting phylogenetic species concept was then applied to known members of the genus, and species descriptions revised to account for additional data collected in the course of this study. The following species of *Otidea* are described in detail in this work: *O. alutacea*, *O. concinna*, *O. leporina*, *O. onotica*, *O. rainierensis*, *O. smithii*, *O. tuomikoskii* and *O. umbrina*. Revised keys to the genus for both fresh and dried material are presented in Chapter Three. *O. alutacea*, *O. leporina*, *O. rainierensis*, *O. smithii* and *O. umbrina* are reported as rare in the Pacific Northwest due to the relatively small number of collections made of each in the course of this study.

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Systematics of the genus *Otidea* in the Pacific Northwest

by

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CONTRIBUTION OF AUTHORS

Dr. Joseph Spatafora was involved in the design, molecular analysis, and writing of each manuscript. Additionally, all molecular work was performed in the lab of Dr. Spatafora. Dr. Nancy Weber was involved in the design, taxonomic analysis and description, and writing of chapter three (Revisional monograph of the genus *Otidea* in the Pacific Northwest).

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SYSTEMATICS OF THE GENUS *OTIDEA* IN THE PACIFIC NORTHWEST

INTRODUCTION

The genus *Otidea* in the Pacific Northwest has been among the many taxa of concern to land managers and mycologists since the publication of the Forest Management and Assessment Team (U.S.D.A. F.S., U.S.D.O.I. B.L.M., 1994) report on the habitat of the Northern Spotted Owl. This document, written to deal with rare and endangered species of animals, plants, and fungi associated with mature and old growth forests of the Pacific Northwestern U.S.A., states that *Otidea smithii*, *O. leporina*, and *O. onotica* are "species of concern" due to their apparent rarity and that a general survey must be taken for all three of these species before federally- and state-owned property slated for forest management activities can be approved. In addition, if *O. smithii* is found, 160 acres surrounding each population must be removed from any ground disturbing activity (U.S.D.A. F.S., U.S.D.O.I. B.L.M., 1994). Implementation of this directive requires accurate identification of specimens of *Otidea*.

The only published North American work solely on the genus, Kanouse (1949), includes descriptions generated primarily from dried collections and original notes on those collections housed in the University of Michigan fungal herbarium. Kanouse's descriptions relied heavily on other worker's assessment of color and shape in the fresh state. She described one new variety and two new species, having previously described *O. smithii* (Kanouse, 1939). *O. alutacea* var. *microspora*, was separated from *O. alutacea* var. *alutacea* by paler apothecial color and slightly smaller spores (characters

that could be attributed to immaturity in collections). Kanouse (1949) separates *O. rainierensis* and *O. kauffmanii* from other members of the genus, but differentiates the pair by "size, shape and color of the apothecia and also differences in spore size" and differences in distribution; *O. kauffmanii* is reported from Michigan, *O. rainierensis* from Washington. However, if one considers the high degree of morphological plasticity and ecological variability attributed to the fungi (Alexopolus, Mims and Blackwell, 1996) and the poorly documented geographic distribution of most species, it is plausible that *O. kauffmanii* and *O. rainierensis* are synonyms. Difficulty associated with identification of these and other species of *Otidea* warranted reassessment of species concepts within the genus.

The working assumption for this study was that combining characters generated from molecular sequence data with morphological characters in phylogenetic studies would allow the generation and testing of robust phylogenetic hypotheses regarding evolution and relationships within the genus. Moreover, by constructing cladistic phylogenies one can infer patterns of character evolution in the genus and establish a phylogenetic species concepts for members of the genus (Donoghue, 1985; Kluge, 1985). The revision of the species concept within *Otidea*, presented in Chapter Two of this work, allows a reassessment of character state distribution within individual species and provide information for the taxonomic revision contained in Chapter Three of this thesis.

This introductory chapter covers a brief summary of the taxonomy of discomycetes in general and the genus *Otidea* specifically, and reviews important aspects of fungal molecular systematics. In addition, I will discuss the idea of a modern synthesis of molecular and morphological methods and how the results of this project

apply to both the genus *Otidea* and other groups of fungi. Details regarding the molecular systematics of the group will be presented in Chapter Two, and those regarding morphology and taxonomy in Chapter Three.

Morphology:

The discomycetes, or "cup-fungi", have been studied since Roman times, when Pliny (23-79 A.D.) described an organism "Belonging to the mushroom kind, also there is a species known to the Greeks by the name 'Pezica' which grows without root or stalk." (Kimbrough, 1970). Among early contributors to information about the cup fungi were Linnaeus (1753) Persoon (1796; 1801; 1822), and Fries (1822). While establishing groups based primarily on morphology of the apothecium, Fries contributed heavily to the study of the discomycetes by establishing an ordinal, subordinal, and familial classification system (Kimbrough, 1970). The Friesian system is still used and advances in the field made clear the importance of microscopic characters. Most notable were the contributions of Nylander (1869), who stressed the importance of the iodine reaction with the tip of the asci, and Crouan and Crouan (1857), who described the operculate nature of the asci. Boudier (1907) proposed a classification based on the presence or absence of ascal operculum, as well as several other macro- and microscopic characters. He was the first to separate the cup-fungi into the operculate and inoperculate discomycetes (Kimbrough, 1970; van Brummelen, 1994). According to van Brummelen (1994), Saccardo abandoned the Friesian system for his own that placed more emphasis on ascospore characters. Numerous rearrangements of taxa at higher levels continued until

Nannfeldt (1932) proposed three main groups of higher Ascomycetes: the Plectascales, Ascoloculares, and the Ascohymeniales. According to Kimbrough (1970), Nannfeldt's work provided a foundation for much of the work done at the generic level from the 1940's to the 1970's (e.g. Le Gal (1947), Rifai (1968), Eckblad (1968), Korf (1973)). Eckblad (1968) divided the Pezizales into the families Thelebolaceae, Ascobolaceae, Pyronemataceae, Pezizaceae, Helvellaceae, Morchellaceae, Rhizinaceae, Sarcoscyphaceae, and Otideaceae based primarily on morphological and anatomical characters of the excipulum. Trappe (1979) emended several families in the Pezizales to include hypogeous fungi in his re-examination of the Tuberales, and distributed most members of this "anachronistic order" in various families of the Pezizales, based primarily upon microscopic characters. A much more thorough treatment of the early history presented above is available in Kimbrough's work, *Current Trends in the Classification of Discomycetes* (1970) and van Brummelen's chapter in *Ascomycete Systematics: Problems and Perspectives in the Nineties* (1994), and a brief, but detailed synopsis of later work is available in Landvik, et al. (1997).

In regard to the operculate discomycetes (Pezizales), of which *Otidea* is a member, definition of some of the basic concepts will make the following chapters more readable. The following information follows Weber, Trappe, and Dennison (1997) and Korf (1973) unless otherwise noted. The ascocarp of the operculate discomycetes is said to be "in its commonest form, a typical apothecium, taking the shape of a saucer, a cup, or a nearly closed sphere" (Korf, 1973). A great deal of variation can be observed within the order, but most epigeous members have an exposed hymenial layer composed of asci surrounded by sterile elements (paraphyses). In most hypogeous members ascribed to the

Pezizales by Trappe (1979) the apothecium is not an open, cup-shaped structure and the ascospores are not, with the exception of *Geopora* (Trappe, 1979), forcibly discharged from the asci at maturity. Rather the asci are cylindric to globose, often enclosed in an epithelium or embedded in tramal tissue, and contained within subglobose to globose fruiting structures of various forms but mostly not apothecia. Several early classification systems were based on the macro-morphology of the ascoma, but this character can vary considerably at lower taxonomic levels, a fact that led Eckblad to conclude that within the Pezizales this character is of "low taxonomic value" (1968). The tissues of the epigeous apothecia are the hymenium, subhymenium, medullary excipulum, and ectal excipulum (from inside to outside). Shape, size, and structure of each of these layers varies a great deal among the discomycetes but their morphology is generally similar among species within a genus. Some authors place importance on the ectal excipulum, especially the presence or absence of hairs (Kimbrough, 1970). The excipular layers can be described as being of seven basic types, *textura globulosa* (Fig. 1.1a), *t. angularis* (Fig. 1.2b), *t. prismatica*, *t. intricata* (Fig. 1.3c), *t. epidermoidea*, *t. oblita*, and *t.*

porrecta, first described by Stårback and diagramed by many authors including Eckblad (1968, his Figure 2) and Korf (1973, his Figure 3).

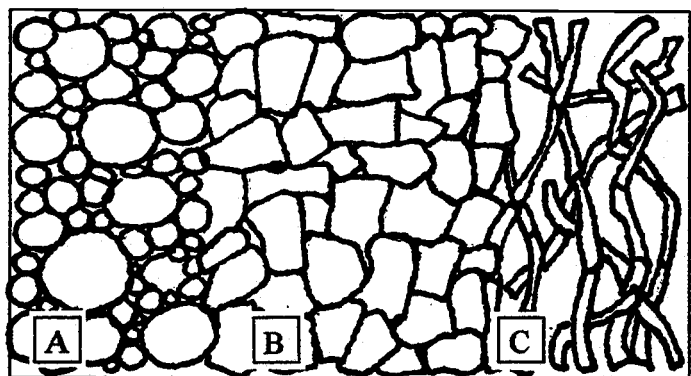


Figure 1.1: Types of excipular layers

The description of ascus dehiscence given by Crouan and Crouan (1857) remains important to the taxonomy of the discomycetes. They described the asci in the Pezizales as typically having an apical or subapical pore that opens like a trap door when the spores are discharged. The asci of the Pezizales are all unitunicate, and, while some authors have indicated that this "single-coated" wall is actually two-layered (Kimbrough, 1970), these layers never separate at spore discharge (Korf, 1973). Additionally, several authors have noted that the apex of the ascus varies enough within the Euascomycetes (ascocarp-forming Ascomycetes) to be phylogenetically informative at higher taxonomic levels (Samuelson, 1978). The ascospores of operculate discomycetes are also a source of extremely important characters, especially to delimit genera or species within a genus. Le Gal emphasized spore characters, believing that "spore characters should take precedence of all other characters" (1947). Eckblad (1968), however, stated that caution is necessary and that no segregation should be made based on spore form only. The spores are unicellular; smooth or variously ornamented; hyaline, brown, or rarely purple; with bipolar or radial symmetry. Many groups possess ascospores with obvious contents, e.g., oil droplets (guttules) (Kimbrough, 1970). Most ascospores of the Pezizales are uninucleate (excepting the Sarcoscyphaceae, Helvellaceae, Rhizinaceae, Discinaceae, Tuberaceae, and Morchellaceae) (Kimbrough, 1970; O'Donnell, et al., 1997). This character is typically consistent within several groups, and thus thought to be phylogenetically informative (Korf, 1973).

Paraphyses are sterile hyphae interspersed among the asci in most operculate discomycetes. They vary in form throughout the group but usually are "filiform to clavate, sometimes lance-shaped, pyriform, curved, hooked or branched, and most always

septate" (Kimbrough, 1970). Within the Otideaceae paraphyses can be extremely useful for differentiating genera and individual species (e.g., the hooked paraphyses of *Otidea*).

Additionally, pigments in the discomycetes are useful for identification at higher taxonomic levels. Arpin (1968) studied carotenoid pigments in nearly 100 species of discomycetes. His work led to the creation of the Aleuriaceae within the Pezizales (from taxa formerly placed in the Ciliariaceae and Humariaceae *sensu* Le Gal) and reported an absence of carotenoid pigments in the Morchellaceae, Helvellaceae, Pezizaceae, and Otideaceae.

Taxonomy and nomenclature of *Otidea*:

Members of the genus *Otidea* are described as having roughly ear-shaped apothecia that are yellow, brown, or orange in color. While ascomal shape varies from species to species, all members of the genus *sensu stricto* have a split in the apothecium on one side giving the ascoma an irregular appearance (Figure 1.2). Microscopically members of the genus typically have smooth, biguttulate ascospores and hooked paraphyses, although exceptions do occur. Additional information regarding the



taxonomy and nomenclature of the genus is presented in Chapter Three.

Figure 1.2: *Otidea tuomikoskii* showing the irregular appearance of the ascoma observed in the genus.

Molecular systematics:

Despite the integral roles fungi play in most terrestrial ecosystems, little is known about their evolutionary history as compared to other groups of eukaryotes (e.g., plants and animals). Problems of assessing characters and character state homology have plagued historical studies of the fungi and have resulted in contradictory classification schemes (Bruns, White and Taylor, 1991). Recently developed methods of molecular systematics offer new approaches to study fungal evolution. Specifically, development of objective criteria for analyzing data, increases in computational power to conduct analyses, and the ability to rapidly generate large data sets of nucleotide characters which are independent of morphology have allowed molecular characters to become integral components of study in fungal systematics (Hibbett and Donoghue, 1998; Bruns, White and Taylor, 1991; Hibbett, 1992; Hillis, Huelsenbeck and Cunningham, 1994). Many different methods are available to compare fungal organisms, including DNA-DNA hybridization, restriction enzyme analysis, electrophoretic karyotyping, fungal diagnostics, and nucleotide sequencing (Hibbett, 1992; Bruns, White and Taylor, 1991). Of these, nucleotide sequencing has been embraced by many authors due to the relative ease of generating large numbers of phylogenetically informative characters. Also, the polymerase chain reaction (PCR, Saiki, et al., 1988; Mullis and Faloona, 1987) relies on a relatively small amount of DNA template (typically around 1-10 μ g), thereby facilitating the study of rare or difficult-to-isolate organisms (Bruns, White and Taylor, 1991). Because many of the genes encoded by genomic DNA are ubiquitous, homologous data can be compared across taxa of varying morphology (Bruns, White and Taylor, 1991).

While phylogenetic studies of nucleotide characters have become commonplace within fungal systematics, Hibbett is careful to point out that "the characters themselves are only as good as the method of analysis" (1992).

Several authors have discussed the need to study a gene or gene region that is appropriate to answer the question of interest (Bruns, White and Taylor, 1991; Hibbett, 1992; Kohn, 1992; Lutzoni and Vilgalys, 1995). Bruns, et al. (1991) cite the following factors to consider when selecting a nucleotide region for phylogenetic analysis: (1) The region should be evolving at an appropriate rate to answer the question of interest. (2) The region should either be present as, or evolve as, a single copy within the genome. (3) The region should have the same function in all the organisms being studied. (4) The effect of codon bias (if applicable) and base composition should be examined, to prevent a distorted estimate of sequence divergence. Both Bruns, et al. (1991) and Hibbett (1992), as well as many others, have suggested the genes which encode for the ribosomal RNA (rDNA) satisfy the above criteria extremely well. rDNA consist of 5.8S, 18S, and 25S subunits that are transcribed along with internal and external transcribed spacer regions (ITS and ETS). The DNA that comprises these units is present in multiple copies as tandem repeats within the genome, but the multiple copies evolve in unison and therefore act as a single copy gene (Hibbett, 1992). In addition, and most importantly, each region of the rDNA unit appears to evolve at a different average rate, thereby providing characters most appropriate to answer questions at different taxonomic levels (Hibbett, 1992; Bruns, White and Taylor, 1991). Hibbett and other authors suggest that, in general, the 18S and 25S regions are most appropriate to answer high to moderate level taxonomic questions (how are families, orders, and perhaps genera related), and that the

ITS regions flanking the 5.8S region are most appropriate to answer lower-level taxonomic questions (how are these species, or populations of a single species, related?) (Hibbett, 1992; Liston, et al., 1996; Downie, et al., 1998). For a much more thorough treatment regarding rDNA see Hibbett (1992).

Numerous workers have used rDNA nucleotide data to answer taxonomic questions about fungi. Molecular characters provide an independent source of data from which phylogenetic hypotheses can be generated to test morphological hypotheses (Blackwell and Spatafora, 1994; Spatafora and Blackwell, 1994; Bruns, White and Taylor, 1991; Lutzoni and Vilgalys, 1995). New hypotheses have been developed regarding relationships amongst the fungi (Bruns, White and Taylor, 1991), classes of ascomycetes (Berbee and Taylor, 1992), the discomycetes (Gargas and Taylor, 1995; O'Donnell, et al., 1997), the origin of the lichen symbiosis (Gargas, et al., 1995), as well as a variety of lower-level taxonomic questions (see Hibbett and Vilgalys, 1993; Vilgalys and Sun, 1994; Lutzoni and Vilgalys, 1995; Hibbett, et al., 1995; Kretzer, et al., 1996; Harrington, 1998). The current trend in fungal systematics is to combine independent data sets, particularly from molecular and morphological sources, to infer the most robust phylogeny possible (Hibbett and Vilgalys, 1993; Lutzoni and Vilgalys, 1995; Tehler, 1994). Many authors are looking critically at the combinability of data and weighting schemes for characters within data sets to better resolve taxonomic relationships (Lutzoni and Vilgalys, 1995; Chippindale and Wiens, 1994; Bull, et al., 1993; Farris, 1969; Cunningham, 1997; Barrett, Donoghue and Sober, 1991). Additionally, molecular tools are now being used to assess rarity within fungal groups (Hibbett, et al., 1995; Kerrigan, et al., 1998).

To return the focus to *Otidea* and related groups, it makes sense to briefly examine how molecular sequence data has been used to examine hypotheses within the cup-fungi. Gargas and Taylor (1995) examined relationships within the "discomycetes" (*sensu* Korf (1973), those fungi having a cup-like apothecium, e.g., the class Discomycetes). Using characters from the rDNA small subunit (SSU), these authors tested the monophyly of the "discomycetes" and high-level taxonomic groups within this artificial taxonomic assemblage. Relevant to my work, they showed that the Pezizales are a monophyletic order (within their sampling) and basal within the discomycetes. The authors speculate, based on their most-parsimonious tree, that the Pezizales as a group may possess ancestral (primitive) characters within the ascomycetes. Spatafora (1995) confirmed the monophyly of the Pezizales, again using nucleotide characters from the rDNA SSU region, although his work did not unequivocally place the Pezizales as basal within the Discomycetes *sensu* Korf (1973). Rather, his work showed that the Pezizales were in a clade that was sister to two groups of cleistothecial and perithecial ascomycetes (Pyrenomycetes and Pleosporales) but that the root from the Saccharomycetes to several Euascomycete groups was equivocal, thereby questioning the ability of SSU rDNA alone to resolve the radiation within the Euascomycetes (Spatafora, 1995).

O'Donnell, et al. (1997) used nucleotide characters from the rDNA tandem repeat to study relationships between epigeous and hypogeous sporocarp-forming genera within a subset of the Pezizales (*sensu* Trappe, 1979). Although it was generally accepted that these hypogeous sporocarp-forming genera belong in the order Pezizales, relationships with epigeous genera were based on few characters, and familial assignments were provisional. These authors combined data from the SSU rDNA and a portion of the LSU

rDNA to test and refine phylogenetic hypotheses of epigeous and hypogeous evolution within the Pezizales. Their data showed a 9.5% nucleotide divergence in the SSU data set, and a 26.9% nucleotide divergence in the LSU data set. These values suggest that within the Pezizales that the SSU and LSU regions can be analyzed to answer questions at different taxonomic levels. Their combination yielded a single most-parsimonious tree with strong bootstrap support for most groupings already recognized based on morphology. The analysis provided a great deal of information regarding the initial question of the relationship between the epigeous and hypogeous Pezizales, enabling several changes in assignment of genera to families.

Addressing a similar problem as O'Donnell, et al. (1997), Landvik, Egger, and Schumacher (1997) evaluated subordinal relationships within the Pezizales. They examined 37 taxa representing as many genera placed within the Pezizales *sensu lato*. Theirs is the most recent work on the Pezizales and the only one that examines hypotheses about relationships within the Otideaceae by use of nucleotide characters. They address the taxonomic difficulties encountered within the Otideaceae, the family being a figurative "dumping ground" for taxa that are not readily classified elsewhere. Within their sampling of the Otideaceae *sensu* Hawksworth, et al. (1995), high bootstrap support was shown for the grouping of *Otidea* with *Trichophaea*, *Aleuria*, *Scutellinia*, *Byssonectria* and *Pyronema*. Additionally, *Otidea* was shown to be basal in this assemblage in one of their four most parsimonious trees (their Figure 1), although this relationship collapsed into unresolved or poorly resolved polytomies in their consensus trees (their Figures 2 & 3). This work provides support for the wide range of characters and character states exhibited by the family as currently recognized. Their work also

suggests that since *Pyronema* is embedded within this assemblage, the proper name for the family is actually Pyronemataceae (since the Pyronemataceae was erected first, in 1842), but they stop short of recommending we use this name preferentially, noting that the group is both large and poorly sampled to date. While these authors sampled *Otidea* in their work no new information about the genus was provided.

Synthesis of morphological and molecular methodologies:

To address the taxonomic problems within the genus *Otidea*, a modern synthesis of morphological and molecular methods was employed in my work. Combining the traditional methods of ascomycete taxonomy with newer methods of molecular systematics will permit a phylogenetically-based system of classification to be proposed and tested for the genus. This new classification will in turn facilitate the refinement of descriptions and tools for identification, making it easier to identify members of the genus. More accurate identifications will allow for better assessments of rarity within the range of the Northern Spotted Owl, and this new combination of systematic methods will then contribute to practical ends, those of conservation biology and land-use concerns.

Phylogenetic analysis:

The synthesis of morphological and molecular methods involves the combining of these two seemingly independent sets of characters into a combined parsimony analysis. Before this combination can be undertaken several potential problems must be considered. The problems of positional homology and gap coding in use of nucleotide

characters and those of definition of characters and character states of morphological characters must be addressed. Additionally, the combination of data sets and the weighting of characters within and between data sets is currently an active area of research in systematics.

The first step after nucleotide data are collected is to generate a sequence alignment for the taxa of interest. The sequence alignment is the basis of the phylogeny, but this step is poorly understood and often overlooked (Swofford, et al., 1996; Wheeler, Gatesy and DeSalle, 1995). For sequences to be useful in phylogenetic analysis *positional homology* must be attained to the highest degree possible. Positional homology is the idea that in a sequence, at any given site, all nucleotides at that position can trace their ancestry to a single character that occurred in a common ancestor. *Homoplasy*, as opposed to homology, is the idea that nucleotides at a site appear to be homologous but have arisen due to parallelism, reversal, or convergence instead of common ancestry (Swofford, et al., 1996). To assure positional homology it is often necessary to place gaps in the alignment. These gaps are hypothesized to have originated from insertion or deletion events in the organism's evolution. Gaps can be treated either by ignoring positions that contain them (in all taxa in the analysis), by coding them as a new state (fifth nucleotide), or by creating multiple sequence alignments and "eliding" (Wheeler, Gatesy and DeSalle, 1995) the sequences to down-weight gaps (as well as ambiguous sites in the alignment). Swofford, et al. (1996) state that since the mechanism that causes insertion and deletion events in nucleotide sequences is not well understood mechanistically, they suggest removing gaps from phylogenetic analysis, either by pairwise deletion (in two taxa being compared) or complete deletion (the site in question

in all taxa). Other authors propose treating insertion/deletion events as a new state, or fifth nucleotide (Downie, et al., 1998; Bruns, et al., 1992). Keeping gaps in the analysis recognizes that, even if we do not fully understand them, the events leading to the insertion or deletion of nucleotides are part of the organism's evolution. Wheeler, et al. (1995) point out that removal of gaps can result in "robust but grossly unresolved hypotheses of relationships" (citing their own work). For this reason they advocate keeping the gaps and creating multiple sequence alignments by assigning different gap penalties, and then combining the alignments into one "grand alignment" (elision, their term).

Conservation concerns:

When the final phylogenetic analysis is complete, and a more robust hypothesis regarding evolutionary relationships within *Otidea* in the Pacific Northwest has been generated, these data can be used to better assess rarity within the genus. By clearly stating a hypothesis about the number of species in the genus and their characteristics, additional steps will have been taken to enable the survey and management of rare and threatened species of *Otidea* and the habitat in which they occur. This work can serve then as a model for taxonomists to use when working with nomenclaturally difficult and morphologically plastic genera.

My research will help to clarify the following taxonomic questions in Chapter Three of this manuscript. (1) What species is *O. leporina* as listed in the FEMAT Record of Decision (U.S.D.A. F.S., U.S.D.O.I. B.L.M., 1994)? The FEMAT report lists *O. leporina* as a strategy three fungus (extensive survey must be taken before forest

management activity can occur), but includes no varietal name. This work will clarify the relationship between what must be *O. leporina* (Batsch) Fuckel var. *leporina* (= var. *typica* Kanouse) and *O. leporina* (Batsch) Fuckel var. *minor* Rehm, as well as help determine which taxon, if either, is actually rare in the range of the Northern Spotted Owl. Preliminary results indicate that the two morphotypes are quite divergent in terms of ITS sequence similarity, suggesting the presence of cryptic species. (2) What names should be applied to the two provisional new species identified in the course of this study? In the course of this work, one species that was unknown to Nancy Smith Weber was collected on several occasions. This fungus is quite distinct morphologically and forms a natural (monophyletic) group separate from other species of *Otidea* in the phylogenetic analysis. A second species, that superficially resembles *O. rainierensis* but has significantly larger spores has also been collected, and this species also forms a monophyletic group in my analysis. Have these species been described from other parts of the world? If so, by what names? If not, what new names should be applied to them? (3) For the rest of the *Otidea* spp. in the Pacific Northwest, what are the best names to apply to each, based on original morphological descriptions? By using the phylogenetic hypotheses in combination with original descriptions (obtained thanks to the staff at the Farlow Herbarium, Harvard University) we hope to answer this question, as well as comment on how names have been misapplied in the past.

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Chapter 2

CLADISTIC ANALYSIS OF THE GENUS *OTIDEA* IN THE PACIFIC NORTHWEST

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Abstract

The genus *Otidea* in the Pacific Northwest is reported to include as many as 10 species. Collections were made over a two year period in Northern California, Idaho, Oregon and Washington to examine morphological diversity in the genus. Sequence data was generated for the ribosomal DNA internal transcribed spacer (ITS) and large subunit (LSU) regions from 37 and 28 collections, respectively. Data were also generated by coding micro- and macroscopic characters. Two different methods were examined for coding continuous data into discrete, phylogenetically useful characters: generalized gap-coding and Duncan's Multiple Range Test. The partition homogeneity test as implemented in PAUP* was used to examine combinability of individual data sets. It was discovered that the ITS and LSU regions were heterogeneous due to the presence of three different LSU types that apparently were derived from at least two ancient gene-duplication events. The ITS and morphological data were determined to be homogenous and combined in our final analysis. Eight phylogenetic species were determined to occur in the Pacific Northwest and relationships between these species are described.

Introduction

The genus *Otidea* in the Pacific Northwest includes eight species that are difficult to identify. Compounding this problem is their rarity. Three species of *Otidea* are currently recognized as being "species of concern" under the U.S. Forest Service Forest Ecosystem Management Assessment Team's 1994 Record of Decision regarding the habitat of the Northern Spotted Owl (U.S.D.A. F.S., U.S.D.O.I. B.L.M., 1994). *O. smithii* Kanouse is listed as a strategy one fungus, requiring that 160 acres surrounding all known populations be excluded from all ground disturbing activities. *O. onotica* (Persoon) Fuckel and *O. leporina* (Batsch) Fuckel are strategy three fungi, requiring active survey for each fungus before any ground disturbing activity can occur. All three species are superficially easy to identify, but this work proves more complicated when one considers the remainder of the genus as it occurs in the Pacific Northwest. The most recent key to all North American material was published in 1949 by Kanouse in which she treated 10 species from the Pacific Northwest.

Our work represents half of a regional monographic revision of members of *Otidea* as they occur in the Pacific Northwest. The working assumption was that combining characters generated from molecular sequence data with morphological characters in phylogenetic studies would allow the generation of robust phylogenetic hypotheses regarding evolution and relationships within the genus. Moreover, by coding and combining characters from both molecular and morphological data sets, one can infer patterns of character evolution in the genus and establish a phylogenetic species concept (Donoghue, 1985). Phylogenetic analysis of data collected from ribosomal DNA (rDNA)

nucleotides and coded from morphological descriptions allows inference of evolutionary relationships within the genus. Support for nomenclatural revision is presented based on the phylogenetic species concept; the results will be presented elsewhere (Peterson, et al., Chapter Three). Little has been written regarding the combination of molecular and morphological data in phylogenetic analysis of the fungi (but see Lutzoni and Vilgalys, 1995; Hibbett and Vilgalys, 1993; and Harrington, 1998). We examine four different strategies to code spore measurements (continuous data), the combination of these data with molecular data and the taxonomic implications of our combined analysis.

Materials and Methods

Materials

Specimens used in this study were collected and examined per Weber, et al. (1997). Fresh material was used whenever possible to minimize errors in measurement caused by distortion due to drying (Baral, 1992). Collections were made throughout the Pacific Northwest in the Fall of 1996 and 1997 and Spring 1998. Fresh collections were supplemented with materials from Nancy Smith Weber's personal herbarium (NSW), the mycological collection of the Oregon State University herbarium (OSC; Holmgren, Holmgren and Barnett, 1990), and The University of Michigan Fungus Collection (MICH). Paratypes of *O. rainierensis* Kanouse, *O. kauffmanii* Kanouse, and *O. alutacea* var. *microspora* Kanouse and the holotype of *O. smithii* Kanouse were made available courtesy of Dr. Robert Fogel, curator of the mycological collection at MICH. GenBank accession numbers for all sequences are given in Table 2.1.

Table 2.1: Collections used in this study. (P) indicates paratype material and (H) indicates holotype. All type material provided by MICH.

Name	Herbarium Accession #	GenBank ITS Accession #	GenBank LSU Accession #
<i>O. concinna</i>	OSC 56749	AF072082	AF086592
	OSC 56760	AF072081	AF086591
	OSC 56809	AF072080	AF086590
	NSW 7574	AF072083	AF086594
<i>O. leporina</i>	OSC 56784	AF072077	AF086597
	OSC 56824	AF072079	AF086589
	OSC 56825	AF072078	AF086588
<i>O. tuomikoskii</i>	OSC 56826	AF072086	AF086596
	OSC 56756	AF072084	AF086594
	OSC 56761	AF072085	AF086595
<i>O. rainierensis</i>	OSC 56829	AF072087	AF086597
	NSW 6354	AF072088	AF086598
	OSC 56745	AF072089	AF086599
<i>O. rainierensis</i> (P)	EGS 2179 (MICH)	AF072093	
<i>O. alutacea</i> var. <i>microspora</i> (P)	AHS 30502 (MICH)	AF072094	
<i>O. kauffmanii</i> (P)	AHS 21147 (MICH)	AF072095	
<i>O. grandis</i>	ML 941947 (MICH)	AF072096	
<i>O. smithii</i> (H)	AHS 8843 (MICH)	AF072065	
<i>O. smithii</i>	OSC 56753	AF072062	AF086574
	OSC 56799	AF072063	AF086575
	OSC 56811	AF072060	AF086572
	OSC 56823	AF072061	AF086573
	OSC 56830	AF072092	
	NSW 7536	AF072064	AF086576
<i>O. onotica</i>	OSC 56734	AF072066	AF086577
	OSC 56759	AF072068	AF086579
	OSC 56801	AF072067	AF086578
<i>O. alutacea</i>	OSC 56747	AF072070	AF086580
	OSC 56754	AF072069	
	OSC 56770	AF072073	AF086585
	OSC 56777	AF072071	AF086582
	OSC 56798	AF072072	AF086583
<i>O. umbrina</i>	OSC 56758	AF072074	AF086581
	OSC 56782	AF072076	AF086586
	OSC 56813	AF072075	AF086584
<i>Aleuria aurantia</i>	OSC 56831	AF072090	AF086600
<i>Scutellinia</i> sp.	NSW 7387	AF072091	AF086601

Molecular data

Thirty-seven individual collections representing 10 species of *Otidea* were examined in this study. Ribosomal DNA (rDNA) internal transcribed spacer (ITS) sequence data was generated for 37 collections. rDNA large subunit (LSU) sequence data were generated for a subset of the collections (28 sequences total). In repeated attempts we were unable to amplify LSU sequences for specimens over 50 years old from MICH. ITS sequence data from these collections were collected by amplifying the ITS1 and ITS2 regions separately.

DNA was extracted from both fresh and dried collections by the following modification of the CTAB technique of Bult, et al. (1992). Thirty to fifty µg of material were carefully cleaned (surface sterilized) in bleach, 70% EtOH, and distilled H₂O. This material was then suspended in 500 µl CTAB (containing 0.5% B-mercaptoethanol) in 1.5 ml Eppendorf tubes (USA Scientific, Ocala, FL) and placed in a 65° C water-bath for 30 minutes. After 30 m the tubes were removed from the bath and the material was macerated with a Ryobi Cordless drill and reusable Kontes Pellet Pestles (Fisher Scientific, Pittsburgh, PA) that had been previously autoclaved. After maceration the material was returned to the water-bath for 30 m. The final step in the process was to further lyse the cells by submerging the Eppendorf tubes in ice-cold EtOH for 5 minutes, then return the tubes to the 65° bath for 5 minutes. The freeze/thaw process was repeated twice.

The resulting material was then extracted by a chloroform:IAA (24:1) extraction as described in Bruns, et al. (1990). When the interface was clear, 500 µl isopropyl alcohol was added to the supernatant and the mixture was spun in a microcentrifuge for

15 m at 12,000 rpm. The supernatant was then poured off and the resulting pellet cleaned by adding 500 μ l 70% EtOH and spinning for 15 m. Cleaned DNA pellets were then resuspended in 20 μ l dd H₂O, heated in a 55° water-bath for 5 m, and vortexed for 30 s.

Specific regions of DNA were amplified via the PCR reaction (Saiki, et al., 1988; Mullis and Faloona, 1987) with the following primer pairs: ITS4 and ITS5, LR0R and LR3 (White, et al., 1990; Vilgalys and Hester, 1990). In a few instances the ITS4/5 primer pair did not amplify suitable product, so another set of primer-pairs (ITS5/2 and ITS4/3) were used to amplify the ITS1 and ITS2 regions separately. In all cases breaking the target region into smaller pieces was successful, and the sequences were easily joined due to the conservation of the rDNA 5.8S region separating ITS1 and ITS2. The few sequences for which we were unable to generate LSU sequence data were 50-plus years old (from the MICH collection). Regardless of primers used, the following program was run on a PTC-100 Programmable Thermocycle Controller (M.J. Research, Inc.) to amplify the target sequence: 35 cycles of denaturation for 45 s at 94° C, annealing for 45 s at 50° C, extension for 1 m at 72° C, followed by incubation for 5 m at 72° C. PCR product mass and concentration was estimated by ethidium bromide staining with Lambda DNA (Gibco BRL, Gaithersburg, MD) that had been cut using restriction enzymes EcoRI and HindIII (New England Biolabs, Beverly, MA). PCR product was purified using NH₄OAc and isopropyl alcohol. For sequencing reactions, PCR product was diluted in dd H₂O to concentrations of 25 - 50 ng/5 μ l, depending upon fragment size, and submitted to Oregon State University's Central Services Lab, where sequences were determined on an ABI Prism 373 or ABI Prism 377 automated DNA sequencer

(Perkin-Elmer Corporation, Norwalk, CT). Bi-directional sequences were generated for all taxa using appropriate primers.

Sequence alignment

Alignment of ITS sequences were performed by direct examination with Genetic Data Environment 2.2 (GDE v. 2.2, Millipore Imaging Systems, Ann Arbor, MI) run on a UNIX workstation with the highly conserved 5.8S region as a guide. Alignment of LSU sequences was initially performed with the CLUSTAL V (Higgins, Bleasby and Fuchs, 1991) option in GDE and then adjusted where necessary. In each region, gaps were inserted as minimally as possible, and in the ITS region the gap coding technique of Bruns, et al. (1992) was used to preserve information contained in these gaps. While sequence similarity was high between morphologically similar taxa, it was quite low between distantly related taxa and alignment was ambiguous and homology difficult to assess, especially in the ITS1 region. Because of this difficulty in assessment, 76 ambiguous sites were excluded from the ITS region, leaving 211 phylogenetically informative characters; this analysis is hereafter termed *culled* ITS (cITS). Additionally, seven taxa representing the *O. concinna* - *O. leporina* group had a 200 b.p. insert in the ITS1 region that was not present in any other members of the genus sampled. This insertion is believed to be a single event and aligned and coded as such. It appears to be highly conserved, differing little within and between the two species (pairwise distances within species having this insertion range from 0.00889 to 0.06730 mean adjusted character differences, and from 0.03561 to 0.08540 mean adjusted character differences between species). These two species did however have larger numbers of total character

differences between collections than species not having the insertion event (see Table 2.2). The 200 base pair insertion event was coded using the technique of Bruns, et al. (1992, see above).

Table 2.2: Raw number of nucleotide changes within species examined in this study. Percentages indicate the maximum amount of within-species sequence divergence. Note extreme values in *O. smithii* and *O. leporina* in LSU region, indicated in **bold** type.

Species	LSU	ITS
<i>O. smithii</i>	5 - 83 (15.6%)	0 - 2 (0.4%)
<i>O. onotica</i>	5 - 13 (2.3%)	4 - 16 (3.3%)
<i>O. leporina</i>	34 - 58 (10.3%)	6 - 27 (4%)
<i>O. alutacea</i>	5 - 18 (3.1%)	0 - 3 (0.5%)
<i>O. concinna</i>	0 - 2 (0.3%)	11 - 43 (6.3%)
<i>O. tuomikoskii</i>	5 - 11 (1.9%)	0 - 1 (0.2%)
<i>O. rainierensis</i>	0 - 2 (0.3%)	2 - 8 (1.6%)
<i>O. umbrina</i>	5 - 10 (1.7%)	0 - 1 (0.2%)

Morphological data

Collections were examined as described in Peterson, et al. (Chapter Three). Morphological characters were coded according to the analysis in Peterson, et al. (Chapter Three) with the exception of characters 16 through 22. Morphological character 16, apothecium color group, was coded per Raitviir's (1972) analysis of the genus *Otidea* as well as fresh notes. The light-colored group included collections colored as some variant of yellow or tan. The dark-colored group included those described as some variant of orange or brown. To code morphological character 17, Duncan's spore ratio (length/width) group, 25 paired length and width measurements were made in distilled water (as described in Chapter Three). These were entered into an Excel spreadsheet (Microsoft Corporation, Redmond, Washington) along with the collection number, which

was then imported into the statistical package SAS 6.12 (SAS Institute, Inc., Cary, North Carolina). In SAS, an entry was created for the ratio of length to width for each paired measurement. This variable was then analyzed with the ANOVA analysis of variance option in SAS Assist. Means for each collection were analyzed with Duncan's Multiple Range Test, a powerful statistical method for detecting differences in means (Montgomery, 1997). Duncan's test orders the groups (species) from lowest mean to greatest mean, then makes all possible comparisons based on the least significant difference (LSD) (Montgomery, 1997). Collections having spore length/width ratios that did not differ significantly at the $\alpha = 0.05$ level were grouped. Multistate, unordered characters were then coded from these groupings, resulting in 3 statistically significant groups. The same general procedure was followed for only the length measurements (character 18) yielding 5 statistically significant groups, and width measurements (character 19) yielding 2 statistically significant groups. Characters 20 through 22 were coded following the generalized gap-coding method proposed by Archie (1985) and expanded by Goldman (1988). Character 20 is the gap-coded ratio of length to width, yielding 5 groups. Characters 21 and 22 are the gap-coded length and width groups, yielding 4 and 3 groups, respectively. Population standard deviations are reported in parentheses with each character and the value of c for each group was 1.0 (per Goldman's suggestion, 1988). Morphological data were analyzed without spore characters included to examine the value of including characters coded from continuous data. All character states are unordered, and missing data is coded as "?". To better examine resolution provided by morphological data, two rounds of successive approximation based on the rescaled consistency index (R.C.) were used to weigh

characters. This approach applies weight to individual characters based on the observed level of character homoplasy in an unweighted analysis, and effectively downweights homoplasious characters (Farris, 1969). It should be noted that in any analysis that only one spore coding strategy was implemented at a time to satisfy the requirement of independence of characters in cladistic analyses. All characters and character states are listed in Table 2.3. Character state distributions for all taxa included in this analysis are presented in Table 2.4.

Table 2.3: Morphological characters and character states for *Otidea* species and outgroup. Characters and character states used in morphological analysis of *Otidea*. Characters with numbers in ***bold-italic*** are phylogenetically uninformative and were excluded from the final analysis. Characters 17 - 22 represent different spore-coding strategies.

Character Number	Character	Character states
1	Apothecium shape	0 = irregular; 1 = short-eared; 2 = long-eared; 3 = spatulate; 3 = cupulate
2	Apothecium apex	0 = truncate; 1 = pointed
3	Split in apothecium	0 = absent; 1 = present
4	Stipe	0 = astipitate; 1 = substipitate; 2 = stipitate
5	Stipe ornamentation	0 = concolorous w/hymenium; 1 = covered w/mycelium (white to cream)
6	Abhymenial ornamentation	0 = absent; 1 = present (pustulate)
7	Abhymenium hygrophanous	0 = not hygrophanous; 1 = hygrophanous
8	Hymenium w/rosy tints	0 = absent; 1 = present
9	Apical cell of paraphyses globose to subglobose	0 = absent; 1 = present
10	Apical cell of paraphyses having "protuberances"	0 = absent; 1 = present
11	<i>Paraphyses coloration</i>	<i>0 = hyaline; 1 = colored somehow</i>
12	Paraphyses containing granulose ornamentation	0 = absent; 1 = present
13	<i>Ascospore shape</i>	<i>0 = subglobose to globose; 1 = ellipsoid</i>
14	Ascospore ornamentation	0 = absent; 1 = present (in some form)
15	<i>Ascospores containing guttules</i>	<i>0 = absent; 1 = present</i>
16	Apothecium color group	0 = light colored; 1 = dark colored
17	Duncan's spore ratio group (length/width) (mean standard error = 0.014)	0 = mean 2.34; 1 = mean 2.19 -- 1.74; 2 = mean 1.24
18	Duncan's spore length group (mean standard error = 0.386)	0 = mean 15.77 -- 15.84; 1 = mean 15.40; 2 = mean 14.93; 3 = mean 14.05 -- 14.14; 4 = mean 11.70 -- 13.39; 5 = mean 10.23 -- 11.31; 6 = mean 8.91
19	Duncan's spore width group (mean standard error = 0.128)	0 = mean 7.18 -- 7.44; 1 = mean 5.48 -- 6.89
20	Generalized gap-code ratio group (length/width) (s = 0.180)	0 = mean 1.25; 1 = mean 1.73 -- 1.89; 2 = mean 1.91 -- 2.06; 3 = mean 2.13 -- 2.19; 4 = mean 2.34
21	Generalized gap-code length group (s = 1.93)	0 = mean 8.912; 1 = mean 10.23 -- 12.10; 2 = mean 12.51 -- 14.14; 3 = mean 14.93 -- 15.80
22	Generalized gap-code width group (s = 0.699)	0 = mean 5.48 -- 6.07; 1 = mean 6.20 -- 6.75; 2 = mean 6.84 -- 7.44

Table 2.4: Character state assignments for morphological data.

Taxon	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
OSC 56826	2	1	1	1	1	1	1	0	0	1	0	0	1	0	1	0	1	5	1	1	1	0
OSC 56758	1,2	0	1	1	0	1	1	0	1	1	0	1	1	0	1	1	1	4	1	2	2	1
OSC 56756	2	1	1	1	1	1	1	0	1	1	0	1	1	0	1	0	1	5	1	2	1	0
NSW 7574	1,4	0	1	2	1	1	?	0	0	1	0	0	1	0	1	1	1	5	1	1	1	1
NSW 6354	4	0	1	0,1	0	1	0	0	1	0	0	1	1	0	1	0	1	5	1	1	1	0
OSC 56734	2	1	1	2	1	1	0	1	0	0	0	0	1	0	1	0	1	4	1	2	1	0
OSC 56745	4	0	1	1	0	0	1	0	1	0	0	1	1	0	1	0	1	5	1	1	1	0
OSC 56747	2,3,4	0,1	1	1,2	0	0	0	0	0	1	0	1	1	0	1	0	1	0	0	3	3	2
OSC 56749	3,4	0	1	2	1	1	?	0	0	1	0	1	1	0	1	1	2	6	0	0	0	2
OSC 56753	2	1	1	1	1	1	1	0	0	1	0	1	1	0	1	1	1	4	1	2	2	2
OSC 56754	1,3	0	1	1	1	1	1	0	0	1	0	1	1	0	1	0	0	0	1	4	3	1
OSC 56759	3	0	1	2	1	1	?	1	0	0	0	1	1	0	1	0	1	4	1	1	1	1
OSC 56760	1	0	1	2	1	1	?	0	0	1	0	1	1	0	1	1	1	5	1	1	1	1
OSC 56761	2	1	1	1,2	1	1	1	0	0	1	0	1	1	0	1	0	1	5	0	1	1	0
OSC 56770	1	0	1	0,1	0	1	1	0	1	0	0	1	1	0	1	1	1	1	1	3	3	2
OSC 56777	1	0	1	1,2	1	1	1	0	0	1	0	1	1	0	1	0	1	2	0	2	3	2
OSC 56782	2,3,4	0	1	0,1	0	1	1	0	0	1	0	1	1	0	1	1	1	4	1	1	1	1
OSC 56784	1	0	1	1,2	1	1	1	0	0	1	0	1	1	0	1	0	1	4	1	1	2	2
OSC 56798	1	0	1	0,1	0	1	1	0	0	1	0	0	1	0	1	1	1	0	0	3	3	2
OSC 56799	1	0	1	2	1	1	1	1	0	1	0	1	1	0	1	0	1	4	1	1	2	2
OSC 56809	1	0,1	1	2	1	1	1	1	0	1	0	1	1	0	1	1	1	5	1	1	1	0
OSC 56813	2,3,4	0	1	0,1	0	1	1	0	0	1	0	1	1	0	1	1	1	4	1	2	2	1
OSC 56820	2	0	1	0,1	0	1	?	0	0	1	0	1	1	0	1	1	1	4	1	2	2	1
OSC 56823	1	0,1	1	1,2	1	1	?	0	0	1	0	1	1	0	1	0	1	4	0	1	2	2
OSC 56824	1	0,1	1	1,2	1	1	0	0	0	1	0	1	1	0	1	0	1	4	0	1	2	2
AHS 30502	1,4	0	1	1,2	1	0	?	0	1	0	0	1	1	0	1	1	1	5	1	1	1	0
OSC 56829	1,4	0	1	1	0	0	?	0	1	0	0	1	1	0	1	0	1	5	1	1	1	0
AHS 21147	1	0	1	2	1	0	1	0	1	0	0	1	1	0	1	?	1	4	1	2	1	0
OSC 56831	0	0	0	0	0	0	0	0	1	0	0	0	1	1	1	0	1	3	0	2	2	2
AHS 8843	1	0	1	1,2	0	1	?	0	0	0	0	1	1	0	1	1	1	3	1	2	2	2
ML 941947	1,4	0	1	0,1	0,1	1	?	0	0	0	0	0	1	1	1	1	1	0	0	3	3	2
EGS 2179	1,4	0	1	1,2	1	0	?	0	1	0	0	1	1	0	1	0	1	5	1	1	1	0

Choice of outgroup

Aleuria aurantia (Persoon : Fries) Fuckel was chosen as an outgroup for this analysis because of its placement in the Otideaceae *sensu lato* and its large, irregular fruiting body. The work of Landvik, et al. show strong support for the relationship between *Otidea* and *Aleuria* (97% bootstrap support, their Figure 1) (Landvik, Egger and Schumacher, 1997). Samuelson (1978) relates these genera on the basis of the apical apparatus of the asci. Microscopically *Aleuria* is similar to *Otidea* in having biguttulate ellipsoid ascospores (although highly ornamented in *Aleuria*) of similar size and having a subglobose to globose apical cells of the paraphyses, as is observed in *O. rainierensis* and *O. kauffmanii*. In the molecular analysis *Scutellinia* sp. was also used as an outgroup based on its placement in the Otideaceae *sensu lato* to examine the placement of the root from outgroup to ingroup.

Combination of data

The incongruence length difference (ILD) test as described by Farris, et al. (1995) as implemented in PAUP* 4d64 (as the partition homogeneity test, Swofford, 1998) was used to examine congruence between the more slowly evolving LSU region and the more quickly evolving ITS region. We also tested the relationship between nucleotide data and morphological data (Cunningham, 1997a; Cunningham, 1997b). To examine the accuracy of the ILD test, the ITS1 region was compared to the ITS2 region. Additionally, where possible, weighting using successive approximation was used to examine the effects of differential weighting on partition homogeneity. ITS sequence

data that was not gap coded was also examined after applying transversion weighting. Fifteen partition comparisons were analyzed (Table 2.5). Partitions were created for each individual data set using the 'charpartition' command in PAUP*4d64, and partition homogeneity was compared using nearest-neighbor interchange (NNI) for branch swapping and the MULPARS option was turned off. 1000 repetitions of the test were performed, and each heuristic search was performed once. All phylogenetically uninformative characters were removed prior to the analysis.

Weighting methods

Characters were weighted by three different methods to examine the relationship between the more conservative LSU gene region and more variable ITS gene region. The methods employed were maximum parsimony, transversion parsimony and successive approximation weighting. Transversion parsimony assumes that transitions are more common than transversions, and therefore gives transitions a weight of zero (Cunningham, 1997). Successive approximation (successive weighting) relies on the set of most parsimonious trees from an equally-weighted analysis to set character weights. Each character is re-weighted based on the degree of homoplasy it had in the equally-weighted analysis (Farris, 1969).

Phylogenetic analysis

All analyses were carried out using PAUP* 4d64 (Swofford, 1997) run on a Sun Sparc 10 (Sun Microsystems, Palo Alto, California). All trees were generated with the

heuristic search option using branch swapping with tree bisection-reconnection (TBR) and ten repetitions of random sequence addition unless otherwise noted. Support for each clade was assessed via the bootstrap (Felsenstein, 1985) implementing the following options: TBR branch swapping, MULPARS option not in effect, five repetitions on each heuristic search and 100 bootstrap replicates (resulting in 500 bootstrap replications). Gaps in the data set were analyzed as missing using the coding scheme of Bruns, et al. (1992). Only parsimonious informative characters were analyzed.

Results

Combinability of data tests

The results of fifteen partition homogeneity test comparisons are presented in Table 2.5. This table lists the type of data compared and the P-value returned by the partition homogeneity test. These results suggest that the LSU and ITS data should not be combined, but the ITS and morphological data are sufficiently homogenous and combination is warranted if successive weighting is applied.

Table 2.5: Results of fifteen partition homogeneity tests. KEY: cLSU (= characters 51 - 100 excluded from LSU analysis; cITS = ambiguous ITS characters excluded; morph (*nn*) indicates that spore-coding character(s) *nn* included in analysis; S.A. = characters weighted in 2nd analysis by successive approximation; Ti/Tv = characters weighted using transition parsimony.

Comparison	p-value	Notes
All ITS - all LSU	p = 0.001	
All ITS - cLSU	p = 0.001	
cITS - all LSU	p = 0.029	* = all taxa representing <i>O. smithii</i> and <i>O. leporina</i> removed
cITS - cLSU	p = 0.001	
cITS - cLSU; S.A.	p = 0.001	
cITS - morph	p = 0.01	
cITS - morph; S.A.	p = 0.22	
cITS - morph (20)	p = 0.01	
cITS - morph (18 & 19)	p = 0.001	
cITS - morph (18 & 19); S.A.	p = 0.219	
cITS - morph (21 & 22)	p = 0.002	
cITS - morph (21 & 22); S.A.	p = 0.192	
All ITS 1 - all ITS 2	p = 0.030	
All ITS 1 - all ITS 2; S.A.	p = 0.021	
All ITS 1 - all ITS 2; Ti/Tv	p = 0.093	All transversions given weight of 1; transitions given weight of 0

Morphological characters

Five of 22 morphological characters proved to be phylogenetically uninformative and were excluded, leaving 17 phylogenetically informative characters. Nine characters were multistate and potentially polymorphic, and coded as such (Table 2.3, characters 1, 2, 4, 5, 18 - 22). The remaining eight characters were binary and scored as present or absent. Care was taken to accurately describe the character states scored in this analysis, and details regarding character states are included in Peterson, et al. (Chapter Three). Four separate analyses of the morphological data were undertaken to examine different spore-size coding strategies.

Excluding all spore coding strategies initially resulted in 407 MPTs, and 787 MPTs of 6.123295 steps (C.I. = 0.804, R.I. = 0.925) after 2 rounds of successive weighting. The strict consensus of these trees was poorly resolved, only a single species was represented by a monophyletic clade (*O. onotica*). When spores are coded by character 20, the generalized gap-coded ratio of length to width, 205 MPTs resulted initially and 3 MPTs of 8.97777 steps (C.I. = 0.611, R.I. = 0.711) after 2 rounds of successive weighting. Resolution in the strict consensus of these trees was worse than that of no spore coding and did not group any species as monophyletic (results not shown). Coding spores using characters 18 and 19, Duncan's spore length and width, initially resulted in 303 MPTs, and 39 MPTs of 10.16348 steps (C.I. = 0.695, R.I. = 0.822) after 2 rounds of successive weighting (Figure 2.1a). The strict consensus of the 39 MPTs resolved the monophyly of *O. umbrina* but no other species. Coding spores using characters 21 and 22, generalized gap-coded spore length and width, initially resulted in 560 MPTs, and 117 MPTs of 9.75533 steps (C.I. = 0.670, R.I. = 0.845) after 2 rounds of successive weighting (Figure 2.1b). The strict consensus tree was well resolved in terms of proximal relationships between species but no monophyletic clades were observed.

The analyses that included spore characters coded by Duncan's Multiple Range Test were as powerful as those characters coded using the more tedious generalized gap-coding technique. We decided to include spore characters 18 and 19, generated with Duncan's MRT, in the combined analysis with cITS data because (1) resolution of MPTs was greater in terms of monophyly of a single clade (*O. umbrina*); (2) fewer MPTs were generated both initially and following the successive weighting; (3) homoplasy values

were similar for both sets of characters (C.I. = 0.500 for character 18 and 0.333 for character 19 vs. C.I. = 0.500 for both characters 21 and 22); (4) the conversion from continuous to discrete data was more easily accomplished with Duncan's MRT than by the generalized gap-coding technique; (5) the P-value reported for the combination of these data with the cITS data (using characters 18 and 19) was higher ($p = 0.219$ vs $p = 0.192$, see Table 2.5).

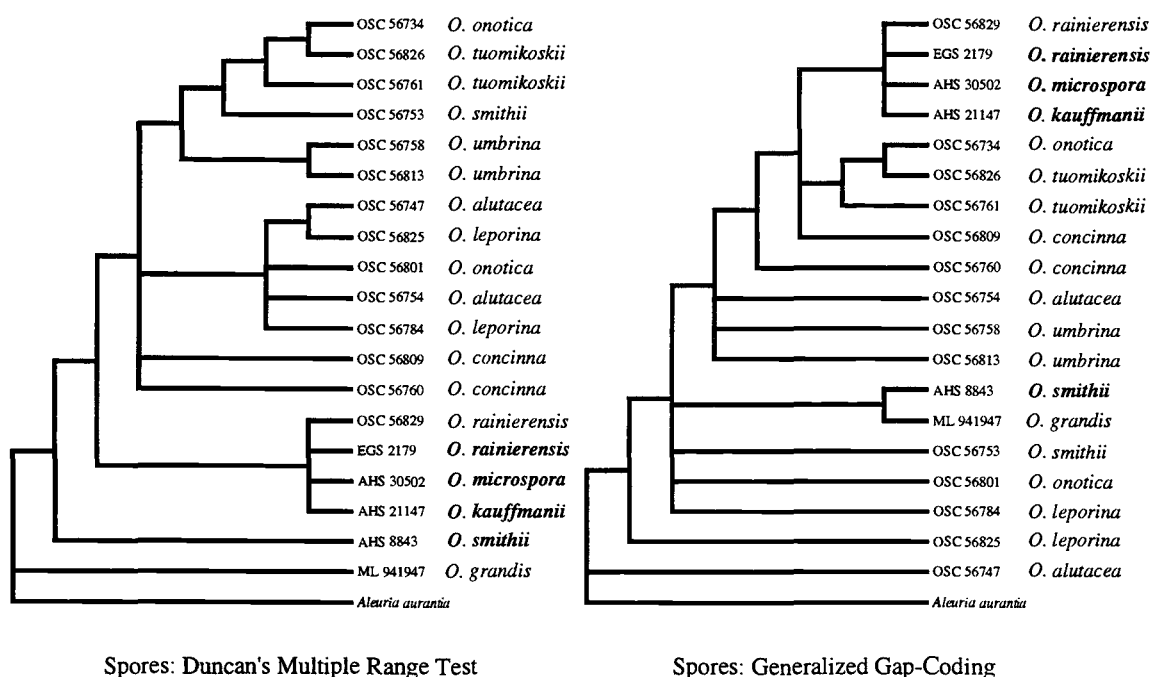


Figure 2.1: Strict consensus trees of morphological data comparing different spore-coding strategies used in this study. **1a** (left): Strict consensus of morphological data coding spores using Duncan's MRT (spore characters 18 & 19). **1b** (right): Strict consensus of morphological data, coding spores by generalized gap-coding technique (spore characters 21 & 22). Names in **bold** indicate type collections (MICH).

Molecular characters

Analysis of 127 phylogenetically informative, equally weighted nucleotide characters from the rDNA LSU region yielded 232 MPTs of 357 steps (C.I. = 0.709, R.I. = 0.869). The strict consensus of these trees is shown in Figure 2.2, with bootstrap values reported above the nodes. The LSU consensus tree has greater resolution than the consensus of either morphological analyses, but there is still little terminal resolution. Additionally, collections representing two morphologically distinct species, *O. smithii* and *O. leporina*, were dispersed throughout the entire tree. Examination of the nucleotide sequence data for these collections reveals a high degree of divergence between same-morphotype collections (up to 10% for *O. smithii* and 16% for *O. smithii*, Table 2.2). Collections representing these two species group together in three different clades and are well supported based on bootstrap values. A single round of successive approximation based on the R.C. values from the previous analysis reduced the number of MPTs to 12 (115.29 steps, C.I. = 0.814, R.I. = 0.948) but did not change the topology of the strict consensus tree. Possible reasons for the ambiguous placement of *O. leporina* and *O. smithii* are discussed below.

The ITS-only analysis included several taxa not sampled in the morphological and LSU analysis, including the holotype of *O. smithii* and paratypes of *O. rainierensis*, *O. kauffmanii*, and *O. alutacea* var. *microspora*, as well as *O. grandis*. Two heuristic searches were performed, one with all nucleotides present and one with all ambiguous sites excluded (culled ITS), to examine the effect of removing characters with questionable positional homology on tree support. Analysis of all nucleotide positions (262 phylogenetically informative characters) yielded 130 MPTs of 629 steps (C.I. =

0.700, R.I. = 0.911). A similar analysis excluding 207 of ambiguously aligned characters from the ITS1 region yielded 88 MPTs of 475 steps (C.I. = 0.680, R.I. = 0.905). The strict consensus of these trees is shown in Figure 2.3, with bootstrap values reported above the nodes. A single round of successive approximation based on the R.C. values from the previous analysis found 23 MPTs of 291.66 steps (C.I. = 0.789, R.I. = 0.942) (results not shown).

A combined analysis of 225 phylogenetically informative sites from unambiguously aligned ITS characters and morphological characters (spore characters 18 and 19 and weighted once using successive approximation after the initial, unweighted analysis) resulted in 12 MPTs of 297.48019 steps (C.I. = 0.784, R.I. = 0.933). The strict consensus of these trees is in agreement with all other topologies presented in this paper with the exception of the LSU analysis, and is presented in Figure 2.4. A phylogram, showing branch lengths but without bootstrap values, is presented in Figure 2.5. In contrast to the LSU analysis, *O. leporina* and *O. smithii* each form monophyletic clades that are well supported by bootstrap values.

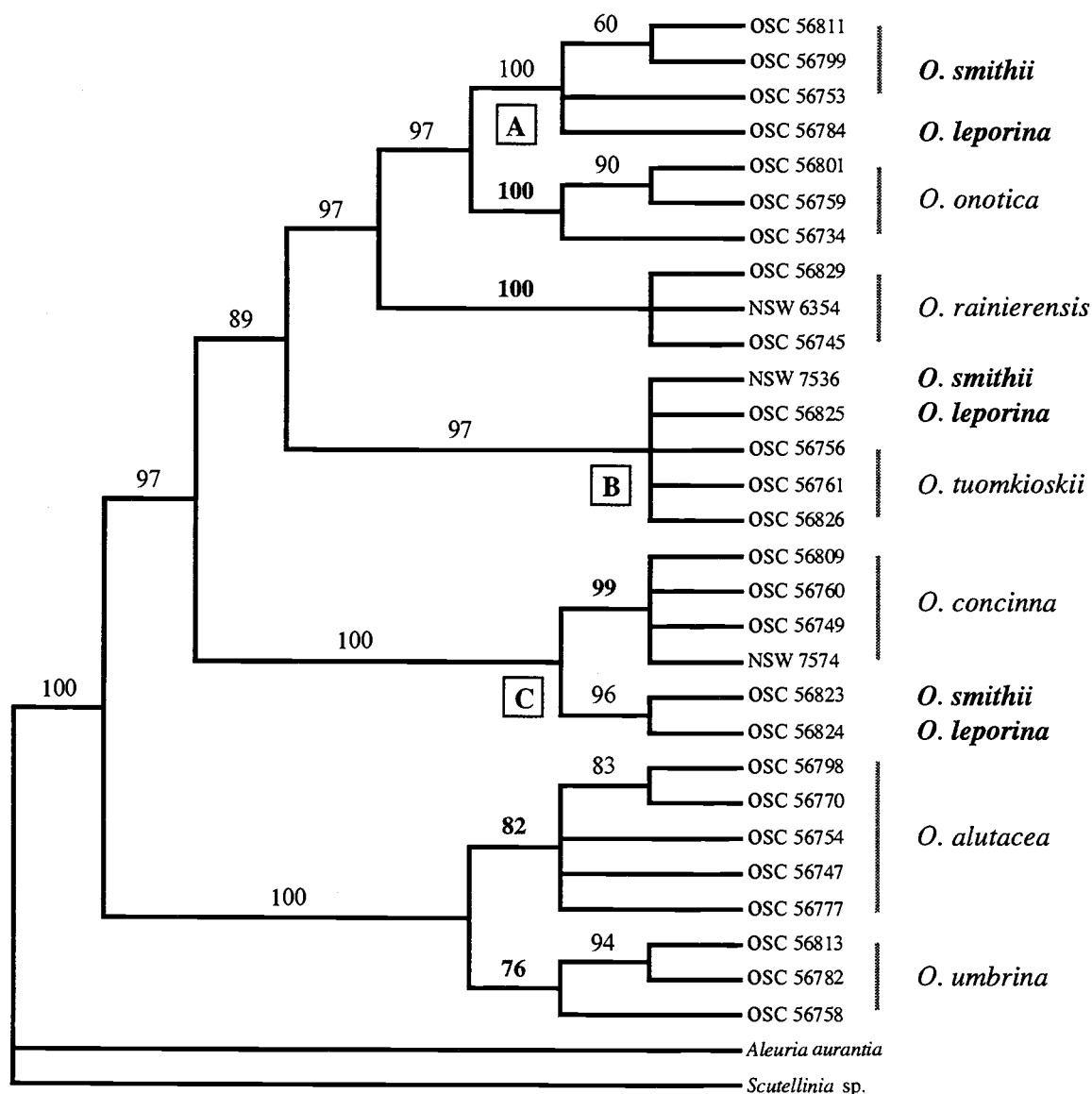


Figure 2.2: Strict consensus 232 MPTs from large subunit (LSU) data with gaps coded and no sites excluded. Trees are 357 steps (C.I. = 0.709, R.I. = 0.869). All characters are equally weighted. Bootstrap values are reported above the node, those supporting monophyletic species are in **bold**. Boxed letters (**A**, **B**, **C**) discussed in text. Paraphyletic species discussed in text are indicated with names in **bold**.

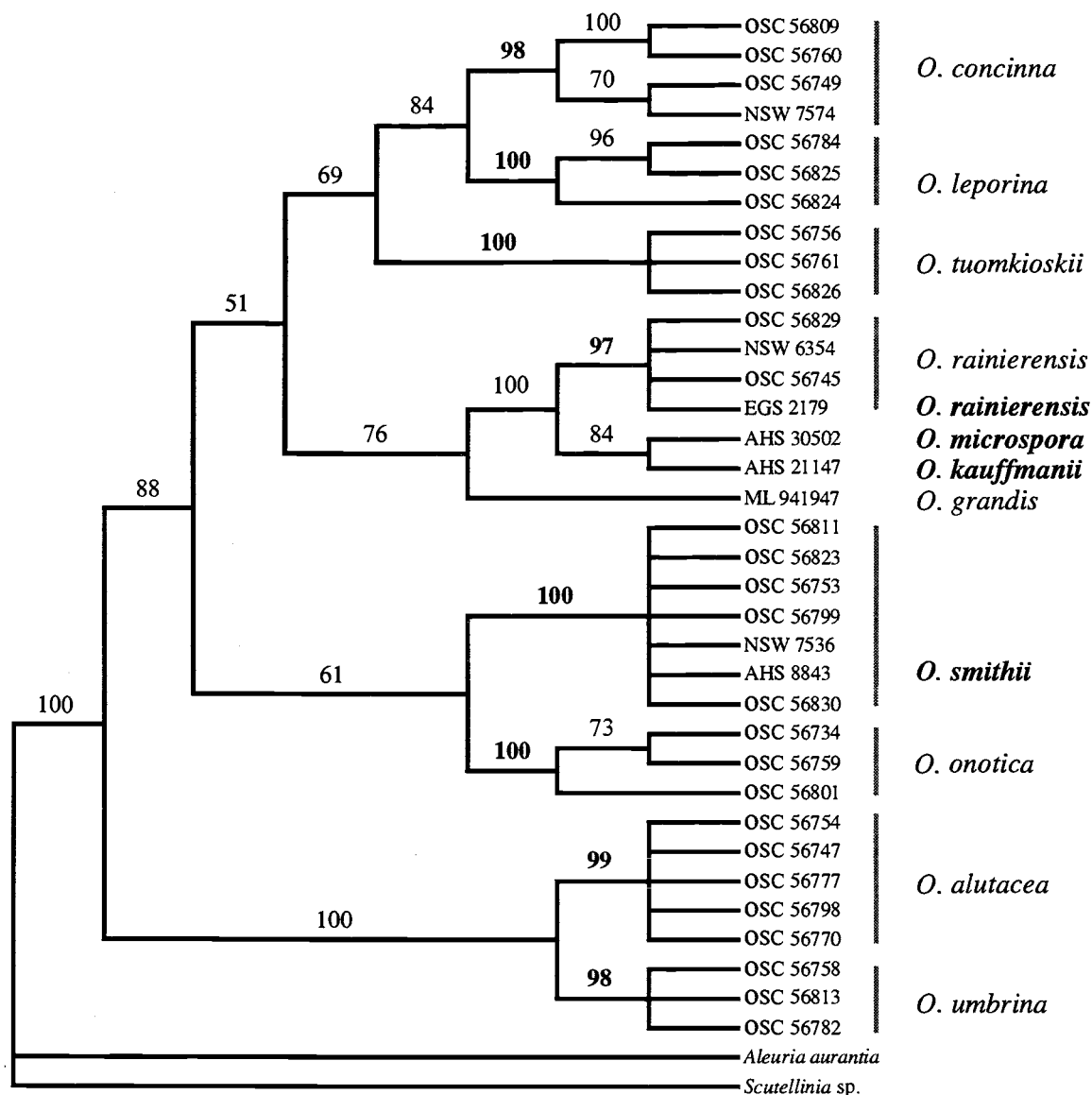


Figure 2.3: Strict consensus of 130 MPTs from internal transcribed spacer (ITS) data with gaps coded and all ambiguous characters excluded. Trees are 638 steps (C.I. = 0.697, R.I. = 0.909). All characters are equally weighted. Bootstrap values are reported above the node. Collections representing type or paratype materials indicated with names in bold.

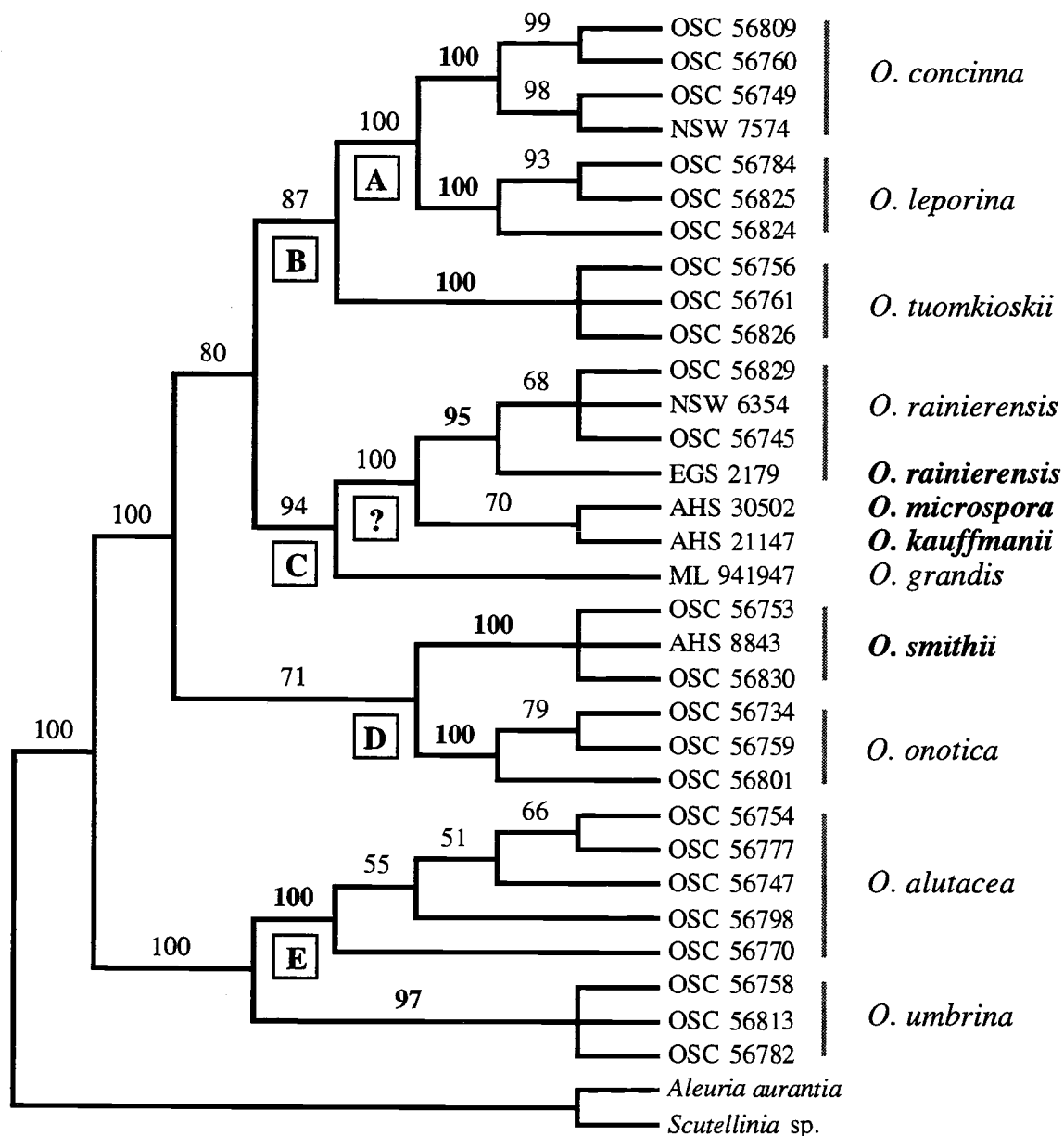


Figure 2.4: Strict consensus of 12 MPTs from combined cITS and morphological data (using spore-coding characters 18 and 19). Trees are 297.48019 steps (C.I. = 0.784, R.I. = 0.933). Bootstrap values are reported above the node, those values in **bold** indicate nodes supporting phylogenetic species. Type material indicated by names in **bold** type. Branches with boxed-letters (*A - E* and *?*) below node are discussed in text.

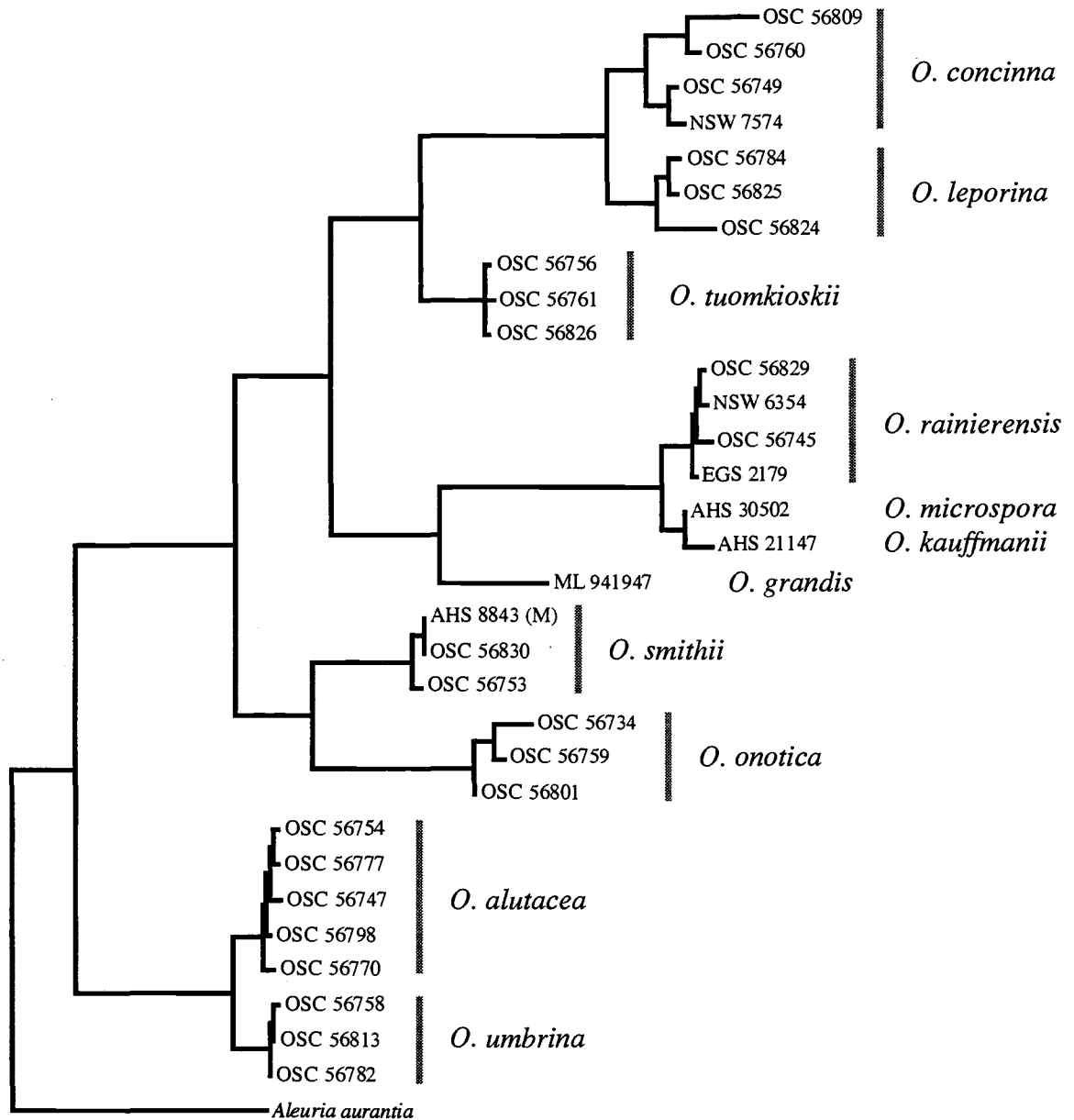


Figure 2.5: Phylogram of 1 of 12 MPTs generated from the combined analysis of cITS and morphological data (including spore-coding characters 18 and 19) weighted using successive approximation (279.56479 steps, C.I. = 0.802, R.I. = 0.941)

Discussion

Large subunit placement of O. leporina and O. smithii.

Careful examination of all LSU sequences of *O. leporina* and *O. smithii* revealed sequences unambiguously aligned with other taxa in this study. This examination also revealed that within-sequence differences scored on a per-nucleotide basis were as high as 10.3% for *O. leporina* and 15.6% for *O. smithii* (Table 2.2). All other LSU conspecific sequences used in this study ranged from 0.3% to 3.1%, the latter value is for the morphologically variable species *O. alutacea*. ITS sequence divergence for these taxa was as expected for conspecifics, 4% for *O. leporina* and 0.4% for *O. smithii*, well within the limits of divergence for other species in this study. Data presented by O'Donnell, et al (1998) show that different ITS2 types have become fixed in populations of *Gibberella fujikuroi* sampled from Africa, Asia, and America. The different ITS2 types are homoplastic in the gene trees presented in their work, and appear to be a result of an ancient gene duplication or interspecies hybridization event, prior to the radiation of the genus. These authors report that sequence divergence in the ITS2 region is as high as 19.4%, comparable to our findings for *O. smithii* and *O. leporina*, especially considering the expected difference in conservation between the ITS and LSU gene regions.

An attempt to map a biogeographical origin onto the placement of taxa in the *O. leporina* - *O. smithii* sequence divergence was inconclusive. Collections in the clade indicated by box A (Figure 2.2) are from Oregon and Washington. Collections in the clade indicated by box B (Figure 2.2) are from Idaho and California, and those in the clade indicated by box C (Figure 2.2) are from California. As in O'Donnell, et al. the

placement of each sequence type appears homoplastic. These data also suggest that different LSU types exist within species of *Otidea*, a condition not previously reported in fungi. Further analysis of the origin of this polymorphism is warranted.

Combinability of data.

The question of whether or not to combine data from independent sources is often debated by systematists. There are three broad opinions on how to handle different sources of data: taxonomic congruence, total evidence, and prior agreement (Chippindale and Wiens, 1994; Bull, et al., 1993; Queiroz, 1993; Rodrigo, 1996; Barrett, Donoghue and Sober, 1991; Tehler, 1994; Nixon and Carpenter, 1996). Methods of taxonomic congruence involve three steps: (1) partitioning of data, (2) separate analysis, and (3) comparison and construction of a consensus topology (Chippindale and Wiens, 1994). The method of total evidence is simple in that all data are combined and a single simultaneous analysis is undertaken (Eernisse and Kluge, 1993). The prior agreement approach is a middle-ground between the first two approaches. First advocated by de Quiroz (1993) and elaborated upon by Bull, et al. (1993) this approach recognizes that more data (i.e., total evidence) have advantages but if the individual data sets are incongruent (e.g., strongly support conflicting phylogenies) that the combined data set has a high probability of inferring the "incorrect" phylogeny. While this approach appears to be the safest route towards phylogenetic reconstruction, data now exist that shows that tests of congruence may in fact be too conservative and therefore prevent combination of data (Cunningham, 1997; Cunningham, 1997; Lutzoni and Vilgalys, 1995; Lutzoni, 1997).

In this analysis three partitions were examined, LSU sequence data, ITS sequence data and morphological characters. The partitioning of the LSU and ITS data is seemingly artificial since these sequences represent continuous, albeit differently constrained, nucleotide data within the rDNA tandem repeat. The decision to partition these data and analyze each subunit separately is based on the expected level of sequence divergence. To answer our major question, how many species of *Otidea* are present in the Pacific Northwest, we needed gene regions that would be evolving quickly enough to resolve intrageneric relationships. The ITS region is appropriate for this type of analysis (Hibbett, et al., 1995; Liston, et al., 1996; Downie, et al., 1998). Large subunit sequence data was initially collected to confirm the appropriateness of the ITS region and to confirm the monophyly of the genus *Otidea* within the Otideaceae and Pezizales.

The phylogenetic relationships inferred in the LSU and ITS appear at least visually to be somewhat congruent (Figures 2.2 and 2.3). Each of the strict consensus trees support the monophyly of a *O. alutacea* - *O. umbrina* clade as sister to all other species and the relationship between of *O. smithii* and *O. onotica*. The major difference between the two topologies is the polyphyletic placement of species in the *O. smithii* and *O. leporina* groups. In the ITS analysis, all sampled members of these two species form monophyletic groups and are well supported (based on bootstrap values). In the LSU analysis, these species are spread throughout the consensus tree, but again their placement is well supported. The partition homogeneity test as implemented in PAUP*4d64 indicated that the LSU and ITS regions are incongruent ($p = 0.001$) and should therefore not be combined. Cunningham (1997) indicates that P-values greater than $p = 0.01$ suggest that combining data will either improve or not effect phylogenetic

accuracy, and that P-values $p < 0.001$ will cause accuracy to suffer. Also, the presence of polymorphic LSU types suggested that these data were not homogeneous. Accordingly we decided not to combine the LSU and ITS data. It is interesting to note however that if the collections representing *O. leporina* and *O. smithii* are excluded, the LSU and ITS data can be combined without causing a decrease in phylogenetic accuracy ($p = 0.029$).

Regarding the combination of the molecular data and morphological data, we analyzed the combinability of the cITS sequence data and morphological data. The partition homogeneity test used as described gave a P-value $p = 0.01$ when all spore-coding character were excluded, $p = 0.001$ and $p = 0.002$ when spore-coding characters 18 & 19 and 21 & 22 were included respectively. However, after a single round of weighting using successive approximation these values changed significantly and all combinations of ITS and morphological data were reported as sufficiently homogenous to combine (Table 2.5).

Our decision to combine ITS and morphological data, and weight these data using successive approximation is supported by our data and the work of other authors who favor combining these types of data (e.g., Hibbett and Vilgalys, 1993; Doyle, 1992; Lutzoni and Vilgalys, 1995; Tehler, 1994; Donoghue and Sanderson, 1992; Harrington, 1998). Arguments in favor of combining molecular and morphological data range from Doyle's (1992) suggestion that morphological data can root "gene trees" with independent characters and provide greater evidence for a species phylogeny that would be available with molecular data alone. Lutzoni and Vilgalys (1995), Hibbett and Vilgalys (1993) and Harrington (1998) all found that the combination of molecular and morphological characters resulted in fewer trees that were more resolved and better supported. Finally,

Donoghue and Sanderson (1992) make the case for total evidence and show quite convincingly that it is "a mistake to set morphological data aside and base phylogeny reconstruction only on molecular evidence." While they recognize limitations inherent in this type of combination -- problems of non-independence, weighting, and the potential swamping effect -- they state these are surmountable problems and *all* evidence should be examined when attempting to infer phylogeny.

In our final analysis we decided to combine the ITS sequence data with the morphological data (using Duncan's Multiple Range Test codes for spore length and width) to infer phylogeny for the genus *Otidea* as it occurs in the Pacific Northwest. In addition to the results of the partition homogeneity test, excluding LSU data from this analysis was decided for the following reasons. First, to resolve *O. smithii* and *O. leporina*, many phylogenetically informative characters would need to be excluded from the analysis. Because the sequences appeared to be free of contamination and they aligned easily with other members of the genus, we have no *a priori* reason to exclude these data. Second, due to the age of the material we failed to amplify LSU sequences for the type and paratypes. By combining LSU and ITS data we would be forced to exclude these valuable sequences, and therefore limit our taxonomic analysis of the genus.

Morphological character coding strategy.

Much has been written regarding the validity of transforming continuous data into discrete units that can be used in cladistic analysis (Pimentel and Riggins, 1987; Cranston and Humphries, 1988; Thiele and Ladiges, 1988; Archie, 1985; Goldman, 1988; Harrington, 1998; Maddison and Maddison, 1992). Archie (1985) and Goldman (1988) present a statistically-based method for coding continuous data into discrete units based on gaps in the data (gap-coding). The major criticism of this technique is the question of the cladistic significance of a mean for a taxon (Pimentel and Riggins, 1987; Cranston and Humphries, 1988). Pimentel and Riggins (1987) critically question the cladistic properties of population means and standard deviations, and recommend that cladists avoid using these types of data. Cranston and Humphries (1988) point out that, because of the questionable validity of using measurements as cladistic data, using ratios is to be further discouraged because you also lose independence of data. It is interesting to us that other authors will follow this line of reasoning and exclude valuable continuous data, while including other characters and coding character states using subjective terms such as "large" and "small" or "rarely" and "frequently" without clearly defining these terms.

Some authors suggest that continuous data need not be modified at all for use in cladistic analysis, but can be used directly without recoding (Maddison and Maddison, 1992; Farris, 1970; Maddison, 1991). In the context of this analysis, to capture important information about spore length and width, this technique seems poor at best. If a group average is used, any addition or exclusion of data from each taxon's population of spore measurements will affect the value of the population mean and thereby change the character state of that character. The gap-coding as implemented in this study minimizes

the effect of addition or removal of data. For this reason we decided not to use spore length and width measurements as continuous data proper.

In contrast to the rejection of continuous data, Thiele and Ladiges (1988), Archie (1985), Goldman (1988) and most notably Stevens (1991) make cases for inclusion of this type of data. Archie (1985) described the generalized gap-coding technique for making continuous data useful in cladistic analysis and analyzed its utility compared to other techniques. One justification for his work, and this type of analysis, is that systematists do collect and rely on continuous data in taxonomic assessments. Goldman (1988) modified Archie's methods and proposed a new method for coding the gap-subsets into discreet character states. Thiele and Ladiges (1988) base the utility of coding quantitative characters based on tree resolution. Their analysis including 18 quantitative characters and 9 qualitative characters yielded one fully-resolved most parsimonious tree, whereas the exclusion produced a little resolved tree (their Figures 2.4 and 2.5). Stevens (1991) in his review of character states, morphological variation, and phylogenetic analysis recognizes the value of including continuous data that has been coded into discreet units if this transformation is carefully undertaken. He recognizes that inclusion of continuous data in phylogenetic analyses often increases the resolution of the analysis, but states that this increase in resolution is accompanied by a decrease significance of the MPT(s) (due to an increase in homoplasy). He offers two general guidelines regarding the use of morphological data: (1) Character states used in phylogenetic analysis should be discreet and without overlap, and (2) characters and character states should be better documented and justified than is generally done. This point returns to our previous criticism of the use of ambiguous terms for character states.

Our decision to use spores coded using Duncan's Multiple Range Test as implemented in SAS Assist 6.12 was because (1) since both strategies for coding continuous data rely on the analysis of populations of measurements it was significantly less time-consuming to use the test in the available software; (2) since the addition of data results in a change in the population standard deviation, the ease-of-use of Duncan's test allowed for quick addition and removal of data that was more cumbersome with the generalized gap-coding technique; (3) each test appeared to have significant resolution, finding between 2 and 7 significant groups. Clearly, the utility of coding continuous data using Duncan's MRT is worth further study with larger data sets than available in this study.

Taxonomic implications.

Based on the final analysis of cITS and morphological data (Figures 2.4 and 2.5) our sampling supports eight species of *Otidea* in the Pacific Northwest (*O. concinna*, *O. leporina*, *O. tuomikoskii*, *O. rainierensis*, *O. smithii*, *O. onotica*, *O. alutacea*, and *O. umbrina*). Each was supported by strong bootstrap support at the terminal or subterminal node, except in the case of *O. alutacea* (discussed below), and morphological characters including ascomal color and ascospore size. Spore measurements are useful in differentiating species of *Otidea* (Raitviir, 1972; Kanouse, 1949; Nannfeldt, 1966). Two major groups of species were observed, the clade formed by *O. umbrina* - *O. alutacea*, and of all other species examined. Within the larger assemblage, two groups were observed. One, *O. concinna* and *O. leporina*, is supported by a 200 b.p. insertion event in the ITS1 region that is absent in all other members of the genus sampled (box A, Figure

2.4). The other, *O. rainierensis*, *O. microspora*, *O. kauffmanii*, and *O. grandis*, is supported by the presence of subglobose or globose apical cells in the paraphyses (box C, Figure 2.4). Each is strongly supported by bootstrap values. Additionally, one reversal is observed regarding the presence of copious white or cream-colored mycelia on the lower portion of the fruiting body in four species. This character state appears to have either arisen twice, once in the *O. onotica* - *O. smithii* clade and again in the *O. concinna* - *O. leporina* - *O. tuomikoskii* clade (boxes B and D, Figure 2.4) or has been lost twice. Other members of the genus have occasional lightening of the lower portion of the fruiting body, but the five listed are the only members of the genus known to have copious white or cream-colored mycelium on the stipe (or an obvious stipe for that matter, with the exception of *O. tuomikoskii*).

Evidence for each species group is supported as well by individual morphological characters, including those listed above. To further support each phylogenetic species we have listed each species or closely related species group below along with characters that support the clade and differentiate it from sister clades. Additional information is provided in Peterson, et al. (Chapter Three).

O. concinna - *O. leporina*: The fruiting bodies vary in shape and color but are generally short-eared with a truncate or pointed apex, and are some shade of orange, tan or brown. Colors in *O. concinna* tend to be the same inside and out whereas the fresh hymenium in *O. leporina* is generally darker than the abhymenium. The spores of *O. concinna* are significantly smaller than those of *O. leporina*. The clade containing these two species is supported by 100% bootstrap support and these are the only species that contain the 200 b.p. insertion event in the ITS1 region (box A, Figure 2.4). Additionally,

as stated previously, both species are generally stipitate and have white or cream-colored hyphae covering the stipe and extending down into the substrate below.

O. tuomikoskii: The fruiting body of *O. tuomikoskii* differs from the previously discussed species by being generally long-eared and slender and yellow or yellowish-brown. It is generally substipitate to astipitate, although the fruiting body may be somewhat constricted towards the base and covered with the previously described white to cream-colored hyphae. *O. tuomikoskii* lacks the 200 b.p. insertion event present in *O. concinna* and *O. leporina*. Workers in the Pacific Northwest have considered *O. tuomikoskii* to be *O. leporina* var. *minor* based on colors and spore sizes described in Kanouse (1949).

O. rainierensis - *O. microspora* - *O. kauffmanii* - *O. grandis*: This entire clade is supported by a 94% bootstrap value and the presence of globose to subglobose apical cells of the paraphyses. *O. grandis* is separated from the remaining three species by its primarily Eastern North American distribution (although reported once from Eastern Washington by E.B. Cooke ca 1955), a darker ascoma, and larger spores that are minutely roughened at maturity. The remaining three species, *O. rainierensis*, *O. microspora* and *O. kauffmanii*, are grouped in a strongly supported clade (100% bootstrap support, box ?, Figure 2.4) and are very closely related (Figure 2.5). Morphologically the three species are quite similar; all have a fruiting body that split down one side, generally cupulate, sessile and often gregarious, with colors some shade of tan or brown. Whereas *O. rainierensis* and *O. microspora* are known and described from Washington, *O. kauffmanii* was described from Michigan collections (Kanouse, 1949). Microscopically the three have spores that overlap in size a great deal. *O. microspora* (Kanouse) Harmaja

(= *O. alutacea* var. *microspora* Kanouse) has spores 9 - 11 x 5.5 - 6.5 μm , *O. rainierensis* has spores 10 - 12 x 6 - 7 (8) μm and *O. kauffmanii* has spores 8 - 10 (12) x 5 - 6 (7) μm . The generalized gap-coding technique grouped collections of these three species together (character 21, group 1, Table 2.3 and 2.4). The Duncan's MRT spore-coding technique grouped *O. rainierensis* and *O. microspora* in group 5 (character 18, Table 2.4 and 2.4) but placed *O. kauffmanii* in group 4 (character 18, Table 2.3 and 2.4). Analysis of morphological characters only with either spore-coding technique found a single unresolved polytomy with these three taxa and another collection identified as *O. rainierensis* (OSC 56829) (Figure 2.1a and b).

Based on cladistic support and morphological similarity one could group these three species into a single species complex and expand the description to cover increased geographical range and morphological variation. Fewer steps separate these differently named taxa than separate morphologically and nomenclaturally identical species (compare this clade to *O. concinna*, Figure 2.5). However, bootstrap support for the *O. microspora* - *O. kauffmanii* clade is high in both the ITS only and combined analysis (84% and 70% respectively), and the sample analyzed is poor, so we suggest that further investigation is warranted. We can conclude that Harmaja's elevation of *O. alutacea* var. *microspora* from variety to species was warranted, based on the phylogenetic distance between this taxon and the clade representing *O. alutacea* var. *alutacea*.

O. smithii - *O. onotica*: These two species, marginally supported in the bootstrap analysis (71%) are well supported individually (100% each). Morphologically they are quite distinct in color and stature. The fruiting body of *O. smithii* is generally firm in texture and purplish-brown inside and out. Conversely, *O. onotica* is generally somewhat

brittle and yellow to bright-yellow (often having pinkish spots or a similar cast in the hymenium). Both species have similarly sized spores, 10 - 12 (14) x 6 - 7 μm vs. 12 - 14 x 6 - 7 (8) μm respectively, as well as a long-eared shape and light colored hyphae covering the stipe (if present).

O. alutacea - *O. umbrina*: These species are also closely related and differ in few morphological characters. Both are darker in color than most other species examined in this study (with the exception of *O. smithii*) and have relatively large spores. *O. alutacea* tends to be lighter in color and more brittle than *O. umbrina* and has slightly larger spores. The abhymenium of *O. umbrina* loses moisture quickly upon collection, especially when young, and often appears quite different in color when compared to the hymenium. This character is observed in *O. alutacea* but generally happens more slowly (slow hygrophanous effect). The major support for separating these species is cladistic. Both the ITS-only analysis and the combined analysis strongly support the monophyly of each terminal clade (99% and 98%, 100% and 97% respectively), as well as the sequence similarity within each species and differences between species (Figure 2.5).

The sampling of *O. alutacea* is larger (5 collections) because collections OSC 56747 and OSC 56754 were lighter in color and more commonly singular in occurrence than other collections described as *O. alutacea*. Initially these were thought to be cryptic or perhaps new species of *Otidea*, however in the LSU-only, ITS-only and combined analysis these two collections grouped with other collections fitting the description of *O. alutacea* with moderate to high bootstrap support (82 - 100%, Figures 2.2, 2.3 and 2.4). Because the LSU-only and ITS-only analyses supported the monophyly of these collections with little or no resolution, we accept the monophyly of the group in the

combined analysis and highlighted the deepest node that was inclusive of these collections as being the point of support for the species (100%, Figure 2.4).

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Chapter 3

REVISIONAL MONOGRAPH OF THE GENUS *OTIDEA* IN THE PACIFIC NORTHWEST

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Abstract

The genus *Otidea* as it occurs in the Pacific Northwest contains three members considered rare throughout the range of the Northern Spotted Owl. *Otidea* has been studied by several authors; the most recent work on North American representatives dates from 1949. This taxonomic reassessment was undertaken due to new information and techniques currently available allowing for the re-evaluation of species concepts. In a separate analysis it was determined that there are eight phylogenetic species of the genus *Otidea* that occur in this range. These species are described in detail and keys to both fresh and dried materials are provided. *O. tuomikoskii* Harmaja and *O. umbrina* (Persoon) Bresadola are reported from North America for the first time.

Introduction

Otidea has long been recognized as a natural genus (Nannfeldt, 1966). It was first erected as a subgenus of *Peziza* by Persoon (1822) for species having an ear-shaped (*otideoid*) apothecium and then elevated to generic status by Bonorden (1851) (although no species were included at that time) According to Kanouse (1949), Cao, Fan and Liu (1990) and Nannfeldt (1966), Fuckel (1869) ascribed four species to the genus, *O. leporina*, *O. onotica*, *O. cochleata*, and *O. abietina*. Boudier (1907) regarded *Peziza abietina* (Persoon : Fries) Fuckel as representing a distinct genus based (presumably) on larger spores and a more regularly cup-like appearance than other members of *Otidea* and made it the type for his new genus *Pseudotis*. Eckblad (1968) reports that a close examination of ascospores, paraphyses, and the medullary and ectal excipula support this species as an *Otidea*, and the *Dictionary of the Fungi* (Hawksworth, et al., 1995) lists *Pseudotis* as a synonym of *Otidea*. Additionally, Kanouse (1949) reported that *O. abietina* is observed to have a split apothecium, and I have seen Canadian material that fits the description of *O. abietina* (*sensu* Kanouse and Cao, et al.) with a split, ear-shaped apothecium (ETP 002, collected near Ontario, Canada by Teresa Lebel).

Boudier considered the straight paraphyses of *O. auricula* to be unique and established the genus *Wynnella* with *W. auricula* as the type species (= *W. silvicola* (Beck in Saccardo) Nannfeldt) (Kanouse, 1949; Harmaja, 1972). Kanouse (1949) did not recognize *Wynnella*. In contrast, Nannfeldt (1966) agreed with Boudier because of the "horny consistency when dry" of the apothecium; spores with one, not two, guttules; straight clavate paraphyses, and differences in the outermost layer of the ectal excipulum.

Harmaja (1972) proposed that *Wynnella* differs from *Helvella* only in form and color, and phylogenetic analysis of nucleotide sequence data (O'Donnell, et al., 1997) support a close relationship between *Helvella* and *Wynnella*.

Rifai (1968), Seaver (1928) and Groves and Hoare (1954), considered the generic name *Scodellina* Gray to be appropriate for *Otidea*. Rifai pointed out that *Scodellina* was originally described as "Thallus fleshy, membranaceous, brittle, sessile, hemispherical, spreading; outside scaly or mealy;" but no unequal split in the apothecium was mentioned. Because of this Rifai (1968) designated "*Peziza vesiculosa* Bull. ex St-Amans" as the lectotype of *Scodellina*, which is now recognized as a synonym of *Peziza*.

Harmaja (1974) moved *O. cantharella* (Fr.) Sacc. and *O. phlebophora* (Berk. & Br.) Saccardo from *Otidea* to his new genus *Flavoscypha* Harmaja with *Peziza phlebophora* Berk. & Br. as the type. He based the change on two minor microscopic and two macroscopic differences, primarily in the outermost layer of the ectal excipulum. He indicates the abhymenium of the apothecium is more or less bright yellow in *Flavoscypha* but this condition is absent in *Otidea sensu stricto*. Additionally he states that the basal parts of the cup are either pitted or ribbed somehow in *Flavoscypha*. Our work indicates that *O. cantharella* and *O. concinna* are closely related, and more information regarding this relationship is presented under the description of *O. concinna*. Cao, et al. (1990) do not mention *Flavoscypha*. Ellis and Ellis (1998) recognize *Flavoscypha* presumably based on the "flesh of ectal excipulum made up of rows of cells at right-angles to the surface."

Originally, apothecial morphology was the primary basis for delimiting *Otidea*. The irregularly split apothecium may either be elongated on one side, giving the fruiting

body a long-eared (donkey-eared) appearance, or symmetrical, giving the apothecium a more short-eared (mouse-eared) appearance (Nannfeldt, 1966). Microscopic and anatomical characters, such as the smooth-walled, ellipsoid, biguttulate ascospores, the slender, hyaline, usually hooked paraphyses, and the structure of the ectal and medullary excipula further reinforce the similarity of taxa within *Otidea* (Nannfeldt, 1966; Kanouse, 1949; Cao, Fan and Liu, 1990). The most recent *Dictionary of the Fungi* includes 15 species in the genus, and describes its distribution as North Temperate (Hawksworth, et al., 1995). The works of Nannfeldt (1966), Kanouse (1949), Cao, et al. (1990), Ellis and Ellis (1998) and Harmaja (1976) yield an extensive list of names proposed for taxa in the genus (Table 3.1).

Table 3.1: Specific epithets used within the genus by Nannfeldt, Kanouse, Cao *et al.*, Ellis and Ellis, and Harmaja since 1949. Authorities are listed verbatim from the listed source, as are past interpretations of the ICBN code (such as var. *typica* in Kanouse, 1949 and the use of "ex" in authority citations) and orthographic errors (such as *Otidea kauffmaniana* in Nannfeldt, 1966).

Specific Epithet	Source(s)
<i>Otidea abietina</i> (Pers. ex Fr.) Fuckel	Kanouse, 1949; Harmaja, 1976; Cao, et al., 1990
<i>Otidea alutacea</i> (Fr.) Bres. var. <i>typica</i>	Kanouse, 1949
<i>Otidea alutacea</i> (Pers. ex Fr.) Bres.	Nannfeldt, 1966
<i>Otidea alutacea</i> var. <i>alutacea</i> (Pers.) Mass.	Cao, et al., 1990; Ellis and Ellis, 1998
<i>Otidea alutacea</i> var. <i>microspora</i> Kanouse	Kanouse, 1949; Nannfeldt, 1966; Cao, et al., 1990
<i>Otidea apophysata</i> (Cooke & Phil.) Sacc.	Nannfeldt, 1966; Cao, et al., 1990
<i>Otidea auricula</i> (Cke.) Mass.	Kanouse, 1949
<i>Otidea bufonia</i> (Pers.) Boud.	Nannfeldt, 1966; Cao, et al., 1990; Ellis and Ellis, 1998
<i>Otidea caligata</i> (Myl.) Sacc.	Nannfeldt, 1966; Cao, et al., 1990
<i>Otidea cantharella</i> var. <i>minor</i> Boud.	Kanouse, 1949
<i>Otidea cochleata</i> (L. ex Fr.) Fuckel	Nannfeldt, 1966; Ellis and Ellis, 1998
<i>Otidea cochleata</i> (L. ex St-Amans) Fuckel	Cao, et al., 1990
<i>Otidea concinna</i> (Pers. ex Fr.) Sacc.	Kanouse, 1949
<i>Otidea felina</i> (Pers.) Bres.	Nannfeldt, 1966
<i>Otidea formicarum</i> Harmaja	Harmaja, 1976
<i>Otidea grandis</i> (Pers.) Boud.	Nannfeldt, 1966
<i>Otidea grandis</i> (Pers.) Rehm.	Kanouse, 1949; Cao, et al., 1990; Ellis and Ellis, 1998
<i>Otidea indivisa</i> (B. & Br.) Sacc.	Nannfeldt, 1966
<i>Otidea indivisa</i> Vel.	Nannfeldt, 1966; Cao, et al., 1990
<i>Otidea kauffmaniana</i> Kanouse	Nannfeldt, 1966
<i>Otidea kauffmanii</i> Kanouse	Kanouse, 1949; Cao, et al., 1990
<i>Otidea lactea</i> Cao et Fan	Cao, et al., 1990
<i>Otidea leporina</i> var. <i>minor</i> (Rehm) Sacc.	Cao, et al., 1990
<i>Otidea microspora</i> (Kanouse) Harmaja	Harmaja, 1976
<i>Otidea myosotis</i> Harmaja	Harmaja, 1976
<i>Otidea nannfeldtii</i> Harmaja	Harmaja, 1976; Cao, et al., 1990
<i>Otidea olivacea</i> Cao et Fan	Cao, et al., 1990
<i>Otidea onotica</i> (Fr.) Fuckel	Kanouse, 1949
<i>Otidea onotica</i> (Pers. ex Fr.) Fuckel	Nannfeldt, 1966
<i>Otidea onotica</i> (Pers.) Fuckel	Cao, et al., 1990; Ellis and Ellis, 1998
<i>Otidea papillata</i> Harmaja	Harmaja, 1976
<i>Otidea phlebophora</i> (B. & Br.) Sacc.	Nannfeldt, 1966
<i>Otidea platyspora</i> Nannf.	Nannfeldt, 1966
<i>Otidea propinquata</i> (Karst.) Harmaja	Harmaja, 1976; Cao, et al., 1990
<i>Otidea purpurea</i> (Zang) Korf et Zhuang	Cao, et al., 1990
<i>Otidea rainierensis</i> Kanouse	Kanouse, 1949; Harmaja, 1976; Cao, et al., 1990
<i>Otidea sinensis</i> Cao et Fan	Cao, et al., 1990
<i>Otidea smithii</i> Kanouse	Kanouse, 1949; Harmaja, 1976; Cao, et al., 1990
<i>Otidea tianshuiensis</i> Cao et Fan	Cao, et al., 1990
<i>Otidea tuomikoskii</i> Harmaja	Harmaja, 1976; Cao, et al., 1990

Table 3.1.

In the Pacific Northwest, *Otidea* fruits mostly on the duff of coniferous forests, especially under Douglas-fir (*Pseudotsuga menziesii*), Pine (*Pinus* spp.) and hemlock (*Tsuga* spp.), but occasionally under cottonwood (*Populus trichocarpa*). *O. tuomikoskii* usually fruits from well-decayed conifer logs, but is also reported from ant hills (Harmaja, 1976). In several species, including *O. tuomikoskii* and *O. concinna*, the hyphae covering the stipe often bind the apothecium to the woody substrate. Whether *Otidea* is mycorrhizal is an open question. The constant association with ectomycorrhizal trees and phenology suggests at least some species may be mycorrhizal. Additionally, a preliminary analysis of carbon-13 signatures of several genera of fungi being conducted at the Environmental Protection Agency (E.P.A.) in conjunction with Oregon State University indicates that *Otidea* may be mycorrhizal (Erik Hobbie, pers. comm.). Little information has been provided by past collectors regarding *Otidea* habitats.

The work presented here is based on phylogenetic analyses of primary nucleotide sequence characters from nuclear ribosomal DNA (rDNA) and morphological characters (Peterson, et al., Chapter Two). Numerous collections and divergent morphotypes were included in the cladistic analysis to examine the morphological variation within a single phylogenetic species. Descriptions presented here complement the work done by Kanouse (1949) and great care has been taken to present accurate descriptions of members of the genus as they occur in the Pacific Northwest of North America.

Materials and Methods

Materials and methods follow Weber, Trappe, and Denison (1997) for fresh material and Baral (1992) for dried material. Unless otherwise noted, all microscopic measurements were on fresh material in water and taken with a Zeiss compound light microscope. Sections were made from innermost layer to outermost layer of the apothecium. Twenty-five spores released from asci were randomly chosen for measurement of length and width. Ten paired ascus length and width measurements were taken from randomly selected asci. Length was measured from the "hooks" at the base of the ascus to the tip, width was measured at the widest point. The ascus in *Otidea* is apically operculate, and the apex is slightly rounded. The spores are ellipsoid, generally 1.5 to 2.7 times longer than wide, and uni- to biguttulate. Most members of the genus have smooth spores, but *O. grandis* (not treated here) has ornamented spores. The terminal cell of the paraphyses in *Otidea* is generally hooked at maturity but may be straight and filiform, clavate, subglobose or globose. The inside of the "hook" of the paraphyses often has small protuberances, often imparting an irregular look to the terminal cell (Figure 3.2). Ten randomly selected paraphyses were measured just below the apex at the broadest point for apical cell width and below the first septa from the apex for "stem" width.

For each ascomata studied, five measurements of the ectal excipulum were taken from the outside of the fruiting body to the point where there appeared to be a significant change in the cell type of the layer (from *textura globosa* or *t. angularis* to *t. intricata* as found in the medullary excipulum). For each ascomata studied, five measurements of the medullary excipulum were made from the previous end point to the often distinct

subhymenium or the base of asci if the subhymenium was indistinct. When dried material was used, samples were taken from the margin to roughly 10 mm towards the center of the ascomata, and rehydrated for 10 minutes in distilled water before measuring. All excipulum measurements were made as near the center of the section as possible from fresh material mounted in distilled water. Squash mounts were used for taking measurements except when measuring the ectal and medullary excipulum, in which case great care was taken not to expand the thickness of the section. In each case the section was made perpendicular to the margin of the apothecium, and three to five apothecia were studied from each collection.

Overall ascomatal measurements are made from the base of the stipe to the top of the fruiting body for height, and at the widest cross-sectional dimension for width and depth. In the following text "in face view" refers to the "front" of the fruiting body, the side having the split in the apothecium. "From above" denotes that the fruiting body is held in face view and then rotated 90° *towards* the viewer, who would then be examining the top of the apothecium. "In side view" or "in profile" denotes that the fruiting body would be held in face view, then rotated 90° *clockwise*. Spore measurements are reported following Huhtinen (1989), giving the 90% confidence interval for each population of measurements as well as the minimum, maximum, and median values. Ascus and paraphysis measurements are reported as minimum and maximum values.

Apothecial shape is referred to as irregular, short-eared, long-eared, spathulate, windswept, or cupulate (Figure 3.1). The apex of the apothecium is either pointed or truncate (Figure 3.1 B & C). In all species presented here the apothecium is split on one side, either to the base or the top of the stipe. The margin of the apothecium is most often

smooth, but occasionally cracks with age and is often inrolled towards the fertile surface when young. The stipe, if present, is often covered with obvious white or cream-colored mycelium. This mycelium may extend into the substrate and bind it together. If the stipe is absent there may still be light-colored hyphae present at the base of the fruiting body.

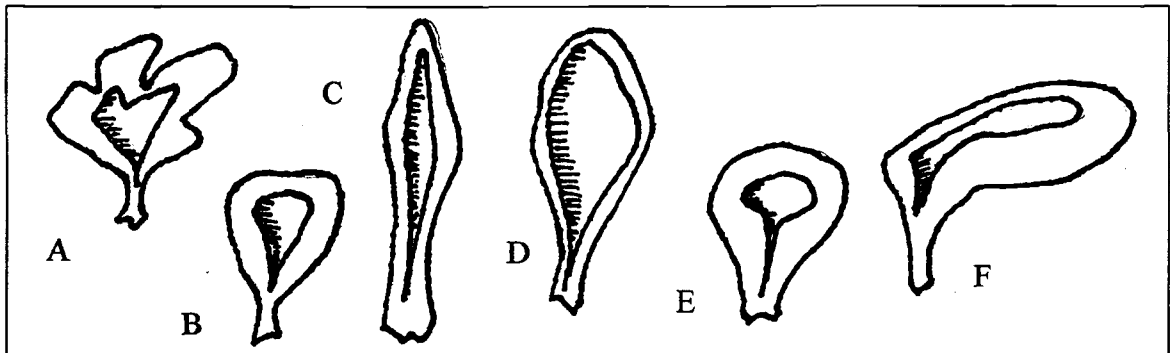


Figure 3.1: Apothecium shapes. A - Irregular; B - Short-eared, apex truncate; C - Long-eared, apex pointed; D - Spathulate; E - Cupulate; F - Windswept. All shapes presented in face-view except windswept, which is presented in profile.

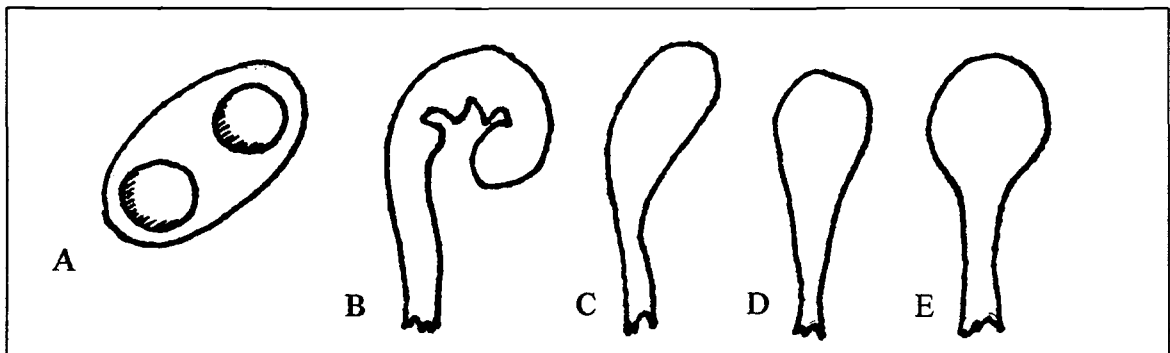


Figure 3.2: Shapes of ascospores and paraphyses apical cells. A - Mature ascospore; B - Hooked paraphysis; C - Clavate paraphysis; D - Subglobose paraphysis; E - Globose paraphysis.

Color names followed by a (Mnnn) designation follow Methuen (Kornerup and Wanscher, 1967) and those followed by a (Snnn) designation follow Smithe (1975) (where nnn is a number that matches plates or pages in each respective color guide). Every attempt has been made to use both sources for color nomenclature, except in the key to dried collections, which cites only the Smithe colors.

Specimens examined in this study were either collected in the course of the study, from the personal collection of Nancy Smith Weber, or loaned by Oregon State University (OSC) or the University of Michigan (MICH). No attempt was made to develop cultures. Specimens have been deposited at Oregon State University.

Generic description

Otidea (Persoon) Bonorden, *Handbuch der allgemeinen Mykologie als Anleitung zum Studium derselben*: 205. 1851.

Apothecia sessile to stipitate, variously shaped, split to base or top of stipe on one side to impart an "ear-shaped" appearance to the fruiting body; apex of apothecium pointed or truncate; margin generally smooth or occasionally cracking in age; colors various, generally some shade of yellow, orange, brown, or tan. Hymenium smooth. Abhymenium smooth to furfuraceous or pustulate. Stipe, if present, often covered with copious light-colored mycelia.

Asci J-; operculate, operculum round, apical; 8-spored; often arising from a darker-colored band in the subhymenium; with a slender base, bearing 1 or 2 well-separated hyphal attachments, cylindric; apex rounded; walls appearing as thick as those of the surrounding paraphyses. Spores smooth to minutely roughened, biguttulate

(infrequently uniguttulate), ellipsoid, generally 1.5 to 2.7 times longer than wide.

Paraphyses hyaline, hooked or straight, occasionally with small protuberances inside the hook, slender to clavate or occasionally subglobose to globose at the tip, septate, branched below usually 3 - 4 times.

Subhymenium and medullary excipulum differentiated by a band of tissue slightly darker than the adjacent medullary excipulum. Medullary excipulum of densely interwoven, hyaline hyphae (*textura intricata*); cells elongate and slightly constricted at septa; entire layer generally thicker than adjacent ectal excipulum in section (measured at thickest point). Ectal excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*); cells slightly constricted at septa; outermost layer smooth or ornamented with irregularly spaced clusters of globose cells and short chains of 3 to 4 globose to subglobose cells that are slightly constricted at the septa.

Type species: *Otidea onotica* (Persoon : Fries) Fuckel

No type species was designated for *Otidea* by Fuckel when he assigned *O. onotica*, *O. leporina*, *O. abietina* and *O. cochleata* to the genus. Kanouse (1949) designated *O. leporina* as the type of the genus, but Saccardo (Saccardo, 1882-1972) indicated *Peziza onotica* as the basionym for *Peziza* subgenus *Otidea*. Eckblad (1968) agreed with Saccardo on this point, as did Rifai (1968), indicating *P. onotica* (S. F. Gray) Persoon as the lectotype species. Neither Cao, et al. (1990) nor Otani (1969) provide any information about the typification of the genus. For the purposes of this work we follow Saccardo, Eckblad and Rifai and accept *O. onotica* as the type of the genus.

Key to *Otidea* (Fresh Material)

1. Ascoma typically light in color, some shade of yellow, orange or tan, or if darker (some shade of brown) then stipitate, stipe covered with white mycelium2
1. Ascoma dark in color, some shade of brown or purplish brown, typically astipitate or short stipitate6
2. Ascoma typically astipitate or substipitate; cupulate or obviously long eared in face view3
2. Ascoma typically stipitate; spathulate, windswept, short-eared, or irregular in face view4
3. Ascoma typically cupulate in face view; lower portion of ascoma may be lighter in color than apothecium, but not covered with copious white mycelium; spores (4.9--5.6--5.7(--6.5) μm broad*O. rainierensis*
3. Ascoma typically long-eared; lower portion of the ascoma covered with copious white mycelium (4.9--6.6--6.7(--6.7) μm *O. tuomikoskii*
4. Ascoma typically much taller than broad, often windswept or spathulate in face view; often with a pinkish cast or pinkish spots on the hymenium; spores (9.2--11.6--11.9(--13.4) x (5.5--6.3--6.4(--8.5) μm *O. onotica*
4. Ascoma not much taller than broad, often short-eared or irregular in face view; rarely with pink spots in the hymenium; spores of different length or width5
5. Hymenium concolorous with abhymenium or nearly so; apothecium generally short-eared or irregular in face view; spores (7.9--10.3--10.6(--12.2) x (5.5--6.2--6.4(--7.3)*O. concinna*
5. Hymenium typically darker than abhymenium; apothecium short-eared to approaching long-eared in face view; spores (12.2--12.8--13.1(--14.6) x (6.7--7.2--7.3(--7.9) μm *O. leporina*
6. Ascoma purplish-brown, drying brown; apex generally pointed but occasionally truncate; spores (12.2--13.4--13.6(--15.5) x (6.0--6.7--6.8(--8.0) μm*O. smithii*
6. Ascoma brown but not purplish-brown, drying tan; apex generally truncate; spores of different length or width7
7. Spores (11.6--12.7--13.1(--14.0) x (6.1--6.6--6.8(--7.3) μm ; abhymenium loses color quickly upon drying*O. umbrina*
7. Spores (13.4--15.4--15.7(--17.7) x (6.1--7.1--7.2(--7.9) μm ; abhymenium loses color slowly upon drying*O. alutacea*

Key to *Otidea* (Dried Material)

1. Spores small, (7.9--10.3--11.9(--13.4) x (4.9--5.6--6.7(--7.3) μm 2
1. Spores large (11.6--12.7--15.7(--17.7) x (6.0--6.6--7.2(--7.9) μm 5
2. Ascoma small, typically less than 2 cm tall, stipe (if present) lighter in color than hymenium; outside near "Raw Umber" (S23), "Cinnamon" (S39), "Brussels Brown" (S121B) or "Mikado Brown" (S121C); inside slightly lighter than "Clay Color" (S26) to "Cinnamon" (S39), "Cream Color" (S54), "Buff" (S124) or "Tawny Olive" (S223D); spores (7.9--10.3--10.6(--12.2) x (5.5--6.2--6.4(--7.3) μm *O. concinna*
2. Ascoma not as above, typically taller than 2 cm or otherwise different3
3. Ascoma medium to large, stipe (if present) lighter in color than above; concolorous inside and out, hymenium often with pink spots or patches; outside near "Clay Color" (S123B) or "Cinnamon" (S123A); inside near "Yellow Ocher" (S123C) or "Chamois" (S123D); spores (9.2--11.6--11.9(--13.4) x (5.5--6.3--6.4(--8.5) μm *O. onotica*
3. Hymenium without pink spots or patches, spores not as above4
4. Ascoma short-eared with apex truncate, typically sub- to astipitate but lower half typically light in color; concolorous inside and out or nearly so; outside "Cream Color" (S54), "Pale Pinkish Buff" (S121D), "Yellow Ocher" (S123C) or "Buff" (S124); inside "Cream Color" (S54), "Buff-Yellow" (S53) or "Buff" (S124); spores (9.2--10.5--10.7(--12.2) x (4.9--5.6--5.7(--6.5) μm *O. rainierensis*
4. Ascoma long-eared, base of ascoma typically lighter than above; concolorous inside and out to slightly lighter inside; outside "Cinnamon" (S123A), "Clay Color" (S123B) or "Verona Brown" (S223B); inside "Cinnamon" (S123A), "Clay Color" (S123B), "Yellow Ocher" (S123C) or "Chamois" (S123D); spores (9.2--10.4--10.6(--11.6) x (4.9--6.6--6.7(--6.7) μm *O. tuomikoskii*
5. Ascoma small, stipe (if present) lighter in color than above; outside "Cinnamon" (S123A), "Clay Color" (S123B), "Yellow Ocher" (S123C) or "Verona Brown" (S223B); inside "Raw Umber" (S223), "Mars Brown" (S223A), near "Vinaceous Pink" (S221C) or lighter to "Light Russet Vinaceous" (S121D); spores (12.2--12.8--13.1(--14.6) x (6.7--7.2--7.3(--7.9) μm *O. leporina*
5. Ascoma medium to large, not stipitate and otherwise different than above6

6. Ascoma large, long-eared with apex pointed or short-ear with apex truncate in shape; outside "Cinnamon" (S121A), "Clay Color" (S121B), near "Raw Umber" (S121), "Mars Brown" (S223A) or lighter to "Sayal Brown" (S223C), purplish cast not obvious in dried collections; inside "Vandyke Brown" (S121), "Prout's Brown" (S121A), "Chamois" (S123D) or "Tawny Olive" (S223D); spores (12.2--13.4--13.6(--15.5) x (6.0--6.7--6.8(--8.0) μm *O. smithii*
6. Dried ascoma lighter in color than above, otherwise similar in shape and size7
7. Abhymenium "Tawny Olive" (S223D) or "Sayal Brown" (S223C); hymenium "Pale Horn Color" (S92), "Drab-Gray" (S119D), lighter than "Chamois" (S123D) or "Tawny Olive" (S223D); spores (11.6--12.7--13.1(--14.0) x (6.1--6.6--6.8(--7.3) μm *O. umbrina*
7. Abhymenium "Tawny Olive" (S223D) or "Sayal Brown" (S223C); hymenium "Tawny Olive" (S223D), "Sayal Brown" (S223C) or "Raw Umber" (S223); spores (13.4--15.4--15.7(--17.7) x (6.1--7.1--7.2(--7.9) μm *O. alutacea*

Descriptions

Otidea alutacea (Persoon : Fries) Masee, *British Fungus Flora IV*: 446. 1895.

≡ *Peziza alutacea* Persoon, *Observationes Mycologicae II*: 78. 1796.

≡ *P. alutacea* Persoon : Fries, *Systema Mycologicum II*: 50. 1822.

Ascoma taller than broad, typically truncate at apex in face view; margins in-rolled towards hymenium when young, shape short-eared to cupulate in face view at maturity. Apothecia split to base, 2.0--6.0 cm tall in face view, 1.5--4.5 x 1.5--4.5 from above; flesh rubbery to firm, without taste. Hymenium smooth, near "Olive-Brown" (S28) or "Walnut-Brown" (S221B) when young to "Drab" (S27) when mature, occasionally with a hint of lilac, towards "Fawn Color" (S25). Margin entire, occasionally cracked at maturity. Abhymenium concolorous with the hymenium or lighter when fresh, near "Olive-Brown" (S28) or "Walnut-Brown" (S221B) when young to "Drab" (S27) when mature, occasionally with a hint of lilac, towards "Fawn Color" (S25); surface sparsely pustulate and minutely tomentose, wrinkled when dried especially

in mature specimens, quickly hygrophanous, and appearing to bruise when handled.

Base of ascoma substipitate to astipitate, often lighter in color than the apothecium.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (13.4--15.4--15.7(--17.7) $\times$ (6.1--7.1--7.2(--7.9) μm , $x = 15.5 \times 7.2 \mu\text{m}$ ($n = 125$), hyaline. Asci J-; operculate, operculum round, apical; 8-spored; 150--207 $\times$ 10.5--12.9 μm . Paraphyses (Figure 3.2) hooked or straight, occasionally having small protuberances inside the hook, hyaline; often clavate at the tip, the clava 3.7--5.5 μm in diameter, below clava 2.4--3.1 μm thick; septate; branched below, usually 3--4 times.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*); entire layer to 400--560 μm thick in section (measured at thickest point); cells elongate and slightly constricted at septa; hyphae 2.4--11.0 μm in diameter at widest point. Ectal excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*), entire layer to 105--135 μm thick in section; cells slightly constricted at septa, 6.1--67.0 μm in diameter at widest point; outer surface with irregularly spaced clusters of globose cells and short chains of 3 to 4 globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to gregarious or caespitose on exposed soil, duff, or in moss under 80-year-old to 150-year-old *Pseudotsuga menziesii*, *Tsuga heterophylla*, and *Calocedrus decurrens* inland; in duff under young *Pinus contorta*, and *Picea sitchensis* on the coast; Oregon, Washington; September to March.

Specimens Examined. U.S.A. OREGON: Lincoln County, Devil's Punchbowl State Park, off Highway 101, 13 Mar. 1997, *T. O'Dell*, *ETP 039* (OSC 56770); same locality, 18 Mar. 1997, *E. T. Peterson*, *ETP 040* (OSC 56771). WASHINGTON: Clallam County, Olympic National Park, Elwha River, 27 Sept. 1941, *A. H. Smith*, *AHS 17338* (MICH); Pierce County, Mt. Rainier National Park, Lower Tahoma Creek, 31 July 1948, *A. H. Smith*, *AHS 29714* (MICH); same locality, 28 July 1948, *A. H. Smith*, *AHS 29507* (MICH); same locality, 29 Oct. 1996, *E. T. Peterson*, *ETP 016* (OSC 56747); same locality, 29 Oct. 1996, *E. T. Peterson*, *ETP 023* (OSC 56754); same locality, 19 Sept. 1997, *E. T. Peterson*, *ETP 203* (OSC 56774); same locality, 19 Sept. 1997, *E. T. Peterson*, *ETP 205* (OSC 56776); same locality, 18 Oct. 1997, *E. T. Peterson*, *ETP 227* (OSC 56798); Snohomish County, Sloan Creek Trail, 24 Sept. 1997, *M. Madsen*, *ETP 206* (OSC 56777).

Observations. Kanouse (1949) referred to the type variety as *O. alutacea* var. *typica* in accordance with the ICBN (Camp, Rickett and Weatherby, 1947) in place at the time when she described the new variety *O. alutacea* var. *microspora*. Cao, et al. (1990) and Otani (1969) refer to this taxon as *O. alutacea* var. *alutacea*, whereas Britenbach and Kränzlin (1984), Tylutki (1993) and Dennis (1981) refer to this species as *O. alutacea* (Tylutki does however recognize *O. alutacea* var. *microspora*). Harmaja (1976) elevated *O. alutacea* var. *microspora* Kanouse to *O. microspora* (Kanouse) Harmaja based on the differences in spore size and ascoma color. Cao, et al. explicitly state that they follow Kanouse (1949) based on a lack of material available for examination. Britenbach and

Kränzlin include *O. alutacea* in their work with no mention of variety nor *O. microspora*. Preliminary molecular analysis by Peterson, et al. (Chapter Two) indicates the two varieties differ significantly phylogenetically, therefore we support Harmaja's conclusions.

This species occurs in two slightly different forms, perhaps depending upon habitat. The gregarious, caespitose, and slightly darker form tends to occur in coastal habitats under pine and spruce. The solitary, substipitate, lighter form tends to occur in inland habitats dominated by 80- to 150-year-old Douglas-fir, hemlock, and cedar. Collections from these divergent habitats have similar microscopic features and form a monophyletic group when analyzed phylogenetically (Peterson, et al., Chapter Two). Dermek (1977) includes a color plate of *O. alutacea* from Europe that resembles the solitary form and has slightly smaller spores than we report here.

Otidea concinna (Persoon : Fries) Saccardo, *Sylloge Fungorum VIII*: 96. 1889.

≡ *Peziza concinna* Persoon, *Mycologia Europea I*: 221. 1822.

≡ *P. concinna* Persoon : Fries, *Systema Mycologicum II*: 49. 1822.

Ascoma stipitate, often as tall as broad, truncate to pointed at apex in face view; margins in-rolled towards hymenium when young, short-eared to cupulate and split to irregular in face view at maturity. Apothecia split to top of stipe or nearly so, 1.0--4.5 cm tall in face view, 1.0--6.5 x 1.0--6.5 cm from above; flesh thin, without taste. Hymenium smooth, "Topaz" (M5C5) to "Clay" (M5D5), "Apricot (Yellow)" (M5C6) to "Oak Brown" (M5D6), or "Linoleum Brown" (M5E7), or "Clay Color" (S123B) to "Yellow Ocher" (S123C), occasionally with a pinkish cast or pink spots. Margin entire, occasionally cracked at maturity. Abhymenium concolorous with the hymenium when

fresh, "Topaz" (M5C5) to "Clay" (M5D5), "Apricot (Yellow)" (M5C6) or "Butter Yellow" (M4A5) to "Oak Brown" (M5D6), or "Bronze (Brown)" (M5E6), or "Cinnamon" (S123A); hygophanous towards "Light Yellow" (M4A4) or "Trogon Yellow" (S153); abhymenial pustulate and minutely tomentose, concolorous with hymenium when moist, often appearing wrinkled when dried. Stipe 3.0--1.2 mm tall, it and the lower portion of the ascoma covered with white or cream-colored hyphae.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (7.9--10.3--10.6(--12.2) x (5.5--6.2--6.4(--7.3) μm , $x = 10.4 \times 6.4 \mu\text{m}$ ($n = 124$), hyaline. Asci 150--212 x 7.5--13.5 μm . Paraphyses (Figure 3.2) hyaline, hooked at the apex, rarely with protuberances inside the hook; some apical cells clavate, the clava 2.4--3.7 μm thick, below clava 2.4--3.1 μm thick; septate; branched below, usually once.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*), entire layer to 400--720 μm thick in section (measured at thickest point); cells elongate, slightly constricted at septa, hyphae 3.9--17.6 μm in diameter at widest point. Ectal excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*), the entire layer to 150--300 μm thick in section; cells slightly constricted at septa, 9.8--30.3 μm in diameter at widest point; outer surface with irregularly spaced clusters of globose cells, or short chains of 3 to 4 globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to gregarious or clustered on exposed soil, duff or moss under *Pseudotsuga menziesii*, *Tsuga heterophylla*; Oregon, Washington, Idaho, California; September to March.

Specimens Examined. U.S.A. CALIFORNIA: Del Norte County, Lake Earl, end of Sand Hill road, 15 Dec 1997, *J. Stockman*, *ETP* 256 (OSC 56827). IDAHO: Idaho County, Seven Devils Mountains, Papoose Creek, 3 Sept 1954, *A. H. Smith* and *H. E. Bigelow*, *AHS* 47346 (MICH). OREGON: Lane County, Hobbit Trail Coastal Area, East side of road, 11 Mar 1996, *E. T. Peterson*, *ETP* 001 (OSC 56732); same locality, 16 Oct. 1996, *E. T. Peterson*, *ETP* 004 (OSC 56735); Lane County, H.G. Andrews Experimental Forest, Lookout Creek Old-growth trail, 20 Oct 1996, *E. T. Peterson*, *ETP* 005 (OSC 56736); same locality, 15 Oct 1997, *J. W. Spatafora*, *ETP* 218 (OSC 56789); Linn County, Hackleman Old-growth trail, Highway 20, just East of Tombstone summit, 6 Oct. 1997, *E. T. Peterson*, *ETP* 209 (OSC 56780); Marion County, Breitenbush Hot Springs Community, near Detroit Reservoir, in woods, 8 Nov. 1997, *J. W. Spatafora*, *ETP* 237 (OSC 56808); same locality, same stand, 8 Nov. 1997, *J. W. Spatafora*, *ETP* 238 (OSC 56809). WASHINGTON: Clallam County, Olympic National Park, Whiskey Bend trailhead, 26 Nov. 1996, *E. T. Peterson*, *ETP* 029 (OSC 56760); Pierce County, Mt. Rainier National Park, Lower Tahoma Creek, 29 Oct 1996, *E. T. Peterson*, *ETP* 018 (OSC 56749); same locality, 22 Sept 1997, *E. T. Peterson*, *ETP* 204 (OSC 56775); same locality, 18 Oct 1997, *E. T. Peterson*, *ETP* 232 (OSC 56803).

Observations. *O. concinna* is the most common species that occurs in the Pacific Northwest. Fruiting in various habitats but most commonly 30 to 80-year-old Douglas-fir stands, it was collected nearly five times more often over this two-year study than the next most common species, *O. tuomikoskii*. Our species concept matches that of

Bresadola (1933), Boudier (1907), Kanouse (1949), Britenbach and Kränzlin (1984) and Cao, et al. (1990). The colors in Bresadola's Tab. 1226 appear lighter than we observed. Dermek (1977) includes *O. concinna* in his work but the color plate resembles *O. rainierensis sensu* Peterson, et al. and has spores much larger than expected for either fungus (19 – 21 x 9 – 12 μm).

Regarding the relationship between *O. concinna* and *O. cantharella sensu* Harmaja (= *O. cantharella* var. *minor sensu* Kanouse), we examined three collections of Alexander Smith and colleagues determined as *O. cantharella* var. *minor* by Kanouse, and in none did we observe the character states that Harmaja describes for *O. cantharella* (= *Flavoscypha cantharella* (Fr.) Harmaja) (AHS 27064, AHS 31033, AHS 56168; MICH). The ectal excipulum was of *textura globosa* and *t. angularis* and had only few short chains and clusters of cells. The dried color of the ascomata was in the range common to the genus, especially in *O. concinna* and *O. tuomikoskii*. No ribs or pits were observed, but the base of the fruiting body had white mycelium present in all three collections. Additionally, spore sizes were 9.8--11.0 x 5.5--6.1 μm . In these three collections it appears that either A) Kanouse misidentified light colored *O. concinna* as *O. cantharella* var. *minor* or B) the two species are synonyms, in which case the appropriate name would be *O. concinna*. It should also be noted that Kanouse (1949) refers to this taxon as *O. cantharella* var. *minor* Boudier and Harmaja (1974) refers to it as *O. cantharella* Fries, although both authors give very similar measurements for spore length and width (10--11(--12) x 6--7 μm in Kanouse, 10--12 x 5--6 μm in Harmaja).

Otidea leporina (Batsch : Fries) Fuckel, *Symbolae Mycologicae*: 329. 1870.

≡ *Peziza leporina* Batsch, *Elenchus Fungorum*: 117. 1783.

≡ *P. leporina* Batsch : Fries, *Systema Mycologicum II*: 47. 1822.

Ascoma stipitate to substipitate, taller than broad, pointed to truncate at apex in face view, short-ear shaped to slightly irregular or occasionally long-eared shaped in face view at maturity. Apothecia split to base or top of stipe, 2.0--6.0 cm tall in face view, 0.5--2.5 x 0.6--2.5 cm from above; taste slightly peppery. Hymenium smooth, "Golden Blonde" (M5C4) to "Topaz" (M5C5), "Oak Brown" (M5D6) to "Golden Brown" (M5D7), "Linoleum Brown" (M5E7) to "Yellowish Brown" (M5E8), or "Yellow Ocher" (S123C) to "Verona Brown" (S223B). Margin entire, in-rolled towards hymenium when young and occasionally cracked at maturity. Abhymenium concolorous with the hymenium or lighter when fresh, near "(Golden) Wheat" (M4B5), or "Pompeian Yellow" (M5C6) to "Oak Brown" (M5D6), very near "Cinnamon" (S123A) or "Clay Color" (S123B); abhymenial surface pustulate and minutely tomentose, not hygrophanous. Stipe, when present, covered with copious light colored hyphae.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (12.2--12.8--13.1(--14.6) x (6.7--7.2--7.3(--7.9) μm , $\bar{x}$ = 13.0 x 7.3 μm (n = 75), hyaline. Asci 165--12 x 9--10.5 μm . Paraphyses (Figure 3.2) hyaline, hooked, occasionally having 2--3 small protuberances inside the hook; often slightly clavate at the tip, the clava 3.7--4.9 μm thick, below clava 2.4--3.1 μm thick; septate; branched below, usually once.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*), entire layer to 320 -- 400 μm thick in section (measured at thickest point); cells elongate and slightly constricted at septa, 2.9--13.7 μm in diameter at widest point. Ectal excipulum of

short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*), the entire layer to 60--90 μ m thick in section; cells slightly constricted at septa; 9.8--23.5 μ m in diameter at widest point; outer surface with irregularly spaced clusters of globose cells and short chains of 3 to 4 globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to gregarious on exposed soil or in needle duff under *Pseudotsuga menziesii*, *Tsuga heterophylla*, or *Picea* spp.; Oregon, California; October to December.

Specimens Examined. U.S.A. CALIFORNIA: Del Norte County, Lake Earl Wildlife Area, 15 Dec. 1997, *J. Stockman ETP 254* (OSC 56825); Humboldt County, Big Lagoon State Park, 16 Dec. 1956, *A. H. Smith, AHS 56799* (MICH); same locality, 23 Dec. 1956, *A. H. Smith, AHS 56954* (MICH); same locality, 14 Dec. 1997, *M. Madsen, ETP 253* (OSC 56824). OREGON: Douglas County, Douglas County Bureau of Land Management, North Bank Habitat Management Unit, 4 Nov. 1997, *J. M. Trappe, JMT 21805* (OSC 60414); Lincoln County, Fogarty Creek State Park, Highway 101 near Depoe Bay, 15 Oct. 1997, *E. T. Peterson, ETP 213* (OSC 56784); same locality, 17 Oct 1997, *E. T. Peterson, ETP 221* (OSC 56792); same locality, 8 Nov 1997, *E. T. Peterson, ETP 235* (OSC 56806).

Observations. *O. leporina* is easily confused with *O. concinna* macroscopically. Both are typically short-eared or irregular in shape and occur in similar habitats. The two species differ slightly in color. *O. concinna* tends to be more orange or brownish-orange

(but displays a wide range of color variation throughout its range and is lighter when faded) and concolorous throughout, whereas *O. leporina* appears to have a lighter colored abhymenium and darker colored hymenial layer than *O. concinna*. An example of this confusion is the description of *O. leporina* in Tylutki (1993). He reports morphological characters that match both fungi, but smaller spore measurements (10 - 14 x 6 - 8 μm) than those attributed to *O. leporina*, which lead us to believe that perhaps Tylutki identified *O. concinna* as *O. leporina* (which he does point out is similar if not identical). The single best character to differentiate the two species is spore size, *O. leporina* has significantly longer spores than *O. concinna*.

O. leporina f. *minor* was proposed by Rehm (1881) and described as follows:

"f. *minor*.

Sporen elliptisch, stumpf, glatt, 1 zellig, mit meist 2 Kernen, -- 12/7; 8 1 reihig in cylindrischen Schlauchen, 120/9; Paraphysen fadig, hackig, Oben kaum etwas dicker, C. 3 mikr. Jod -."

The key and description in Kanouse (1949) will lead one to *O. leporina* var. *minor* (Rehm) Saccardo when trying to identify all light-colored, small spored, ear-shaped members of the genus having hooked apical cells of the paraphyses. Cao, et al. (1990) recognize this variety of *O. leporina* but state that they have not seen an authentic specimen and have viewed only one collection from China. In our work, collections that key to *O. leporina* var. *minor* with Kanouse (1949) are easily identified as *O. tuomikoskii* using the key in Cao, et al. (1990). Additionally, collections that were thought to be *O.*

leporina var. *minor* also keyed to *O. concinna*, which is the older of the two names. With the above in mind, we propose that *O. leporina* var. *minor* be regarded as a *nomen dubium*. Our interpretation of this species agrees visually with that of Boudier (1907) and Bresadola (1933). Dahncke and Dahncke (1979) include a photo of *O. leporina* from Europe that is closer to *O. concinna sensu* Peterson, et al. but has spores as expected for *O. leporina*. Lincoff's (1981) *O. leporina* fits our concept very well, and the color difference from hymenium to abhymenium is visible in the smaller fruiting body included in his work. Peter's (1964) photo of *O. leporina* from Europe again resembles *O. concinna* but has spores that fit our concept (12 – 15 x 6 – 8 μ m).

Otidea onotica (Persoon : Fries) Fuckel, *Symbolae Mycologicae*: 329. 1870.

≡ *Peziza onotica* Persoon, *Synopsis Methodica Fungorum*: 637. 1801.

≡ *P. onotica* Persoon : Fries, *Systema Mycologicum II*: 48. 1822.

Ascoma stipitate, taller than broad, truncate to pointed at apex in face view; often semi-spathulate in face view or windswept in profile at maturity, split to top of stipe or nearly so, 1.0--7.0 cm tall in face view, 1.0--3.0 x 1.0--3.0 cm from above; flesh thin, without taste. Hymenium smooth, "Butter yellow" (M4A5) to "Maize" (M4A6) to "Sunflower" (M4A7) or "Saffron" (M4A8), slightly lighter than "Orange Yellow" (S18), often having a pinkish cast or pink spots throughout the layer at maturity. Margin entire, in-rolled towards hymenium when young and occasionally cracked at maturity. Abhymenium concolorous with the hymenium when fresh, to slightly darker, towards "Indian Yellow" (M5B7) to "Golden Brown" (M5D7), or slightly lighter than "Orange Yellow" (S18), slightly darker than "Buff-Yellow" (S53), very near "Trogon Yellow" (S153) when fresh, fading quickly when drying, especially in young specimens and then

"Pastel Yellow" (M3A4) to "Yellow" (M3A6) or "Buff-Yellow" (S53); abhymenial surface pustulate and minutely tomentose, concolorous with hymenium when moist, often appearing wrinkled when dried, hygrophanous. Stipe covered with white to cream colored hyphae.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (9.2--11.6--11.9(--13.4) x (5.5--6.3--6.4(--8.5) μm , $\bar{x}$ = 11.8 x 6.3 μm (n = 100), hyaline. Asci 150--180 x 9.0--10.5 μm . Paraphyses (Figure 3.2) hyaline, hooked at the apex, rarely having protuberances inside the hook; some apical cells clavate, the clava 2.4--3.1 μm thick, below clava 2.0--2.4 μm thick; septate; branched below, usually once.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*), entire layer to 400 μm thick in section (measured at thickest point); cells elongate and slightly constricted at septa; hyphae 2.5--15.7 μm in diameter at widest point. Ectal excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*), the entire layer to 120 - 160 μm thick in section; cells slightly constricted at septa, 11.8--40.0 μm in diameter at widest point; outer surface with irregularly spaced clusters of globose cells, or short chains of globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to scattered or gregarious on exposed soil, duff or moss under 40-year-old to 150-year-old *Pseudotsuga menziesii*-dominated stands; Oregon, Washington; August to December.

Specimens Examined. U.S.A. OREGON: Benton County, Philomath, Woods Creek road, 18 Nov. 1996, *E. T. Peterson*, *ETP* 028 (OSC 56759); Josephine County, Oregon Caves road, 1 Dec. 1937, *A. H. Smith*, *AHS* 9322 (MICH); Lane County, Lamb Butte, 30 Sept. 1997, *T. O'Dell*, *ETP* 208 (*TOD* 4273) (OSC 56779). WASHINGTON: Pierce County, Mt. Rainier National Park, Lower Tahoma Creek, Westside road, near highway 709, 27 Aug. 1948, *A. H. Smith*, *AHS* 30674 (MICH); same locality, 8 Sept. 1948, *A. H. Smith*, *AHS* 30990 (MICH); same locality, 18 Oct. 1997, *E. T. Peterson*, *ETP* 230 (OSC 56801); same locality, 18 Oct. 1996, *E. T. Peterson*, *ETP* 229 (OSC 56800); same locality, 1 Oct. 1996, *E. T. Peterson*, *ETP* 003 (OSC 56734); same locality, 29 Oct. 1996, *Thom O'Dell*, *ETP* 019 (OSC 56750); same locality, 30 Oct. 1996, *E. T. Peterson*, *ETP* 024 (OSC 56755); same locality, 22 Sept. 1997, *E. T. Peterson*, *ETP* 201 (OSC 56772); same locality, 22 Sept. 1997, *E. T. Peterson*, *ETP* 202 (OSC 56773);

Observations. *O. onotica* has been considered easy to identify since the time of Fries and Persoon because of the characteristic pink hue often observed in the hymenium. This character can be absent or present either as spots in the hymenium or as large patches appearing pink throughout the hymenium. We have observed specimens with a slight pink hue in the hymenium that otherwise clearly match *O. concinna*. Careful examination differentiates the two based primarily on apothecium color and size and spore length. *O. concinna* is generally smaller and rarely as yellow, and has shorter spores than *O. onotica*. Our species concept is in general agreement with most previous authors, including Dahncke and Dahncke (1979), Dermek (1977) and Maublanc (1971). Exceptions include Romagnesi (1962) who includes a photo that resembles *O. leporina*

but has spores that fit our concept, and Schalkwijk-Barendsen (1991) who includes a fungus that resembles *O. tuomikoskii* and is described as a “lopsided cup, like donkey ears, edges inrolled; up to 10 cm tall.”

Otidea rainierensis Kanouse, *Mycologia* 41: 674. 1949.

Ascoma substipitate to astipitate, taller than broad, usually truncate at apex in face view; split-cupulate in face view at maturity. Apothecia split to base, 1.0--5.0 cm tall in face view, 1.0--5.0 x 1.0--5.0 cm from above; flesh thin, without taste. Hymenium smooth, "Drab" (S27) to "Drab-Gray" (S119D) or lighter, approaching "Fawn Color" (S25). Margin entire and occasionally cracked and darker colored than the abhymenium proper at maturity. Abhymenium concolorous with the hymenium or lighter when fresh, "Drab" (S27) to "Drab-Gray" (S119D) or lighter, approaching "Fawn Color" (S25); abhymenial surface smooth, apparently lacking pustules. Lower portion of ascoma lacking light colored superficial hyphae but occasionally is lighter in color than the apothecium.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (9.2 --) 10.5 -- 10.7 (-- 12.2) x (4.9--) 5.6 -- 5.7 (--6.5) μm , $x = 10.6 \times 5.7 \mu\text{m}$ ($n = 100$) hyaline. Asci 140 -- 160 x 10.0 μm . Paraphyses (Figure 3.2) hyaline, straight or slightly hooked, often globose to subglobose (Figure 3.2) or clavate at the tip; the clava 3.7--7.3 μm thick, below clava 2.4--3.1 μm thick; septate; branched below, usually 3--4 times.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*), entire layer to 560--800 μm thick in section (measured at thickest point); cells elongate and slightly constricted at septa, hyphae 2.4--11.0 μm in diameter at widest point. Ectal

excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*), the entire layer to 200--400 μm thick in section; cells slightly constricted at septa, 6.1--67.0 μm in diameter at widest point; outer surface with irregularly spaced clusters of globose cells and short chains of 3 to 4 globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to gregarious and caespitose on exposed soil, duff or moss under 80-year-old to 150-year-old *Pseudotsuga menziesii*, *Tsuga heterophylla*; Oregon, Washington, Idaho; August to October.

Specimens Examined. U.S.A. IDAHO: Bonner County, Priest River Experimental Forest, 26 Sept. 1968, *N. J. Smith*, *NJS 2067* (MICH). OREGON: Jackson County, Rogue River National Forest, off Forest Service road 37, 27 Oct. 1990, *D. McKay*, *NSW 6354*; Marion County, near Breitenbush Hot Springs Community, 27 Oct. 1996, *J. M. Trappe*, *ETP 014* (OSC 56745). WASHINGTON: Pierce County, Mt. Rainier National Park, Lower Tahoma Creek, 23 Aug. 1948, *A. H. Smith*, *AHS 30553* (MICH, HOLOTYPE); same locality, 5 Sept. 1948, *E. G. Simmons*, *EGS 2179* (MICH, PARATYPE); Lewis County, Gifford-Pinchot National Forest, Camp Creek Falls Trail, 6 Nov. 1997, *M. Castellano*, *ODELL 4680* (OSC 56829).

Observations. Kanouse (1949) based *O. rainierensis* primarily on subglobose to globose apical cells of paraphyses, a character state not previously reported for the genus. Often an equal or greater number of regularly hooked apical cells occur on the

paraphyses. We speculate that there are two modes of apical cell formation present in the genus. One, observed here, has apical cells subglobose to globose or clavate when young and become hooked or bent at maturity. Another has apical cells that are slender (filiform) to slightly clavate when young becoming regularly hooked or bent at maturity. Careful examination of a large number of paraphyses is necessary to observe the states of this character. One may question the value of this character, especially considering that Kanouse described two new taxa based primarily on this feature and minor color variations that she did not observe directly (notes of C. H. Kauffman and A. H. Smith). However, the molecular analysis by Peterson, et al. (Chapter Two) supports the monophyly of this species, and the two character states map onto two distinct clades in rDNA ITS analysis (their Figure 4). *O. rainierensis*, *O. kauffmanii*, *O. microspora*, and *O. grandis* form a monophyletic, basal lineage within *Otidea*, and all have subglobose to globose apical cells in the paraphyses.

Otidea smithii Kanouse, *Papers of the Michigan Academy of Science, Arts & Letters* 24: 28. 1939.

Ascoma stipitate to substipitate, taller than broad, usually pointed at apex in face view; short-ear or long-ear shaped in face view at maturity. Apothecia always split to top of stipe, 3.0--9.0 cm tall in face view, 3.0--5.0 x 3.0--5.0 cm from above; flesh thick, without taste. Hymenium smooth, "Brown" (M6E4) to "Dark Brown" (M7F7 to M7F8), or "Dark Greyish Brown" (S20) or "Drab" (S27), often with a purplish cast. Margin entire and occasionally cracked at maturity. Abhymenium concolorous with the hymenium or lighter when fresh, "Brown" (M6E4) to "Chestnut Brown" (M6F7) or "Brownish Grey" (M6F8) or "Burnt Umber" (S22) to "Raw Umber" (S23), hygrophanous

to "Reddish Golden" (M6C7) or "Raw Sienna" (M6D7); abhymenial surface pustulate and minutely tomentose, wrinkled in appearance when dried especially in mature specimens, hygrophanous. Stipe, when present, covered with light colored hyphae.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (12.2--13.4--13.6(--15.5) x (6.0--6.7--6.8(--8.0) μm , $\bar{x}$ = 13.5 x 6.7 μm (n = 100), hyaline. Asci 170--203 x 10.5 μm . Paraphyses (Figure 3.2) hyaline, hooked, occasionally having 2--3 small protuberances inside the hook; often slightly clavate at the tip, the clava 3.1--4.9 μm thick, below clava 2.4--3.7 μm thick; septate; branched below, usually once.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*), entire layer to 480--560 μm thick in section (measured at thickest point); cells elongate and slightly constricted at septa, hyphae 5.0--7.3 μm in diameter at widest point. Ectal excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*), the entire layer to 90--120 μm thick in section; cells slightly constricted at septa, 6.1--18.4 μm in diameter at widest point; outer surface with irregularly spaced clusters of globose cells and short chains of 3 to 4 globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to gregarious on exposed soil, duff or moss under 80-year-old to 150-year-old *Pseudotsuga menziesii*, 100-year-old *Populus trichocarpa*, 150-year-old *Tsuga heterophylla*; California, Idaho, Oregon, Washington; September to December.

Specimens Examined. U.S.A. CALIFORNIA: Del Norte County, Crescent City, 18 Nov. 1937, *A. H. Smith*, *AHS* 8843 (MICH, HOLOTYPE); Earl Lake State Park, 15 Dec. 1997, *M. Madsen* and *R. Davis*, *ETP* 252 (OSC 56823). IDAHO: Bonner County, Priest Lake area, 27 Sept. 1968, *N. J. Smith*, *NJS* 2076 (MICH); Priest River Experimental Forest, 27 Sept. 1995, *T. Lebel*, *NSW* 7536. OREGON: Benton County, Philomath, Woods Creek road, 15 Nov. 1997, *E. T. Peterson* and *T. Lebel*, *ETP* 240 (OSC 56811). WASHINGTON: Pierce County, Mt. Rainier National Park, Lower Tahoma Creek, 8 Sept. 1948, *A. H. Smith*, *AHS* 30994 (MICH); same locality, 30 Oct. 1996, *E. T. Peterson*, *ETP* 022 (OSC 56753); same locality, 18 Oct. 1997, *E. T. Peterson*, *ETP* 228 (OSC 56799); same locality, 18 Oct. 1997, *E. T. Peterson*, *ETP* 226 (OSC 56797); Lewis County, Gifford-Pinchot National Forest, Camp Creek Falls Trail, 6 Nov. 1997, *E. Hathaway* and *E. Milliman*, *ODELL* 4455 (OSC 56830).

Observations. *O. smithii* is relatively easy to identify when fresh by its overall shape, size, and color (purplish-brown hymenium, unique within the genus). Habitat for this species is quite variable as observed in the course of this study. Kanouse (1939) described the species as under pine in Crescent City, California. In this study we collected *O. smithii* under pine, Douglas-fir, cottonwood, and hemlock. *O. smithii* does appear to have an association with older forests, although one collection (ETP 240) was made in a 60- to 80-year-old Douglas-fir stand in Oregon. Miller (1977) includes a photo of a fungus he refers to as *O. smithii* having spores 18 – 24 x 12 – 14 μm and colors much more red than purple. We believe Miller's *O. smithii* to actually be *Wynnella silvicola*.

Otidea tuomikoskii Harmaja, *Karstenia* 15: 30. 1976.

Ascoma stipitate to substipitate, much taller than broad, usually pointed at apex in face view; narrowly long-ear shaped in face view at maturity. Apothecia always split to the base or nearly so, 6.0--8.5 cm tall in face view, 1.0--2.5 x 1.0--2.5 cm from above; flesh thick, without taste. Hymenium smooth, slightly lighter than "Butter Yellow" (M4A5) or "Buff-Yellow" (S53) to "Yellow-Ocher" (S123C). Margin entire, in-rolled towards hymenium when young and occasionally cracked at maturity. Abhymenium concolorous with the hymenium when fresh, "Butter Yellow" (M4A5) to slightly darker, "Maize (Yellow)" (M4A6) or "(Golden) Wheat" (M4B5), or "Buff-Yellow" (S53) or "Cream Color" (S54) to "Yellow-Ocher" (S123C), slowly hygrophanous to "Butter Yellow" (M4A5) or lighter; abhymenial surface pustulate and minutely tomentose, concolorous with hymenium when moist, hygrophanous. Lower portion of the apothecium often covered with light colored superficial hyphae.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (9.2--10.4--10.6(--11.6) x (4.9--6.6--6.7(--6.7) μm , $x = 10.5 \times 5.7 \mu\text{m}$ ($n = 100$), hyaline. Asci 150--201 x 9.0--10.5 μm , arising from a band in the subhymenium slightly darker than adjacent tissue (approximately 80 μm thick in section). Paraphyses (Figure 3.2) hyaline, hooked at the apex, often having 2-3 protuberances inside the hook; the tip 1.8--3.7 μm thick, below tip 1.8--2.4 μm thick; septate; branched below, usually once.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*), entire layer to 400--480 μm thick in section (measured at thickest point); cells elongate and slightly constricted at septa, hyphae 6.7--11.6 μm in diameter at widest point. Ectal excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or

± irregular (*textura globosa* to *t. angularis*), the entire layer to 120--150 µm thick in section; cells slightly constricted at septa; 9.8--49.0 µm in diameter at widest point; outermost layer with irregularly spaced clusters of globose cells, or short chains of globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to gregarious on exposed soil, duff or well-decayed conifer logs, under 40-year-old to 80-year-old *Pseudotsuga menziesii*; Oregon, Washington, California; September to December.

Specimens Examined. U.S.A. CALIFORNIA: Del Norte County, Earl Lake State Park, off Sand Hill road, 15 Dec. 1997, *M. Madsen & R. Davis*, ETP 255 (OSC 56826); Humboldt County, Big Lagoon Park, 16 Dec. 1956, *A. H. Smith*, AHS 56799 (MICH); same locality, 23 Dec. 1956, *A. H. Smith*, AHS 56954 (MICH). OREGON: Benton County, Corvallis, MacDonald-Dunn Research Forest, Road 580, stand 050907, 1 Nov. 1996, *E. T. Peterson*, ETP 025 (OSC 56756); same locality, 2 Dec. 1996, *E. T. Peterson*, ETP 030 (OSC 56761); same locality, 23 Oct. 1996, *E. T. Peterson*, ETP 011 (OSC 56742); same locality, 15 Oct. 1997, *E. T. Peterson*, ETP 212 (OSC 56783); same locality, 11 Oct. 1997, *E. T. Peterson*, ETP 222 (OSC 56793); same locality, stand 060510, 17 Oct. 1997, *L. Grubisha*, ETP 219 (OSC 56790); same locality, stand 080801 near intersection of roads 680 and 700, 25 Nov. 1997, *E. T. Peterson*, ETP 247 (OSC 56818); Columbia County, Tillamook BLM Resource Area, Pig's Puzzle Timber sale, 10 Dec. 1997, *M. Madsen* and *L. R. Scofield*, ETP 251 (OSC 56822). WASHINGTON: Clallam County, Olympic National Park, Elwha River, 27 Sept. 1941, *A. H. Smith*, AHS

17338 (MICH); Pierce County, Mt. Rainier National Park, Lower Tahoma Creek, 18 Oct. 1997, E. T. Peterson, ETP 231 (OSC 56802).

Observations. *O. tuomikoskii* was described from Finland (Harmaja, 1976); this is the first report of it from North America. Numerous collections of this taxon have been ascribed to *O. leporina* var. *minor* based loosely on color and spore size, especially when identified with descriptions in Kanouse (1949). Cao, et al. (1990) include *O. tuomikoskii* in their descriptions and differentiate it from *O. leporina sensu stricto* and *O. leporina* var. *minor* based on having a "yellowish to clear yellow" hymenium and a "brown to dull brown" exterior. Harmaja is careful to note that the apothecia of *O. tuomikoskii* are "gregarious to caespitose, pronouncedly and rather narrowly ear-shaped", this morphology being unique to the genus as it occurs in the Pacific Northwest. Additionally, Harmaja notes that under ultraviolet light (UV₂₅₄) there is a stark contrast between abhymenial and hymenial colors, being dark outside but bright pale yellow internally. This character was checked and his description is quite good. Considering Harmaja's work and the distinctive morphology of this taxon we now recognize *O. tuomikoskii* as occurring in the Pacific Northwest, primarily in 40- to 80-year-old Douglas-fir stands in-or-near well decayed conifer logs. Schalkwijk-Barendsen (1991) describes a fungus as *O. onotica* that we believe to be *O. tuomikoskii* and in her description states that this fungus is "said to be a good edible with an almond taste."

Otidea umbrina (Persoon) Bresadola, *Fungi Tridentini II*: 68. 1898.

≡ *Peziza umbrina* Persoon, *Observationes Mycologicae II*: 77. 1796.

Ascoma substipitate to astipitate, taller than broad, usually truncate at apex in face view; semi-spathulate, occasionally deep-cupulate in face view at maturity. Apothecia always split to the base or nearly so, 2.0--7.0 cm tall in face view, 1.0--5.5 x 1.0--5.5 cm from above; flesh thick, without taste. Hymenium smooth, milk-chocolate-brown when fresh, slightly lighter than "Mustard Brown" (M5E6) or "Linoleum Brown" (M5E7) or "Cinnamon-Brown" (S33), or "Ground-Cinnamon" (S239), or slightly lighter than "Raw Umber" (S123). Margin entire, in-rolled towards hymenium when young and occasionally cracked at maturity. Abhymenium concolorous with the hymenium when fresh, to slightly darker, towards "Snuff (Brown)" (M5F6) or "Coffee" (M5F7) or "Cinnamon-Brown" (S33), slightly darker than "Raw Umber" (S223), or slightly lighter than "Prout's Brown" (S121A), fading quickly when drying, especially in young specimens, towards "Ivory" (M4B3) or "Champagne" (M4B4); abhymenial surface pustulate and minutely tomentose, concolorous with hymenium when moist, hygrophanous. Lower portion of ascoma rarely covered with light colored superficial hyphae.

Ascospores (Figure 3.2) smooth, biguttulate, ellipsoid, (11.6--12.7--13.1(--14.0) x (6.1--6.6--6.8(--7.3) μm , $\bar{x}$ = 12.9 x 6.7 μm (n = 25), hyaline. Asci 180--245 x 9.0--12.0 μm . Paraphyses (Figure 3.2) hyaline, hooked, often irregularly so, at the apex, often having 2--3(--5) protuberances inside the hook; often slightly clavate at the tip, the clava 3.1--5.5 μm thick, below clava 2.4--3.1 μm thick; septate; branched below, usually once.

Medullary excipulum of densely woven hyaline hyphae (*textura intricata*), entire layer to 400--440 μm thick in section (measured at thickest point); cells elongate and slightly constricted at septa, hyphae 5.0--6.0 μm in diameter at widest point. Ectal excipulum of short, hyaline, versiform to globose or pyriform cells varying to angular or $\pm$ irregular (*textura globosa* to *t. angularis*), the entire layer to 120 μm thick in section; cells slightly constricted at septa, cells 6.1--24.5 μm in diameter at widest point; outer surface with irregularly spaced clusters of globose cells, or short chains of globose to subglobose cells that are slightly constricted at the septa.

Habit, Habitat and Distribution. Solitary to gregarious or occasionally caespitose on exposed soil, occasionally in duff, under 40-year-old to 80-year-old *Pseudotsuga menziesii* often mixed with *Acer* spp. and *Quercus garryana*; Oregon, Washington; October to November.

Specimens Examined. OREGON: Benton County, Corvallis, north of Corvallis in McDonald-Dunn Research Forest, stand 080801, 25 Oct. 1996, *E. T. Peterson*, ETP 013 (OSC 56744); same locality, 9 Nov. 1996, *E. T. Peterson*, ETP 026 (OSC 56757); same locality, 18 Nov. 1996, *E. T. Peterson*, ETP 027 (OSC 56758); same locality, 13 Oct. 1997, *E. T. Peterson*, ETP 210 (OSC 56781); same locality, stand 060210, 10 Oct. 1997, *S. Holmes*, ETP 211 (OSC 56782); same locality, stand 060510, 8 Nov 1997, *R. Hamill*, ETP 239 (OSC 56810); Corvallis, Witham Hill, back of Witham Oaks apartments, 25 Nov 1997, *L. Wilson*, ETP 242 (OSC 56813). WASHINGTON: Pierce

County, Mt. Rainier National Park, Lower Tahoma Creek, 13 Sept. 1954, *A. H. Smith*, AHS 47471 (MICH); same locality, 15 Sept. 1954, *A. H. Smith*, AHS 47514 (MICH).

Observations. We initially thought this was a new species of *Otidea*; however careful examination of herbarium material and the works of Boudier (1907) and Bresadola (1933) reveal that this species matches *O. umbrina*. Both the description of the internal and external color, down to the perhaps unintentional description of a lighter colored exterior without noting the quick hygrophanous effect, as well as the spore size, fits Bresadola's interpretation very well. Very little has been written about *O. umbrina* regarding habitat or distribution, and in the literature it has not been noted to occur in North America. In fact, the name *O. umbrina* appears to have not been used recently.

Several names have been used when discussing dark-brown-colored members of the genus including *O. cochleata*, *O. bufonia*, and *O. alutacea*. Cao, et al. (1990) report that *O. alutacea* is lighter in color than *O. cochleata* and *O. bufonia* (dull brown vs. dark brown). *O. cochleata* is reported to have larger spores than *O. umbrina* (16 - 19 μm x 7.5 - 8.0 μm vs. 11.6 - 15 μm x 6.1 - 7.3 μm). The photograph of *O. cochleata* in Breitenbach and Kränzlin (1984) shows the color of *O. cochleata*, reported as reddish-brown to dark-brown by Cao, et al. (1990), and in our opinion the two species are quite different in this respect. Romagnesi (1962) includes *O. umbrina* from France and his concept very closely matches our own.

O. bufonia is considered to be a synonym of *O. umbrina* by Dennis (1981), and his color plate (VIII C.) superficially matches fresh material collected in the course of this study, except for the obvious light-colored hyphae at the base of the apothecium.

Additionally, Dennis describes the spores of *O. bufonia* as elliptic-fusiform, a character state that was not observed in the taxa in this study. Because of the lack of conspicuous light-colored hyphae near the base of the apothecium and the difference in shape of the ascospores, we choose not to recognize the synonymy of *O. umbrina* and *O. bufonia sensu* Dennis (1981).

The apparent difference between *O. umbrina* and *O. alutacea* is very slight, dull-brown versus dark-brown. Otherwise they share many characters states including those of stipe, stature, and shape. The two major differences between these two closely related taxa as observed in this study are those of ascospore size and abhymenial ornamentation. The ascospores of *O. alutacea* are slightly longer than those of *O. umbrina*, 13.4--17.7 x 6.1--7.9 μm vs. 11.6--14.0 x 6.1--7.3 μm . The exterior of *O. umbrina* becomes lighter very quickly upon drying, a visible change is obvious in under five minutes, especially in younger specimens, and this effect is easily observed in dried specimens. This quickly-hygrophanous effect was not observed and has not been reported for *O. alutacea*. Additionally, although *O. umbrina* and *O. alutacea* form a monophyletic group in the analysis of Peterson, et al. (Chapter Two), each individual species is well supported as a distinct monophyletic taxon (97%, their Figure 4).

O. umbrina has been collected quite frequently in the vicinity of Corvallis, Oregon, primarily due to the activity of Dr. J. W. Spatafora's Introductory Mycology class. Outside of Corvallis, this species is very poorly known and has been reported less than five times during this study from inadequate collections. More data needs to be collected regarding this fungus, its distribution, and habitat. To confirm the identification of this name specimens from MICH were examined, and in every case a near exact match was made.

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Chapter 4

CONCLUSIONS

Molecular analysis described in Chapter Two of this work indicates that there are eight species of *Otidea* that occur commonly in the Pacific Northwest. This number may be as high as ten with the inclusion of *O. microspora* and *O. abietina*, which were not collected in the course of this study. The information presented in Chapter Two also indicates that nucleotide data from the internal transcribed spacer (ITS) region of the ribosomal DNA (rDNA) repeat unit is adequate to allow for the differentiation of phylogenetic species, especially when these data are combined with characters coded from morphology. Additionally, molecular analysis of the large subunit (LSU) of several species of *Otidea* indicates that there are at least three different LSU types present in *Otidea* as sampled in this study. The origin of these divergent types is speculated to be multiple ancient gene duplication events. The result is multiple LSU rDNA types (ancestral LSU rDNA polymorphisms) present within both *O. leporina* and *O. smithii* that have somehow not been homogenized by lineage sorting and concerted evolution (Zimmer, et al., 1980).

The phylogenetic species inferred in Chapter Two have been described in Chapter Three and new keys to both fresh and dried materials have been written. Pending additional information, the species of *Otidea* known to occur in the Pacific Northwest are as follows: *O. smithii*, *O. onotica*, *O. leporina*, *O. concinna*, *O. tuomikoskii*, *O. alutacea*, *O. umbrina* and *O. rainierensis*. Kanouse (1949) indicates that *O. abietina* is known to

occur in Washington and *O. microspora* was described from this range, although neither was found in the course of this study.

Regarding conservation of *Otidea* species and their habitat, while I have no way to make a formal statement about rarity I can comment on the number of occurrences of individual species. A graph of the total number of collections for each species examined in the course of this study is presented in Figure 4.1. The numbers on this graph represent all collections made in the course of this two-year study. Clearly, the small number of collections of the species represented on the right side of the graph indicates that *O. microspora*, *O. rainierensis*, and *O. smithii* are rare. For a fungus to be collected less than five times in two years, especially when a group of experts is looking for it, must surely be some indication of rarity. Castellano (1997) defines rare as “species known from 10 or less vouchered occurrences” and gives a range of 1 km for the boundary of collection. The 1996 R.E.D. list for Oregon Macrofungi only indicates that *O. onotica* is rare in Oregon (Castellano, 1997). The 1994 FEMAT list includes *O. onotica* along with *O. smithii* and *O. leporina* as rare or endangered in the range of the Northern Spotted Owl (U.S.D.A. F.S., U.S.D.O.I. B.L.M., 1994). In the course of this study *O. onotica* has been found quite often and now I question whether or not this listing is warranted. *O. onotica* aside, it is clear that under Castellano’s definition of rare that *O. umbrina*, *O. leporina*, *O. alutacea*, *O. smithii*, *O. rainierensis*, and *O. microspora* are quite rare.

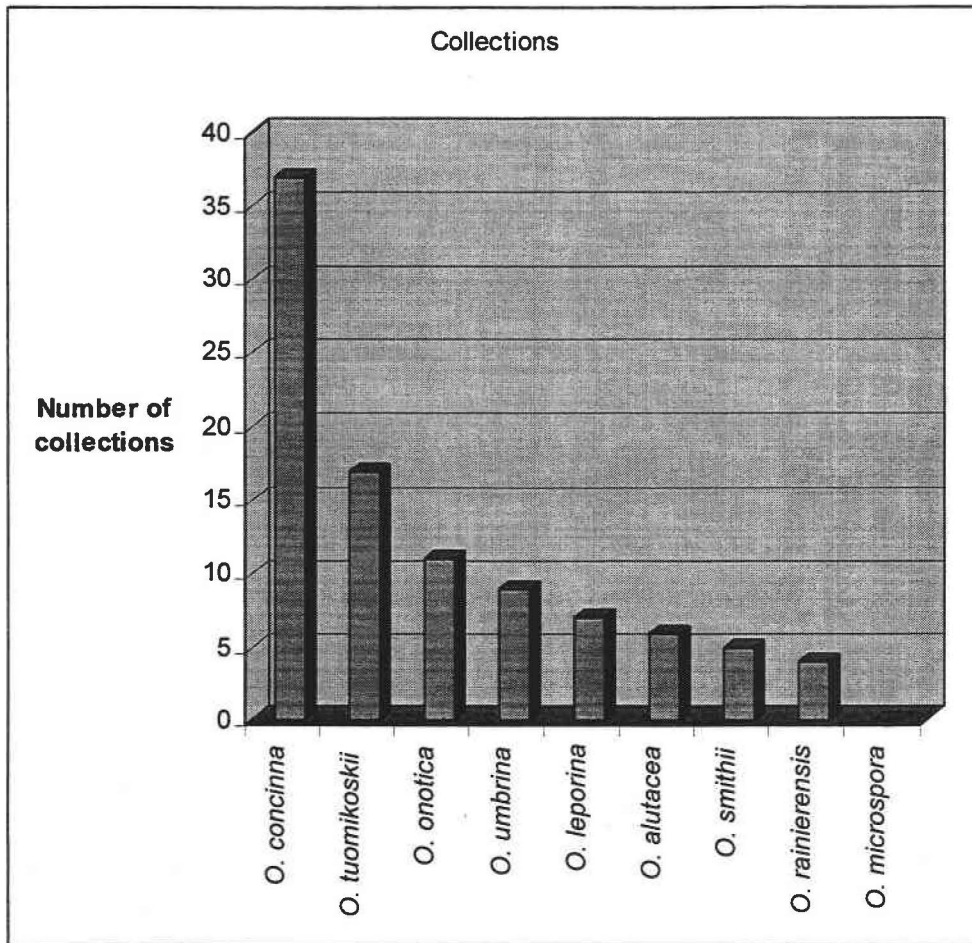


Figure 4.1: Number of collections by species made during the course of this study (1996 – 1998).

In addition to being infrequently collected, several of the aforementioned species are limited in their distribution, at least in this study. *O. leporina* is only known from two localities, *O. rainierensis* from three localities, and *O. alutacea* from four. Before this study was undertaken *O. smithii* was extremely poorly known, and still is excepting the relatively large number of collections made in 1997. *O. umbrina* is almost unknown except in and around Corvallis, Oregon, which must surely be an artifact of the

distribution of mycologists. *Otidea microspora* was not collected once in the course of this two-year study in the Pacific Northwest.

Of the species under discussion, while there is no quantifiable evidence to this point, it is clear to this author that old-growth habitat is necessary for these fungi. Few collections of any of the aforementioned species, with the exception of *O. umbrina*, were made in habitat that did not contain coniferous trees older than 150 years. A single collection of *O. smithii* was made near Corvallis, Oregon in a stand seemingly devoid of any trees older than 80 years but little is known to us about the history of this stand and it is adjacent to stands containing older trees. The remaining collections of *O. smithii* made in the course of this study were made near if not immediately underneath old-growth trees. The continued destruction of old-growth forests throughout the Pacific Northwest will surely lead to a reduction in populations of *Otidea* species.

As part of the effort to catalogue and conserve fungi known to be rare in the Pacific Northwest, under the definition of rarity defined by Castellano (1997) and the Federal Government (U.S.D.A. F.S., U.S.D.O.I. B.L.M., 1994), I recommend that the following species be added where appropriate to the FEMAT strategy one and three listings:

Table 4.1: FEMAT listing recommendations for rare *Otidea* species.

Species	Recommended FEMAT listing
<i>O. microspora</i>	Strategy One
<i>O. rainierensis</i>	Strategy One
<i>O. smithii</i>	Strategy One
<i>O. leporina</i>	Strategy One
<i>O. alutacea</i>	Strategy One
<i>O. umbrina</i>	Strategy Three

As additional information is collected regarding these species a better assessment of their rarity and the habitat relationship with the Northern Spotted Owl will be possible. Until that time I believe that it is better to be conservative and attempt to preserve the habitat of these fungi and associated organisms.

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APPENDIX

	51	61	71	81	91	100	
50	TTGAAATCTG	ACGtTTTT-G	ACGTTCGAAT	TGTAATTTGG	AGGGATATCT		98 OSC 56811
50	TTGAAAACCG	GCAACACC--	AGCCGGCAG-	TGTAATTTGA	AGGGACATCT		96 OSC 56823
50	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAAT	TGTAATTTGG	AGG-ATATCT		97 OSC 56753
50	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAAT	TGTAATTTGG	AGGGATATCT		98 OSC 56799
49	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAGT	TGTAATTTGG	AGGGATATCT		97 NSW 7536
50	TTGAAATCTG	ACGTTTTT-G	ACGTCCGAGT	TGTAATTTGG	AGGGATATCT		98 OSC 56734
50	TTGAAATCTG	ACGTTTTT-G	ACGTCCGAGT	TGTAATTTGG	AGGGATATCT		98 OSC 56801
50	TTGAAATCTG	ACGTTTTT-G	ACGTCCGAGT	TGTAATTTGG	AGGGATA-CT		97 OSC 56759
50	TTGAAATCTG	ACGTCACCTG	GCGTTCGAAT	TGTAATTTGG	AGGGGCATTT		99 OSC 56754
50	TTGAAATCTG	ACGTCACCTG	GCGTTCGAAT	TGTAATTTGG	AGGG-CATTT		98 OSC 56747
50	TTGAAATCTG	ACGTCTTT-G	GCGTTCGAAT	TGTAATTTGG	AGGG-CATTT		97 OSC 56758
50	TTGAAATCTG	ACGTCACCTG	GCGTTCNAAT	TGTAATTTGG	ANGGGCATTT		99 OSC 56777
50	TTGAAATCTG	ACGTCACCTG	GCGTTCGAAT	TGTAATTTGG	AGGGGCATTT		99 OSC 56798
50	TTGAAATCTG	ACGTCTTT-G	GCGTTCGAAT	TGTAATTTGG	AGGGGCATTT		98 OSC 56813
50	TTGAAATCTG	ACGTCACCTG	GCGTTCGAAT	TGTAATTTGG	AGGGGCATTT		99 OSC 56770
50	TTGAAATCTG	ACGTCTTT-G	GCGTTCGAAT	TGTAATTTGG	AGGGGCATTT		98 OSC 56782
50	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAAT	TGTAATTTGG	AGGGATATCT		98 OSC 56784
49	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAAT	TGTAATTTGG	AGGGATATCT		97 OSC 56825
50	TTGAAAACCG	GCAACACC--	AGCCGGCAG-	TGTAATTTGA	AGGGACATCT		96 OSC 56824
50	TTGAAAACCG	GCAACCCC--	AGCCGGCAG-	TGTAATTTGA	AGGGACATCT		96 OSC 56809
50	TTGAAAACCG	GCAACCCC--	AGCCGGCAG-	TGTAATTTGA	AGGGACATC-		95 OSC 56760
50	TTGAAAACCG	GCAACCCC--	AGCCGGCAG-	TGTAATTTGA	AGGGACATC-		95 OSC 56749
50	TTGAAAACCG	GCAACCCC--	AGCCGGCAG-	TGTAATTTGA	AGGGACATCT		96 NSW 7574
50	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAGT	TGTaATTTGG	AGGGATATCT		98 OSC 56756
51	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAGT	TGTAATTTGG	AGGGATATCT		99 OSC 56761
50	TTGAAATCTG	ACGTTTTT-G	ACGTTCGAGT	TGTAATTTGG	AGGGATATCT		98 OSC 56826
50	TTGAAATCTG	ACGTTTTT-G	ACGTCCGAGT	TGTAATTTGG	AGGGATATCT		98 OSC 56829
50	TTGAAATCTG	ACGTTTTT-G	ACGTCCGAGT	TGTAATTTGG	AGGGATATCT		98 NSW 6354
51	TTGAAATCTG	ACGTTTTT-G	ACGTCCGAGT	TGTAATTTGG	AGGGATA-CT		98 OSC 56745
51	TTGAAATCTG	GCGTCTTC-G	GCNTCCNANT	TNTAATTTNN	ANGGATATCT		99 OSC 56831
50	TTGAAATCTG	GCGTCTTC-G	ACGTCCGANT	TGTAATTTGG	AGGGATATCT		98 <i>Scutellinia</i>
51	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		100 AHS 8843
51	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		100 OSC 56830
51	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		100 EGS 2179
51	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		100 AHS 30502
51	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		100 AHS 21147
51	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		100 ML 941947

	101	111	121	131	141	150			
99	TCGGAGCTGG	CGCTGTTCTA	AGTTCTTTGG	AACCAGACAT	CAAAGAGGGT		148	OSC	56811
97	TCGGAGCTGG	CGCCGTCTTA	AGTTCTTTGG	AACCGGACAT	CATAGAGGGT		146	OSC	56823
98	TCGGAGCTGG	CGCTGTTCTA	AGTTCTTTGG	AACCAGACAT	CAAAGAGGGT		147	OSC	56753
99	TCGGAGCTGG	CGCTGTTCTA	AGTTCTTTGG	AACCAGACAT	CAAAGAGGGT		148	OSC	56799
98	TCGGAGCTGG	CACCGTCCTA	AGTTCTTTGG	AACCGGACAT	CATAGAGGGT		147	NSW	7536
99	TCGGAGCTGG	CGCTGTCCTA	AGTTCTTTGG	AACCAGACAT	CATAGAGGGT		148	OSC	56734
99	TCGGAGCTGG	CGCTGTCCTA	AGTTCTTTGG	AACCAGACAT	CATAGAGGGT		148	OSC	56801
98	TCGGAGCTGG	CGCTGTCCTA	AGTTCTTTGG	AACCAGACAT	CATAGAGGGT		147	OSC	56759
100	TCGGAGCTGG	CGTCGTCCCTA	AGTTCCTTGG	AACAGGACGT	CACAGAGGGT		149	OSC	56754
99	TCGGAGCTGG	CGTCGTCCCTA	AGTTCCTTGG	AACAGGACGT	CACAGAGGGT		148	OSC	56747
98	TCGGAGCTGG	CGTCGTCCCTA	AGTTCCTTGG	AACAGGACGT	CACAGAGGGT		147	OSC	56758
100	TCGGAGCTGG	CGTCGTCCCTA	AGTTCCTTGG	AACAGGACGT	CACAGAGGGT		149	OSC	56777
100	TCGGAGCTGG	CGTCGTCCCTA	AGTTCCTTGG	AACAGGACGT	CACAGAGGGT		149	OSC	56798
99	TCGGAGCTGG	CGTCGTCCCTA	AGTTCCTTGG	AACAGGACGT	CACAGAGGGT		148	OSC	56813
100	TCGGAGCTGG	CGTCGTCCCTA	ANTTCCTTGG	AACAGGACGT	CACANAGGGT		149	OSC	56770
99	TCGGAGCTGG	CGTCGTCCCTA	AGTTCCTTGG	AACAGGACGT	CACAGAGGGT		148	OSC	56782
99	TCGGAGCTGG	CGCTGTTCTA	AGTTCTTTGG	AACCAGACAT	CAAAGAGGGT		148	OSC	56784
98	TCGGAGCTGG	CACCGTCCTA	AGTTCTTTGG	AACCGGACAT	CATAGAGGGT		147	OSC	56825
97	TCGGAGCTGG	CGCCGTCTTA	AGTTCTTTGG	AACCGGACAT	CATANAGGGT		146	OSC	56824
97	TCGGAGCTGG	CGCCGTCTTA	AGTTCTTTGG	AACCGGACAT	CATAGAGGGT		146	OSC	56809
96	TCGGAGCTGG	CGCCGTCTTA	AGTTCTTTGG	AACCGGACAT	CATAGAGGGT		145	OSC	56760
96	TCGGAGCTGG	CGCCGTCTTA	AGTTCTTTGG	AACCGGACAT	CATAGAGGGT		145	OSC	56749
97	TCGGAGCTGG	CGCCGTCTTA	AGTTCTTTGG	AACCGGACAT	CATAGAGGGT		146	NSW	7574
99	TCGGAGCTGG	CACCGTCCTA	AGTTCCTTGG	AACCGGACAT	CaTAgAGGGT		148	OSC	56756
100	TCGGAGCTGG	CACCGTCCTA	AGTTCCTTGG	AACCGGACAT	CATAGAGGGT		149	OSC	56761
99	TCGGAGCTGG	CACCGTCCTA	AGTTCCTTGG	AACCGGACAT	CATAGAGGGT		148	OSC	56826
99	TCGGAGCTGG	CGCTGTCCTA	AGTTCTTTGG	AACCAGACAT	CATAGAGGGT		148	OSC	56829
99	TCGGAGCTGG	CGCTGTCCTA	AGTTCTTTGG	AACCAGACAT	CATAGAGGGT		148	NSW	6354
99	TCGGAGCTGG	CGCTGTCCTA	AGTTCTTTGG	AACCAGACAT	CATAGAGGGT		148	OSC	56745
100	GCGGAGTTGG	CGCCGNCCTA	AGTTCCTTGG	AACANGACNT	CATANAGGGT		149	OSC	56831
99	TCGGGGATGG	CGCCGTCCCTA	ANTTCCTTGG	AACAGGACNT	CATANAGGGT		148	<i>Scutellinia</i>	
101	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		150	AHS	8843
101	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		150	OSC	56830
101	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		150	EGS	2179
101	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		150	AHS	30502
101	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		150	AHS	21147
101	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		150	ML	941947

	151	161	171	181	191	200		
149	GAGAATCCCG	TGCCTGAACG	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56811
147	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCGTGTGAA	GTGTCTCCGA		196	OSC 56823
148	GAGAATCCCG	TGCCTGAACG	GCTGTCCCGC	TCCATGTGAA	-TGTCTCCGA		196	OSC 56753
149	GAGAATCCCG	TGCCTGAACG	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56799
148	GAGAATCCCG	TGCCTGGATG	GCTGTCAAGC	TCCATGTGAA	GTGTCTCCGA		197	NSW 7536
149	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56734
149	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56801
148	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		197	OSC 56759
150	GAGAATCCCG	TGCCTGGATG	GCTGTCCAGC	TCCATGTGAG	GTGTCTCCGA		199	OSC 56754
149	GAGAATCCCG	TGCCTGGATG	GCTGTCCAGC	TCCATGTGA-	GTGTCTCCGA		197	OSC 56747
148	GAGAATCCCG	TGCCTGGATG	GATGTCCAGC	TCCATGTGAG	GTGTCTCCGA		197	OSC 56758
150	GAGAATCCCG	TGCCTGGATG	GCTGTCCAGC	TCCATGTGAG	GTGTCTCCGA		199	OSC 56777
150	GAGAATCCCG	TGCCTGGATG	GCTGTCCAGC	TCCATGTGAG	GTGTCTCCGA		199	OSC 56798
149	GAGAATCCCG	TGCCTGGATG	GATGTCCAGC	TCCATGTGAG	GTGTCTCCGA		198	OSC 56813
150	GANAATCCCG	TGCCTGGATG	GCTGTCCAGC	TCCATGTGAG	GTGTCTCCGA		199	OSC 56770
149	GAGAATCCCG	TGCCTGGATG	GATGTCCAGC	TCCATGTGAG	GTGTCTCCGA		198	OSC 56782
149	GAGAATCCCG	TGCCTGAACG	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56784
148	GAGAATCCCG	TGCCTGGATG	GCTGTCAAGC	TCCATGTGAA	GTGTCTCCGA		197	OSC 56825
147	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCGTGTGAA	GTGTCTCCGA		196	OSC 56824
147	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCGTGTGAA	GTGTCTCCGA		196	OSC 56809
146	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCGTGTGAA	-TGTC-CCGA		193	OSC 56760
146	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCGTGTGAA	-TGTCTCCGA		194	OSC 56749
147	GAGAATCCCG	TGCCTGGGTG	GCTGTCCCGC	TCCGTGTGAA	GTGTCTCCGA		196	NSW 7574
149	GAGAATCCCG	TGCCTGGATG	GCTGTCAAGC	TCCATGTGAA	GTGTCTCCgA		198	OSC 56756
150	GAGAATCCCG	TGCCTGGATG	GCTGTCAAGC	TCCATGTGAA	GTGTCTCCGA		199	OSC 56761
149	GAGAAAtCCCG	TGCCTGGATG	GCTGTCAAGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56826
149	GAGAATCCCG	TGCCTGGATA	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56829
149	GAGAATCCCG	TGCCTGGATA	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	NSW 6354
149	GAGAATCCCG	TGCCTGGATA	GCTGTCCCGC	TCCATGTGAA	GTGTCTCCGA		198	OSC 56745
150	GAGAATCCCG	TGCCTGGATG	GCTGTCCATC	TCCATGTGAA	GTGTCTCCGA		199	OSC 56831
149	GAGAATCCCG	TGCCTGGATG	GCTGTCCATC	TCCATGTGAA	NTGTCTCCGA		198	Scutellinia
151	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		200	AHS 8843
151	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		200	OSC 56830
151	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		200	EGS 2179
151	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		200	AHS 30502
151	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		200	AHS 21147
151	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		200	ML 941947

	351	361	371	381	391	400			
349	AAAGGGAAGC	GCTTGAGACT	AGATTTCGACC	GGCGGTGCATC	AGCTGCGTTT		398	OSC	56811
346	AAAGGGAAGC	GCTTGAGACT	ACATTTCAGCC	GGCGGTGCATC	AGCTATGCTT		395	OSC	56823
346	AAAGGGAAGC	GCTTGAGACT	AGATTTCGACC	GGCGGTGCATC	AGCTGCGTTT		395	OSC	56753
349	AAAGGGAAGC	GCTTGAGACT	AGATNCGACC	GGCGGTGCATC	AGCTGCGTTT		398	OSC	56799
348	AAATGGAACG	C-NNGACACT	AANATCGGAC	CGTGGTGANC	GNCCCAGCTC		396	NSW	7536
349	AAAGGGAAGC	GCTTGAGACC	AGATTTCAGCC	GGCGGTGCATC	AGCTACATTT		398	OSC	56734
349	AAAGGGAAGC	GCTTGAGACC	AGATTTCAGCC	GGCGGTGCATC	AGCTACATTT		398	OSC	56801
348	AAAGGGAAGC	GCTTGAGACC	AGATTTCAGCC	GGCGGTGCATC	AGCTACATTT		397	OSC	56759
350	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	AgCCGTGCTT		399	OSC	56754
348	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	AGCCGTGCTT		397	OSC	56747
348	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	AGCTGCGCTT		397	OSC	56758
350	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	AGCCGTGCTT		399	OSC	56777
350	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	AGCCGTGCTT		399	OSC	56798
349	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	AGCTGCGCTT		398	OSC	56813
350	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	ACCG-TGCTT		398	OSC	56770
349	AAAGGGAAGC	GCTTGAGACC	AGACTCAACC	TTCGGTGATC	AGCTGCGCTT		398	OSC	56782
347	AAAGGGAAGC	GCTTGAGACT	AGATTTCGACC	GGCGGTGCATC	AGCTGCGTTT		396	OSC	56784
348	AAAGGGAAGC	GCTTGAGACT	AGAT-CGGCC	GGTGGTGATC	AGCCATGCTT		396	OSC	56825
347	AAAGGGAAGC	GCTTGAGACT	AGATTTCAGCC	GGCGGTGCATC	AGCTATGCTT		396	OSC	56824
347	AAAGGGAAGC	GCTTGAGACT	AGATTTCAGTC	GGCGGTGCATC	AGCTATGCTT		396	OSC	56809
344	AAAGGGAAGC	GCTTGAGACT	AGATTTCAGTC	GGCGGTGCATC	AGCTATGCTT		393	OSC	56760
345	AAAGGGAAGC	GCTTGAGACT	AGATTTCAGTC	GGCGGTGCATC	AGCTATGCTT		394	OSC	56749
346	AAAGGGAAGC	GCTTGAGACT	AGATTTCAGTC	GGCGGTGCATC	AGCTATGCTT		395	NSW	7574
349	AAAGGGAAtC	GCTTGATACT	AgATTTCGGCC	GGTGGTGATC	AGCCATGCTT		398	OSC	56756
350	AAAGGGAAGC	GCTTGAGACT	AGATTTCGGCC	GGTGGTGATC	AGCCATGCTT		399	OSC	56761
349	AAAGGGAAGC	GCTTGAGACT	AGATTTCGGCC	GGTGGTGATC	AGCCATGCTT		398	OSC	56826
349	AAAGGGAAGC	GCTTGGGACT	ATATACAGCC	GGCTGTGATC	AGCCACGTTT		398	OSC	56829
348	AAAGGGAAGC	GCTTGGGACT	ATATACAGCC	GGCTGTGATC	AGCCACGTTT		397	NSW	6354
349	AAAGGGAAGC	GCTTGGGACT	ATATACAGCC	GGCTGTGATC	AGCCACGTTT		398	OSC	56745
350	AAAGGGAAGC	GCTTGAGACC	AGACTCAATC	TTTGGTGATC	AGCTGTGCTT		399	OSC	56831
349	AAAGGGAAGC	GCTTGCNACC	AGACTCGATC	TTTGGTGATC	AGCCGGGCTT		398	<i>Scutellinia</i>	
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		400	AHS	8843
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		400	OSC	56830
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		400	EGS	2179
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		400	AHS	30502
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		400	AHS	21147
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		400	ML	941947

	401	411	421	431	441	450		
399	TTACGTGGTG	CACTTGCCGT	CGGTTGAACC	AGCATCGGTT	TCGATGGCAG	448	OSC	56811
396	CTGCGTGGTG	CACTTGCCGT	CGGTTGAACC	ANCATCGGTT	TTGATGGCGG	445	OSC	56823
396	TTACGTGGTG	CACTTGCCGT	CGGTTGAGCC	AGCATCGGTT	TCGATGGCAG	445	OSC	56753
399	TTACGTGGTG	CACTTGCCGT	CGGTTGAACC	ANCATCCGTT	TCTATGGCAG	448	OSC	56799
397	CGTCTTGNNG	TNCTTGCCCT	CCGNTCAGNC	-G-ACCCCN	TTCTGATTCT	444	NSW	7536
399	CTATGTGGTG	CACTTGCCGT	CGGTTGAGCC	AGCATCGGTT	TTGATGGTGG	448	OSC	56734
399	CTATGTGGTG	CACTTGCCGT	CGGTTGANCC	AGCATCGGTT	TTGATGGTGG	448	OSC	56801
398	CTATGTGGTG	CACTTGCCGT	CGGTTGA _g CC	AGCATCGGTT	TTGATGGTGG	447	OSC	56759
400	TTGTGCGGTG	CACTTGCCGG	GGGTTGGGCC	AACATC _g GTT	TTGACGGTGG	449	OSC	56754
398	TTGTGCGGTG	CACTTGCCGG	GGGTTGGGCC	AGCATC _g GTT	TTGACGGTGG	447	OSC	56747
398	CTGTGCGGTG	CACTTGCCGT	GGGTTGGGCC	AGCATCGGTT	TTGACGGTGG	447	OSC	56758
400	TTGTGCGGTG	CACTTGCCGG	GGGTTGGGCC	AGCATCGGTT	TTGACGGTGG	449	OSC	56777
400	TTGTGCGGTG	CACTTGCCGG	GGGTTGGGCC	AGCATCCGTT	TTGACGGTGG	449	OSC	56798
399	CTGTGCGGTG	CACTTGCCGT	GGGTTGGGCC	ANCATCGGTT	TTGACGGTGG	448	OSC	56813
399	TTGTGCGGTG	CACTTGCCGG	GGGTTGGGCC	ANCATCNGTT	TTGACGGTGG	448	OSC	56770
399	CTGTGCGGTG	CACTTGCCGT	GGGTTGGGCC	AGCATCGGTT	TTGACGGTGG	448	OSC	56782
397	TTACGTGGTG	CACTTGCCGT	CGGTTGAGCC	AGCATCGGTT	TCGATGGCAG	446	OSC	56784
397	TTGCGTGGTG	CACTTGCCGT	CGGTTGAGCC	AGCATCGGTT	CTGATGGTGG	446	OSC	56825
397	CTGCGTGGTG	CACTTGCCGT	CGGTTGANCC	AGCATCNGTT	TTGATGGCGG	446	OSC	56824
397	CTGCGTGGTG	CACTTGCCGT	CGATTGAGCC	AGCATCGGTT	TTGATGGCGG	446	OSC	56809
394	CTGCGTGGTG	CACTTGCCGT	CGATTGAGCC	AGCATCGGTT	TTGATGGCGG	443	OSC	56760
395	CTGCGTGGTG	CACTTGCCGT	CGATTGAGCC	AGCATCGGTT	TTGATGGCGG	444	OSC	56749
396	CTGCGTGGTG	CACTTGCCGT	CGATTGAGCC	AGCATCGGTT	TTGATGGCGG	445	NSW	7574
399	TTGCGTGGTG	CACTTGCCGT	CGGTTGAGCC	AGCATCGGTT	CTGATGGTGG	448	OSC	56756
400	TTGCGTGGTG	CACTTGCCGT	CGGTTGAGCC	AGCATCGGTT	CTGATGGTGG	449	OSC	56761
399	TTGCGTGGTG	CACTTGCCGT	CGGTTGAGCC	AGCATCGGTT	CTGATGGTGG	448	OSC	56826
399	TTACGTGGTG	CACTACAAGT	CGGTTGAGCC	AGCATCGGTT	CTGACGGCGG	448	OSC	56829
398	TTACGTGGTG	CACTACAAGT	CGGTTGA _g CC	AGCATCGGTT	CTGACGGCGG	447	NSW	6354
399	TTACGTGGTG	CACTACAAGT	CGGTTGAGCC	AGCATCGGTT	CTGACGGCGG	448	OSC	56745
400	CTGTACAGTG	CACTTGCCAT	TGATTGGGCC	AGCATCGGTT	CTGACGGTGG	449	OSC	56831
399	CTGTCCGGTG	CACTTGCCAC	TGATCGGGCC	AGCATCGGTT	CTGANGGCGG	448	<i>Scutellinia</i>	
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	450	AHS	8843
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	450	OSC	56830
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	450	EGS	2179
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	450	AHS	30502
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	450	AHS	21147
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	450	ML	941947

	451	461	471	481	491	500	
449	GATAAAGGTT	TCAGGAATGT	GGCNCCTCAA	TTT-CGAGGA	GTGTTATAGC		497 OSC 56811
446	GATAAAGGTT	TGAGGAATGT	GGCTCCCCG-	TTT-CGGGGA	ATGTTATANC		493 OSC 56823
446	GATAAAGGTT	TCAGGAATGT	GGCTCCTCAA	TTT-CGAAGA	gTGTTATAgC		494 OSC 56753
449	GATAAAAGTT	-CAGGAATGT	GGCTCCTCCN	NT--CGANGA	GTNTTATA-C		494 OSC 56799
445	NNGNNANGAG	TNCGGTGACN	GNAGTGTCCA	TT-GCGGGGA	GTGTTATANC		493 NSW 7536
449	GATAAAGGTT	TCAGGAATGT	GGgTCTTCGA	TTT-CGAGGA	GTGTTATAGC		497 OSC 56734
449	GATAAANGTT	C-AGGAATGT	GGCTCCTCCA	TTT-CGAAGA	ATGTTATT-C		495 OSC 56801
448	GATAAAGGTT	TCAGGAATGT	GGCTCCTCgA	TTT-CGAAGA	GTGTTATAGC		496 OSC 56759
450	GATAAAGGTT	CGAAGAATGT	GGCTCCCCGA	TTT-CGGGGA	GTGTTATAGC		498 OSC 56754
448	GATAAAGGTT	CGAAGAATGT	GGCTCCCCGA	TTT-CGGGGA	gTGTTATAGC		496 OSC 56747
448	GATAAAGGTT	CGAGGAATGT	GGCTCCCCGA	TT-CCGGGGA	gTGTTATAgC		496 OSC 56758
450	GATAAAG-TT	CGAGGAATGT	GGCTCCCCGA	TTT-CGGGGA	GTGTTATAGC		497 OSC 56777
450	GATAAANGTT	CNAAGAATGT	GGCTCCCCNA	TTT-CGGGGA	ATGTTATANC		498 OSC 56798
449	GATAAANGTT	CGAAGAATGT	GGCTCCCCGA	TT-CCGGGGA	NTGTTATANC		497 OSC 56813
449	GATAAANGTT	CGAAGAATGT	GGCTCCCN-A	TTTCCGGG-A	ATGTTATA-C		495 OSC 56770
449	GATAAAGGTT	CGAAGAATGT	GGCTCCCCGA	T--CCGGGGA	GTGT-ATA-C		494 OSC 56782
447	GATAAAGGTT	TCAGGAATGT	GGCTCCTCAT	TTT-CGAGGA	GTGTTATAAC		495 OSC 56784
447	GATAAAGGTT	CNANGAATGT	GGCTCCCCAA	TT-GCGGGGA	GTGTTATA-C		494 OSC 56825
447	GATAAANGTT	TGAAGAATGT	GGCTCCCCG-	TTT-CGGGGA	ATGTTATA-C		493 OSC 56824
447	GATAAAGGTT	TGAGGAATGT	GGCTCCCCGA	TT-CTGGGGA	GTGTTATAGC		495 OSC 56809
444	GATAAAGGTT	TGAGGAATGT	GGCTCCCCGA	TT-CTGGGGA	GTGTTATAGC		492 OSC 56760
445	GATAAAGGTT	TGAGGAATGT	GGCTCCCCGA	TT-CTGGGGA	GTGTTATAGC		493 OSC 56749
446	GATAAAGGTT	TGAAGAATGT	TGCTCCCCGA	TT-CTGGGGA	GTGTTATAGC		494 NSW 7574
449	GATAAAGGTT	CGAGGAATGT	GGCTCCCCAA	TT-GCGGGGA	GTGTTATAGC		497 OSC 56756
450	GATAAAGGTT	CGAGGAATGT	GGCTCCCCAA	TT-GCGGGGA	GTGTTATAGC		498 OSC 56761
449	GATAAAGGTT	CGAGGAATGT	GGCCCCCACC	TT-GCGGGGA	GTGTTATAGC		497 OSC 56826
449	GATAAAGGTT	TCAGGAATGT	GGCTCCCCAA	TTATC-GGGA	GTGTTAAAGC		497 OSC 56829
448	GATAAAGGTT	TCAGGAATGT	GGCTCCCCAA	TTATC-GGGA	GTGTTAAAGC		496 NSW 6354
449	GATAAAGGTT	TCAGGAATGT	GGCTCCCCAA	TTATC-GGGA	GTGTTAAAGC		497 OSC 56745
450	GATAAAATTT	-GAGGAATGT	GGCTCTC---	TT--CGGGGA	GTGTTATANC		493 OSC 56831
449	GATAAAAGGT	TGGGGAATGT	ACCTTCTCT-	----CGGGGA	ATGTTATACC		493 <i>Scutellinia</i>
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		500 AHS 8843
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		500 OSC 56830
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		500 EGS 2179
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		500 AHS 30502
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		500 AHS 21147
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		500 ML 941947

	501	511	521	531	541	550	
498	CTGGAGCGCA	ATGCTGCCTG	TTGGGACCCG	AGGACCGCGC	---TTNTGCT		544 OSC 56811
494	CTCNAACGTA	ATGCCGCCTG	TTGGGACC-G	AAGAACGCGC	---TTCNGCT		539 OSC 56823
495	CTGGAGCGCA	ATGCTGCCTG	TTGGGACC-G	AAGACCGCGC	---TTTTGCT		540 OSC 56753
495	CTNGAACGCA	ATGCTGCCTG	TTGGGAAC-G	AGGAACGCGC	---TTTTGCT		540 OSC 56799
494	CTGGAACGCA	ATNCCACCTG	TTGGGAAC-G	NGGACCGCGA	C--NTCCGCT		540 NSW 7536
498	CTGGAGCGCA	ATGCCGCCTG	TCGGGACC-G	AGGACCGCGC	---TTTTGCT		543 OSC 56734
496	CTGGANCGCA	ATGCCGCCTG	TCGGGAACCA	AGGACCCCCC	----TTTGCT		541 OSC 56801
497	CTGGAGCGCA	ATGCCGCCTG	TCGGGAAC-G	AAGACCGCGC	---TTTTGCT		542 OSC 56759
499	CCTGAGCGCA	ATGCCACCTG	TTGGGACC-G	AGGACCGCGC	---TTCCGCT		544 OSC 56754
497	CCTGAGCGCA	ATGCCACCTG	TTGGGACC-G	AgGACCGCGC	---TTCCGCT		542 OSC 56747
497	CCTGAGCGCA	ATGCCACCTG	TTGGGACC-G	AGGACCGCGC	---TTCCGCT		542 OSC 56758
498	CCTGAGCGCA	ATGCCACCTG	TTGGGACC-G	AAGGACCGCG	---CTCCGCT		543 OSC 56777
499	C-TGANCCCA	ATGCC-CCTG	TTNGGACC-A	AGGACCGCCC	---TCCCCCT		542 OSC 56798
498	C-TGANCGCA	ATGCC-CCTG	TTGGGACC-A	AGGACCGCCC	----TCCCCT		540 OSC 56813
496	CCTGAACGCA	ATGCC-NCTG	TTNGGACC-N	AGGACCCNC-	----TCCCCT		538 OSC 56770
495	CCTGANCGCA	ATGCCCCCTG	TTGGGAAC-G	AAGAACGCCC	C--TCCCCCT		541 OSC 56782
496	CTGGAGCGCA	ATGCT-CCTG	TTGGGACC-N	AGGACCNCGC	---TTTTGCT		540 OSC 56784
495	CTGGAACGCA	ATGCC-CCTG	TTGGGACC-N	AGGACCGCCC	----TCCGCT		538 OSC 56825
494	CTCCAACGTT	ATGCCGCCTG	TTNGGAAC-G	AAGACCCCCC	----TCCGCT		538 OSC 56824
496	CTTGAGCGTA	ATGCCGCCTG	TCGGGACCCG	AGGACCGCGC	---TTCGGCT		542 OSC 56809
493	CTTGAGCGTA	ATGCCgCCTG	TCGGGACC-G	AGGACCGCGC	---TTCGGCT		538 OSC 56760
494	CTTGAGCGTA	ATGCCGCCTG	TCGGGACC-G	AgGACCGCGC	---TTCGGCT		539 OSC 56749
495	CTTGAGCGTA	ATGCCGCCTG	TCGGGACC-G	AGGACCGCGC	---TTCGGCT		540 NSW 7574
498	CTGGAGCGCA	ATGCCACCTG	TTGGGACC-G	AGGACCGCGC	---TTCGGCT		543 OSC 56756
499	CTGGAGCGCA	ATGCCACCTG	TTGGGACC-G	AGGACCGCGC	---TTCGGCT		544 OSC 56761
498	CTGGAGCGCA	ATGCCNCCTG	TTGGGACC-G	AGGACCGCGC	--TTTCGGCT		544 OSC 56826
498	CTGGAGCGCA	ATGCCGCCAG	TTGGGACC-G	AGGCTAGCGC	GGATTTCGCAT		546 OSC 56829
497	CTGGAGCGCA	ATGCCGCCAG	TTGGGACC-G	AGGCTAGCGC	GGATTTCGCAT		545 NSW 6354
498	CTGGAGCGCA	ATGCCGCCAG	TTGGGACC-G	AGGCTAGCGC	GGATTTCGCAT		546 OSC 56745
494	CTCGATCATA	ATGCTGCCAG	TTGGGACC-G	AAGACCGCGC	---TTCGGCT		539 OSC 56831
494	C-CAGTCATA	ATGCC-CCA-	TCGGGACC-N	AGGACCGCCC	---TNCGC-T		535 <i>Scutellinia</i>
501	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		550 AHS 8843
501	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		550 OSC 56830
501	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		550 EGS 2179
501	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		550 AHS 30502
501	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		550 AHS 21147
501	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		550 ML 941947

	551	561	571	581	591	600	
545	AGGATGCTGG	CTAAAA-GTC	TCAATTCTAA	CACACTCTGC	GTACCTTTCC	593	OSC 56811
540	AAGATGCTGG	CNAAAANGTC	TCAATTcTAA	CACAcTcTGC	GTACCTTTCC	589	OSC 56823
541	AGGATGCTGG	CTAAAAGGTC	TCAATTCTAA	CACACTCTGC	GTACCTTTCC	590	OSC 56753
541	AGGAT-CTGG	CTAAAAAGTC	TCAATTCTAA	CACAcTcTGC	GTACCTTTCC	589	OSC 56799
541	ANGAT-CTGG	CCAAGAGGTC	TCAATTCTAA	CACACTCTGC	GTACCTTTCC	589	NSW 7536
544	AGGATGCTGG	CTAAAAGGTC	TCAATTCCAA	CCCATTcAGC	GAATCATTCC	593	OSC 56734
542	ANGATGCTGG	CTAAAAAGTC	TCAATTCCAA	CCCATTCTGC	GTATCATTCC	591	OSC 56801
543	AGGATGCTGG	CTAAAAGGTC	TCAATTCCAA	CCCATTCTGC	GTATCATTCC	592	OSC 56759
545	AGGATGCTGG	CGCAATGGTC	TCAATTCAAA	CACACTCTGC	GTACCTTTCC	594	OSC 56754
543	AGGATGCTGG	CGCAATGGTC	TCAATTCAAA	CACACTCTGC	GTACCTTTCC	592	OSC 56747
543	AGGATGCTGG	CGCAATGGTC	TCAATTcTAA	C-CACTCTGC	GTACCTTTCC	591	OSC 56758
544	AGGATGCTGG	CGCAATGGTC	TCAATTCAAA	CACACTCTGC	GTACCTTTCC	593	OSC 56777
543	ANGATGCTNG	CGCCATNGTC	TCAATTCAAA	CACACTCTGC	GTACCTTTCC	592	OSC 56798
541	AGGAT-CTGG	CGCCATNGTC	TCAATTCAAA	CCCCTCTGC	GTACCTTTCC	589	OSC 56813
539	AGGATGCTGG	CC-CATGGTC	TNNNNNNNNN	NNNNNTCTGN	GTGCCTTACC	587	OSC 56770
542	AGGATGCTGG	CGCCATGGTC	TCAATTCAAA	CCCCTCTGC	GTACCTTTCC	591	OSC 56782
541	AGGATGCTGG	CTTNAAGGTC	TCAATTCTAA	CACACACTGT	GTACCATTCC	590	OSC 56784
539	AGGAT-CTGG	CGAAAANGTC	TCAaTTcTAA	cAcAcAcTgT	GTACCATTCC	587	OSC 56825
539	ANGANGCTNG	CCAAAAAGTC	TCAATTCTAA	CACACACTGT	GTACCATTCC	588	OSC 56824
543	AGGATGCTGG	CGAAAA-GTC	TCAATTCTAA	CACACACTGC	GTACCATTCC	591	OSC 56809
539	AGGATGCTGG	CGAAAAGGTC	TCAATTCTAA	CACACACTGC	GTACCATTCC	588	OSC 56760
540	AGGATGCTGG	CGAAAAGGTC	TCAATTCTAA	CACACACTGC	GTACCATTCC	589	OSC 56749
541	AGGATGCTGG	CGAAAAGGTC	TCAATTCTAA	CACACACTGC	GTACCATTCC	590	NSW 7574
544	AGGATGCTGG	CGAAAAGGTC	TCAATTCTAA	CACATTCTGC	GTACCATTCC	593	OSC 56756
545	AGGATGCTGG	CGAAAAGGTC	TCAATTCTAA	CACATTCTGC	GTACCATTCC	594	OSC 56761
545	AGGATGCTGG	CGAAAA-GTC	TCAATTcTAA	CACATTcTGC	GTACCATTCC	593	OSC 56826
547	-GGATGCTGG	CTAAT--GTA	TCAGTTCAAA	CACACCcTGC	GTACCCTTCC	593	OSC 56829
546	-GGATGCTGG	CTAAATGGTC	TCAGTTCAAA	CACACCCTGC	GTACCCTTCC	594	NSW 6354
547	-GGATGCTGG	CTAAATGGTC	TCAGTTCAAA	CACACCCTGC	GAACCCTTCC	595	OSC 56745
540	ANGATGCTGG	CGTAATGGTC	TACATTAAAA	GATAT---GC	ATACTCT-CC	585	OSC 56831
536	ANGAT-CTGG	CGTA-TGGTC	TACATTATAA	ACCCATCTGT	GTATCTTACC	583	<i>Scutellinia</i>
551	nnnnnnnnnn	nnnnnnnnnn	nCAATTCTAA	CACACTCTGC	GTACCTTTCC	600	AHS 8843
551	nnnnnnnnnn	nnnnnnnnnn	nCAATTCTAA	CACACTCTGC	GNACCTTTCC	600	OSC 56830
551	nnnnnnnnnn	nnnnnnnnnn	nCAGTTCAAA	CACACCCTGC	GTACCCTTCC	600	EGS 2179
551	nnnnnnnnnn	nnnnnnnnnn	nCAGTTCAAA	CACACCCTGT	GTACCCTTCC	600	AHS 30502
551	nnnnnnnnnn	nnnnnnnnnn	nCAGTTCAAA	CACACCCTGT	GtACCCTTCC	600	AHS 21147
551	nnnnnnnnnn	nnnnnnnnnn	nCAATTCTAA	CACACTCTGC	GTATCATTCC	600	ML 941947

	601	611	621	631	641	650	
594	TGTTGCTTCC	-----	-----	-----	-----	-----	603 OSC 56811
590	TGTTGCTTCC	-----	-----	-----	-----	-----	599 OSC 56823
591	TGTTGCTTCC	-----	-----	-----	-----	-----	600 OSC 56753
590	TGTTGCTTCC	-----	-----	-----	-----	-----	599 OSC 56799
590	TGTTGCTTCC	-----	-----	-----	-----	-----	599 NSW 7536
594	TGATGCTTCC	-----	-----	-----	-----	-----	603 OSC 56734
592	TGTTGCTTCC	-----	-----	-----	-----	-----	601 OSC 56801
593	TGTTGCTTCC	-----	-----	-----	-----	-----	602 OSC 56759
595	TGTTGCTTCC	-----	-----	-----	-----	-----	604 OSC 56754
593	TGTTGCTTCC	-----	-----	-----	-----	-----	602 OSC 56747
592	CGTTGCTTCC	-----	-----	-----	-----	-----	601 OSC 56758
594	TGTTGCTTCC	-----	-----	-----	-----	-----	603 OSC 56777
593	TGTTGCTTCC	-----	-----	-----	-----	-----	602 OSC 56798
590	CGTTGCTTCC	-----	-----	-----	-----	-----	599 OSC 56813
588	TGTTGCTNCC	-----	-----	-----	-----	-----	597 OSC 56770
592	CGTTGCTTCC	-----	-----	-----	-----	-----	601 OSC 56782
591	TGTCGCTTCC	GTGGGGTGA	GCTGCTGTCT	TGGGAAGCTT	CAACCGTAGC		640 OSC 56784
588	TGTTGCTTCC	GTGGgGtGGA	GCTGCTgTCT	TGGGAaGCTT	CAaCCGTAGc		637 OSC 56825
589	TGTTGCTTCC	GTGGGGTGA	GCTGCTGTCT	TGGGAAGCTT	CAACCGTAGC		638 OSC 56824
592	TGTTGCTTCC	GTGGGGTGGG	GCTGCTGTCT	TGGGAATCTT	CAACCGTAGC		641 OSC 56809
589	TGTTGCTTCC	GTGGGGTGGG	GCTGCTGTCT	TGGGAATCTT	CAACCGTAGC		638 OSC 56760
590	TGTTGCTTCC	GTGGGGTGGG	GCTGCTGTCT	TGGGAATCTT	CAACCGTAGC		639 OSC 56749
591	TGTTGCTTCC	GTGGGGCGGG	GCTGCTGTCT	TGGGAATCTT	CAACCGTAGC		640 NSW 7574
594	TGTTGCTTCC	-----	-----	-----	-----	-----	603 OSC 56756
595	TGTTGCTTCC	-----	-----	-----	-----	-----	604 OSC 56761
594	TGTTGCTTCC	-----	-----	-----	-----	-----	603 OSC 56826
594	TGTTGCTTCC	-----	-----	-----	-----	-----	603 OSC 56829
595	TGTTGCTTCC	-----	-----	-----	-----	-----	604 NSW 6354
596	TGTTGCTTCC	-----	-----	-----	-----	-----	605 OSC 56745
586	GGA-GC----	-----	-----	-----	-----	-----	590 OSC 56831
584	CGTTGCTTCC	-----	-----	-----	-----	-----	593 <i>Scutellinia</i>
601	TGTTGCTTCC	-----	-----	-----	-----	-----	610 AHS 8843
601	TGTTGCTTCC	-----	-----	-----	-----	-----	610 OSC 56830
601	TGTTGCTTCC	-----	-----	-----	-----	-----	610 EGS 2179
601	TGTTGCTTCC	-----	-----	-----	-----	-----	610 AHS 30502
601	TGTTGCTTCC	-----	-----	-----	-----	-----	610 AHS 21147
601	TGTTGCTTCC	-----	-----	-----	-----	-----	610 ML 941947

	801	811	821	831	841	850	
604	-GTGGTGGTC	GGGTTCGTGC	AAGTTAGGCC	ACGTTCCCCA	GATGCTTCTT		652 OSC 56811
600	-GTGGTGGTC	GGGTTCGTGC	AAGTTAGGCC	ACGTTCCCCA	GATGcTTcTT		648 OSC 56823
601	-GTGGTGGTC	GGGTTCGTGC	AAGTTAGGCC	ACGTTCCCCA	GATGCTTCTT		649 OSC 56753
600	-GTGGTGGTC	GGGTTCGTGC	AAGTTAGGCC	ACGTTCCCCA	GATGcTTcTT		648 OSC 56799
600	-GTGGTGGTC	GGGTTCGTGC	AAGTTAGGCC	ACGTTCCCCA	GATGCTTCTT		648 NSW 7536
604	-GNGG-GGAG	GGGATCGAGC	ATGATTCGGN	TCGCTCCGAC	TAGN-CAGTT		650 OSC 56734
602	-GTGG-GGTG	GAGTTCGAGC	ATGTTTCGGA	TCGCTCCGAC	TAGT-CAGTT		648 OSC 56801
603	-GTGG-GGTG	GAGTTCGAGC	ATGTTTCGGA	TCGCTCCGAC	TAGT-CAGTT		649 OSC 56759
628	TGTGCGGGG	AGGTCCCCCG	AGACAAGCCC	CTGCCAT-GG	TGTAGGCGGT		676 OSC 56754
626	-----	-----	-----GCCC	CTGCCATCGG	TGTAGGCGGT		649 OSC 56747
625	TGTG-TGGGG	AGGTCCCCCG	AGACAAGCCC	CTGCCATCGT	TGCAGGCGGT		673 OSC 56758
627	TGTGCGGGG	AGGTCCCCCG	AGACAAGCCC	CTGCCATCGG	TGTAGGCGGT		676 OSC 56777
626	TGTGCGGGG	AGGTCCCCCG	AGACAAGCCC	CTGCCATCGG	TGTAGGCGGT		675 OSC 56798
623	TGTG-TGGGG	AGGTCCCC-G	ANACAAGCCC	CTGCCATCGT	TGCAGGCGGT		670 OSC 56813
621	TGTGCGGGG	AGGTCCCCCG	AGACAAGCCC	CTGCCATCGG	TGTAGGCGGT		670 OSC 56770
625	TGTGTGGGG	AGGTCCCCCG	AGACAAGCCC	CTGCCATCGT	TGCAGGCGGT		673 OSC 56782
791	-GTTGGTGGC	TGGC-----G	ACG-----	--GTT-GAGT	GTTCTGGGGA		824 OSC 56784
788	-GTTGGTGGC	TGGC-----G	ACG-----	--GTT-GAGG	GTTCTGGGGA		821 OSC 56825
789	-GTTGGTGGC	TGGC-----G	ACG-----	--GTT-GAGG	GTTCTGGGGA		822 OSC 56824
791	-GTTGGTGGC	TGGC-----A	ACG-----	--GTT-GANG	ATTCTGGGGA		824 OSC 56809
788	-GTTGGTGGC	TGGC-----A	ACG-----	--GTT-GAGG	ATTCTGGGGA		821 OSC 56760
789	-GTTGGTGGC	TGGC-----G	ACG-----	--GTT-GAGG	ATTCTGGGGA		822 OSC 56749
790	-GTTGGTGGC	TGGC-----G	ACG-----	--GTT-GAGG	ATTCTGGGGA		823 NSW 7574
604	-GTGGGGTAT	-GGA-----G	CT-GT----C	CTG---GACA	G--CTTCGG-		635 OSC 56756
605	-GTGGGGTAT	-GGA-----G	CT-GT----C	CTG---GACA	G--CTTCGG-		636 OSC 56761
604	-GTGGGGTAT	-GGA-----G	CT-GT----C	CTG---GACA	G--CTTCGG-		635 OSC 56826
604	-----GC	-GGTTGGGGG	CTTGT----C	ACT---GACA	GTCCT----A		633 OSC 56829
605	-----GC	-GGTTGGGGG	CTTGT----C	ACT---GACA	GTCCT----A		634 NSW 6354
625	-GAGACAAGC	-GGTTGGGGG	CTTGT----C	ACT---GACA	GTCCT----A		661 OSC 56745
606	T-CCGAGTAC	C--TTACCTG	-TTGC----T	TCC---GTAN	AnCANTAAC-		643 OSC 56831
594	-----GC	GAGGCAG-TG	-ATCTCGG-	-----TCA	CCTCCGAAC-		623 <i>Scutellinia</i>
611	-GTGGTGGTC	GGGTTCGTGC	AAGTTAGGCC	ACGTTCCCCA	NATGCTTCTT		659 AHS 8843
611	-GTGGTGGTC	GGGNTCGTGC	AAGTTAG-CC	ACGTTCCCCA	GNTGCTTCTT		658 OSC 56830
611	-----GC	-GGTTGGGGG	CTTGTCACT-	-----GACA	GTCCT----A		640 EGS 2179
611	-----GC	-GGTTGGGGG	CTCGTCACT-	-----GACA	GTCCT----A		640 AHS 30502
611	-----GC	-GGTTGGGGG	CTCGTCACT-	-----GACA	GTCCT----A		640 AHS 21147
611	-GTGGGGT--	GGAAGC---T	GTCCTG----	-----GACA	G-CCT----C		639 ML 941947

	851	861	871	881	891	900	
653	TATTGCTACC	TG-CCAGCCC	CTACTGGC-T	TG-TCCCTAC	-GGGAGG---		695 OSC 56811
649	TATTGcTACC	TG-CCAGCCC	cTAcTGGC-T	TG-TCCcTAC	-GGGAGG---		691 OSC 56823
650	TATTGCTACC	TG-CCAGCCC	CTACTGGC-T	TG-TCCCTAC	-GGGAGG---		692 OSC 56753
649	TATTGcTACC	TG-CCAGCCC	cTAcTGGC-T	TG-TCCcTAC	-GGGAGG---		691 OSC 56799
649	TATTGCTACC	TG-CCAGCCC	CTACTGGC-T	TG-TCCCTAC	-GGGAGG---		691 NSW 7536
651	T-GG-CT-GG	TC-CC-----	-----	----CGC--G	-GGGAGA---		671 OSC 56734
649	T-GG-CT-GG	TC-CC-----	-----	----CGC---	-GGGAGG---		668 OSC 56801
650	T-GG-CT-GG	TC-CC-----	-----	----CGC---	-GGGAGG---		669 OSC 56759
677	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		715 OSC 56754
650	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		688 OSC 56747
674	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		712 OSC 56758
677	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		715 OSC 56777
676	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		714 OSC 56798
671	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		709 OSC 56813
671	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		709 OSC 56770
674	GTGGTCTTGG	T--CCATGAA	-GAC--GCCT	T-----CCTGC	-GG-AGGGTG		712 OSC 56782
825	GCGG--TTCA	GA-CCAGCCA	--TTG-CGCT	GGGCT-CTGC	-GGGAGG---		863 OSC 56784
822	GTGG--TTCA	GA-CCAGCCA	--TTGTGC-T	GGGCT-CTGC	-GGGAGG---		860 OSC 56825
823	ACGG--TTCA	GA-CCAGCCA	--TTGCGC-T	GGGCT-CTGC	-GGGAGG---		861 OSC 56824
825	GCGG--TTCC	GA-CCAGCCA	--TTGTGCCT	GGGCT-CTGC	-GGGAG---		863 OSC 56809
822	GCGG--TTCC	GA-CCAGCCA	--TTGTGCCT	GGGCT-CTGC	-GGGAGG---		861 OSC 56760
823	GCGG--TTCC	GA-CCAGCCA	--TTGTGCCT	GGGCT-CTGC	-GGGAGG---		862 OSC 56749
824	GCGG--TTCC	GA-CCAGCCA	--TTGTGCCT	GGGCT-CTGC	-GGGAAG---		863 NSW 7574
636	-----	---CCGGCCA	--GCAGGC-T	GG-TTCCCAC	-GGGAGG---		664 OSC 56756
637	-----	---CCGGCCA	--GCAGGC-T	GG-TTCCCAC	-GGGAG---		664 OSC 56761
636	-----	---CCGGCCA	--GCAGGC-T	GG-TTCCCAC	-GGGAGG---		664 OSC 56826
634	GCTGA-----	---CCAAGAA	-----GGT-T	GGCTTCCGT-	-----		658 OSC 56829
635	GCTGA-----	---CCAAGAA	-----GGT-T	GGCTTCCGT-	-----		659 NSW 6354
662	GCTGA-----	---CCAAGAA	-----GGN-T	GGCTTCCGT-	-----		686 OSC 56745
644	TCTGA--TTAC	CTCTGATCAT	GGTCTTGATC	ATCTTCA---	-GGGAGTCTC		688 OSC 56831
624	GCTGG--CGA	CAGCCGT---	-----	-----CCGAC	GGGGAGCACT		653 <i>Scutellinia</i>
660	TATTGCTACC	TG-CCAGCCC	CTACTGGC-T	TG-TCCCTAC	-GGGAGG---		702 AHS 8843
659	TATTGCTACC	TG-CCAGCCC	CTACTGGC-T	TG-TCCCTAC	-GGGNGG---		701 OSC 56830
641	GCTGA-----	---CCAAGAA	-----GGT-T	GGCTTCCGT-	-----		665 EGS 2179
641	GCTGG-----	---CCAAGAA	-----GGT-T	GGCTTCTGT-	-----		665 AHS 30502
641	GCTGG-----	---CCTAGAA	-----GgT-T	GGCTTCCGT-	-----		665 AHS 21147
640	AGCCA-----	--GCC-GGCA	-----GGT-T	GG-TTCC-TG	C-----		664 ML 941947

	901	911	921	931	941	950			
696	-----T	CCCCC-GCAA	ACCATTTGTA	TTTATTTTGC	CTTCTGTCTG		735	OSC	56811
692	-----T	CCCCC-GCAA	ACCATTTGTA	TTTATTTTGC	CTTCTGTCTG		731	OSC	56823
693	-----T	CCCCC-GCAA	ACCATTTGTA	TTTATTTTGC	CTTCTGTCTG		732	OSC	56753
692	-----T	CCCCC-GCAA	ACCATTTGTA	TTTATTTTGC	CTTCTGTCTG		731	OSC	56799
692	-----T	CCCCC-GCAA	ACCATTTGTA	TTTATTTTGC	CTTCTGTCTG		731	NSW	7536
672	-----	ACCCT-ACAA	ACCATTTGCA	TTTATTTTGC	CTTCTGACTG		710	OSC	56734
669	-----T	ACCCT-ACAA	ACCATTTGCA	TTTATTTTGC	CTTCTGTCTG		708	OSC	56801
670	-----T	ACCCT-ACAA	ACCATTTGCA	TTTATTTTGC	CTTCTGTCTG		709	OSC	56759
716	T--GAA-GA-	-----AA	ACCATTTGCA	TT-ATCTTGC	CATCAGTCTG		752	OSC	56754
689	T--GAA-GA-	-----AA	ACCATTTGCA	TT-ATCTTGC	CATCAGTCTG		725	OSC	56747
713	T--GAA-GA-	-----AA	A-CATTTGCA	TT-ATCTTGC	CATCAGTCTG		748	OSC	56758
716	T--GAA-GA-	-----AA	ACCATTTGCA	TT-ATCTTGC	CATCAGTCTG		752	OSC	56777
715	T--GAA-GA-	-----AA	ACCATTTGCA	TT-ATCTTGC	CATCAGTCTG		751	OSC	56798
710	T--GAA-GA-	-----AA	ACCATTTGCA	TT-ATCTTGC	CATCAGTCTG		746	OSC	56813
710	T--GAA-GA-	-----AA	ACCATTTGCA	TT-ATCTTGC	CATCAGTCTG		746	OSC	56770
713	T--GAA-GA-	-----AA	ACCATTTGCA	TT-ATCTTGC	CATCAGTCTG		749	OSC	56782
864	-----T	ATCCTGT-AA	ACATTGAGCA	TTTATTTTAC	CTTCCGTCTG		903	OSC	56784
861	-----T	ATCCTGT-AA	ACATTGAGCA	TTTATTTTAC	CTTCCGTCTG		900	OSC	56825
862	-----T	ATCCTGT-AA	ACATTGAGCA	TTTATTTTAC	CTTCCGTCTG		901	OSC	56824
864	-----T	ATCCTGT-AA	ACATTGAGCT	TTTATTTAAN	CTTCTGTCTG		903	OSC	56809
862	-----T	ATCCTGT-AA	ACATTGAGCT	TTTATTTTAC	CTTCTGTCTG		901	OSC	56760
863	-----T	ATCCTGT-AA	ACATTGAGCT	TTTATTTTAC	CTTCTGTCTG		902	OSC	56749
864	-----T	ATCCTGT-AA	ACATTGAGCT	TTTATTTTAC	CTTCTGTCTG		903	NSW	7574
665	-----T	ATTCT-ACAA	ACCATTTGTA	TATAT-TTGC	CTTCTGTCTG		703	OSC	56756
665	-----T	ATTCT-ACAA	ACCATTTGTA	TATAT-TTGC	CTTCTGTCTG		703	OSC	56761
665	-----T	ATTCT-ACAA	ACCATTTGTA	TATAT-TTGC	CTTCTGTCTG		703	OSC	56826
659	---GAAAGAT	ATTTT-ACAA	ACTATTTGCA	TTTGTCTTGC	CTTCTGTCTG		704	OSC	56829
660	---GAAAGAT	ATTTT-ACAA	ACTATTTGCA	TTTGTCTTGC	CTTCTGTCTG		705	NSW	6354
687	---GAAAGAT	ATTTT-ACAA	ACTATTTGCA	TTTGTCTTGC	CTTCTGTCTG		732	OSC	56745
689	TGCGGGAGGT	ATACATT-AA	ACTC-TTGCA	TT-ACCATGT	CATCTGTCTG		735	OSC	56831
654	CGCGGGAGGT	ATACAT-CAA	ACTC-TTGCA	TTT-TTATGT	CATCTGTCTG		700	<i>Scutellinia</i>	
703	-----T	CCCCC-GCAA	ACCATTTGTA	TTTATTTTGC	CTTCTGTCTG		742	AHS	8843
702	-----T	CCCCC-GCAA	ACCATTTGTA	TTTATTTTGC	CTTCTGTCTG		741	OSC	56830
666	---GAAAGAT	ATTTT-ACAA	ACTATTTGCA	TTTGTCTTGC	CTTCTGTCTG		711	EGS	2179
666	---GGAAGAT	ATTTT-TACAA	ACCATTTGCA	TTTGTCTTGC	CTTCTGTCTG		712	AHS	30502
666	---GGAAGAT	ATTTT-TACAA	ACCATTTGCA	TTTGTCTTGC	CTTCTGTCTG		712	AHS	21147
665	---GGGAGGT	ATTTT-ACAA	ATCATTTGCA	TTCATTTTGC	CTTCTGTCTG		710	ML	941947

	951	961	971	981	991	1000			
736	AATCATGTTA	ATAACAATCG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		785	OSC	56811
732	AATCATGTTA	ATAACAATCG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		781	OSC	56823
733	AATCATGTTA	ATAACAATCG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		782	OSC	56753
732	AATCATGTTA	ATAACAATCG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		781	OSC	56799
732	AATCATGTTA	ATAACAATCG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		781	NSW	7536
711	AATAATGATT	ATAACAATTG	CTAAAACTTT	CAACAACGGA	TCTCTTGGTT		760	OSC	56734
709	AATAATGTTT	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		758	OSC	56801
710	AATAATGTTT	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		759	OSC	56759
753	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		802	OSC	56754
726	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		775	OSC	56747
749	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		798	OSC	56758
753	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		802	OSC	56777
752	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		801	OSC	56798
747	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		796	OSC	56813
747	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		796	OSC	56770
750	AATTTTGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		799	OSC	56782
904	AATTATATCA	ATAACATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		953	OSC	56784
901	AATTATATCA	ATAACATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		950	OSC	56825
902	AATTATATCA	ATAACATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		951	OSC	56824
904	AATTATATCA	ATAANANTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		953	OSC	56809
902	AATTATATCA	ATAACATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		951	OSC	56760
903	AATTATATCA	ATAACATTG	TTAAAAATTT	CAACAACGGA	TCTCTTGGTT		952	OSC	56749
904	AATTATATCA	ATAACATTG	TTAAAAATTT	CAACAACGGA	TTTTTTGGTT		953	NSW	7574
704	AATTATGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		753	OSC	56756
704	AATTATGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		753	OSC	56761
704	AATTATGTTA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		753	OSC	56826
705	AATCATGTTT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		754	OSC	56829
706	AATCATGTTT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		755	NSW	6354
733	AATCATGATT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		782	OSC	56745
736	AATC-TGTTT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		784	OSC	56831
701	AA-C-TGTTT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		748	<i>Scutellinia</i>	
743	AATCATGTTA	ATAACAATCG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		792	AHS	8843
742	AATCATGTTA	ATAACAATCG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		791	OSC	56830
712	AATCATGTTT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		761	EGS	2179
713	AATCATGTTT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		762	AHS	30502
713	AATCATGTTT	ATAACAAATG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		762	AHS	21147
711	AATCTGTAA	ATAACAATTG	TTAAAACTTT	CAACAACGGA	TCTCTTGGTT		760	ML	941947

	1001	1011	1021	1031	1041	1050	
786	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	835	OSC 56811
782	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	831	OSC 56823
783	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	832	OSC 56753
782	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	831	OSC 56799
782	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	831	NSW 7536
761	CTCGCATCGA	TGAAGGACGC	AGCGAAATGC	GATAAGAAGT	GTGAATTGCA	810	OSC 56734
759	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	808	OSC 56801
760	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	809	OSC 56759
803	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	852	OSC 56754
776	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	825	OSC 56747
799	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	848	OSC 56758
803	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	852	OSC 56777
802	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	851	OSC 56798
797	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	846	OSC 56813
797	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	846	OSC 56770
800	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	849	OSC 56782
954	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	1003	OSC 56784
951	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	1000	OSC 56825
952	CTCGCATCNA	TAAAAAACGC	ACCGAAATGC	GATAAGTANT	GTGAATTGCA	1001	OSC 56824
954	CTC-CATCGA	TCAAGAACGC	ANCNAAATGC	GANAACTACT	GTGAATTGCA	1002	OSC 56809
952	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	1001	OSC 56760
953	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	1002	OSC 56749
954	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	1003	NSW 7574
754	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	803	OSC 56756
754	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	803	OSC 56761
754	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	803	OSC 56826
755	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	804	OSC 56829
756	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	805	NSW 6354
783	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	832	OSC 56745
785	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	834	OSC 56831
749	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	798	<i>Scutellinia</i>
793	CTCGCATCGA	TGAAGAAcgc	agcGAAAtgc	gataagtagt	gtgaaTTGCA	842	AHS 8843
792	CTCGCATCGA	TNAAGAACGC	AGCGAAATGC	GATAAGTAGT	GTGAATTGCA	841	OSC 56830
762	CTCGCATCGA	TGAAGAACGC	nnnnnnnnnn	nnnnnnnnnn	nnnAATTGCA	811	EGS 2179
763	CTCGCATCGA	TGAAGAACgc	agcgaaatgc	gataagtagt	gtGAATTGCA	812	AHS 30502
763	CTCGCATCGA	TAAAGAACGC	nnnnnnnnnn	nnnnnnnnnn	nnGAAtTGCA	812	AHS 21147
761	CTCGCATCGA	TGAAGAACGC	AGCAGNNNNN	NNNNNNNNNN	NNNNNNNGCA	810	ML 941947

	1051	1061	1071	1081	1091	1100	
836	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	885	OSC 56811
832	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	881	OSC 56823
833	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	882	OSC 56753
832	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	881	OSC 56799
832	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	881	NSW 7536
811	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	860	OSC 56734
809	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	858	OSC 56801
810	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	859	OSC 56759
853	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	902	OSC 56754
826	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	875	OSC 56747
849	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	898	OSC 56758
853	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	902	OSC 56777
852	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	901	OSC 56798
847	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	896	OSC 56813
847	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	896	OSC 56770
850	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	899	OSC 56782
1004	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCATGGTAT	1053	OSC 56784
1001	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCATGGTAT	1050	OSC 56825
1002	NAAT-CAGTG	AATCATCNAA	TCTTN-AACN	CACATTGCCC	CTCATGGTAT	1049	OSC 56824
1003	CAATTCATTN	AATCATCCAA	TCTTTGAACG	C-CATTNCGC	CCCATGGTAT	1051	OSC 56809
1002	GAATTCAGTG	AATCATCGAA	TCTTTGA-CG	CACATTGCGC	CCCATGGTAT	1050	OSC 56760
1003	GAATTCAGTG	AATCATCGAA	TTTTTGAACG	CACATTGCGC	CCCATGGTAT	1052	OSC 56749
1004	GAATTCAGTG	AATCATCGAA	TTTTTGAACG	CACATTGCGC	CCCATGGTAT	1053	NSW 7574
804	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	853	OSC 56756
804	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	853	OSC 56761
804	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGCAT	853	OSC 56826
805	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	854	OSC 56829
806	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	855	NSW 6354
833	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	882	OSC 56745
835	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	884	OSC 56831
799	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	848	<i>Scutellinia</i>
843	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	892	AHS 8843
842	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	891	OSC 56830
812	GAnTTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	861	EGS 2179
813	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	862	AHS 30502
813	GAATTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCcTGGTAT	862	AHS 21147
811	GAGTTCAGTG	AATCATCGAA	TCTTTGAACG	CACATTGCGC	CTCCTGGTAT	860	ML 941947

	1101	1111	1121	1131	1141	1150	
886	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AGGAGATATT	TCAAGCTCTT	935	OSC 56811
882	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AGGAGATATT	TCAAGCTCTT	931	OSC 56823
883	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AGGAGATATT	TCAAGCTCTT	932	OSC 56753
882	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AGGAGATATT	TCAAGCTCTT	931	OSC 56799
882	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AGGAGATATT	TCAAGCTCTT	931	NSW 7536
861	TCCGGGAAGC	ATGCCTGTTC	GAGCGTCATG	AAGAAAATTT	-CAAGCTCTT	909	OSC 56734
859	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AAGACAATTT	-CAAGCTCTT	907	OSC 56801
860	-CCGGGAAGC	ATGCCTGTTC	GAGCGTCATG	AAGAACAATT	TCAAGCTCTT	908	OSC 56759
903	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CAAGCTCTT	951	OSC 56754
876	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CAAGCTCTT	924	OSC 56747
899	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CA-GCTCTT	946	OSC 56758
903	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CAAGCTCTT	951	OSC 56777
902	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CAAGCTCTT	950	OSC 56798
897	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CAAGCTCTT	945	OSC 56813
897	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CAAGCTCTT	945	OSC 56770
900	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATA	AAAACCCACT	-CAAGCTCTT	948	OSC 56782
1054	CCCATGGGGC	ATGCCTTCCG	GA-CGTCGGG	AAAACCCCTT	TCAAGCATTT	1102	OSC 56784
1051	CCCATGGGGC	ATGCCTTCCG	GAGCGTCgGG	AAAACCCCTT	TCAAGCATTT	1100	OSC 56825
1050	CCCATGGGGC	ATCNTN-CG	GAACGTCGGG	AAAACCCCTT	-CAANCATTT	1097	OSC 56824
1052	CCCATGGGGC	ATGCCTTCCG	GAACGTCGCG	AAAACCCCTT	-CAANCTTTA	1100	OSC 56809
1051	CCCATGGGGC	ATGCCTTCCG	GAGCGTCGGG	AAAACCCCTT	-CAAGCTTTT	1098	OSC 56760
1053	CCCATGGGGC	ATGCCTTCCG	GAGCGTCGGG	AAAACCCCTT	-CAAGCTTTT	1101	OSC 56749
1054	CCCATGGGGC	ATGCCTTCCG	GAGCGTCGGG	AAAACCCCTT	-CAAGCTTTT	1102	NSW 7574
854	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AAGACCATTT	-CAAGCTCTT	902	OSC 56756
854	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AAGACCATTT	-CAAGCTCTT	902	OSC 56761
854	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AAGACCATTT	-CAAGCTCTT	902	OSC 56826
855	TCCGGGAGGC	ATGCCTGTCC	GCGC-ACAAA	ATGGCTCATT	-CAGGGTGAC	902	OSC 56829
856	TCCGGGAGGC	ATGCCTGTCC	GCGC-ACAAA	ATGGCTCATT	-CAGGGTGAC	903	NSW 6354
883	TCCGGGAAGC	ATGCCTGTCC	GCGC-ACAAA	ATGGCTCATT	-CAGGGTGAC	930	OSC 56745
885	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATT	AAAAACCACT	-CAAGCTCTT	933	OSC 56831
849	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATT	AAAAACCACT	-CAAGCTCTT	897	<i>Scutellinia</i>
893	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AGGAGATATT	TCAAGCTCTT	942	AHS 8843
892	TCCGGGAGGC	ATGCCTGTTC	GAGCGTCATG	AGGAGATATT	TCAAGCTCTT	941	OSC 56830
862	TCCGGGAGGC	ATGCCTGTCC	GCGC-AcAAA	ATGGCTCATT	-CAGGGTGAC	909	EGS 2179
863	TCCGGGAGGC	ATGCCTGTCC	GCGC-ACAAA	ATGGCTCATT	-CAGGGTGAC	910	AHS 30502
863	TCCGGGATGC	ATGCTTtTCC	GCGC-ACAAT	ATGGCTCATT	-CAGGGTGAC	910	AHS 21147
861	TCCGGGAGGC	ATGCCTGTTC	NANCTTCATN	AANACAACCT	-CGGGCTCTT	909	ML 941947

	1151	1161	1171	1181	1191	1200			
936	TTTT---GCT	TGGTCTT-GG	AGGTTGAGTG	TTGCTCTTGT	A-CTCATTCA	980	OSC	56811	
932	TTTT---GCT	TGGTCTT-GG	AGGTTGAGTG	TTGCTCTTGT	A-CTCATTCA	976	OSC	56823	
933	TTTT---GCT	TGGTCTT-GG	AGGTTGAGTG	TTGCTCTTGT	A-CTCATTCA	977	OSC	56753	
932	TTTT---GCT	TGGTCTT-GG	AGGTTGAGTG	TTGCTCTTGT	A-CTCATTCA	976	OSC	56799	
932	TTTT---GCT	TGGTCTT-GG	AGGTTGAGTG	TTGT-CTTGT	A-CTNANTCA	975	NSW	7536	
910	TT-----GCT	TGGTTTT-GA	AGGTTGAGTG	TTGCGCTTGC	G-CTCGTTCA	952	OSC	56734	
908	TT-----GCT	TGGTTTT-GA	AGGTTGAGTG	TTGCGCTTGC	G-CTCGTTCA	950	OSC	56801	
909	TT-----GCT	TGGTTTT-GA	AGGTTGAGTG	TTGCGCTTGC	G-CTCGTTCA	951	OSC	56759	
952	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ACGTCCTTCG	GTGACC-TCA	994	OSC	56754	
925	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ACGTCCTTCG	GTGACC-TCA	967	OSC	56747	
947	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ATGCCCTTCG	GTAACC-TCA	989	OSC	56758	
952	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ACGTCCTTCG	GTGACC-TCA	994	OSC	56777	
951	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ACGTCCTTCG	GTGACC-TCA	993	OSC	56798	
946	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ATGCCCTTCG	GTAACC-TCA	988	OSC	56813	
946	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ACGTCCTTCG	GTGACC-TCA	988	OSC	56770	
949	T-----GGCT	TGGTTAT-GG	AGGTTGAGCT	ATGCCCTTCG	GTAACC-TCA	991	OSC	56782	
1103	TTTT---GCT	TGGTTGT-GG	AGGCTGAGCG	TTGCCCTGCGT	G-CACGTTTG	1147	OSC	56784	
1101	TTTT---GCT	TGGTTGT-GG	AGGCTGAGCG	TTGCCCTGCGT	G-CACGTTTG	1145	OSC	56825	
1098	TTTT---GCT	TGGTTGTGGA	AGCT-GAACN	TTGCCCTCCTT	--CNCCTTTG	1141	OSC	56824	
1101	TTNT---GTC	-GGAGCT-GG	AGCT-GAACC	TTGCTTGCTT	--CACTTTCC	1142	OSC	56809	
1099	TTTTTTT-GCT	TGgTTCT-GG	AgGT-GAACg	TTtCTTGCTT	TTCACTTTcG	1145	OSC	56760	
1102	TTTTTTT-GCT	TGGTTCT-GG	AGGCTGAGCG	TTGCTTGCGT	G-CACGTTTCG	1148	OSC	56749	
1103	TTTTTTT-GCT	TGGTTCT-GG	AGGCTGAGCG	TTGCTTGCGT	G-CACGTTTCG	1149	NSW	7574	
903	TT-----GCT	TGGTTGT-GG	AGGTTGAGCG	TTGCCCGCGT	G-CTCGTTCC	945	OSC	56756	
903	TT-----GCT	TGGTTGT-GG	AGGTTGAGCG	TTGCCCGCGT	G-CTCGTTCC	945	OSC	56761	
903	TT-----GCT	TGGTTGT-GG	AGGTTGAGCG	TTGCCCGCGT	G-CTCGTTCC	945	OSC	56826	
903	CAGGGTTGCT	TTGGTACTGA	AGGTCGAATG	TTGCTCATAT	G-TTTGTTCG	951	OSC	56829	
904	CA----GGCT	TTGGTACTGA	AGGTCGAATG	TTGCTCATAT	G-TTTGTTCG	948	NSW	6354	
931	CAGGGTTGCT	TTGGTACTGA	AGGTCGAATG	TTGCTCATAT	G-TTTGTTCG	979	OSC	56745	
934	TT-----GCT	TGGTCATGGA	AGAG-GAGGG	T-GC--CTGT	GTACTC-TCC	973	OSC	56831	
898	TT-----GCT	TGGTATTGGG	AGAG-GAGTG	CACTCGTTGC	CCTCCCTTCC	941	<i>Scutellinia</i>		
943	TTTT---GCT	TGGTCTT-GG	AGGTTGAGTG	TTGCTCTTGT	A-CTCATTCA	987	AHS	8843	
942	TTTT---GCT	TGGTCTT-GG	AGGTTGAGTG	TTGCTCTTGT	A-CTCATTCA	986	OSC	56830	
910	CAGGGTTGCT	TTGGTACTGA	AGGTCAAATG	TTGCTCATAT	G-TTTGTTCG	958	EGS	2179	
911	CAGGGTTGCC	TTGGTATTGA	AGGTCGAATG	TTGCTCATAT	G-TTTGTTCG	959	AHS	30502	
911	CAGGGTTGCC	TTGGTATTGA	AgGTCGAATG	TTGCTCATAT	G-TTTGTTCG	959	AHS	21147	
910	TTGCTTGCTT	CTGAAGGCT-	-GATGTAAT-	----CCATAT	A-CTCATTCA	951	ML	941947	

	1201	1211	1221	1231	1241	1250	
981	CCTTTGAAAT	TTACAGGCGG	GATTGCGTCG	TGTTCCTTTT	--GGCGTTAT	1028	OSC 56811
977	CCTTTGAAAT	TTACAGGCGG	-ATTGCGTCG	TGTTCCTTTT	--GGCGTTAT	1023	OSC 56823
978	CCTTTGAAAT	TTACAGGCGG	-ATTGCGTCG	TGTTCCTTTT	--GGCGTTAT	1024	OSC 56753
977	CCTTTGAAAT	TTACAGGCGG	-ATTG-GTCG	TGTTCCTTTT	--GGCGTTAT	1022	OSC 56799
976	CCTTTGAAAT	TTACAGGCGG	-ATTGCGTCG	TGTTCCTTTT	--GGCGTTAT	1022	NSW 7536
953	CCATTGAAAT	TCACAGGCGG	-ACGTTTCG	TGTTCCTTCT	--GGCGTTAT	999	OSC 56734
951	CCATTGAAAT	TCACAGGCGG	-ACGTTTCG	TGTTCCTTCT	--GGCGTTAT	997	OSC 56801
952	CCATTGAAAT	TCACAGGCGG	-ACGTTTCG	TGTTCCTTCT	--GGCGTTAT	998	OSC 56759
995	CCTTCGAAAT	TCAGAGGCGG	-ATCGTCCAT	TGTTGCCCT-	--GGCGTTAT	1040	OSC 56754
968	CCTTCGAAAT	TCAGAGGCGG	-ATCGTCCAT	TGTTGCCCT-	--GGCGTTAT	1013	OSC 56747
990	CCTTCGAAAT	TCAGAGGCGG	-ATTGCCCCG	TGTTGCCCT-	--GGCGTTAT	1035	OSC 56758
995	CCTTCGAAAT	TCAGAGGCGG	-ATCGTCCAT	TGTTGCCCT-	--GGCGTTAT	1040	OSC 56777
994	CCTTCGAAAT	TCAGAGGCGG	-ATCGTCCAT	TGTTGCCCT-	--GGCGTTAT	1039	OSC 56798
989	CCTTCGAAAT	TCAGAGGCGG	-ATTGCCCCG	TGTTGCCCT-	--GGCGTTAT	1034	OSC 56813
989	CCTTCGAAAT	TCAGAGGCGG	-ATCGTCCAT	TGTTGCCCT-	--GGCGTTAT	1034	OSC 56770
992	CCTTCGAAAT	TCAGAGGCGG	-ATTGCCCCG	TGTTGCCCT-	--GGCGTTAT	1037	OSC 56782
1148	CCTTCGAAAT	TCATTGGCGG	-ACTGTTTCA	TGTTCCATTT	--GGCGTTAT	1194	OSC 56784
1146	CCTTCGAAAT	TCATTGGCGG	-ACTGTTTCA	TGTTCCATTT	--GGCGTTAT	1192	OSC 56825
1142	CCTTCCAAAA	TCAT-GGCCG	GANTGTTTNN	TGTTCCATTT	--GGCGTTAT	1188	OSC 56824
1143	CCNCCNNANA	TCCATGGCGG	-AC-GTTTCA	TTTTCCATTT	--GGCGTTAT	1188	OSC 56809
1146	CCTCCAAAAAT	TCATTGGCGG	-AgTGTTC	TNTTCCATTT	--GGCGTTAT	1192	OSC 56760
1149	CCTCCGAAAT	TCATTGGCGG	-ACTGTTTCA	TGTTCCATTT	--GGCGTTAT	1195	OSC 56749
1150	CCTCCGAAAT	TCATTGGCGG	-AcTGTTC	TGTTCCATTg	--GGcGTTAT	1196	NSW 7574
946	CCTTTGAAAT	TTGCTGGCGG	-ATCGCTCCA	TGTTCCATTT	--GGCGTTAT	992	OSC 56756
946	CCTTTGAAAT	TTGCTGGCGG	-ATCGCTCCA	TGTTCCATTT	--GGCGTTAT	992	OSC 56761
946	CCTTTGAAAT	TTGCTGGCGG	-ATCGCTCCA	TGTTCCATTT	--GGCGTTAT	992	OSC 56826
952	TCTTTAAAAAT	TTACAGGCGG	GCGACTTCAA	-GT-CCTTTC	ATAGCGTTGT	999	OSC 56829
949	TCTTTAAAAAT	TTACAGGCGG	GCGACTTCAA	-GT-CCTTTC	ATAGCGTTGT	996	NSW 6354
980	TCTTTAAAAAT	TTACAGGCGG	GCGACTTCAA	-GT-CCTTTC	ATAGCGTTGT	1027	OSC 56745
974	CTTTTGAAAT	CAAATGGCGG	AAAGC-TCCA	TGT-GCCCC-	--GGCGTAGT	1018	OSC 56831
942	G-----AAAT	TCAATGGCGG	AAAGCC-CCA	TGT-GCCCC-	--GGCGTAGT	981	<i>Scutellinia</i>
988	CCTTTGAAAT	TTACAGGCGG	-ATTGCGTCG	TGTTCCTTTT	--GGCGTTAT	1034	AHS 8843
987	CCTTTGAAAT	TTACAGGCGG	-ATTGCGTCG	TGTTCCTTTT	--GGCGTT-T	1032	OSC 56830
959	TCTTTAAAAAT	TTACAGGCGG	GCGACTTCAA	--TTCCTTTC	ATAGCGTTGT	1006	EGS 2179
960	TCTTTAAAAAT	TTACAGGCGG	GCGACTTCAA	-GT-CCTTTT	TCAGCGTTGT	1007	AHS 30502
960	TCTTTAAAAAT	TTACAGGCGg	GCGACTTCAA	-GT-CCTTTT	TTAGCGTTGT	1007	AHS 21147
952	CCTTTGAAAT	TTACAGGCGG	-ACTCTTCCA	TGTTCCATTT	--GGCGTTAT	998	ML 941947

	1251	1261	1271	1281	1291	
1029	AAGANAAC	TTTCGCTT-G	GACTCGGTG	TC-TGTCCTG	CCCTA	1071 OSC 56811
1024	AGGATAAC	TTTCG-TT-G	GACTCGGTG	TC-TGTCctG	CCcTA	1065 OSC 56823
1025	AGGATAAC	TTTCGCTT-G	GACTCGGTG	TC-TGTCCTG	CCCTA	1067 OSC 56753
1023	AGGATAAC	TTTCGCTT-G	GACTCGGTG	TC-TGTCCTG	CCCTA	1065 OSC 56799
1023	AGGATAAC	TTTCGCTT-G	GACTCGGTG	TC-TGTCCTG	CCCTA	1065 NSW 7536
1000	AGGTTANCT	TCTCGCTT-G	GATN-CGTGA	GCCTGTCTG	CCCCA	1042 OSC 56734
998	AGGTTAACT	TCTCGCTT-G	GATA-CGTGA	AC-TGTCCTG	CCCCA	1039 OSC 56801
999	A-GTTAACT	TCTCGCTT-G	GATA-CGTGA	ACCTGTCTG	CCCCA	1040 OSC 56759
1041	AAGTTTTCT	TTTCGCTT-G	GATTACATG	TCATCTC--G	CCACA	1082 OSC 56754
1014	AAGTTTTCT	TTTCGCTT-G	GATTACATG	TCATCTC--G	CCACA	1055 OSC 56747
1036	AAGTTTGCT	TTTCGCTC-G	GATTACATG	CCATCTC--G	CCGCA	1077 OSC 56758
1041	AAGTTTTCT	TTTCGCTT-G	GATTACATG	TCATCTC--G	CCACA	1082 OSC 56777
1040	AAGTTTTCT	TTTCGCTT-G	GATTACATG	TCATCTC--G	CCACA	1081 OSC 56798
1035	AAGTTTGCT	TTTCGCTC-G	GATTACATG	CCATCTC--G	CCGCA	1076 OSC 56813
1035	AAGTTTTCT	TTTCGCTT-G	GATTACATG	TCATCTC---	CCACA	1075 OSC 56770
1038	AAGTTTGCT	TTTCGCTC-G	GATTACATG	CCATCTC--G	CCGnn	1079 OSC 56782
1195	AGGATAACT	TTTCGCTT-G	GACTTATGAG	GC-TGTCCAG	CCC-A	1236 OSC 56784
1193	AGGATAACT	TTTCGCTT-G	GACTTATGAG	GC-TGTCCAG	CCC-A	1234 OSC 56825
1189	AGGAAAAC	TT-CCCTT-G	GANTTATGAA	GC-TTTCCA-	CCCnn	1229 OSC 56824
1189	AGGANAAC	TTNC-CTT-G	GAATTATNNA	GN-TNTCTN	CC--A	1228 OSC 56809
1193	ANGAtAACaC	TTTCCCTT-G	GAATTAATAA	AGCTGTCTG	CCCCA	1236 OSC 56760
1196	AGGATAACT	TTTCGCTT-G	GACTTATGAG	GC-TGTCNTG	CCC-A	1237 OSC 56749
1197	AGGATAATNT	TTGGGNN--G	GACTATTGAG	GN-TGTNGNG	CCC-A	1237 NSW 7574
993	AGGATAACT	TTTCGCTT-G	GACTCATGAG	GC-TGTCCTG	CCCCA	1035 OSC 56756
993	AGGATAACT	TTTCGCTT-G	GACTCATGAG	GC-TGTCGTG	CCCCA	1035 OSC 56761
993	AGGATAACT	TTTCGCTT-G	GACTCATGAg	GC-TGTCCTG	CCCCA	1035 OSC 56826
1000	AAGTTAACT	TTTCGCTTAG	GACTTGGTGG	AT-TGTCCAG	CCTCG	1043 OSC 56829
997	AAGTTAACT	TTTCGCTTAG	GACTTGGTGG	CT-TGTCCAG	CCTCG	1040 NSW 6354
1028	AAGTTAGCT	TTTCGCTTAG	GACTTGGTGG	CT-TGTCCAG	CCTCG	1071 OSC 56745
1019	AAGTTTTTC--	TTTCGCTT-G	GAACATGAGG	TG--ATCCTG	CCCCn	1058 OSC 56831
982	AAGTTTTTC--	TTTCGCTT-G	GAACGTGAGG	TG--ATCCTG	CCGCA	1021 <i>Scutellinia</i>
1035	AGGATAACT	TTTCGCTT-G	GACTCGGTG	TC-TGTCCTG	CCCTA	1077 AHS 8843
1033	AGGATNACT	TTTCGCTT-G	GACTCGGTG	TC-TGTCCTG	CCCTA	1075 OSC 56830
1007	AAGTTAACT	TTTCGCTTAa	GACTTGGTGG	CT-TGTCCAg	CCTCG	1050 EGS 2179
1008	AAGTTAACT	TTTCGCT-AG	GACTTTGTGG	CT-TGTCCAG	CCTTG	1050 AHS 30502
1008	AAGTTAACT	TTTCGCT-AG	GACTTTGTGG	TT-TGTCCAG	CCTTG	1050 AHS 21147
999	AAGATTACT	TTTCNCTT-G	GACTCATGGG	TTCTGTCTN	CCnnn	1042 ML 941947