A PRELIMINARY INVESTIGATION OF MARINE YEAST BIODIVERSITY
IN NEW ZEALAND WATERS

BY

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Abstract

This is the first known investigation of marine yeast biodiversity from waters surrounding New Zealand's main Islands. Marine yeasts were cultured onto agar plates from algae sampled at three locations in the Wellington Region. DNA extractions and PCR amplifications of the internal transcribed spacer (ITS) regions were conducted, and resultant sequence data were used for isolate identification and phylogenetic analysis. Yeasts isolated during this investigation were not unique; seventy-four isolates were identified from a range of genera that are frequently detected in marine and terrestrial environments worldwide. Furthermore, high ITS sequence similarity was observed between yeasts isolated during this investigation and those from geographically distant locations. These findings may indicate that marine yeasts are ubiquitous at a global level, although evidence is insufficient as to whether yeasts also demonstrate biogeographic distribution patterns. Yeasts isolated during this investigation may have ecological implications in New Zealand's marine environment; marine yeasts are likely to play a general saprophytic role and certain genera are pathogenic. Isolates were also identified from genera that have previously demonstrated beneficial properties and applications, including the production of useful compounds and highly nutritious yeast biomass, biocontrol potential against the postharvest decay of produce, and degradation abilities that may enable bioremediation of polluted marine environments.

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1. Introduction

1.1 Background

1.1.1 History

Yeasts are unicellular, eukaryotic microorganisms, consisting of two phyla in the kingdom Fungi: Ascomycota and Basidiomycota (Kutty and Philip 2008). Yeasts have historical significance in most societies worldwide due to their role in the production of fermented food and beverages (Legras et al. 2007). A letter written by Antony van Leeuwenhoek in 1680 described yeast cells in beer and is the first known record of their observation (Dobell 1932). Current literature searches reveal vast amounts of research on terrestrial yeast species, in particular *Saccharomyces cerevisiae* Meyen ex E.C. Hansen which is a useful model for the study of eukaryotic cell biology (Botstein et al. 1997). In comparison, few studies have focused on marine yeasts; most investigations from the 1940's and earlier were either incidental or provided incomplete information for yeast identification (Fell et al. 1960). Nevertheless, irregular accounts and descriptions of marine fungi exist from as early as 1850 (Kohlmeyer 1963). The first known record of marine yeasts was not until 1894 when Fischer isolated yeasts from waters of the Atlantic Ocean, the majority of which were identified as white and red "Torula" species (Phaff et al. 1952). By the mid 1960's, several researchers had isolated over 30 different yeast species from various marine environments (Fell and Van Uden 1963). Yeasts from both the Ascomycota and the Basidiomycota were isolated in early studies, even though it was originally thought that the sea was nearly devoid of the

Basidiomycota (Wilson 1960). For example, multiple species from the genera *Candida* (Ascomycota) and *Rhodotorula* (Basidiomycota) were isolated from Biscayne Bay, Florida (Fell et al. 1960). Recent investigations have isolated yeasts from a wide range of marine substrates and habitats, but many locations have yet to be surveyed (Kutty and Philip 2008).

1.1.2 Marine Yeasts versus Terrestrial Yeasts

Yeasts considered to have terrestrial origins have been regularly isolated from marine and brackish environments (Fell et al. 1960; Singh et al. 2010). This has raised questions: what distinguishes marine yeasts from terrestrial ones? are yeasts isolated from marine environments obligate marine forms, or terrestrial contaminants passively surviving in the sea? (Van Uden and Castelo Branco 1963; Kohlmeyer and Kohlmeyer 1979). Marine fungi are adaptable (Kohlmeyer 1963), so the answers to these two questions are not obvious. Genetically, there is no specific group that makes up the marine yeasts; yeasts from marine and terrestrial sources are distributed over many genera, such as *Candida* and *Debaryomyces* (Kurtzman 1994). Physiologically, no defining characteristics are known to explain the habitation of marine yeasts in marine environments (Kohlmeyer and Kohlmeyer 1979). The majority of marine yeasts isolated during one investigation were physiologically similar to their terrestrial counterparts (Fell et al. 1960). *Rhodotorula* species from marine and terrestrial sources were also similar in terms of their metabolic attributes, although exceptions such as the additional nutrients required by marine strains of *Rhodotorula aurantiaca* (Saito) Lodder occurred in some situations (Ahearn et al. 1962). Salinity tolerance is not exclusive to marine yeasts, as the growth of most species is not inhibited by sodium chloride concentrations greater than those of the ocean (Kohlmeyer and Kohlmeyer 1979). Since yeasts isolated from

marine sources generally grow equally well on media prepared with saltwater or freshwater, they cannot be distinguished as marine or terrestrial simply based on which media elicits optimal growth (Fell and Van Uden 1963). Overall, currently available information does not enable straightforward differentiation of marine and terrestrial yeasts, or great improvement to Kohlmeyer's original definition of marine fungi as "those that grow and reproduce submerged in the sea or on the seashore on intertidal substrates" (Kohlmeyer 1963).

1.2 Microorganism Distribution

1.2.1 Ubiquity

There is currently debate as to whether microorganisms are ubiquitous, or if they exhibit biogeographic patterns (Martiny et al. 2006). Early studies by Baas Becking and Beijerinck shaped concepts that are still relevant when studying microorganism biogeography and Baas Becking's original theory from 1934, "everything is everywhere, but, the environment selects", is commonly cited (Baas Becking 1934; De Wit and Bouvier 2006). There is suggestion and evidence that microbial eukaryotes are generally cosmopolitan, and do not have biogeographies (Finlay 2002; Finlay and Fenchel 2004). The small physical size and huge abundance of microorganisms raises the probability that they may be transported over large distances simply by chance (Finlay and Esteban 2001). Dispersal of microorganisms is thought to occur via essentially random forces, including both physical means such as ocean currents and hurricanes, and biological means such as transport via other organisms (Finlay 2002). Dispersal may result in the introduction of microorganisms to new locations, where

their subsequent colonisation could overwhelm any tendency towards genetic differentiation (Martiny et al. 2006). However, random dispersal does not necessarily result in relocation of microorganisms to their preferred habitat. One suggestion is that microorganisms are generally ubiquitous and will grow wherever their preferred habitat is realised (Boenigk et al. 2006, plus references therein). A ubiquitous seed bank may exist, in which a large reservoir of microbial species occur in a given environment; some microorganisms may thrive and others may persist only as spores or cysts (Finlay and Esteban 2001). This theory implies the existence of a pool of undetected microorganisms and that local extinction of specific species is rare (Fenchel and Finlay 2004). The number of microbial species worldwide would be small relative to local species richness (Finlay 2002), and ecosystem functions would never be compromised by a lack of microbial diversity (Finlay et al. 1997). Various investigations support the theory of microorganism ubiquity; bacterial sequences from peat sampled in Germany demonstrated similarity with sequences from marine and terrestrial habitats in distant locations including New Zealand (Rheims et al. 1996). Furthermore, an increase in the proportion of cosmopolitan species was observed as organism size decreased in two habitats that have been extensively sampled for eukaryotes: Nivå Bay, an estuary-like habitat near Copenhagen; and Priest Pot, a eutrophic freshwater pond in England (Finlay and Fenchel 2004).

1.2.2 Biogeography

In contrast to the theory of ubiquity, certain evidence suggests that free-living microorganisms demonstrate biogeographic distribution patterns (Martiny et al. 2006). “The environment selects” is the second part of Baas Becking and Beijerinck’s tenet (Baas Becking 1934; De

Wit and Bouvier 2006), and rather than existing environmental conditions it is argued that past events or geographic factors are responsible for shaping spatial variation in microorganism diversity (Baas Becking 1934; Martiny et al. 2006). Data from various investigations support the theory that geographic barriers influence the distribution of eukaryotic microorganisms. *Spumella* morphospecies typically demonstrate a positive linear trend between heat tolerance and the ambient air temperature of their isolation site, however, *Spumella* isolates from Antarctica possessed a lower maximum tolerated temperature (Boenigk et al. 2006). These findings support the idea of restricted geographic transport; *Spumella* migration to Antarctica was sufficiently restricted to allow adaptation of local populations to the environmental conditions present (Boenigk et al. 2006). Minimal gene flow between populations was also observed during an investigation of the hyperthermophilic archaeon *Sulfolobus* (Whitaker et al. 2003). The specific growth requirements of *Sulfolobus* may have prevented dispersal, or perhaps immigrants were unable to persist in locations with established microorganism populations (Whitaker et al. 2003). Since current evaluations of biodiversity may overlook endemic ecophysiological traits and genomic variance, additional evidence of geographic barriers on microorganism distribution might become apparent if finer taxonomic resolution is considered (Boenigk et al. 2006; Gazis et al. 2011).

1.2.3 A Compromise between Ubiquity and Biogeography

Since there is supporting evidence for both theories of microorganism distribution, a potential alternative could include aspects of ubiquity and biogeography. An investigation of the freshwater heterokont alga *Synura* morphotaxon found that species in the *Synura petersenii* complex could be either endemic or cosmopolitan; neither the ubiquity nor the biogeography

theory was individually sufficient to explain the distribution of microbial eukaryotes observed worldwide (Boo et al. 2010). It was suggested that the existing theories of microbial distribution may not be mutually exclusive, assuming the *Synura petersenii* complex is generally representative of non-marine microbial eukaryotes (Boo et al. 2010). One proposal is that microbial eukaryotes are mainly ubiquitous, although the possibility of some endemics is also recognised (Finlay and Esteban 2001). Even though restricted migration is thought to occur, geographic barriers to microbial eukaryotes may have resulted in some cases of endemism in *Spumella*; Antarctic *Spumella* isolates differed from the global trend in terms of their maximum tolerated temperature and were thus more strongly adapted to their environment (Boenigk et al. 2006). Despite uncertainty as to whether microorganisms follow a biogeographic distribution pattern or demonstrate ubiquity, it seems that Baas Becking and Beijerinck's original statement is still relevant; "everything is everywhere" describes the situation if microorganisms are ubiquitous, as does "the environment selects" if they demonstrate biogeography (Baas Becking 1934; De Wit and Bouvier 2006).

1.2.4 Yeast Distribution

The extremely widespread distribution of yeasts has been recognised from as early as 1960 (Van Uden 1960). Yeasts have been isolated from a range of environments, including terrestrial sources such as soils and aquatic sources such as rivers, lakes and oceans (Van Uden 1960, plus references therein). During early investigations of marine environments yeasts were isolated from various substrates: seawater, sediments, vegetation and vertebrates (Roth et al. 1962). By 1963, multiple authors had isolated over 30 yeast species from marine sources including isolates from both the Ascomycota and the Basidiomycota (Fell and Van

Uden 1963). For example, *Candida* species (*Candida tropicalis* (Castell.) Berkhout and *Candida parapsilosis* (Ashford) Langeron & Talice) from the Ascomycota and *Rhodotorula* species (*Rhodotorula mucilaginosa* (A. Jörg.) F.C. Harrison and *Rhodotorula glutinis* (Fresen.) F.C. Harrison) from the Basidiomycota were frequently isolated from Biscayne Bay, Florida (Fell et al. 1960). During an investigation of Biscayne Bay and additional marine areas, the most commonly isolated genera were *Candida* and *Debaryomyces* (from the Ascomycota), plus *Trichosporon*, *Rhodotorula* and *Cryptococcus* (from the Basidiomycota) (Roth et al. 1962). In California, *Metschnikowia zobellii* (Van Uden & Cast.-Branco) Van Uden and *Candida pulcherrima* (Lindner) Windisch were isolated from beach cast algae (*Macrocystis pyrifera* (L.) C. Agardh) (Van Uden and Castelo Branco 1963). Further sampling from coastal USA yielded an assortment of marine yeast genera similar to those isolated from the coast of Portugal at around the same time (Taysi and Van Uden 1964). Although some regions have not been extensively sampled, recent evidence suggests that marine yeasts have a widespread distribution; yeasts from a range of genera (including *Candida*, *Cryptococcus*, *Debaryomyces* and *Rhodotorula*) have been isolated from various substrates in marine and estuarine waters worldwide (Kutty and Philip 2008, plus references therein).

Although microorganisms are generally ubiquitous, existing environmental factors may also influence microbial distribution. The availability and concentration of organic material is known to affect the character of yeast populations (Fell and Van Uden 1963), as are environmental conditions such as temperature, light, pressure and pH (Dix and Webster 1995; Deák 2006). Terrestrial runoff and pollution are also influential on the character of yeast populations in coastal areas (Fell and Van Uden 1963; Hagler and Mendonça-Hagler 1981). An investigation of both polluted and unpolluted waters in Rio de Janeiro found an increase in

the number and variation in the type of yeasts isolated in polluted areas; pink yeasts made up a lower proportion of the total number of yeasts isolated in polluted water (Hagler and Mendonça-Hagler 1981). However, it is difficult to distinguish whether the influence of pollution is due to the introduction of terrestrial yeasts into marine environments, the effect of pollution on yeasts already present in the environment, or both. Factors such as thermoclines, eddies, plankton blooms and surface slicks also influence yeast distribution (Gadanhó et al. 2003). Furthermore, an increase in water depth or distance from land is generally associated with a decrease in the size of marine yeast populations (Gadanhó et al. 2003). The low organic content of sediments may also contribute to the high proportion of oxidative yeasts observed in the deep sea (Fell et al. 1960). Even though marine yeasts are suggested to have a widespread distribution at a global level, existing environmental conditions may govern their numbers and distribution (Kutty and Philip 2008, plus references therein).

1.3 Fungal Systematics and Molecular Techniques

1.3.1 Phylogenetic Techniques

Fungal systematics was originally based on phenotypic characteristics, but recently developed molecular techniques have contributed DNA sequence data as an alternative source of information (Seifert 2009). Like fungi, yeasts were primarily identified using phenotypic characteristics such as morphology and physiology, however, certain tests are laborious and may give ambiguous results due to strain variability (Kurtzman and Robnett 1998). Techniques developed based on DNA-DNA reassociation, restriction fragment length

polymorphisms (Kurtzman and Blanz 1998), and recently obtained DNA sequence data have enabled yeast classification to be based directly on evolutionary relationships (Kurtzman and Piškur 2006). Hence, the use of molecular data as the main source of information for yeast identification is increasing (Kurtzman and Robnett 1998). Analysis of sequence divergence has been used to resolve many phylogenetic relationships (Kurtzman and Fell 2006), and this novel source of information has led to major alterations in yeast taxonomy (Deák 1999). Although it is recognised that relying solely on physiological traits to establish yeast taxonomy can create errors, molecular and conventional taxonomies need not be exclusive as they may complement each other in polyphasic taxonomy (Valente et al. 1999). Macroscopic descriptions of colony colour are still helpful when describing yeasts; a pink or red colony is usually indicative of a species from the Basidiomycota, and a white colony could belong to either the Basidiomycota or the Ascomycota (Gadanhó et al. 2003).

1.3.2 Internal Transcribed Spacer Region

Fungal species delineation is now primarily based on relatedness of the rRNA gene region; ribosomal nucleic acid sequences are of particular interest because they allow evaluation of phylogenetic and evolutionary relationships at multiple taxonomic levels (Deák 1999; Valente et al. 1999). White et al. (1990) described primers for amplification of the nuclear and mitochondrial rRNA genes in fungi. The nuclear gene component of rRNA consists of a small subunit (SSU) and a large subunit (LSU), separated by two internal transcribed spacer regions (ITS1 and ITS2) which are interrupted by a conserved 5.8S region (White et al. 1990). Henceforth, the term ITS will be used to refer to both the ITS1 and ITS2 regions, and includes the 5.8S region. The conserved areas of rRNA sequences enable alignment, and the more

variable regions enable estimation of evolutionary relationships (Kurtzman 1994), thus, unequally conserved ITS components allow resolution at various scales (Nilsson et al. 2008). James et al. (1996) analysed ITS and SSU rRNA sequence data and found that the patterns of relationships were generally in agreement, although ITS sequences were superior for assessment of very close relationships due to greater interspecies sequence divergence. Additional advantages of the rRNA region for species identification include its occurrence in multiple copies in all living cellular organisms (Kurtzman and Piškur 2006), plus its ~550 bp size and ease of amplification from low quantity samples (Nilsson et al. 2008). Consequently, the use of ITS in yeast sequencing studies is increasing and ITS collections in online databases are expanding (Valente et al. 1999). A growing sequence database is advantageous since the more taxonomic coverage a database has, the greater the chance that any particular sequence obtained from the environment will yield a close database match (O'Brien et al. 2005).

ITS sequence data appear to be the default choice for species level fungal studies (Seifert 2009), but use of the ITS region also has limitations (Nilsson et al. 2008). The ITS region is variable in length, and although beneficial for providing superior resolution and identification in groups with longer amplicons, abundant insertion-deletions generate difficulties for alignment and phylogenetic construction (Seifert 2009). For example, ITS sequences from the genera *Zygosaccharomyces* and *Torulaspora* included extensive insertions and deletions, limiting the use of sequence alignment programs and assessment of more distant relationships (James et al. 1996). Establishment of a cut-off point or variation limit for species delimitation based on ITS sequences is also difficult due to the variable level of intraspecific ITS variation in fungi (O'Brien et al. 2005). ITS also has limitations for assessment of biodiversity; an investigation into the definition of species boundaries in tropical terrestrial endophytes found

that sole use of the ITS region generally underestimated the predicted number of species, compared with estimates made using other nuclear loci (Gazis et al. 2011).

1.3.3 Alternative Regions

Molecular systematics and extensive databases have focused on the non-coding ITS region, however, coding regions such as the SSU and the D1/D2 variable domain of the LSU have also been used to analyse close and distant relationships (Kurtzman and Blanz 1998; Scorzetti et al. 2002). For example, the LSU enabled reliable identification of the majority of yeasts investigated due to its combination of conserved and variable regions (Fell and Kurtzman 1990; Kurtzman and Robnett 1998). One investigation examined yeasts from the Basidiomycota via sequence analysis of the ITS region and the D1/D2 region of the LSU; identification of most yeasts was possible with either sequence, but there were instances where ITS was able to separate closely related species when D1/D2 could not, and vice versa (Scorzetti et al. 2002). Although the LSU generally allows reliable identification of marine yeasts, analysis of additional regions may improve the confidence of identification procedures (Fell and Kurtzman 1990). The use of sequence data from multiple regions (including ITS and D1/D2) appears to be beneficial when comparing closely related sequences (James et al. 1996; Kurtzman and Fell 2006). Since phylogenetic analysis using a single gene can create uncertainty when assessing distant relationships, a multigene sequence approach has been used to analyse yeasts (Kurtzman and Robnett 2003); multigene analyses can be used to strengthen support for phylogenetic trees, which are often weak when constructed with single genes (Kurtzman and Fell 2006). Although they do not always enable separation of species,

single gene sequences are still valuable for the rapid identification of some isolates via database searches (Kurtzman and Piškur 2006).

1.4 Applications

1.4.1 Overview

It has been suggested that marine fungi may have unusual physiological adaptations which have arisen from the distinct physio-chemical properties of marine environments (Raghukumar 2008). These adaptations have been exploited and developed for biotechnological uses (Raghukumar 2008), thus, marine yeasts have a wide range of current and potential applications (Chi et al. 2010). For example, the immunostimulatory abilities of marine yeasts have potential for use in aquaculture settings (Sajeevan et al. 2006; Reyesbecerril et al. 2008), and the biocontrol abilities of live marine yeasts can protect fruit against postharvest decay caused by pathogenic fungi (Wang et al. 2008). The biodegradative abilities of marine yeasts enable production of yeast biomass, which is of high nutritional quality and can be used in aquaculture or animal feed (Rhishipal and Philip 1998). Production of degradative extracellular enzymes is the main mode in which microorganisms take part in detrital processes, and can also be manipulated for biotechnological uses (Raghukumar 2008). Certain marine yeast species also produce various extracellular enzymes, including inulinase and killer toxin (Chi et al. 2009). Yeast byproducts or biomass can be produced efficiently due to the short generation time and limited requirements of yeasts (Kutty and Philip 2008, plus references therein). If marine yeasts are used instead of terrestrial yeasts for the

production of byproducts or biomass, the freshwater required for these processes could be replaced with seawater, which is an abundant resource in many areas (Chi et al. 2006).

1.4.2 Biomass

Yeasts efficiently biodegrade organic matter or waste into yeast biomass (Rhishipal and Philip 1998). For example, certain marine yeasts isolated from the coast of India demonstrated efficient biotransformation of prawn shell waste into single cell protein; the biotransformation process conserved protein from the raw material and displayed additional protein enrichment (Rhishipal and Philip 1998). Marine yeasts have good amino acid composition plus high protein and carbohydrate levels, indicating potential for use as a dietary component in aquaculture (Brown et al. 1996). A marine strain of *Yarrowia lipolytica* (Wick., Kurtzman & Herman) Van der Walt & Arx contained more than 47 g of protein per 100 g of dry cell weight, and would be an excellent candidate for single cell protein production in the mariculture industry (Chi et al. 2007). During another investigation, two marine yeast species (*Debaryomyces hansenii* (Zopf) Lodder & Kreger-van Rij and *Candida austromarina* (Fell & I.L. Hunter) S.A. Mey. & Yarrow, originally isolated from the coast of Korea) were fed to cladoceran *Moina macrocopa* (Straus), which has potential as a dietary component for fish larvae (Kang et al. 2006). In terms of nutritional quality, *Candida austromarina* was especially superior to the commercial diet *Erythrobacter sp.* Sπ-I used as a control (Kang et al. 2006). On a large scale, production and concentration of yeast cells is easy to manage, and certain species thrive on cheap agricultural byproducts (Chi et al. 2007). Overall, yeast single cell biomass is of high nutritional quality and would be a cost effective choice for

supplementing animal or aquaculture feed, while utilizing a waste product (Rhishipal and Philip 1998).

1.4.3 Immunostimulation and Biocontrol

Bacteria and fungi have potential for use as prophylactic probiotics in aquaculture settings, where fish are susceptible to infections but antibiotic use is not appropriate for various reasons (Reyesbecerril et al. 2008). Yeasts are generally considered to be a commensal part of the gut flora in fish; live yeasts bind to the intestine and have potential probiotic activity (Gatesoupe 2007, plus references therein). When given as a dietary supplement, marine yeast *Debaryomyces hansenii* (originally isolated from the digestive system of rainbow trout) demonstrated adherence to the intestine and stimulation of some aspects of innate immunity in the seabream *Sparus aurata* L. (Reyesbecerril et al. 2008). Non-viable marine yeasts can also demonstrate immunostimulatory ability; one study investigated the effect of autoclaved marine yeast *Candida sake* (Saito & Oda) Van Uden & H.R. Buckley ex S.A. Mey. & Ahearn (originally isolated from the coast of India) in the diet of shrimp *Fenneropenaeus indicus* (Milne-Edwards) (Sajeevan et al. 2006). Shrimps fed a diet with a *Candida sake* component of 10 % exhibited a significant increase in immune response when challenged with white spot syndrome virus (Sajeevan et al. 2006). It was proposed that in penaeid shrimp, yeasts may simultaneously act as a nutritional supplement and an immunostimulant, and that the role of yeasts in immunostimulation is due to their nucleotides and cell wall glucan contents (Sajeevan et al. 2006). Data suggest that the β -glucan component of yeasts accounts for much of their immunostimulatory ability in fish, and that yeast extracts such as β -glucan can also be used as immunostimulants (Gatesoupe 2007, plus references therein). *Penaeus monodon*

Fabrizius demonstrated an enhanced survival rate and disease resistance when its diet was supplemented with β -1, 3-glucan from mushroom *Schizophyllum commune* Fr. (Chang 2000). If used for their immunostimulatory abilities, the halotolerant properties of marine yeasts would enable ease of application in brackish and seawater aquaculture systems (Sajeevan et al. 2006).

In addition to their immunoprotective abilities, marine yeasts have biocontrol potential against postharvest fungal disease (Wang et al. 2008). A *Rhodosporidium paludigenum* Fell & Tallman isolate from the East China Sea was able to control black rot caused by *Alternaria alternata* (Fr.) Keissl. on cherry tomato fruit, possibly via competition for space and nutrition (Wang et al. 2008). The biocontrol ability of marine yeast species against postharvest grey mold caused by *Botrytis cinerea* Pers. on cherry tomatoes was also investigated; a washed cell suspension of *Rhodosporidium paludigenum* was the most efficacious treatment for decreasing disease incidence (Wang et al. 2010). An increase in *Rhodosporidium paludigenum* concentration was correlated with a decrease in disease incidence, suggesting that the mechanism of action was competition for nutrients, however, culture filtrate and autoclaved cultures also had some effect *in vivo* and may indicate further mechanisms (Wang et al. 2010). *Rhodosporidium paludigenum* is a suitable candidate for use in commercial processes due to its biocontrol abilities and resistance to osmotic stress, features that may be correlated with its isolation from the marine environment (Wang et al. 2010). Marine and terrestrial strains of *Debaryomyces hansenii* (originally isolated from Mexico) also demonstrated effective inhibition of postharvest blue mold caused by *Penicillium italicum* Wehmer on limes (Hernández-Montiel et al. 2010). These strains had an antagonistic nature, and competition for space and nutrients was suggested as a possible mechanism (Hernández-Montiel et al. 2010).

1.4.4 Yeast Products

Potential applications of marine yeasts include their utilization in the production of compounds such as pharmaceuticals, cosmetics, and chemicals for industry (Chi et al. 2006). Reviews describe a range of valuable products from marine yeasts, including bioemulsifiers (Nerurkar et al. 2009) and compounds such as vitamin c, glutathione and β -carotenoids (Chi et al. 2006). Marine yeasts from genera including *Aureobasidium*, *Cryptococcus*, *Metschnikowia*, *Pichia* and *Yarrowia* produce many extracellular enzymes: lipase, phytase, inulinase, alkaline protease, acid protease and killer toxin (Chi et al. 2009). Optimal conditions for the production of various enzymes were determined, and the presence of Na^+ ions enhanced production in some cases (Chi et al. 2009). Certain enzymes have been purified and characterised, and have had their encoding genes cloned, sequenced and expressed (Chi et al. 2009). Certain enzymes have unique characteristics or encoding genes compared with homologous enzymes from their terrestrial counterparts (Chi et al. 2009). For example, marine yeast derived inulinase, lipase and phytase demonstrated higher activity than equivalent enzymes derived from terrestrial sources (Chi et al. 2009, plus references therein).

Inulinase is produced by many microorganisms, and is able to hydrolyse inulin to 95 % pure fructose in one step (Gao et al. 2007). Inulinase can transform inulin (high levels of which are found in plants) into high fructose syrup, inulooligosaccharides and bioethanol (Chi et al. 2009). Microorganisms, particularly yeasts, are excellent producers of inulinases due to their high yields and ease of cultivation (Chi et al. 2009). Four marine yeasts (originally isolated from algae sampled in China, or sediment from the South China Sea) secreted large amounts of inulinase when grown on inulin containing media: *Pichia guilliermondii* Wick., *Cryptococcus aureus* (Saito) Takash., Sugita, Shinoda & Nakase, *Yarrowia lipolytica* and

Debaryomyces hansenii (Gao et al. 2007). Exoinulinase levels were highly variable between the yeasts isolated, as were the levels of monosaccharides, disaccharides and oligosaccharides produced by their crude inulinases (Gao et al. 2007). The pH and temperature required for optimal growth of these isolates was established, and although there was some variation between strains the ranges were in accordance with those from corresponding terrestrial yeasts (Gao et al. 2007). Nevertheless, some physical and biochemical differences have been observed between inulinases produced by marine and terrestrial yeasts (Chi et al. 2009).

Some marine yeasts produce killer toxin, which kills yeast of the same or related species but does not harm the killer strain itself (Magliani et al. 1997). Killer yeast strains are common and have been detected from a variety of genera: *Debaryomyces*, *Candida*, *Pichia*, *Cryptococcus* and *Williopsis* (Magliani et al. 1997). For example, marine yeast *Pichia anomala* (E.C. Hansen) Kurtzman (originally isolated from the gut of ascidians on the coast of China) produced killer toxin against *Metschnikowia bicuspidata* (Metschn.) T. Kamiński (Wang et al. 2007). *Metschnikowia bicuspidata* causes milky disease in the crab *Portunus trituberculatus* (Miers) and is responsible for great economic losses (Wang et al. 2007). Natural killer strains, such as *Pichia anomala*, have potential for controlling the growth of pathogenic yeasts including *Metschnikowia bicuspidata* in aquaculture settings, and may also be of use in other animals and plants (Wang et al. 2007). These unique properties are encouraging for further investigation of marine yeasts, which may be novel or enable production of compounds with novel characteristics (Chi et al. 2009).

1.4.5 Bioremediation

Microorganisms take part in detrital processes via production of extracellular degradative enzymes (Raghukumar 2008). The degradation abilities of marine yeasts may enable bioremediation of contaminated marine environments by removing pollutants such as heavy metals and organic substances, especially hydrocarbons (Chi et al. 2010). For example, untreated palm oil mill effluent has a high chemical oxygen demand and is a source of pollution when released into rivers and lakes (Oswal et al. 2002). A marine strain of *Yarrowia lipolytica* (originally isolated from India) demonstrated degradation of raw palm oil mill effluent without dilution or nutrient addition, and reduced the chemical oxygen demand by around 95 % (Oswal et al. 2002). This *Yarrowia lipolytica* strain was able to grow in saltwater or freshwater and over a wide range of pH levels, making it an excellent candidate for waste management (Oswal et al. 2002). *Yarrowia lipolytica* also enables the biotransformation of trinitrotoluene into less toxic products that can subsequently be utilized by other microorganisms (Jain et al. 2004), and has potential for the bioremediation of soil or water contaminated by heavy metals (Strouhal 2003). Marine yeasts may facilitate bioremediation via alternative mechanisms; a marine strain of *Debaryomyces hansenii* has potential as a sorbent for uranium removal due to its high sorption capacity, low biomass cost and ease of accessibility (Sarri et al. 2009).

1.5 New Zealand

Most investigations of New Zealand fungi have focused on the food and beverage industry, soils and pasture, plant pathogens and terrestrial ecosystems (Di Menna 1955; Fleet 2001;

McKenzie 2001; Serjeant et al. 2008). Some information has been published regarding New Zealand's marine fungi (Lintott and Lintott 1982; Parsons and Fenwick 1984; Lintott and Lintott 2002), but no investigations are known to have surveyed marine yeast biodiversity from waters surrounding New Zealand's main Islands. Marine yeasts have been isolated from the Chatham Islands (Fell and Hunter 1968), which are geographically distant from the North and South Islands of New Zealand (Heath 1985). Twelve isolates of *Candida natalensis* Van der Walt & Tscheuschner and a single isolate of *Metschnikowia zobellii* were collected from Chatham Island tidal pools, and six further isolates of *Metschnikowia zobellii* were found in a small freshwater lake (Fell and Hunter 1968). Isolates were identified based on their biochemical properties and mating characteristics with yeast type strains (Fell and Hunter 1968). The isolates from the freshwater ponds on Chatham Island were originally identified as *Metschnikowia zobellii*, but redesignated as *Metschnikowia bicuspidata* var. *chathamia* after further mating tests (Fell and Pitt 1969).

1.6 Research Question

There is a lack of information regarding the biodiversity of marine yeasts in New Zealand, yet they play an important ecological role and may have useful applications. The shortage of information has led to this investigation: the aim was to determine the marine yeast species present and their biodiversity in New Zealand.

2. Materials and Methods

2.1 Algal Collections

Four algal collections were carried out in the Wellington Region (Fig. 1). Collection 1 was from Tarakena Bay on 18/12/09, Collections 2 and 3 were from Waitaha Cove on 29/01/10 and 25/02/10, and Collection 4 was from Onehunga Bay on 19/03/10. Sampling was carried out at low tide, and only completely submerged algae attached to the sea bed were collected. Where possible, two algal species were collected from each group: Rhodophyta, Chlorophyta and Phaeophyceae (Table 1). In Collection 1, five samples of each of the following algae were collected: *Pachymenia lusoria* (Greville) J. Agardh, *Cladhymenia oblongifolia* J.D. Hooker & Harvey, *Ulva* sp. L., *Macrocystis pyrifera* and *Carpophyllum maschalocarpum* (Turner) Greville. In Collection 2, ten samples of each of the following algae were collected: *Psaromenia berggernii* (J. Agardh) D'Archino, W.A. Nelson & Zuccarello, *Champia novae-zelandiae* (J.D. Hooker & Harvey) Harvey, *Codium convolutum* (Dellow) P.C. Silva, *Caulerpa brownii* (C. Agardh) Endlicher, *Cystophora scalaris* (J. Agardh) and *Macrocystis pyrifera*. In Collection 3, five samples were collected of the same algae that were sampled in Collection 2. In Collection 4, five samples were collected of the same algae that were sampled in Collections 2 and 3, with exception of the Rhodophyta. The same species belonging to the Rhodophyta could not be found in Collection 4 (except for an individual *Psaromenia berggernii*, which was sampled), so five samples from each of the species *Cladhymenia oblongifolia* and *Pachymenia lusoria* were collected. Each algal sample consisted of a ~10 x 10 cm sized piece taken from the blade (except for samples of *Codium convolutum* and *Champia novae-zelandiae* which consisted of a ~3 x 3 x 3 cm sized algal mass). Each sample

was collected in a sterile resealable plastic bag and given a code to reflect its origin, then transported to the lab on ice and processed on the same day.

Figure 1. Map illustrating the location of algal collections conducted in the Wellington Region (Google Maps 2011).

2.2 Initial Culture Techniques

Based on positive growth results from trial investigations, two different nutrient media were chosen for marine yeast isolation (Appendix 5.2). These were Difco Standard Marine Agar Plus 1 (STD) and Difco Potato Dextrose Agar Plus (PDA), both with additional nutrients and PDA with additional salt (Appendix 5.1). Media was made up with the ingredients as specified, autoclaved and poured into Petri dishes one or two days prior to use. Sterile microbiological techniques were used at all times during preparation of the agar plates.

To prevent bacterial overgrowth, filter-sterilised antibiotic solutions of streptomycin sulfate (in distilled water) and rifampicin (in methanol) were applied in a thin layer to each agar plate with a sterile disposable plastic spreader. During Collection 1, 100 μl of streptomycin sulfate solution with concentration 10 mg ml^{-1} and 100 μl of rifampicin solution with concentration 5 mg ml^{-1} were applied to each plate. During Collections 2, 3 and 4, 100 μl of streptomycin sulfate solution with concentration of 9 mg ml^{-1} and 100 μl of rifampicin solution with concentration of 4.5 mg ml^{-1} were applied to each plate. The combination of streptomycin sulfate and rifampicin demonstrated effective inhibition of bacterial colony formation in trial investigations (Appendix 5.2). Antibiotics were applied to agar plates the day before collection, then covered with aluminium foil and left at room temperature overnight to prevent degradation of the antibiotics by light.

For Collection 1, three methods were used to inoculate agar plates with yeasts from the algae sampled. These were the sterile swabbing method (algal surface was rubbed with a sterile cotton swab which was transferred to an agar plate), the agitation of alga method (algal sample was shaken vigorously for 2 minutes in its original collection bag with ~30 ml of autoclaved sterile seawater, and a 100 μl aliquot of the resultant solution was transferred to an agar plate) and the homogenisation of alga method (a ~2 x 2 cm algal sample was homogenised with a mini-blender in a falcon tube with ~10 ml of sterile seawater, and a 100 μl aliquot of the resultant solution was transferred to an agar plate). However, the homogenisation method was more time consuming than the other inoculation techniques and it was difficult to process the samples via all three methods within a single day. The homogenisation method was also thought to be the most prone to contamination, so it was not used for the remainder of the collections. For Collections 2, 3 and 4, only the sterile swabbing

method and the agitation of alga method were used. Two agar plates were created for each transfer method per algal sample: one using STD and one using PDA. Thus, for each algal sample a total of four agar plates were created: a STD and a PDA plate using the sterile swabbing method, plus a STD and a PDA plate using the agitation of alga in sterile seawater method. A few plates were treated with an application of sterile seawater or rubbed with a sterile swab as a control. Agar plates were inverted and incubated at 18 °C, then checked for colonies at one week and again at three weeks after inoculation.

2.3 Isolate Processing

In order to reduce the number of yeast isolates that were studied, individual colonies were selected for investigation. Selection was based on colony morphology; the criteria were colour, wet or dry surface, and colony elevation. One isolate from each morphological group was selected per algal sample, per collection. For example, if a plate had two pink colonies, two matt white colonies and two shiny white colonies, one colony from each group was selected. The isolates were given codes to reflect their alga of origin and which media they were isolated from: STD or PDA. Selected colonies were then subcultured onto fresh agar plates to eliminate possible fungal contamination (no antibiotics were required at this stage). Plates were incubated at 18 °C and checked after five days.

In order to ascertain that each yeast isolate was pure, a wet mount was made with a single colony taken from each subculture plate and viewed under an Olympus microscope. To establish purity, yeast isolates were required to have cells with a homogenous appearance and no observable contaminants, such as bacteria or filamentous fungi. Colony morphology and

microscopic characteristics such as cell size and shape were observed and recorded. Photographs of agar plates were also taken with a Nikon D90 SLR camera, using automatic settings for conditions with fluorescent white light. If there were any doubts about the purity of an isolate it was subcultured again until pure. When the purity of an isolate was established, a liquid culture was made by inoculating a sample of the individual colony into 1 ml of Difco Marine Broth Plus and incubating for five days at 18 °C. During later collections, Difco Luria Broth was used as it was an equally effective liquid media for yeast growth and contained less sediment which was beneficial for microscopy. After incubation, a sample of broth from each isolate was checked via microscopy to ensure that the liquid culture was pure. A Leica DM IL inverted microscope was used and images were taken with an attached Olympus C5060WZ camera. A 1.5 ml aliquot of broth from each isolate was taken for DNA extraction. An additional 600 µl aliquot of broth was taken from each isolate, mixed with 550 µl of an autoclaved glycerol solution (45 % glycerol in aged seawater) and preserved at -80 °C. This method was tested and found to ensure the survival of yeast isolates; frozen samples were placed on ice while yeasts were resuscitated onto fresh agar plates.

2.4 DNA Extraction

A 1.5 ml aliquot of each yeast liquid culture was spun down for 2 minutes at 12,000 G in a 1.5 ml Eppendorf tube to produce a pellet. The supernatant was discarded and DNA extraction was carried out. 500 µl of CTAB extraction buffer (2 % CTAB, 0.1 M Tris-HCl (pH 8.0), 1.4 M NaCl, 20 mM EDTA, 1 % PVP) plus 2 µl of RNase A (100 mg ml⁻¹) and 5 µl of Proteinase K (20 mg ml⁻¹) were added to each pellet. Samples were incubated at ~57 °C overnight, with occasional mixing. An equal volume of chloroform:isoamyl alcohol (24:1)

was added to each sample. Samples were gently mixed on a rocking table for 2 minutes and spun at 12,000 G for 10 minutes. The supernatant (aqueous phase) was extracted and reserved in a new tube. An equal volume of chloroform:isoamyl alcohol (24:1) was added to the samples, which were gently rocked for 2 minutes then spun at 12,000 G for 5 minutes. The aqueous phase was retained in a new tube, to which an equal volume of 100 % isopropanol was added. Samples were inverted a few times, then placed at room temperature for 30 minutes and spun at 12,000 G for 20 minutes. The liquid phase was decanted and 500 µl of 70 % ethanol was added to each pellet. Samples were inverted a few times and spun at 12,000 G for 5 minutes. The liquid phase was decanted and the pellet allowed to air dry before 50 µl of a 0.1X TE (Tris/EDTA) buffer was added. Samples were stored at -20 °C until required.

2.5 PCR and Sequencing

For each isolate, the ITS rRNA gene region was amplified from an aliquot of the DNA extraction samples using ITS1 (TCCGTAGGTGAACCTGCGG) and ITS4 (TCCTCCGCTTATTGATATGC) primers (White et al. 1990). The reaction mixture had a total volume of 30 µl, and was comprised of a 1X New England BioLabs Buffer (including 2 mM MgCl₂), 208 µM dNTPs, 0.00833 % bovine serum albumin, 250 pM ITS1, 250 pM ITS4, and included 1U New England BioLabs *Taq polymerase*. 1µl of DNA extraction product was used for each PCR reaction and is included in the total volume of 30 µl. A touchdown PCR was carried out and the amplification conditions were as follows: preliminary denaturation at 94 °C for 5 minutes, followed by five cycles of denaturation at 94 °C for 1 minute, annealing at 55 °C for 45 seconds and extension at 72 °C for 1 minute. The annealing temperature was decreased by 1 °C every cycle. This was followed by a further 28 cycles with denaturation at

94 °C for 1 minute, annealing at 50 °C for 45 seconds and extension at 72 °C for 1 minute. Final extension was at 72 °C for 5 minutes. An aliquot of each PCR product (4 µl) was electrophoresed on a 1 % agarose gel made with 0.5X TBE (Tris/Borate/EDTA) in a buffer of 0.5X TBE. The gel was stained in an ethidium bromide solution for 15 minutes and viewed under ultraviolet light to ensure that the PCR products were of the expected size and that the DNA was of sufficient quantity for sequencing. The remainder of the successful PCR products (volume ~26 µl) were purified by adding 0.5 µl of ExoSAP-IT to each sample and incubating as per manufacturer's instructions (15 minutes at 37 °C followed by 15 minutes at 80 °C for inactivation (Affymetrix)). PCR products were sequenced commercially by Macrogen Inc.

2.6 Data Analysis

ITS sequences from yeast isolates were imported into Geneious version 5.4.5 (Drummond et al. 2011). The ITS1 and ITS4 sequence for each isolate were assembled into a contig (a consensus sequence created with overlapping DNA segments) using default settings. For isolates that did not form a contig or formed one with little overlap, the sequence with the best quality and length was chosen for further analysis (this was always the sequence from the ITS4 primer side). The few ITS sequences that were very short or had poor quality were removed from this investigation. ITS sequences were manually checked by eye for errors, and any ambiguities were replaced with the correct nucleotide if it was possible to do so with confidence. The ends of the ITS sequences were manually trimmed to remove primers and regions of poor quality sequence as required; most sequences had poor quality ends that did not contain the full primer sequence so required removal of primer fragments. The lengths of

ITS sequences that formed contigs (after removal of primers and poor quality sequences) were generally in agreement with corresponding PCR product lengths from agarose gel electrophoresis and expected ITS lengths from the literature (CBS-KNAW 2012; MycoBank 2012). ITS sequences were exported in FASTA format in order to carry out database searches.

Each edited ITS sequence was queried against the National Center for Biotechnology Information sequence database: GenBank (Benson et al. 2005). The Basic Local Alignment Search Tool (BLAST) was used, with selection of the Nucleotide collection (nr/nt) and Megablast (optimised for highly similar sequences) (Altschul et al. 1990). For each sequence queried, the BLAST result with the highest identity plus four additional high identity sequences (from different sources if possible) were selected and recorded from GenBank in order of their appearance (data not shown). Parameters such as E-values were also recorded. Selected ITS sequences from GenBank and the literature were imported into Geneious for further analysis, and divided into groups representing four subphyla: Pezizomycotina, Saccharomycotina (both from the Ascomycota), Agaricomycotina and Pucciniomycotina (both from the Basidiomycota). Yeasts isolated during this investigation were assigned to the subphylum they shared the highest ITS sequence similarity with. ITS sequence alignments were created for each subphylum using the standard Geneious alignment procedure (Drummond et al. 2011). The option of global alignment with free end gaps and associated default settings were used. Alignments were checked and edited for accuracy manually and the ends trimmed where appropriate. Neighbour-joining phylogenetic trees were constructed using the Tamura-Nei genetic distance model (Tamura and Nei 1993). Bootstrap values were obtained via resampling with default bootstrap settings and 100 replicates.

3. Results

3.1 Collection Data

3.1.1 Algal Collections

Four algal collections were carried out during this investigation (Table 1). Collection 1 was from Tarakena Bay on 18/12/09 where the sea surface temperature was 14.8 °C. Collections 2 and 3 were from Waitaha Cove. Collection 2 was on 29/01/10 where the sea surface temperature was 14.0 °C and Collection 3 was on 25/02/10 where the sea surface temperature was 17.9 °C. Collection 4 was from Onehunga Bay on 19/03/10 where the sea surface temperature was 16.2 °C. A range of different algal species from Rhodophyta, Chlorophyta and Phaeophyceae were sampled during these collections. The algal species sampled and the total number of yeasts isolated from each alga was variable between collections.

3.1.2 Inoculation Plates

Marine yeasts were isolated from algal samples as described above. After inoculation from algae and one week of incubation at 18 °C, agar plates displayed an assortment of yeasts and filamentous fungal colonies (Fig. 2). Yeast colonies were selected for isolation and subcultured as described above. The control plate, which was treated with a sterile swab and sterile seawater, yielded no visible colonies.

Table 1. Particulars regarding algae sampled in the Wellington Region.

Algal Code	Algal Group	Algal Species	Number of Algal Samples Collected	Number of Individual Yeasts Isolated
Collection 1: 18/12/09 from Tarakena Bay (14.8 °C)				
B	Rhodophyta	<i>Pachymenia lusoria</i>	5	1
C		<i>Cladhymenia oblongifolia</i>	5	1
D	Chlorophyta	<i>Ulva sp.</i>	5	1
E	Phaeophyceae	<i>Macrocystis pyrifera</i>	5	3
F		<i>Carpophyllum maschalocarpum</i>	5	0
Collection 2: 29/01/10 from Waitaha Cove (14.0 °C)				
H	Rhodophyta	<i>Psaromenia berggernii</i>	10	4
I		<i>Champia novae-zelandiae</i>	10	6
J	Chlorophyta	<i>Codium convolutum</i>	10	5
KK		<i>Caulerpa brownii</i>	10	3
L	Phaeophyceae	<i>Cystophora scalaris</i>	10	7
M		<i>Macrocystis pyrifera</i>	10	2
Collection 3: 25/02/10 from Waitaha Cove (17.9 °C)				
N	Chlorophyta	<i>Caulerpa brownii</i>	5	8
O		<i>Codium convolutum</i>	5	8
P	Phaeophyceae	<i>Macrocystis pyrifera</i>	5	7
Q		<i>Cystophora scalaris</i>	5	7
R	Rhodophyta	<i>Champia novae-zelandiae</i>	5	6
S		<i>Psaromenia berggernii</i>	5	6
Collection 4: 19/03/10 from Onehunga Bay (16.2 °C)				
T	Phaeophyceae	<i>Macrocystis pyrifera</i>	5	3
U		<i>Cystophora scalaris</i>	5	4
V	Rhodophyta	<i>Cladhymenia oblongifolia</i>	5	4
W		<i>Pachymenia lusoria</i>	5	1
X2		<i>Psaromenia berggernii</i>	1	1
Y	Chlorophyta	<i>Codium convolutum</i>	5	3
Z		<i>Caulerpa brownii</i>	5	3

Figure 2. Photographs illustrating the appearance of agar plates, after inoculation with yeasts from algae and one week of incubation at 18 °C. These agar plates have been created to reflect the appearance of original isolation plates, which were not photographed. The recreated agar plates were inoculated with yeasts from a fresh algal sample using the same isolation techniques, media, antibiotics and incubation conditions employed during this investigation. Plate A was inoculated with a sterile swab and sterile seawater only, as a control. Plates B, C and D display small cream coloured yeast colonies, and large filamentous fungal colonies coloured black, white and green.

3.1.3 Yeast Isolation

During this investigation, 106 individual yeasts were selected for isolation from original algal-inoculated agar plates. Ninety-four of these yeasts were successfully isolated and found to be pure via the methods described above. ITS PCR products from 86 yeast isolates were sent away for sequencing.

3.2 Isolate Identification

3.2.1 ITS Sequences

ITS PCR products from 86 of 94 successfully isolated yeasts were sent away for sequencing. ITS sequences from 12 of these isolates were omitted due to poor quality sequence data. The remaining 74 isolates yielded ITS sequences of sufficient quality for yeast identification to at least the genus level and sometimes to the species level (Table 2). Based on their similarity with ITS sequences obtained from GenBank, good quality ITS sequences could be confidently separated into four subphyla: Pezizomycotina, Saccharomycotina, Agaricomycotina and Pucciniomycotina. ITS sequences from three isolates in the subphylum Pezizomycotina were obtained, all of which were of good quality and formed contigs ranging from 526 to 541 bp in length. ITS sequences from 50 isolates in the subphylum Saccharomycotina were obtained, but only one contig was generated (383 bp). ITS sequences from the remaining 49 Saccharomycotina isolates did not form contigs; since they were of better quality than sequences from the ITS1 primer side, partial sequences from the ITS4

primer side (159 to 247 bp) were used during further analysis. ITS sequences from 12 isolates in the subphylum Agaricomycotina were obtained, all of which were of good quality and formed contigs ranging from 421 to 603 bp in length. Similarly, ITS sequences from nine isolates in the subphylum Pucciniomycotina were obtained, all of which were of good quality and formed contigs ranging from 539 to 599 bp in length.

3.2.2 GenBank

A BLAST search queried good quality ITS sequences from 74 isolates against the sequence database GenBank, and most sequences yielded BLAST results with high sequence identity (97 - 100 %) (Table 2). For some ITS sequences, the BLAST result with the highest sequence identity was from a named species, allowing confident identification of the corresponding isolate based on GenBank search results alone. However, further information was required as GenBank results did not enable confident identification of all isolates.

3.2.3 Phylogenetic Analysis

Phylogenetic analysis was carried out using ITS sequences from yeasts isolated during this investigation and selected ITS sequences from GenBank search results. For each isolate with good quality ITS sequence data, a comparison was made between GenBank search results and the closest neighbouring organism from phylogenetic trees (Table 2). For isolates from the Basidiomycota, phylogenetic trees demonstrated good species separation; phylogenetic trees containing Agaricomycotina or Pucciniomycotina isolates were generally in agreement with

results from GenBank searches, providing confident isolate identification. Most isolates from the Ascomycota were in the subphylum Saccharomycotina and did not demonstrate good species separation in phylogenetic trees; phylogenetic trees could not confirm GenBank search results or identify many Saccharomycotina isolates further than the genus level.

3.2.4 Culture Studies

Although sequence data were the main source of information for isolate identification, observations made during culture studies were useful for confirmation of these results. A range of features including colony colour and surface appearance, plus microscopic size and shape were recorded. Observations made during this investigation were compared to descriptions of yeast species from the literature, particularly from fungal databases MycoBank (MycoBank 2012) and Centraalbureau voor Schimmelcultures (CBS-KNAW 2012). For most isolates, features observed during this investigation and descriptions from the literature were in agreement with initial isolate identifications made based on ITS sequence data.

Table 2. Isolate identification based on GenBank search results and phylogenetic analysis using ITS sequence data.

Isolate Code	Isolate Sequence Type	Highest Identity Sequence from GenBank				Closest Neighbouring Organism from Phylogenetic Tree	Assigned Organism
		Organism Name	Accession Number	E-Value	Identity (%)		
Pezizomycotina							
L10S-PDA	Contig (537 bp)	Uncultured Dothioraceae	FM178237	0	100	<i>Aureobasidium pullulans</i>	<i>Aureobasidium pullulans</i>
P5S-PDA	Contig (541 bp)	Uncultured Dothioraceae	FM178237	0	100	<i>Aureobasidium pullulans</i>	<i>Aureobasidium pullulans</i>
N2M-PDA	Contig (526 bp)	Uncultured Dothioraceae	FM178237	0	100	<i>Aureobasidium pullulans</i>	<i>Aureobasidium pullulans</i>
Saccharomycotina							
D5S-STD	Partial ITS Sequence (224 bp)	<i>Metschnikowia bicuspidata</i>	U51436	2.00E-104	97	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
E1M-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	9.00E-113	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
H8-PDA	Partial ITS Sequence (237 bp)	<i>Metschnikowia zobellii</i>	U51433	5.00E-96	91	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
H10-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	2.00E-114	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
I1S-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E-112	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
I2-STD	Partial ITS Sequence (238 bp)	<i>Metschnikowia zobellii</i>	U51433	2.00E-120	100	Unresolved via Phylogenetic Tree	<i>Metschnikowia sp.</i>
I3-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	7.00E-114	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
I6-STD	Partial ITS Sequence (240 bp)	<i>Metschnikowia zobellii</i>	U51433	3.00E-113	97	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
J1S-PDA	Partial ITS Sequence (237 bp)	<i>Metschnikowia zobellii</i>	U51433	8.00E-114	97	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>

J3S-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	1.00E -116	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
J5S-PDA	Partial ITS Sequence (165 bp)	<i>Metschnikowia reukaufii</i>	HQ221884	5.00E -79	99	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
J8S-STD	Partial ITS Sequence (238 bp)	<i>Metschnikowia zobellii</i>	U51433	6.00E -100	93	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
KK5S-STD	Partial ITS Sequence (215 bp)	<i>Metschnikowia bicuspidata</i>	U51436	5.00E -105	100	<i>Metschnikowia bicuspidata</i> (Possibly var. <i>bicuspidata</i> or var. <i>chathamia</i>)	<i>Metschnikowia sp.</i>
KK8S-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -112	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
L2S-2-PDA	Partial ITS Sequence (185 bp)	<i>Metschnikowia bicuspidata</i>	EF643581	8.00E -88	98	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
L10S-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -113	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
M7-STD	Partial ITS Sequence (230 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -108	98	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
N1M-PDA	Partial ITS Sequence (211 bp)	<i>Metschnikowia bicuspidata</i>	EF643581	3.00E -102	99	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
N2M-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	2.00E -103	100	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
N4M-STD	Partial ITS Sequence (159 bp)	<i>Metschnikowia reukaufii</i>	HQ221884	5.00E -74	98	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
N5M-PDA	Partial ITS Sequence (229 bp)	<i>Metschnikowia bicuspidata</i>	EF643581	6.00E -110	97	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
N5M-STD	Partial ITS Sequence (245 bp)	<i>Metschnikowia zobellii</i>	U51433	1.00E -112	99	<i>Metschnikowia zobellii</i>	<i>Metschnikowia zobellii</i>
O1M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	2.00E -114	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
O1M-STD	Partial ITS Sequence (210 bp)	<i>Metschnikowia bicuspidata</i>	U51436	9.00E -103	99	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>

O3M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -113	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
O5M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	7.00E -114	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
O5M-STD	Partial ITS Sequence (244 bp)	<i>Metschnikowia zobellii</i>	U51433	6.00E -95	89	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
O5S-PDA	Partial ITS Sequence (210 bp)	<i>Metschnikowia bicuspidata</i>	U51436	1.00E -101	99	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
O5S-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -112	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
P1M-2-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	2.00E -114	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
P3S-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -112	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
Q1M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	2.00E -104	100	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
Q1M-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -113	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
Q2M-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	7.00E -114	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
Q4S-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -113	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
Q5S-(1)-PDA	Partial ITS Sequence (245 bp)	<i>Metschnikowia zobellii</i>	U51433	1.00E -91	89	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
R1M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	EF643581	2.00E -88	100	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
R2M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	7.00E -114	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
R2S-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	4.00E -106	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
R4M-STD	Partial ITS Sequence (247 bp)	<i>Metschnikowia zobellii</i>	U51433	3.00E -118	97	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>

R5M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	9.00E -113	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
S1M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	4.00E -111	99	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
S1M-STD	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	5.00E -105	100	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
S2S-PDA	Contig (383 bp)	<i>Metschnikowia zobellii</i>	U51433	9.00E -170	98	<i>Metschnikowia zobellii</i>	<i>Metschnikowia zobellii</i>
S3M-PDA	Partial ITS ^x Sequence (218 bp)	<i>Metschnikowia bicuspidata</i>	U51436	1.00E -101	100	<i>Metschnikowia bicuspidata</i>	<i>Metschnikowia sp.</i>
S5S-PDA	Partial ITS Sequence (223 bp)	<i>Metschnikowia bicuspidata</i>	U51436	3.00E -108	98	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
U3S-1-STD	Partial ITS Sequence (203 bp)	<i>Metschnikowia bicuspidata</i>	U51436	8.00E -98	99	<i>Metschnikowia bicuspidata</i> (Possibly var. <i>bicuspidata</i> or var. <i>chathamia</i>)	<i>Metschnikowia sp.</i>
U5S-PDA	Partial ITS Sequence (225 bp)	<i>Metschnikowia bicuspidata</i>	U51436	6.00E -110	99	<i>Metschnikowia bicuspidata</i> (Possibly var. <i>bicuspidata</i> or var. <i>chathamia</i>)	<i>Metschnikowia sp.</i>
X21S-STD	Partial ITS Sequence (227 bp)	<i>Metschnikowia zobellii</i>	U51433	3.00E -98	93	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
Y2S-STD	Partial ITS Sequence (237 bp)	<i>Metschnikowia zobellii</i>	U51433	8.00E -104	94	Omitted from Phylogenetic Tree due to Poor Quality	<i>Metschnikowia sp.</i>
Agaricomycotina							
V5M-PDA	Contig (507 bp)	<i>Bullera unica</i>	AF444441	0	100	<i>Bullera unica</i>	<i>Bullera unica</i>
Z2S-STD	Contig (473 bp)	<i>Cryptococcus sp.</i>	HM849618	0	100	Uncultured Fungus AM901777 (Second Closest Organism was <i>Cryptococcus carnescentis</i>)	<i>Cryptococcus carnescentis</i>
U3S-PDA	Contig (603 bp)	<i>Cryptococcus chernovii</i>	AF444354	0	99	Uncultured Fungus AJ875389 (Second Closest Organism was <i>Cryptococcus chernovii</i>)	<i>Cryptococcus chernovii</i>

Y5S-PDA	Contig (460 bp)	Uncultured Basidiomycete	AM901805	0	100	Uncultured Fungus AM901805 (Second Closest Organism was <i>Cryptococcus dimennae</i>)	<i>Cryptococcus dimennae</i>
T1S-3-PDA	Contig (421 bp)	Uncultured Basidiomycete	AM901805	0	100	Uncultured Fungus AM901805 (Second Closest Organism was <i>Cryptococcus dimennae</i>)	<i>Cryptococcus dimennae</i>
Z4S-1-STD	Contig (455 bp)	Uncultured Basidiomycete	AM901805	0	99	Uncultured Fungus AM901805 (Second Closest Organism was <i>Cryptococcus dimennae</i>)	<i>Cryptococcus dimennae</i>
P4M-STD	Contig (582 bp)	Uncultured Fungus	AB520402	0	100	<i>Cryptococcus macerans</i>	<i>Cryptococcus macerans</i>
T1S-1-PDA	Contig (582 bp)	<i>Cystofilobasidium macerans</i> (A Teleomorph of <i>Cryptococcus macerans</i>)	AF444317	0	100	<i>Cryptococcus macerans</i>	<i>Cryptococcus macerans</i>
S4S-PDA	Contig (481 bp)	<i>Cryptococcus victoriae</i>	AY040654	0	100	<i>Cryptococcus victoriae</i>	<i>Cryptococcus victoriae</i>
W5S-4-STD	Contig (480 bp)	<i>Cryptococcus sp.</i>	HM589279	0	100	<i>Cryptococcus sp.</i> (Second Closest Organism was <i>Cryptococcus victoriae</i>)	<i>Cryptococcus victoriae</i>
L2S-1-PDA	Contig (481 bp)	<i>Cryptococcus sp.</i>	HM589279	0	100	<i>Cryptococcus sp.</i> (Second Closest Organism was <i>Cryptococcus victoriae</i>)	<i>Cryptococcus victoriae</i>
Y2M-PDA	Contig (460 bp)	Uncultured Basidiomycete	AM901805	0	100	Unresolved via Phylogenetic tree	<i>Cryptococcus sp.</i>
Pucciniomycotina							
H10S-PDA	Contig (599 bp)	<i>Kondoa aeria</i>	AF444595	0	99	<i>Kondoa aeria</i>	<i>Kondoa aeria</i>
B4M-STD	Contig (542 bp)	<i>Rhodotorula minuta</i>	AB078501	0	100	<i>Rhodotorula minuta</i>	<i>Rhodotorula minuta</i>

E3M-STD	Contig (576 bp)	<i>Rhodotorula mucilaginosa</i>	HQ702343	0	100	<i>Rhodotorula mucilaginosa</i>	<i>Rhodotorula mucilaginosa</i>
E5S-PDA	Contig (571 bp)	<i>Rhodotorula mucilaginosa</i>	EU871492	0	99	<i>Rhodotorula mucilaginosa</i>	<i>Rhodotorula mucilaginosa</i>
Q5S-2-PDA	Contig (572 bp)	<i>Rhodotorula mucilaginosa</i>	HQ702343	0	100	<i>Rhodotorula mucilaginosa</i>	<i>Rhodotorula mucilaginosa</i>
I1-STD	Contig (543 bp)	<i>Rhodotorula slooffiae</i>	AB025994	0	99	<i>Rhodotorula slooffiae</i>	<i>Rhodotorula slooffiae</i>
J3S-STD	Contig (543 bp)	<i>Rhodotorula slooffiae</i>	AF444589	0	100	<i>Rhodotorula slooffiae</i>	<i>Rhodotorula slooffiae</i>
P2S-PDA	Contig (539 bp)	<i>Rhodotorula sp.</i>	FJ238090	0	99	<i>Rhodotorula sp.</i>	<i>Rhodotorula sp.</i>
Z4S-1-PDA	Contig (564 bp)	<i>Sakaguchia dacryoidea</i>	AF444597	0	98	<i>Sakaguchia dacryoidea</i>	<i>Sakaguchia dacryoidea</i>

X denotes 25 individual and identical partial ITS sequences which had *Metschnikowia bicuspidata* (possible varieties include *Metschnikowia bicuspidata* var. *bicuspidata* and *Metschnikowia bicuspidata* var. *chathamia*) as their closest phylogenetic neighbour.

3.3 Ascomycota

3.3.1 Isolates Identified

A total of 53 isolates were identified from the Ascomycota. Three isolates were identified as *Aureobasidium pullulans* (De Bary) G. Arnaud ex Cif., Ribaldi & Corte in the subphylum Pezizomycotina. Fifty isolates were identified from the genus *Metschnikowia* in the subphylum Saccharomycotina.

3.3.2 Pezizomycotina

3.3.2.1 Identification via Molecular Techniques

Three isolates were identified as the yeast-like fungus *Aureobasidium pullulans* in the subphylum Pezizomycotina (Table 2). ITS sequences obtained from Pezizomycotina isolates were of good quality and formed contigs ranging from 526 to 541 bp in length. The ITS contig from each isolate was queried against GenBank and all three gave excellent sequence identity (100 %) to an Uncultured Dothioraceae (FM178237), *Aureobasidium pullulans* (HM992505, HQ115720 and HM849619) and an Uncultured Fungus (GQ851743). A Geneious alignment also confirmed that all three isolates shared a pairwise identity of 100 % with the above ITS sequences, so

construction of a phylogenetic tree was unnecessary (Appendix 5.3). Results from GenBank searches and the Geneious alignment were in agreement, allowing confident identification of all three isolates as *Aureobasidium pullulans*.

3.3.2.2 Morphological Observations

All three isolates from the Pezizomycotina had circular, peach coloured colonies with a slightly raised shiny surface and a filamentous margin (Fig. 3 and Table 3). Microscopically, the cells of all three isolates were cylindrical and two isolates displayed clustering or formation of chains of cells (as indicated in Fig. 3). Isolates from the Pezizomycotina had the largest cells in this investigation, ranging from 9.8 to 11.8 μm , with an average of 10.7 μm (Table 3). Descriptions of *Aureobasidium pullulans* from the literature were generally in agreement with observations made during this investigation, thus, data from culture studies support the identification of these isolates (CBS-KNAW 2012; MycoBank 2012). Although not technically a yeast, the yeast-like appearance of *Aureobasidium pullulans* (Zalar et al. 2008) may be responsible for its isolation during this investigation.

Table 3. Morphology of Pezizomycotina isolates.

Assigned Organism	Isolate Code	Alga of Origin	Colony Colour	Colony Surface	Additional Notes: Colony Appearance	Average Cell Size (µm)	Cell Shape	Additional Notes: Cellular Appearance
<i>Aureobasidium pullulans</i>	L10S-PDA	<i>Cystophora scalaris</i>	Peach	Shiny	Slightly Raised with Filamentous Margin	11.8	Cylindrical	Cluster Formation
<i>Aureobasidium pullulans</i>	N2M-PDA	<i>Caulerpa brownii</i>	Peach	Shiny	Slightly Raised with Filamentous Margin	10.6	Cylindrical	
<i>Aureobasidium pullulans</i>	P5S-PDA	<i>Macrocystis pyrifera</i>	Peach	Shiny	Slightly Raised with Filamentous Margin	9.8	Cylindrical	Cluster Formation

Figure 3. A, B, C: Photographs of colonies formed by Pezizomycotina isolates on agar plates. A=L10S-PDA, B=N2M-PDA, C=P5S-PDA. D, E, F: Corresponding microscopic images of the same Pezizomycotina isolates. D=L10S-PDA, E=N2M-PDA, F=P5S-PDA. All isolates were identified as *Aureobasidium pullulans*.

3.3.3 Saccharomycotina

3.3.3.1 Identification via Molecular Techniques

Fifty isolates were identified from the genus *Metschnikowia* in the subphylum Saccharomycotina (Table 2). A contig (383 bp) was formed by ITS sequences from only one Saccharomycotina isolate. For the remaining 49 isolates, the ITS4 primer side yielded some partial sequences (159 to 247 bp) which were sufficient for use in molecular identification procedures. The partial ITS sequence or contig from each isolate was queried against GenBank and gave good sequence identity (89 – 100 %) to *Metschnikowia bicuspidata*, *Metschnikowia zobellii* or *Metschnikowia reukaufii* (Pitt & M.W. Mill.).

A phylogenetic tree was constructed with ITS sequences from Saccharomycotina isolates plus selected sequences from GenBank and the literature (Fig. 4). Overall, the Saccharomycotina phylogenetic tree did not demonstrate good separation of species. One isolate (I2-STD) was unresolved and identified as *Metschnikowia sp.* An unsupported group contained sequences from isolates obtained during this investigation plus sequences from *Metschnikowia bicuspidata* and its varieties: *Metschnikowia bicuspidata* var. *bicuspidata* and *Metschnikowia bicuspidata* var. *chathamia*. Isolates situated in this unsupported group were X (which represents 25 individual isolates with identical partial ITS sequences), KK5S-STD, U5S-PDA and U3S-1-STD. All isolates in this unsupported group were suspected to be from the species *Metschnikowia bicuspidata* (or possibly one of its varieties: *Metschnikowia bicuspidata* var. *bicuspidata* or

Metschnikowia bicuspidata var. *chathamia*), but were identified as *Metschnikowia* sp. due to the lack of support. Sequences from U5S-PDA and U3S-1-STD formed a supported group by themselves (bootstrap support 88 %). Only two isolates in the Saccharomycotina phylogenetic tree were resolved to a species level: S2S-PDA and N5M-STD formed a well-supported group (bootstrap support 98 %) with two *Metschnikowia zobellii* sequences (U51433 and CBS4821). N5M-STD had a partial ITS sequence of 245 bp and S2S-PDA had an ITS contig of 383 bp. The poor resolution of species in the Saccharomycotina phylogenetic tree did not contradict or support results obtained from GenBank searches.

3.3.3.2 Morphological Observations

All isolates from the Saccharomycotina had circular, cream coloured colonies with an entire margin (Fig. 5 and Table 4). Colony surface was glistening, shiny or heterogeneous (both shiny and matt colony textures were apparent). The majority of colonies appeared to have a slightly raised or convex surface, although some were flat and spread out. The cell morphology of Saccharomycotina isolates was variable; most isolates had an ellipsoidal cell shape, some were elongated ellipsoids (Fig. 6), and many formed clusters or chains of cells (some of which are indicated in Fig. 6). Cell size ranged from 3.8 to 6.0 μm , with an average of 4.8 μm (Table 4). Literary descriptions of yeasts from the *Metschnikowia* were generally in agreement with observations made during this investigation, supporting the identification of these isolates as *Metschnikowia* sp. or *Metschnikowia zobellii* (CBS-KNAW 2012; MycoBank 2012).

3.3.3.3 Isolate Identification Summary

ITS sequence data and supporting morphological observations enabled confident species identification of just two isolates from the Saccharomycotina: both isolates were identified as *Metschnikowia zobellii* (Table 2). The remaining 48 isolates were identified as *Metschnikowia sp.* and included 28 isolates that formed an unsupported phylogenetic group with *Metschnikowia bicuspidata* (all 28 isolates had partial ITS sequences, 25 of which were identical) plus 19 isolates omitted from phylogenetic tree construction due to poor quality partial ITS sequences.

Figure 4. Neighbour-joining phylogenetic tree based on ITS sequences from Saccharomycotina isolates (shown in bold), using the Tamura-Nei model. Bootstrap values are shown for nodes supported by >70 % of 100 replicates. Scale bar represents 0.05 substitutions per site. For simplicity, X represents 25 individual isolates with identical partial ITS sequences.

Table 4. Morphology of Saccharomycotina isolates.

Assigned Organism	Isolate Code	Alga of Origin	Colony Colour	Colony Surface	Additional Notes: Colony Appearance	Average Cell Size (µm)	Cell Shape	Additional Notes: Cellular Appearance
<i>Metschnikowia sp.</i>	D5S-STD	<i>Ulva sp.</i>	Cream	Shiny		4.2	Ellipsoidal	
<i>Metschnikowia sp.</i>	E1M-STD	<i>Macrocystis pyrifera</i>	Cream	Glistening		5.0	Ellipsoidal	Cluster Formation
<i>Metschnikowia sp.</i>	H8-PDA	<i>Psaromenia berggernii</i>	Cream	Shiny	Flat	6.0	Elongate Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	H10-STD	<i>Psaromenia berggernii</i>	Cream	Shiny		4.4	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	I1S-PDA	<i>Champia novae-zelandiae</i>	Cream	Heterogeneous		4.2	Ellipsoidal	
<i>Metschnikowia sp.</i>	I2-STD	<i>Champia novae-zelandiae</i>	Cream	Shiny		4.8	Elongate Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	I3-STD	<i>Champia novae-zelandiae</i>	Cream	Shiny		5.4	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	I6-STD	<i>Champia novae-zelandiae</i>	Cream	Heterogeneous		5.6	Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	J1S-PDA	<i>Codium convolutum</i>	Cream	Heterogeneous	Flat			
<i>Metschnikowia sp.</i>	J3S-PDA	<i>Codium convolutum</i>	Cream	Glistening		4.8	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	J5S-PDA	<i>Codium convolutum</i>	Cream	Glistening		4.0	Ellipsoidal	
<i>Metschnikowia sp.</i>	J8S-STD	<i>Codium convolutum</i>	Cream	Shiny		4.6	Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	KK5S-STD	<i>Caulerpa brownii</i>	Cream			4.2	Ellipsoidal	Possible Clustering

<i>Metschnikowia sp.</i>	KK8S-STD	<i>Caulerpa brownii</i>	Cream	Shiny	Flat	5.4	Ellipsoidal	Cluster Formation
<i>Metschnikowia sp.</i>	L10S-STD	<i>Cystophora scalaris</i>	Cream	Shiny		4.4	Ellipsoidal	Cluster Formation
<i>Metschnikowia sp.</i>	L2S-2-PDA	<i>Cystophora scalaris</i>	Cream	Glistening		4.0	Ellipsoidal	
<i>Metschnikowia sp.</i>	M7-STD	<i>Macrocytis pyrifera</i>	Cream	Glistening		4.6	Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	N1M-PDA	<i>Caulerpa brownii</i>	Cream			4.6	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	N2M-STD	<i>Caulerpa brownii</i>	Cream	Glistening		5.4	Ellipsoidal	
<i>Metschnikowia sp.</i>	N4M-STD	<i>Caulerpa brownii</i>	Cream	Glistening		4.4	Ellipsoidal	Cluster Formation
<i>Metschnikowia sp.</i>	N5M-PDA	<i>Caulerpa brownii</i>	Cream	Shiny		5.6	Ellipsoidal	
<i>Metschnikowia zobellii</i>	N5M-STD	<i>Caulerpa brownii</i>	Cream	Shiny		5.4	Elongate Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	O1M-PDA	<i>Codium convolutum</i>	Cream	Shiny		5.2	Ellipsoidal	Cluster Formation
<i>Metschnikowia sp.</i>	O1M-STD	<i>Codium convolutum</i>	Cream	Shiny		6.0	Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	O3M-PDA	<i>Codium convolutum</i>	Cream	Shiny		4.4	Ellipsoidal	
<i>Metschnikowia sp.</i>	O5M-PDA	<i>Codium convolutum</i>	Cream	Shiny		4.2	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	O5M-STD	<i>Codium convolutum</i>	Cream	Glistening		5.6	Elongate Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	O5S-PDA	<i>Codium convolutum</i>	Cream	Shiny		4.6	Ellipsoidal	
<i>Metschnikowia sp.</i>	O5S-STD	<i>Codium convolutum</i>						

<i>Metschnikowia sp.</i>	P1M-2-PDA	<i>Macrocystis pyrifera</i>	Cream	Heterogeneous		4.2	Ellipsoidal	
<i>Metschnikowia sp.</i>	P3S-STD	<i>Macrocystis pyrifera</i>	Cream			4.6	Ellipsoidal	
<i>Metschnikowia sp.</i>	Q1M-PDA	<i>Cystophora scalaris</i>	Cream	Shiny			Elongate Ellipsoidal	
<i>Metschnikowia sp.</i>	Q1M-STD	<i>Cystophora scalaris</i>	Cream	Heterogeneous		5.6	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	Q2M-STD	<i>Cystophora scalaris</i>	Cream			5.0	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	Q4S-STD	<i>Cystophora scalaris</i>	Cream	Shiny		4.8	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	Q5S-(1)-PDA	<i>Cystophora scalaris</i>	Cream	Heterogeneous	Flat	5.4	Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	R1M-PDA	<i>Champia novae-zelandiae</i>	Cream	Glistening		4.0	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	R2M-PDA	<i>Champia novae-zelandiae</i>	Cream	Shiny		4.4	Ellipsoidal	
<i>Metschnikowia sp.</i>	R2S-PDA	<i>Champia novae-zelandiae</i>	Cream	Shiny		4.6	Ellipsoidal	Cluster Formation
<i>Metschnikowia sp.</i>	R4M-STD	<i>Champia novae-zelandiae</i>	Cream	Glistening		5.2	Elongate Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	R5M-PDA	<i>Champia novae-zelandiae</i>	Cream	Glistening		4.4	Ellipsoidal	
<i>Metschnikowia sp.</i>	S1M-PDA	<i>Psaromenia berggernii</i>	Cream	Glistening		4.6	Ellipsoidal	
<i>Metschnikowia sp.</i>	S1M-STD	<i>Psaromenia berggernii</i>	Cream			3.8	Ellipsoidal	
<i>Metschnikowia zobellii</i>	S2S-PDA	<i>Psaromenia berggernii</i>	Cream	Shiny	Flat	5.4	Elongate Ellipsoidal	Cluster Formation
<i>Metschnikowia sp.</i>	S3M-PDA	<i>Psaromenia berggernii</i>	Cream	Shiny		5.2	Ellipsoidal	Cluster Formation

<i>Metschnikowia sp.</i>	S5S-PDA	<i>Psaromenia berggernii</i>	Cream	Shiny		4.4	Ellipsoidal	
<i>Metschnikowia sp.</i>	U3S-1-STD	<i>Cystophora scalaris</i>	Cream	Glistening		4.4	Ellipsoidal	
<i>Metschnikowia sp.</i>	U5S-PDA	<i>Cystophora scalaris</i>	Cream	Glistening		4.0	Ellipsoidal	Possible Clustering
<i>Metschnikowia sp.</i>	X21S-STD	<i>Psaromenia berggernii</i>	Cream	Glistening		5.0	Elongate Ellipsoidal	Chain Formation
<i>Metschnikowia sp.</i>	Y2S-STD	<i>Codium convolutum</i>	Cream	Heterogeneous		5.0	Elongate Ellipsoidal	Chain Formation

Figure 5. Photographs of colonies formed by Saccharomycotina isolates on agar plates. A=J3S-PDA, B=J5S-PDA, C= L2S-2-PDA, D=O3M-PDA, E=R5M-PDA, F=S2S-PDA, G=D5S-STD, H=I3-STD, I=I6-STD, J=L10S-STD, K=N2M-STD, L=N4M-STD. All isolates were identified as *Metschnikowia sp.*, except for S2S-PDA which was identified as *Metschnikowia zobellii*.

Figure 6. Microscopic images of *Saccharomycotina* isolates. A=J3S-PDA, B=J5S-PDA, C= L2S-2-PDA, D=O3M-PDA, E=R5M-PDA, F=S2S-PDA, G=D5S-STD, H=I3-STD, I=I6-STD, J=L10S-STD, K=N2M-STD, L=N4M-STD. All isolates were identified as *Metschnikowia sp.*, except for S2S-PDA which was identified as *Metschnikowia zobellii*.

3.4 Basidiomycota

3.4.1 Isolates Identified

A total of 21 isolates were identified from the Basidiomycota. Twelve isolates were identified from a range of species in the subphylum Agaricomycotina, and nine isolates were identified from the subphylum Pucciniomycotina.

3.4.2 Agaricomycotina

3.4.2.1 Identification via Molecular Techniques

Twelve isolates were identified from the subphylum Agaricomycotina (Table 2). These were comprised of 11 isolates from the genus *Cryptococcus* and a single isolate of *Bullera unica* (Hamam. & Nakase). ITS sequences obtained from Agaricomycotina isolates were of good quality and formed contigs ranging from 421 to 603 bp in length. The ITS contig from each isolate was queried against GenBank and gave excellent sequence identity (99 – 100 %) to a named *Cryptococcus* species, *Cryptococcus sp.*, *Bullera unica* or an uncultured fungus. Contigs without a named species as their primary GenBank result typically demonstrated excellent sequence identity (99 – 100 %) to another named *Cryptococcus* species.

A phylogenetic tree was constructed with ITS sequences from Agaricomycotina isolates plus selected sequences from GenBank and the literature (Fig. 7). Overall, the Agaricomycotina phylogenetic tree demonstrated good separation of ITS sequences from named species and Agaricomycotina isolates into distinct clades. Sequences from uncultured fungi were also distributed within these clades and are not mentioned further as they did not contribute to isolate identification. One isolate (V5M-PDA) was in a well-supported clade with, and identified as, *Bullera unica* (bootstrap support 89 %). Two isolates (P4M-STD and T1S-1-PDA) in a well-supported clade with *Cryptococcus macerans* (Frederiksen) Phaff & Fell and *Cystofilobasidium macerans* (a teleomorph of *Cryptococcus macerans*) (bootstrap support 100 %) were identified as *Cryptococcus macerans*. Due to their position in a well-supported clade with the species, three isolates (T1S-3-PDA, Y5S-PDA and Z4S-1-STD) were identified as *Cryptococcus dimennae* Fell & Phaff (bootstrap support 100 %). A further three isolates (L2S-1-PDA, W5S-4-STD and S4S-PDA) were in a well-supported clade with, and identified as, *Cryptococcus victoriae* (M.J. Montes et al.) (bootstrap support 99 %). Although it was in an unsupported clade, one isolate (Z2S-STD) was identified as *Cryptococcus carnescens* (Verona & Luchetti) Takash., Sugita, Shinoda & Nakase. Finally, a well-supported clade (bootstrap support 100 %) consisted of an unsupported and a moderately supported group of sequences. The unsupported group contained sequences from *Cryptococcus magnus* (Lodder & Kreger-van Rij) Baptist & Kurtzman, *Cryptococcus oeirensis* Á. Fonseca, Scorzetti & Fell, and one isolate (Y2M-PDA) which was in an unresolved position and identified as *Cryptococcus sp.* The moderately supported group (bootstrap support 79 %) was comprised of two well-supported clades (bootstrap support 100 % for both clades): one clade contained sequences from *Cryptococcus chernovii* Á. Fonseca,

Scorzetti & Fell, and the other clade contained sequences from uncultured fungi plus an isolate (U3S-PDA) identified as *Cryptococcus chernovii*. Overall, the Agaricomycotina phylogenetic tree displayed good resolution of isolates to a species level, with the exception of one isolate (Y2M-PDA) which was identified as *Cryptococcus sp.* Results from this phylogenetic tree were in agreement with those obtained from GenBank searches, and the combination of these two methods allowed confident identification of isolates from the Agaricomycotina.

3.4.2.2 Morphological Observations

All isolates from the Agaricomycotina had circular colonies with an entire margin (Fig. 8 and Table 5). Colonies were shiny or glistening and displayed a range of colours including cream, peach and bright pink. Colony elevation was slightly raised or convex, except for one isolate identified as *Cryptococcus macerans* which was umbonate (T1S-1-PDA) (B in Fig. 8). The cell morphology of Agaricomycotina isolates was variable; most isolates had an ellipsoidal cell shape, although a small number had elongated ellipsoidal cells (Fig. 9). A couple of isolates displayed what appeared to be a clustering of cells, but distinct chains of cells were not observed (as indicated in Fig. 9). Cell size ranged from 4.2 to 7.8 μm , with an average of 5.3 μm (Table 5). Literary descriptions of yeasts from the Agaricomycotina were generally in agreement with observations made during this investigation, thus, data from culture studies support the identification of these isolates (CBS-KNAW 2012; MycoBank 2012).

Figure 7. Neighbour-joining phylogenetic tree based on ITS sequences from Agaricomycotina isolates (shown in bold), using the Tamura-Nei model. Bootstrap values are shown for nodes supported by >70 % of 100 replicates. Scale bar represents 0.05 substitutions per site. The outgroup contains ITS sequences from the genus *Rhodotorula*.

Table 5. Morphology of Agaricomycotina isolates.

Assigned Organism	Isolate Code	Alga of Origin	Colony Colour	Colony Surface	Additional Notes: Colony Appearance	Average Cell Size (µm)	Cell Shape	Additional Notes: Cellular Appearance
<i>Bullera unica</i>	V5M-PDA	<i>Cladhymenia oblongifolia</i>	Peach	Shiny		5.0	Ellipsoidal	
<i>Cryptococcus carnescens</i>	Z2S-STD	<i>Caulerpa brownii</i>	Peach	Glistening		4.4	Ellipsoidal	
<i>Cryptococcus chernovii</i>	U3S-PDA	<i>Cystophora scalaris</i>	Cream			5.2	Ellipsoidal	
<i>Cryptococcus dimennae</i>	T1S-3-PDA	<i>Macrocystis pyrifera</i>	Peach	Shiny		4.2	Ellipsoidal	
<i>Cryptococcus dimennae</i>	Y5S-PDA	<i>Codium convolutum</i>	Peach	Shiny		4.4	Ellipsoidal	
<i>Cryptococcus dimennae</i>	Z4S-1-STD	<i>Caulerpa brownii</i>	Peach	Glistening		5.0	Ellipsoidal	Possible Clustering
<i>Cryptococcus macerans</i>	P4M-STD	<i>Macrocystis pyrifera</i>	Bright Pink			7.8	Elongate Ellipsoidal	
<i>Cryptococcus macerans</i>	T1S-1-PDA	<i>Macrocystis pyrifera</i>	Bright Pink	Shiny	Umbonate	7.6	Elongate Ellipsoidal	
<i>Cryptococcus sp.</i>	Y2M-PDA	<i>Codium convolutum</i>	Peach	Glistening		5.4	Elongate Ellipsoidal	
<i>Cryptococcus victoriae</i>	L2S-1-PDA	<i>Cystophora scalaris</i>	Cream	Shiny		5.0	Ellipsoidal	
<i>Cryptococcus victoriae</i>	S4S-PDA	<i>Psaromenia berggernii</i>	Cream	Shiny		4.6	Ellipsoidal	Possible Clustering
<i>Cryptococcus victoriae</i>	W5S-4-STD	<i>Pachymenia lusoria</i>	Peach	Shiny		4.6	Elongate Ellipsoidal	Possible Clustering

Figure 8. Photographs of colonies formed by Agaricomycotina isolates on agar plates. A=Z2S-STD (*Cryptococcus carnescentis*), B=T1S-1-PDA (*Cryptococcus macerans*), C=Y2M-PDA (*Cryptococcus sp.*), D=T1S-3-PDA, E=Y5S-PDA, F=Z4S-1-STD (D, E, F all *Cryptococcus dimennae*), G=L2S-1-PDA, H=S4S-PDA, I=W5S-4-STD (G, H, I all *Cryptococcus victoriae*), J=V5M-PDA (*Bullera unica*).

Figure 9. Microscopic images of Agaricomycotina isolates. A=Z2S-STD (*Cryptococcus carnescentis*), B=T1S-1-PDA (*Cryptococcus macerans*), C=P4M-STD (*Cryptococcus macerans*), D=T1S-3-PDA, E=Y5S-PDA, F=Z4S-1-STD (D, E, F all *Cryptococcus dimennae*), G=L2S-1-PDA, H=S4S-PDA, I=W5S-4-STD (G, H, I all *Cryptococcus victoriae*), J=U3S-PDA (*Cryptococcus chernovii*), K=Y2M-PDA (*Cryptococcus sp.*), L=V5M-PDA (*Bullera unica*).

3.4.3 Pucciniomycotina

3.4.3.1 Identification via Molecular Techniques

Twelve isolates were identified from the subphylum Pucciniomycotina (Table 2). These were comprised of seven isolates from the genus *Rhodotorula* and one isolate from each of the species *Sakaguchia dacryoidea* (Fell, I.L. Hunter & Tallman) Y. Yamada, K. Maeda & Mikata and *Kondoa aeria* Á. Fonseca, Samp. & Fell. ITS sequences obtained from Pucciniomycotina isolates were of good quality and formed contigs ranging from 539 to 599 bp in length. The ITS contig from each isolate was queried against GenBank and gave excellent sequence identity (98 – 100 %) to a named *Rhodotorula* species, *Rhodotorula* sp., *Kondoa aeria* or *Sakaguchia dacryoidea*.

A phylogenetic tree was constructed with ITS sequences from Pucciniomycotina isolates plus selected sequences from GenBank and the literature (Fig. 10). Overall, the Pucciniomycotina phylogenetic tree separated ITS sequences from named species and Pucciniomycotina isolates into distinct clades with good fidelity. Sequences from uncultured fungi were also distributed within these clades and are not mentioned further as they did not contribute to isolate identification. One isolate (H10S-PDA) was situated in a well-supported clade with, and identified as, *Kondoa aeria* (bootstrap support 100 %). Due to their position in a well-supported clade with the species, three isolates (E5S-PDA, E3M-STD and Q5S-2-PDA) were identified as *Rhodotorula mucilaginosa* (bootstrap support 100 %). A single isolate (B4M-STD) was in a well-supported clade with, and identified as, *Rhodotorula minuta* (Saito) F.C. Harrison (bootstrap

support 100 %). Two isolates (J3S-STD and I1-STD) were identified as *Rhodotorula slooffiae* E.K. Novák & Vörös-Felkai due to their position in a well-supported clade with this species (bootstrap support 92 %). One isolate (P2S-PDA) was situated in a well-supported clade with, and identified as, *Rhodotorula sp.* (bootstrap support 100 %). Due to its position in a well-supported clade with the species, one isolate (Z4S-1-PDA) was identified as *Sakaguchia dacryoidea* (bootstrap support 82 %). Overall, the Pucciniomycotina phylogenetic tree displayed good resolution of isolates to a species level, with the exception of one isolate (P2S-PDA) which was identified as *Rhodotorula sp.* Results from this phylogenetic tree were in agreement with those obtained from GenBank searches, and the combination of these two methods allowed confident identification of isolates from the Pucciniomycotina.

3.4.3.2 Morphological Observations

All isolates from the Pucciniomycotina had slightly raised or convex circular colonies with an entire margin (Fig. 11 and Table 6). Colonies ranged in colour from peach to bright pink and were shiny or glistening. The cell morphology of Pucciniomycotina isolates was variable; most isolates had an ellipsoidal cell shape, although a small number had elongated cells (A, B & H in Fig. 12). A couple of isolates displayed what appeared to be a clustering of cells, but distinct chains of cells were not observed (as indicated in Fig. 12). Cell size ranged from 4.0 to 5.4 μm , with an average of 4.4 μm (Table 6). Literary descriptions of yeasts from the Pucciniomycotina were generally in agreement with observations made during this investigation, thus, data from culture studies support the identification of these isolates (CBS-KNAW 2012; MycoBank 2012).

Figure 10. Neighbour-joining phylogenetic tree based on ITS sequences from Pucciniomycotina isolates (shown in bold), using the Tamura-Nei model. Bootstrap values are shown for nodes supported by >70 % of 100 replicates. Scale bar represents 0.05 substitutions per site. The outgroup contains ITS sequences from the genus *Cryptococcus*.

Table 6. Morphology of Pucciniomycotina isolates.

Assigned Organism	Isolate Code	Alga of Origin	Colony Colour	Colony Surface	Average Cell Size (µm)	Cell Shape	Additional Notes: Cellular Appearance
<i>Kondoa aerea</i>	H10S-PDA	<i>Psaromenia berggernii</i>	Peach	Glistening	4.0	Elongate Ellipsoidal	
<i>Rhodotorula minuta</i>	B4M-STD	<i>Pachymenia lusoria</i>	Bright Pink	Shiny	4.4	Ellipsoidal	Cluster Formation
<i>Rhodotorula mucilaginosa</i>	E3M-STD	<i>Macrocystis pyrifera</i>	Bright Pink	Shiny	4.6	Ellipsoidal	Cluster Formation
<i>Rhodotorula mucilaginosa</i>	E5S-PDA	<i>Macrocystis pyrifera</i>	Bright Pink	Shiny	4.2	Ellipsoidal	Possible Clustering
<i>Rhodotorula mucilaginosa</i>	Q5S-2-PDA	<i>Cystophora scalaris</i>	Bright Pink	Glistening	4.2	Ellipsoidal	
<i>Rhodotorula slooffiae</i>	I1-STD	<i>Champia novae-zelandiae</i>	Bright Pink	Glistening	4.0	Ellipsoidal	Possible Clustering
<i>Rhodotorula slooffiae</i>	J3S-STD	<i>Codium convolutum</i>	Peach	Glistening	4.4	Elongate Ellipsoidal	
<i>Rhodotorula sp.</i>	P2S-PDA	<i>Macrocystis pyrifera</i>	Peach	Glistening	4.8	Ellipsoidal	
<i>Sakaguchia dacryoidea</i>	Z4S-1-PDA	<i>Caulerpa brownii</i>	Bright Pink	Shiny	5.4	Elongate Ellipsoidal	Possible Clustering

Figure 11. Photographs of colonies formed by Pucciniomycotina isolates on agar plates. A=H10S-PDA (*Kondoa aeria*), B=Z4S-1-PDA (*Sakaguchia dacryoidea*), C=B4M-STD (*Rhodotorula minuta*), D=E3M-STD, E=E5S-PDA, F=Q5S-2-PDA (D, E, F all *Rhodotorula mucilaginosa*), G=I1-STD (*Rhodotorula slooffiae*), H=J3S-STD (*Rhodotorula slooffiae*), I=P2S-PDA (*Rhodotorula* sp.).

Figure 12. Microscopic images of Pucciniomycotina isolates. A=H10S-PDA (*Kondoa aeria*), B=Z4S-1-PDA (*Sakaguchia dacryoidea*), C=B4M-STD (*Rhodotorula minuta*), D=E3M-STD, E=E5S-PDA, F=Q5S-2-PDA (D, E, F all *Rhodotorula mucilaginosa*), G=I1-STD (*Rhodotorula slooffiae*), H=J3S-STD (*Rhodotorula slooffiae*), I=P2S-PDA (*Rhodotorula sp.*).

3.5 Isolate Distribution

3.5.1 Isolate Distribution by Subphylum

3.5.1.1 Pezizomycotina

Yeasts identified as *Aureobasidium pullulans* were isolated on PDA (Table 7) from three algal species (Table 8) sampled during Collections 2 and 3 (Waitaha Cove) (Fig. 13). However, only three *Aureobasidium pullulans* isolates were obtained so no distribution patterns were apparent.

3.5.1.2 Saccharomycotina

Metschnikowia isolates did not demonstrate a preferential association with any particular media (Table 7) or alga (Table 8). Yeasts from the genus *Metschnikowia* occurred frequently and made up over half of the isolates obtained during Collections 2 and 3 (Waitaha Cove) (Fig. 13). *Metschnikowia* isolates made up less than a third of the yeasts obtained during Collections 1 (Tarakena Bay) and 4 (Onehunga Bay), however, it was unclear whether this represented a distribution pattern or was simply due to the low number of yeasts isolated during these collections.

3.5.1.3 Agaricomycotina

No distribution trends could be determined for *Bullera unica* since only one isolate was obtained; V5M-PDA was isolated on PDA from *Cladhymenia oblongifolia* sampled during Collection 4 (Onehunga Bay) (Table 7, Table 8 and Fig. 13). Low numbers of *Cryptococcus* isolates were found on six of the algae sampled and did not demonstrate an obvious association with any particular alga (Table 8). In terms of media, *Cryptococcus* isolates were found more frequently on PDA (7) than STD (4) (Table 7). The number of *Cryptococcus* isolates obtained was variable between collections; no *Cryptococcus* isolates were found during Collection 1 (Tarakena Bay), a small number were obtained during Collections 2 and 3 (Waitaha Cove), and *Cryptococcus* made up 42 % of the yeasts isolated during Collection 4 (Onehunga Bay) (Fig. 13). However, it was unclear whether variation in the number of *Cryptococcus* isolates obtained between collections was representative of a distribution pattern, since only 11 isolates were obtained from this genus.

3.5.1.4 Pucciniomycotina

No distribution trends could be determined for *Sakaguchia dacryoidea* and *Kondoa aeria*, since only one isolate was obtained from each species (Table 7, Table 8 and Fig. 13). *Kondoa aeria* was isolated on PDA from *Psaromenia berggernii* during Collection 2 (Waitaha Cove), and *Sakaguchia dacryoidea* was isolated on PDA from *Caulerpa brownii* during Collection 4 (Onehunga Bay). *Rhodotorula* isolates did not demonstrate a clear preference for any particular media (Table 7). Furthermore, it was unclear whether *Rhodotorula* isolates demonstrated an

association with any particular alga, since isolates were found on *Champia novae-zelandiae*, *Codium convolutum*, *Cystophora scalaris*, *Pachymenia lusoria* and *Macrocystis pyrifera* (Table 8). The number of *Rhodotorula* isolates obtained was highly variable between collections; *Rhodotorula* made up half the isolates from Collection 1 (Tarakena Bay), a small proportion of the isolates from Collections 2 and 3 (Waitaha Cove), and was not detected during Collection 4 (Onehunga Bay) (Fig. 13). However, only seven *Rhodotorula* isolates were obtained during this investigation, an inadequate number to reveal any distribution patterns.

3.5.2 Possible Influences on Isolate Biodiversity

3.5.2.1 Isolation Media

Out of 94 successfully isolated yeasts, 52 were found on PDA and 42 on STD media (Table 7). The isolation frequency of yeasts from the genera *Metschnikowia*, *Cryptococcus* and *Rhodotorula* was similar on both STD and PDA. Yeasts from the genera *Aureobasidium*, *Bullera*, *Kondoa* and *Sakaguchia* were only isolated on PDA, although they occurred infrequently.

3.5.2.2 Algal Host

Ten different algal species were sampled during four collections (Table 8). *Champia novae-zelandiae*, *Cladhymenia oblongifolia* and *Pachymenia lusoria* were sampled during two collections, whereas *Ulva sp.* and *Carpophyllum maschalocarpum* were only sampled during Collection 1. For the purposes of detecting any trends, algae sampled during three or all four collections were considered: *Macrocystis pyrifera*, *Cystophora scalaris*, *Caulerpa brownii*, *Codium convolutum* and *Psaromenia berggernii*. *Champia novae-zelandiae* was also considered as it yielded 12 isolates despite being sampled in just two collections. On average, 4.8 yeasts were isolated from each of the six algae considered per collection, and no alga yielded considerably fewer or more isolates. Fifty isolates were obtained from the genus *Metschnikowia* and the number isolated from each algal species was reasonably constant. The eleven *Cryptococcus* isolates were equally distributed between all algal species considered except for *Champia novae-zelandiae*, and the seven *Rhodotorula* isolates were equally distributed between *Macrocystis pyrifera*, *Cystophora scalaris*, *Codium convolutum* and *Champia novae-zelandiae*. *Caulerpa brownii*, *Cystophora scalaris* and *Macrocystis pyrifera* each yielded a single *Aureobasidium pullulans* isolate. The single *Sakaguchia dacryoidea* isolate was found on *Caulerpa brownii*, and the *Kondoa aerea* isolate was found on *Psaromenia berggernii*. Yeasts were also isolated from infrequently sampled algae; *Cladhymenia oblongifolia* yielded a *Bullera unica* isolate plus four unidentified yeasts, *Pachymenia lusoria* yielded one isolate each from *Cryptococcus* and *Rhodotorula*, and *Ulva sp.* yielded one *Metschnikowia* isolate. Although data were insufficient to draw conclusions regarding infrequently sampled yeasts or algae, yeasts from frequently isolated genera did not demonstrate a clear preference for any particular alga.

3.5.2.3 Location

Differences were observed in the types of yeasts isolated between algal collections (Fig. 13). Around half of the yeasts isolated during Collection 1 (Tarakena Bay on 18/12/09, sea surface temperature of 14.8 °C) were from *Rhodotorula*, a third were from *Metschnikowia* and the rest were unidentified. During Collection 2 (Waitaha Cove on 29/01/10, sea surface temperature of 14 °C), the majority of the isolates were from *Metschnikowia*, a quarter were unidentified, and one or two yeasts were isolated from *Rhodotorula*, *Cryptococcus*, *Kondoa* and *Aureobasidium*. Despite the higher temperature, the yeast species isolated during Collection 3 (Waitaha Cove on 25/02/10, sea surface temperature of 17.9 °C) were very similar to those from Collection 2: the majority of the isolates were from *Metschnikowia*, 16 % were unidentified, and one or two yeasts were isolated from *Rhodotorula*, *Aureobasidium* and *Cryptococcus*. During Collection 4 (Onehunga Bay on 19/03/10, sea surface temperature of 16.2 °C), 42 % of the yeasts isolated were from *Cryptococcus*, around one quarter were unidentified, less than one quarter were from *Metschnikowia*, and one yeast was isolated from each of the following genera: *Bullera* and *Sakaguchia*.

Table 7. Isolation frequency of different yeast genera on two types of media.

Yeast Genus	Number of Colonies on Difco Potato Dextrose Agar Plus (PDA)	Number of Colonies on Difco Standard Marine Agar Plus (STD)
<i>Aureobasidium</i>	3	0
<i>Metschnikowia</i>	24	26
<i>Bullera</i>	1	0
<i>Cryptococcus</i>	7	4
<i>Kondoa</i>	1	0
<i>Sakaguchia</i>	1	0
<i>Rhodotorula</i>	3	4
Unidentified	12	8
Total	52	42

Table 8. Isolation frequency of different yeast genera from ten algal species.

Yeast Genus	<i>Caulerpa brownii</i>	^x <i>Champia novae-zelandiae</i>	^x <i>Cladhymenia oblongifolia</i>	<i>Codium convolutum</i>	<i>Cystophora scalaris</i>	<i>Macrocystis pyrifera</i>	^x <i>Pachymenia lusoria</i>	<i>Psaromenia berggerii</i>	^x <i>Ulva</i> sp.	^x <i>Carpophyllum maschalocarpum</i>
<i>Aureobasidium</i>	1	0	0	0	1	1	0	0	0	0
<i>Metschnikowia</i>	7	9	0	12	9	4	0	8	1	0
<i>Bullera</i>	0	0	1	0	0	0	0	0	0	0
<i>Cryptococcus</i>	2	0	0	2	2	3	1	1	0	0
<i>Kondoa</i>	0	0	0	0	0	0	0	1	0	0
<i>Sakaguchia</i>	1	0	0	0	0	0	0	0	0	0
<i>Rhodotorula</i>	0	1	0	1	1	3	1	0	0	0
Unidentified	3	2	4	1	5	4	0	1	0	0
Total	14	12	5	16	18	15	2	11	1	0

X denotes algae sampled during only one or two collections.

18/12/09 - Collection 1
Tarakena Bay (14.8 °C)
Number of yeasts isolated = 6

29/01/10 - Collection 2
Waitaha Cove (14.0 °C)
Number of yeasts isolated = 27

25/02/2010 - Collection 3
Waitaha Cove (17.9 °C)
Number of yeasts isolated = 42

19/03/2010 - Collection 4
Onehunga Bay (16.2 °C)
Number of yeasts isolated = 19

Figure 13. Pie graphs illustrating the isolation frequency of different yeast genera during four algal collections.

Figure 14. Summary of isolates identified at three taxonomic levels. The number of isolates in each category is given in brackets.

3.6 Summary of Results

During this investigation, 106 yeasts were selected from original inoculation plates, 94 of which were successfully isolated and found to be pure. ITS PCR products from 86 isolates were sent away for sequencing and 74 of these were of sufficient quality for yeast identification. ITS sequence data allowed identification via phylogenetic analysis and GenBank searches. Data regarding colony morphology and the microscopic appearance of cells generally confirmed isolate identity. Out of 74 yeasts identified, 53 isolates were from the Ascomycota and 21 were from the Basidiomycota. Yeasts identified from the Ascomycota were from two subphyla: 50 isolates were identified from the Saccharomycotina and three isolates were from the Pezizomycotina. All three isolates from the Pezizomycotina were confidently identified as the yeast-like fungus *Aureobasidium pullulans*. All 50 isolates from the Saccharomycotina were identified from the genus *Metschnikowia*: two isolates were identified as *Metschnikowia zobellii* but the remaining 48 isolates could not be identified further than the genus level. Isolates from the Basidiomycota were also from two subphyla: 12 isolates were identified from the Agaricomycotina and nine isolates were from the Pucciniomycotina. Yeasts obtained from the Agaricomycotina consisted of a single *Bullera unica* isolate plus 11 isolates from the genus *Cryptococcus* (three isolates each from *Cryptococcus dimennae* and *Cryptococcus victoriae*, two from *Cryptococcus macerans*, one each from *Cryptococcus carnescens* and *Cryptococcus chernovii*, and an unresolved *Cryptococcus* sp.). Yeasts obtained from the Pucciniomycotina consisted of single isolates from *Sakaguchia dacryoidea* and *Kondoa aeria* plus seven isolates from the genus *Rhodotorula* (three isolates from *Rhodotorula mucilaginosa*, two from *Rhodotorula slooffiae*, one from *Rhodotorula minuta* and an unresolved *Rhodotorula* sp.).

4. Discussion

4.1 Observations

There is currently debate as to whether microorganisms are ubiquitous or if they exhibit biogeographic patterns (Martiny et al. 2006). To address these questions of biodiversity, results from this investigation are discussed in light of evidence from the literature. Yeasts isolated during this investigation were from similar genera and demonstrated high ITS sequence similarity with yeasts from diverse substrates and environments worldwide. Similarity observed between the isolates obtained and yeasts from other sources may be suggestive of marine yeast ubiquity at a global level, or as proposed by Baas Becking and Beijerinck's widely accepted tenet, "everything is everywhere, but, the environment selects" (Baas Becking 1934; De Wit and Bouvier 2006).

Although this was the first known investigation of marine yeast biodiversity from waters surrounding New Zealand's main Islands, the species isolated were not unique. Ninety-four yeasts were isolated from algae sampled in the Wellington Region, 74 of which were identified from a variety of previously recognised species in seven genera and four subphyla (Fig. 14). Most isolates belonged to *Metschnikowia*, *Rhodotorula* or *Cryptococcus*, a similar range of genera to those detected from diverse habitats worldwide. *Candida*, *Cryptococcus*, *Rhodotorula* and *Debaryomyces* are regularly detected from various marine environments (Kutty and Philip 2008, plus references therein), such as the deep sea of the Pacific Ocean (Yamasato et al. 1974;

Nagahama 2006) and the fresh, estuarine and marine waters of Florida (Ahearn et al. 1968). Many yeasts isolated during this investigation also demonstrated high identity to previously documented ITS sequences (Table 2); the high level of ITS sequence identity indicates similarity between the isolates obtained and yeasts from diverse marine and terrestrial substrates worldwide. For example, one isolate identified as *Rhodotorula mucilaginosa* (E3M-STD) had 100 % identity to ITS sequences obtained from New Zealand oak trees (unpublished sequence in GenBank, submitted by H. Zhang, R. C. Gardner, A. Skelton and M. R. Goddard) and seawater from the coast of Taiwan (unpublished sequence in GenBank, submitted by C. F. Chang and S. M. Liu). One isolate identified as *Cryptococcus carnescens* (Z2S-STD) had 99 - 100 % identity to ITS sequences from a range of different sources: grapevines (Al Rwahnih et al. 2011), indoor dust (Pitkaranta et al. 2008), plus soils and historic wood from the Ross Sea Region of Antarctica (Arenz et al. 2006).

Yeasts obtained during this investigation also demonstrated high ITS sequence similarity with strains originally isolated from the Chatham Islands. Twelve isolates of *Candida natalensis* and a single *Metschnikowia zobellii* isolate were collected from tidal pools on the Chatham Islands, and six further *Metschnikowia zobellii* isolates were found in a small freshwater lake (Fell and Hunter 1968). Although originally identified by morphological features as *Metschnikowia zobellii*, further morphological investigation and results from mating tests indicated that some isolates from the Chatham Islands should be redesignated as *Metschnikowia bicuspidata* var. *chathamia* (Fell and Pitt 1969). Original type strains of *Metschnikowia bicuspidata* var. *chathamia* from the Chatham Islands now have ITS sequence data available (CBS-KNAW 2012), and some demonstrated high ITS sequence similarity with isolates obtained during this investigation. An

unsupported group in the Saccharomycotina phylogenetic tree contained ITS sequences from strains of *Metschnikowia bicuspidata* var. *chathamia* and yeasts isolated during this investigation (Fig. 4); 25 individual isolates with identical partial ITS sequences shared a pairwise identity of 99.1 % with strain CBS5980 and a pairwise identity of 99.5 % with strain CBS5903.

Results from this investigation and limited evidence from the literature suggest that marine yeasts are ubiquitous at a global level, or as proposed by Baas Becking and Beijerinck's widely accepted tenet, "everything is everywhere, but the environment selects" (Baas Becking 1934; De Wit and Bouvier 2006). The distribution of marine yeasts is recognised as widespread (Van Uden 1960) and they have been detected from various substrates: seawater, sediments, algae, vertebrates and invertebrates (Roth et al. 1962; Kohlmeyer and Kohlmeyer 1979). Marine yeasts have also been observed in diverse habitats including tropical (Zinjarde and Pant 2002), Antarctic (Vishniac 2006) and extreme environments (Raspor and Zupan 2006), the deep sea (Yamasato et al. 1974; Nagahama 2006), and now from waters surrounding New Zealand's main Islands. The South Pacific Ocean has not been extensively sampled for marine yeasts (Kutty and Philip 2008) so the results of this investigation provide a valuable source of information. Data collected during this investigation did not reveal any biogeographic patterns or novel species; the isolates obtained were similar to previously recognised yeasts. Most marine yeasts isolated during this investigation belonged to *Metschnikowia*, *Rhodotorula* or *Cryptococcus*, a comparable range of genera to those detected from diverse habitats worldwide. Many isolates also demonstrated high ITS sequence similarity with yeasts from distant environments, or isolates obtained from the Chatham Islands in the 1960's (Fell and Hunter 1968). The high level of similarity observed, despite the large geographic distances between yeasts detected during this and other

investigations, may reflect a widespread distribution of yeasts at a global level. High sequence similarity between yeasts from diverse sources and the isolates obtained during an investigation has been recorded previously (Singh et al. 2010), and may contribute to evidence which suggests marine yeast ubiquity. Furthermore, 20 types of filamentous marine fungi that were previously known from the Northern Hemisphere have been detected in New Zealand, suggesting that New Zealand's marine mycoflora is similar to that of comparable regions (Lintott and Lintott 1982).

The seemingly ubiquitous distribution of marine yeasts from diverse substrates and locations worldwide may be due to their ease of dispersal and adaptable nature, under the influence of existing environmental conditions. The small size and huge abundance of microorganisms may facilitate their dispersal over large distances by essentially random forces (Finlay and Esteban 2001; Finlay 2002) and result in the introduction of microorganisms to new locations (Martiny et al. 2006). For example, it has been suggested that frequent dispersal occurs between terrestrial and deep sea habitats (Bass et al. 2007); waterlogged wood and particulate organic matter from the sea surface may sink, contributing species to the deep sea (Singh et al. 2010, plus references therein). The similarities observed between yeasts isolated during this investigation and those from elsewhere may be partially due to simple dispersal processes such as ocean currents, which appear to move from the main Islands of New Zealand towards the Chatham Islands (Heath 1985). It has been suggested that the common presence of filamentous marine fungi *Halosphaeria mediosetigera* Cribb & J.W. Cribb and *Ceriosporopsis halima* Linder in Queensland and New Zealand waters is in agreement with the flow of warm ocean currents from Queensland to New Zealand (Lintott and Lintott 1982). The adaptable nature of marine yeasts may also contribute to their ubiquitous distribution; fungi are known to be ecologically successful

and occupy a wide range of niches due to their highly versatile physiological adaptations (Nagano et al. 2010). Marine fungi are generally recognised as an adaptable group (Kohlmeyer 1963), and yeast cells have mechanisms that allow them to withstand the diverse range of stress inducing conditions to which they are continuously exposed (Tanghe et al. 2006). For example, halophilic marine yeasts such as *Debaryomyces hansenii* are often found in shallow seawater and other salty environments (Raspor and Zupan 2006, plus references therein). Certain yeasts are even known as extremophiles due to their ability to thrive under various extreme conditions (Raspor and Zupan 2006). This ease of microbial dispersal and their subsequent colonisation of new environments may lead to increased gene flow and overcome any tendency towards genetic and spatial differentiation (Martiny et al. 2006). Despite their generally adaptable nature, existing environmental conditions such as temperature, light, pressure, pH, water and nutrient availability are known to influence yeast populations (Dix and Webster 1995; Deák 2006). Pollution, terrestrial runoff and the availability and concentration of organic material may also modify the character of yeast populations in coastal waters (Fell and Van Uden 1963; Kohlmeyer and Kohlmeyer 1979; Hagler and Mendonça-Hagler 1981). The selective survival of certain marine yeasts in various aquatic environments has been suggested (Ahearn et al. 1968). Existing environmental conditions may act upon a large reservoir or seed bank of microbial species in a given environment, allowing certain species to thrive while others persist only as spores or cysts until suitable conditions arise (Finlay and Esteban 2001; Fenchel and Finlay 2004). One suggestion is that microorganisms are generally ubiquitous, and will grow wherever their preferred habitat is realised (Boenigk et al. 2006, plus references therein). Yeast genera such as *Cryptococcus* could contribute to a dormant marine yeast seed bank because they produce chlamydospores and very thick capsules, which protect against and ensure survival in extreme

environments (Raspor and Zupan 2006, plus references therein). Yeasts have also been detected from piles of decomposing kelp, which may act as a reservoir of microbial populations that are released when the kelp is washed back into the sea (Van Uden and Castelo Branco 1963).

In contrast to previously mentioned evidence, certain research supports the idea that free-living microorganisms demonstrate biogeographic distribution patterns, and that past events or geographic barriers may be responsible for shaping spatial variation in microorganism biodiversity (Boenigk et al. 2006; Martiny et al. 2006). One suggestion is that most microbial eukaryotes are ubiquitous, although the possibility of subtle cases of endemism is recognised (Finlay and Esteban 2001; Boenigk et al. 2006). For example, geographic isolation was found to be primarily responsible for the global population structure of the archaeon *Sulfolobus*, which demonstrated clustering by geographic locale rather than current environmental conditions (Whitaker et al. 2003). It was suggested that gene flow between *Sulfolobus* populations is restricted over large distances, and that the highly specialized growth requirements of *Sulfolobus* limit their introduction and persistence in new locations with established microorganism populations (Whitaker et al. 2003). Marine yeasts appear to be widespread (Kutty and Philip 2008, plus references therein), but further investigation might reveal biogeographic distribution patterns at a local level. Certain oceanic yeasts are thought to demonstrate ubiquity or occur by chance, although other rare yeasts are restricted biologically and geographically (Fell 1976). If the distribution of marine yeasts is restricted, it could be due to their nutritional requirements or saprophytic or parasitic dependence on a specific group of marine plants or animals (Fell 1976).

4.2 Limited Isolate Identification

Although they were the primary source of information used for isolate identification, ITS sequences did not enable confident identification of all isolates obtained during this investigation. Yeasts are frequently identified based on phylogenetic construction with rRNA sequence data (Valente et al. 1999; Nagahama et al. 2001; Kurtzman and Robnett 2003; Singh et al. 2010), and high ITS sequence identity (97 – 100 %) between yeasts isolated during this investigation and named yeast sequences available in GenBank enabled identification of many isolates (Table 2). However, 48 *Metschnikowia* isolates could not be confidently identified further than the genus level. The identification difficulties demonstrated by *Metschnikowia* isolates may be because their ITS sequences were of insufficient quality for phylogenetic analysis; ITS sequences from some *Metschnikowia* isolates displayed several undetermined nucleotides, which often occurred at the same positions within this gene region. The frequent occurrence of poor quality ITS sequences among *Metschnikowia* isolates may be due to low quantity PCR products, or a technical problem such as sequence primer mismatch during the PCR reaction, although no mention of this is apparent in the literature. *Metschnikowia* sequences that were of sufficient quality for contig construction and use in phylogenetic analysis also had limitations (Fig. 4); poor separation and support of branches in the Saccharomycotina phylogenetic tree meant that phylogenetic data were unable to confirm isolate identifications based on GenBank search results. Poor branch separation may be due to the high level of ITS sequence similarity among previously recognised yeasts from the genus *Metschnikowia* and isolates obtained during this investigation. For example, 25 individual isolates with identical partial ITS sequences (represented by X in the Saccharomycotina phylogenetic tree) shared a pairwise identity of up to 99.5 % with ITS

sequences from *Metschnikowia bicuspidata* (U51436), *Metschnikowia bicuspidata* var. *bicuspidata* (CBS5575) and *Metschnikowia bicuspidata* var. *chathamia* (CBS5903). *Metschnikowia bicuspidata*, *Metschnikowia zobellii* and *Metschnikowia australis* (Fell & I.L. Hunter) Mend.-Hagler, Hagler, Phaff & Tredick are closely related, as demonstrated by their production of asci in cross matings (Fell and Hunter 1968) and by the grouping of these species in a consensus tree constructed with LSU sequence data (Nguyen et al. 2006). *Metschnikowia bicuspidata* var. *bicuspidata* and *Metschnikowia australis* appear to be more closely related to each other than to *Metschnikowia zobellii*, despite an intermediate level of base sequence complementarity in DNA-DNA reassociation experiments indicating some genomic divergence between the former two species (Mendonça-Hagler et al. 1985). Analysis of additional rRNA regions that demonstrate sequence divergence, such as the LSU or SSU, might enable further resolution of isolate identity (Mendonça-Hagler et al. 1993; Kurtzman and Fell 2006).

Morphological and physiological descriptions are frequently used to support initial isolate identifications based on rRNA sequence data (Nagahama et al. 2001; Singh et al. 2010). The primary identification of yeasts isolated during this investigation was based on ITS sequence data and typically supported by morphological observations (Tables 3-6); morphological features of yeast isolates were generally in agreement with descriptions of corresponding yeast type strains from the databases MycoBank and CBS-KNAW (CBS-KNAW 2012; MycoBank 2012). For example, isolate B4M-STD was identified as *Rhodotorula minuta* based on ITS sequence data, and descriptions which indicate that this species has pink coloured colonies support this identification (CBS-KNAW 2012). However, the subjective nature of describing yeast cell morphology at a microscopic level limited the extent to which morphological observations were

able to support the identification of isolates. For example, difficulties were experienced when determining whether the shape of a cell should be described as ellipsoidal or an elongated ellipsoid, or whether the chains or clusters of cells displayed by isolates such as *Cryptococcus dimennae* and *Cryptococcus victoriae* (as indicated in Fig. 9) were indicative of cells which did not detach after budding, cells clustered together via sedimentation, or possibly the formation of pseudohyphae. Certain strains of yeast are known to produce pseudohyphae (CBS-KNAW 2012; MycoBank 2012), but clear pseudohyphae formation was not observed during microscopic analysis in this investigation. The use of morphological and physiological observations to support isolate identification has further limitations; results from morphological and physiological analysis may be ambiguous due to strain variability (Kurtzman and Robnett 1998) and can demonstrate variable results both between and within species (Fell et al. 2000). Although there were no obvious contradictions, slight discrepancies occurred between morphological descriptions from the literature and the morphology demonstrated by some isolates. For example, isolates identified as *Rhodotorula mucilaginosa* had an ellipsoidal cell shape, although yeasts from the genus *Rhodotorula* demonstrate natural variation in cell morphology (Hasegawa et al. 1960). It is recommended that isolate identification be based on more than two techniques (Singh et al. 2010), and further identification of isolates might be possible via analysis of additional rRNA regions, morphological or physiological characteristics. Although recognised as a physiologically homogenous genus (Giménez-Jurado et al. 1995) more accurate identification of *Metschnikowia* isolates might be achieved via analysis of certain characteristics, such as biochemical properties (Mendonça-Hagler et al. 1985), maximum growth temperature, ascus length (Fell and Hunter 1968) and the number of ascospores produced per ascus (Fell and Pitt 1969).

4.3 Limited Representation of Biodiversity

Due to limitations of the collection procedures used, this investigation is likely to be only partially representative of marine yeast biodiversity in New Zealand. In terms of yeast isolation from algal samples, the experimental procedures used were in accordance with other studies (Van Uden and Castelo Branco 1963; Seshadri and Sieburth 1971; Kohlmeyer and Demoulin 1981). However, this was a preliminary investigation; a limited number of algae were sampled during four collections conducted in the Wellington Region and only 94 yeasts were isolated in total (Fig. 13). Accordingly, the amount of data obtained with regards to marine yeast populations was limited and the results of this investigation are likely to represent just some of New Zealand's marine yeast biodiversity. Data limitations also hindered the development of conclusions as to whether experimental procedures, the type of alga sampled, or other environmental factors were influential on the yeasts isolated; slight differences were observed in the type and frequency of yeasts isolated between algal collections, but the significance of these differences was unclear. The number of new species detected generally decreases each time an area is sampled (Fenchel and Finlay 2004; Lachance 2006), but more extensive sampling would still be expected to reveal further marine yeast species in New Zealand. Sampling additional algae, substrates, locations, and during different seasons might allow a more accurate representation of New Zealand's marine yeast biodiversity, and possibly reveal biogeographic distribution patterns.

Limitations of culture techniques used to isolate yeasts from algae mean that the isolates obtained during this investigation only represent some of New Zealand's marine yeast biodiversity. Yeast isolation procedures were similar to those from other investigations in terms of the culture

techniques and isolation media used (Nagahama et al. 2001; Nagahama 2006). However, yeast isolation techniques have limitations for capturing biodiversity; a range of isolates were obtained using culture-based detection methods, but standard culture techniques are unable to detect “nonculturable” yeasts (Boundy-Mills 2006). It is unclear how much biodiversity has been overlooked, since the numbers of non-viable and nonculturable yeasts in marine environments are unknown (Fell 2001) and may be almost impossible to estimate (Boundy-Mills 2006). Experimental procedures used during this investigation also involved selecting yeast colonies for isolation based on their morphology, and discarding colonies with duplicate morphologies for each alga sampled in a given collection. Although essential for reducing the total number of isolates obtained, this approach is likely to have caused further misrepresentation of the biodiversity of marine yeasts, since different yeast species may exhibit identical morphologies and an individual species may have multiple morphologies (Boundy-Mills 2006). Certain yeasts may have been overlooked because culture-based detection techniques may bias isolate recovery towards rapidly growing strains, influencing the apparent diversity present in the community being analysed (Boundy-Mills 2006). These limitations mean that the yeast isolates obtained were only partially representative of the biodiversity present on each algal sample, and may also have contributed to the relatively similar range of marine yeasts isolated between collections. Additional culture-independent and PCR-based techniques allow direct sequencing of nonculturable fungi from environmental samples and may improve understanding of yeast biodiversity (Deák 2006; Singh et al. 2010); evaluation of even limited diversity might be possible with the use of group-specific environmental PCR plus cloning and gene library construction (Bass et al. 2007). It has also been recommended that a polyphasic approach using both culture-based and culture-independent methods be used to maximise the advantages of both

techniques (Boundy-Mills 2006). Thus, additional biodiversity might be revealed upon further investigation of marine yeasts from the algal samples collected, particularly if nonculturable varieties are analysed (sterile seawater washings of original algal samples have been frozen and retained for this purpose).

The sole use of ITS sequence data is unlikely to have captured the full biodiversity of marine yeasts isolated during this investigation. The ITS region is often used for species delimitation, even though assessment of marine yeast biodiversity using genetic sequence data from just one region such as ITS is limited (Gazis et al. 2011, plus references therein). During an investigation into the delimitation of species boundaries in tropical terrestrial endophytes, it was noted that the choice of molecular marker, the way the molecular marker is used and subjective placement of species boundaries are influential on estimates of biodiversity (Gazis et al. 2011). Sole use of the ITS region for species delimitation has been recognised as restricted, since it generally underestimates the predicted number of species present compared with predictions made using other nuclear loci (Gazis et al. 2011). Yeasts may also possess diversity that is not apparent in genetic analysis; one investigation found that homology between the ITS and LSU sequences of an isolate and those in GenBank do not imply identity, and that fungi isolated from deep sea sediments may have physiological differences which were not detected via analysis of these sequences (Singh et al. 2010). Thus, use of the ITS region for analysis of isolates obtained during this investigation is likely to have resulted in an underestimate of their biodiversity, and assumption of homology between potential species may have contributed to the apparent absence of biogeographic patterns. It has been suggested that analysing isolates with multiple primers is essential when evaluating their biodiversity and ecology, and might reveal patterns of

biogeography (Nagano et al. 2010; Gazis et al. 2011). Further investigation of isolates with more than one gene or a higher ITS similarity threshold might resolve yeasts into units which more accurately reflect their genetic affinities, and provide a more accurate estimate of biodiversity (Gazis et al. 2011). Since the current taxonomic resolution used can overlook endemic ecophysiological traits and genomic variance, analysis of isolates at a finer taxonomic level might reveal evidence of geographic barriers on microorganism distribution which have so far been overlooked (Boenigk et al. 2006; Gazis et al. 2011).

4.4 Implications

Fungi are recognised as principal degraders of biomass in terrestrial ecosystems (Bass et al. 2007) and marine yeasts are suggested to have a similar saprophytic role (Fell 2001). Fungi play a vital role in decomposition and have also been recognised as symbionts or parasites associated with plants and algae (Dix and Webster 1995; Hawksworth 1998). Marine fungi have previously been detected from a range of ecosystems and interact with many components of their environment, including their hosts, competitors and substrates (Dix and Webster 1995). In addition to playing a role in the detrital food web, marine yeasts may contribute to various ecological activities: decomposition of plant substrates, biodegradation of pollutants such as oils, nutrient-recycling, and parasitism of marine animals (Kutty and Philip 2008, plus references therein). Due to the limited information available on the role of individual yeast species, the ecological implications of specific marine yeasts isolated during this investigation are unclear. However, the species of

yeast present may not be important (Fell 1976); marine yeasts might play a collective, saprophytic role in New Zealand waters.

Certain marine yeast species have been recognised as pathogens or killer yeasts, both of which may have implications in aquaculture settings. Many isolates obtained during this investigation were from the *Metschnikowia*; *Metschnikowia* is one of many pathogenic yeast genera (Fell 1976) and includes yeasts known to actively attack their host via forcible spore discharge (Lachance et al. 1976). For example, various species from the genus *Metschnikowia* parasitize marine copepods (Seki and Fulton 1969) and have been identified as the cause of fry mortality in Chinook salmon *Oncorhynchus tshawytscha* (Walbaum) (Moore and Strom 2003). Pathogenic marine yeasts have the potential to cause damage and are of particular concern in immunocompromised hosts or stressful situations such as aquaculture settings (Wang et al. 2007). For example, *Metschnikowia bicuspidata* causes milky disease in the crab *Portunus trituberculatus* and is responsible for great economic losses (Wang et al. 2007). In contrast, marine yeasts from a wide variety of genera have the ability to produce killer toxin, which kills yeasts of the same or related species without harming the killer strain itself (Magliani et al. 1997). For example, marine yeasts from *Williopsis saturnus* (Klöcker) Zender and the genus *Pichia* produce killer toxin against *Metschnikowia bicuspidata* (Wang et al. 2007; Peng et al. 2010). The killer toxin produced by *Williopsis saturnus* degrades the cell wall of sensitive yeasts and may be suitable for biocontrol purposes against pathogenic yeasts in organisms such as animals, which are not affected by the toxin due to their lack of a cell wall (Peng et al. 2010). Further information on pathogenic and killer marine yeasts from New Zealand may be valuable to the aquaculture industry; killer marine yeasts might provide potential strategies for countering pathogenic yeasts

and reducing economic losses (Peng et al. 2010). If marine yeasts with the killer phenotype are isolated in New Zealand, they are likely to be suited to local conditions and would not pose any biosecurity risks if applied in the aquaculture industry.

Potential biocontrol ability against postharvest fungal disease has been demonstrated by marine yeasts (Wang et al. 2008), such as those from genera frequently isolated during this investigation. Yeasts are generally preferred over bacteria for biocontrol purposes, as they are unlikely to cause disease when consumed by humans (Demain et al. 1998). The application of marine yeasts appears to effectively control postharvest disease and avoids the development of fungicide resistance by pathogens (Chi et al. 2009). Marine *Rhodosporidium paludigenum*, *Cryptococcus laurentii* (Kuff.) C.E. Skinner and *Rhodotorula glutinis* demonstrated biocontrol ability against postharvest grey mold caused by *Botrytis cinerea* on cherry tomatoes, and *Rhodosporidium paludigenum* was the most effective at decreasing disease incidence (Wang et al. 2010). Certain terrestrial strains of *Aureobasidium pullulans* also demonstrated activity against postharvest decay on a range of fruits (Schena et al. 1999). *Cryptococcus*, *Rhodotorula*, and *Aureobasidium* isolates obtained during this investigation may have similar biocontrol abilities, and could be used in New Zealand to protect fresh produce from postharvest decay.

A range of marine yeast genera, similar to those detected during this investigation, have previously demonstrated biodegradation abilities that could enable bioremediation of pollutants such as hydrocarbons (Chi et al. 2010). Yeasts and other fungi have been readily detected in oil contaminated environments, giving rise to the suggestion that they may play an important role in the degradation of oil (Fedorak et al. 1984; Zinjarde and Pant 2002; Raghukumar 2008).

Although no single microorganism is known to be capable of completely degrading crude oil, certain yeast species may contribute to the degradation of oil in marine environments (Ahearn and Meyers 1976). For example, *Cryptococcus neoformans* (San Felice) Vuill. and species from the genus *Rhodotorula* were found to degrade hydrocarbons (Da Costa and D'Souza 1979), and a range of genera including *Rhodotorula* have potential for the biotransformation of polycyclic aromatic hydrocarbons (MacGillivray and Shiaris 1993). It has been suggested that fungi from polluted marine environments are well suited for bioremediation of these conditions (Raghukumar 2002); although unable to compete with hydrocarbon-degrading bacteria under normal conditions, yeasts may have the advantage in challenging environments where the nutrient and oxygen content is low (Fedorak et al. 1984). Fungi are known to be tolerant of challenging conditions such as the high salt concentrations present in marine environments (Raghukumar 2002). Certain marine yeasts also possess heavy metal tolerance and have potential for bioremediation of waters contaminated with toxic metals (Abe et al. 2001). For example, high tolerance against Cu^{2+} was demonstrated by a deep sea yeast from the genus *Cryptococcus* (Abe et al. 2001). Thus, the biodegradation abilities of marine yeasts and their tolerance to challenging environmental conditions indicate potential for use in the remediation of various polluted marine environments.

The biodegradation of organic matter into yeast biomass has also been demonstrated by marine yeasts (Rhishipal and Philip 1998), such as those from genera frequently isolated during this investigation. Single cell yeast biomass is of high nutritional quality and a cost effective choice for supplementing animal or aquaculture feed (Rhishipal and Philip 1998). For example, *Cryptococcus aureus* is considered to be an excellent candidate for single cell protein production

due to its ease of cultivation, good growth on inulin and beneficial nutritional properties (Chi et al. 2008). Yeast biomass production is efficient due to their short generation time, limited nutrient requirements (Kutty and Philip 2008, plus references therein), and the ease of managing production and concentration of yeast cells on a large scale (Chi et al. 2007). Certain yeasts also thrive on cheap waste products; yeasts from the genus *Rhodotorula* were excellent candidates for the production of single cell protein from prawn shell waste (Rhishipal and Philip 1998). Some marine yeasts produce biomass more efficiently in seawater rather than distilled water (Singh et al. 2010), so marine yeast biomass production has the advantage of using seawater, which is an abundant resource (Chi et al. 2006). Due to their various advantages, marine yeasts may have potential for development as a low cost feed supplement for use in New Zealand's aquaculture industry.

Many marine yeasts produce compounds with potential applications as pharmaceuticals, cosmetics and industrial chemicals (Chi et al. 2006). Applications have previously been described for all marine yeast genera frequently isolated during this investigation: *Cryptococcus*, *Rhodotorula*, *Metschnikowia* and *Aureobasidium* (Chi et al. 2009, plus references therein). For example, a marine strain of *Cryptococcus aureus* demonstrated secretion of large amounts of inulinase, which can be used for the production of ultra high fructose syrups and high concentrations of ethanol (Gao et al. 2007, plus references therein). *Aureobasidium pullulans* is also biotechnologically important due to its ability to produce various extracellular enzymes: proteinase, amylase, lipase, cellulase, xylanase, mannanase and transferases (Chi et al. 2009, plus references therein). Enzymes produced by marine yeasts may have unique properties; subtle physical and chemical differences were observed between inulinases produced by marine and

terrestrial strains of the same species (Chi et al. 2009, plus references therein). Production of marine yeast byproducts has the advantage of using seawater (Chi et al. 2006), and their short generation time and limited nutrient requirements make marine yeasts an excellent economic choice (Kutty and Philip 2008, plus references therein). Screening fungi from extreme marine environments may yield additional novel enzymes and bioactive molecules which could be exploited for use in biotechnological processes (Raghukumar 2008).

4.5 Conclusions

Although this was the first known investigation of marine yeast biodiversity from waters surrounding New Zealand's main Islands, the yeasts isolated were not unique. Marine yeasts were isolated and identified from a diverse range of species that have been described during previous investigations. High ITS sequence similarity was observed between yeasts isolated during this investigation and those from diverse marine and terrestrial substrates worldwide; the high level of similarity may suggest that marine yeasts are ubiquitous at a global level. However, data regarding marine yeasts is insufficient to support or dispute whether they also demonstrate biogeographic distribution patterns. Limitations of the experimental procedures used mean that results obtained during this investigation are only partially representative of New Zealand's marine yeast biodiversity. The marine yeasts isolated may have ecological implications; marine yeasts are generally considered to be saprophytes but some genera are recognised as pathogenic and may have negative implications for aquaculture in New Zealand. Many marine yeast genera isolated during this investigation have previously described applications, including the

production of nutritionally valuable yeast biomass or useful compounds, biocontrol abilities against postharvest decay, and potential abilities for bioremediation of polluted marine environments. More extensive investigation of new and existing marine yeasts from New Zealand may provide further information regarding their biodiversity, ecological role and potential applications.

5. Appendix

5.1 Media Components

Difco Potato Dextrose Agar Plus (PDA):

40 g Difco Potato Dextrose Agar

10 g Oxoid Yeast Extract

5 g Oxoid Peptone

Prepared with 1 L aged seawater

Difco Standard Marine Agar Plus (STD):

37.5 g Difco Marine Agar

5 g Sigma-Aldrich D+ Galactose

10 g Oxoid Yeast Extract

5 g Oxoid Beef Extract

5 g Oxoid Peptone

Prepared with 1 L ddH₂O

Difco Standard Marine Agar Plus 2:

20 g Difco Marine Agar

10 g Sigma-Aldrich D+ Glucose

1 g Oxoid Yeast Extract

4 g Oxoid Beef Extract

4 g Pancreatic Digest of Gelatin

2.5 g NaCl

Prepared with 1 L ddH₂O

Difco Standard Marine Agar Plus 3:

13.3 g Difco Marine Agar

15 g Sigma-Aldrich D+ Glucose

0.5 g Oxoid Yeast Extract

0.5 g Oxoid Peptone

0.5 g Gelatin Hydrolysate

Prepared with 1 L ddH₂O

Difco Marine Broth Plus:

30 g Difco Marine Broth

5 g Sigma-Aldrich D+ Galactose

10 g Oxoid Yeast Extract

5 g Oxoid Beef Extract

5 g Oxoid Peptone

Prepared with 1 L ddH₂O

Sigma Luria Broth:

Prepared according to manufacturer's instructions with aged seawater

5.2 Optimisation of Culture Techniques

Prior to Collections 1-4, a preliminary investigation was conducted in order to determine which culture techniques yielded the highest number of marine yeast colonies. Various media, antibiotics and inoculation methods were trialled using a piece of miscellaneous alga. More colonies were observed on agar plates inoculated using the homogenisation of alga method (a ~2 x 2 cm algal sample was homogenised with a mini-blender in a falcon tube with ~10 ml of sterile seawater, and a 100 μ l aliquot of the resultant solution was transferred to an agar plate) than agar plates inoculated with a 100 μ l aliquot of seawater (Table 9). The number of colonies obtained on each agar plate was not excessive, rendering sample dilution unnecessary. More colonies were observed on Difco Standard Marine Agar Plus (STD) and Difco Potato Dextrose Agar Plus (PDA) than the other two media trialled (Table 10). Antibiotic Treatment B (100 μ l of 10 mg ml⁻¹ streptomycin sulfate solution (in distilled water) plus 100 μ l of 5 mg ml⁻¹ rifampicin solution (in methanol)) was found to be the most effective for suppression of bacterial overgrowth (Table 10). Due their efficacy in preliminary investigations, STD and PDA plates treated with both antibiotics (streptomycin sulfate and rifampicin) were used for yeast isolation in Collections 1-4. During Collection 1, 100 μ l of streptomycin sulfate solution with concentration 10 mg ml⁻¹ and 100 μ l of rifampicin solution with concentration 5 mg ml⁻¹ were applied to each plate. During Collections 2, 3 and 4, 100 μ l of streptomycin sulfate solution with concentration of 9 mg ml⁻¹ and 100 μ l of rifampicin solution with concentration of 4.5 mg ml⁻¹ were applied to each plate.

Table 9. Appearance of agar plates after inoculation with seawater or the solution resulting from homogenisation of an algal sample in sterile seawater.

Aliquot Applied to Agar Plate	Number of Colonies on Agar Plate 1 (STD)	Number of Colonies on Agar Plate 2 (STD)	Number of Colonies on Agar Plate 3 (STD)	Average Number of Colonies per Agar Plate
100 µl Seawater	17	13	16	15
100 µl Seawater (1 in 10 Dilution)	3	2	1	2
100 µl Homogenised Alga Solution	~7069	~7304	~7854	~7383
100 µl Homogenised Alga Solution (1 in 10 Dilution)	~2592	~2278	~3142	~2670

Table 10. Appearance of agar plates after treatment with antibiotics and inoculation with the solution resulting from homogenisation of an algal sample in sterile seawater.

Antibiotic Treatment	Difco Potato Dextrose Agar Plus (PDA)	Difco Standard Marine Agar Plus (STD)	Difco Standard Marine Agar Plus 2	Difco Standard Marine Agar Plus 3
<u>Treatment A:</u> 50 µl Vancomycin Solution (25 mg ml ⁻¹ in Distilled Water)	Heavy Bacterial Lawn	Heavy Bacterial Lawn	Light Bacterial Lawn	Light Bacterial Lawn
<u>Treatment B:</u> 100 µl Streptomycin Sulfate Solution (10 mg ml ⁻¹ in Distilled Water) +100 µl Rifampicin Solution (5 mg ml ⁻¹ in Methanol)	Many Fungal Colonies	Many Fungal Colonies	Some Fungal Colonies	Some Fungal Colonies
<u>Treatment C:</u> Control (No Antibiotic Treatment)	Very Heavy Bacterial Lawn	Very Heavy Bacterial Lawn	Heavy Bacterial Lawn	Light Bacterial Lawn

5.3 Geneious Alignments by Subphylum

5.3.1 Pezizomycotina

		1	10	20	30	40	50	60
Aureobasidium pullulans	HM992505	GAAGGATCATTAAAGAGTAAGGGTGCTCAGCGCCCGACCTCCAACCCCTTTGTTGTTAAAA						
Aureobasidium pullulans	HQ115720	-AAGGATCATTAAAGAGTAAGGGTGCTCAGCGCCCGACCTCCAACCCCTTTGTTGTTAAAA						
	L10S-PDA	-----TCATTAAAGAGTAAGGGTGCTCAGCGCCCGACCTCCAACCCCTTTGTTGTTAAAA						
	N2M-PDA	--AGGATCATTAAAGAGTAAGGGTGCTCAGCGCCCGACCTCCAACCCCTTTGTTGTTAAAA						
	P5S-PDA	--AGGATCATTAAAGAGTAAGGGTGCTCAGCGCCCGACCTCCAACCCCTTTGTTGTTAAAA						
Aureobasidium pullulans	HM992505	CTACCTTGTGCTTTGGCGGGACCGCTCGGTCTCGAGCCGCTGGGGATTGTCCTCCAGGCG						
Aureobasidium pullulans	HQ115720	CTACCTTGTGCTTTGGCGGGACCGCTCGGTCTCGAGCCGCTGGGGATTGTCCTCCAGGCG						
	L10S-PDA	CTACCTTGTGCTTTGGCGGGACCGCTCGGTCTCGAGCCGCTGGGGATTGTCCTCCAGGCG						
	N2M-PDA	CTACCTTGTGCTTTGGCGGGACCGCTCGGTCTCGAGCCGCTGGGGATTGTCCTCCAGGCG						
	P5S-PDA	CTACCTTGTGCTTTGGCGGGACCGCTCGGTCTCGAGCCGCTGGGGATTGTCCTCCAGGCG						
Aureobasidium pullulans	HM992505	AGCGCCCGCCAGAGTTAAACCAAACCTCTTGTTATTTAACCGGTCGTCTGAGTTAAAAATTT						
Aureobasidium pullulans	HQ115720	AGCGCCCGCCAGAGTTAAACCAAACCTCTTGTTATTTAACCGGTCGTCTGAGTTAAAAATTT						
	L10S-PDA	AGCGCCCGCCAGAGTTAAACCAAACCTCTTGTTATTTAACCGGTCGTCTGAGTTAAAAATTT						
	N2M-PDA	AGCGCCCGCCAGAGTTAAACCAAACCTCTTGTTATTTAACCGGTCGTCTGAGTTAAAAATTT						
	P5S-PDA	AGCGCCCGCCAGAGTTAAACCAAACCTCTTGTTATTTAACCGGTCGTCTGAGTTAAAAATTT						
Aureobasidium pullulans	HM992505	TGAATAAATCAAACTTTCAACAACGGATCTCTGGTTCTCGCATCGATGAAGAACGCAG						
Aureobasidium pullulans	HQ115720	TGAATAAATCAAACTTTCAACAACGGATCTCTGGTTCTCGCATCGATGAAGAACGCAG						
	L10S-PDA	TGAATAAATCAAACTTTCAACAACGGATCTCTGGTTCTCGCATCGATGAAGAACGCAG						
	N2M-PDA	TGAATAAATCAAACTTTCAACAACGGATCTCTGGTTCTCGCATCGATGAAGAACGCAG						
	P5S-PDA	TGAATAAATCAAACTTTCAACAACGGATCTCTGGTTCTCGCATCGATGAAGAACGCAG						
Aureobasidium pullulans	HM992505	CGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA						
Aureobasidium pullulans	HQ115720	CGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA						
	L10S-PDA	CGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA						
	N2M-PDA	CGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA						
	P5S-PDA	CGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA						
Aureobasidium pullulans	HM992505	CATTGCGCCCTTGGTATTCGAGGGGCATGCCTGTTGAGCGCTATTACACCACTCAAG						
Aureobasidium pullulans	HQ115720	CATTGCGCCCTTGGTATTCGAGGGGCATGCCTGTTGAGCGCTATTACACCACTCAAG						
	L10S-PDA	CATTGCGCCCTTGGTATTCGAGGGGCATGCCTGTTGAGCGCTATTACACCACTCAAG						
	N2M-PDA	CATTGCGCCCTTGGTATTCGAGGGGCATGCCTGTTGAGCGCTATTACACCACTCAAG						
	P5S-PDA	CATTGCGCCCTTGGTATTCGAGGGGCATGCCTGTTGAGCGCTATTACACCACTCAAG						
Aureobasidium pullulans	HM992505	CTATGCTTGGTATTGGGCGTCGTCCTTAGTTGGGCGCGCCTTAAAGACCTCGGCGAGGCC						
Aureobasidium pullulans	HQ115720	CTATGCTTGGTATTGGGCGTCGTCCTTAGTTGGGCGCGCCTTAAAGACCTCGGCGAGGCC						
	L10S-PDA	CTATGCTTGGTATTGGGCGTCGTCCTTAGTTGGGCGCGCCTTAAAGACCTCGGCGAGGCC						
	N2M-PDA	CTATGCTTGGTATTGGGCGTCGTCCTTAGTTGGGCGCGCCTTAAAGACCTCGGCGAGGCC						
	P5S-PDA	CTATGCTTGGTATTGGGCGTCGTCCTTAGTTGGGCGCGCCTTAAAGACCTCGGCGAGGCC						
Aureobasidium pullulans	HM992505	ACTCCGGCTTTAGGCGTAGTAGAATTTATTCGAACGTCTGTCAAAGGAGAGGAACTCTGC						
Aureobasidium pullulans	HQ115720	ACTCCGGCTTTAGGCGTAGTAGAATTTATTCGAACGTCTGTCAAAGGAGAGGAACTCTGC						
	L10S-PDA	ACTCCGGCTTTAGGCGTAGTAGAATTTATTCGAACGTCTGTCAAAGGAGAGGAACTCTGC						
	N2M-PDA	ACTCCGGCTTTAGGCGTAGTAGAATTTATTCGAACGTCTGTCAAAGGAGAGGAACTCTGC						
	P5S-PDA	ACTCCGGCTTTAGGCGTAGTAGAATTTATTCGAACGTCTGTCAAAGGAGAGGAACTCTGC						
Aureobasidium pullulans	HM992505	CGACTGAAACCTTTATTTTCTAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACT						
Aureobasidium pullulans	HQ115720	CGACTGAAACCTTTATTTTCTAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACT						
	L10S-PDA	CGACTGAAACCTTTATTTTCTAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACT						
	N2M-PDA	CGACTGAAACCTTTATTTTCTAGGTTGACCTCGGATCAGGTAGGGAT-----						
	P5S-PDA	CGACTGAAACCTTTATTTTCTAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACT						
Aureobasidium pullulans	HM992505	TAAGCATAT						
Aureobasidium pullulans	HQ115720	TAA-----						
	L10S-PDA	TAA-----						
	N2M-PDA	-----						
	P5S-PDA	TAA-----						

5.3.2 Saccharomycotina

	1	10	20	30	40	50	60
I2-STD	1	10	20	30	40	50	60
M. zobellii U51433	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. zobellii CBS4821 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
S2S-PDA	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. australis CBS5847 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
N5M-STD	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. noctiluminum DQ002495	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. corniflorae FJ810507	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
C. chrysomelidarum FJ623613	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. zobellii DQ659336	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii CBS8174 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
C. gelsemii DQ988045	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
C. gelsemii DQ988046	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
C. gelsemii DQ988047	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii CBS8978 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
Metschnikowia sp. AY188370	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii CBS5554 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii EF568059	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii CBS8994 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii CBS5834	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii HQ221884	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. reukaufii AY188383	AAAAC	TTTCA	ACAAC	GGATC	-TTT	GGTTCT	CGCATCGATGAAGA
M. cibodasensis AB236924	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. cibodasensis AB236925	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. bicuspidata EF643581	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. bicuspidata U51436	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. bicuspidata var. bicuspidata CBS5575 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. bicuspidata var. chathamia CBS5903 (reversed)	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. bicuspidata DQ534407	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
KK5S-STD	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
M. bicuspidata var. chathamia CBS5980	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
X	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
U5S-PDA	AAAAC	TTTCA	ACAAC	GGATC	-TCTT	GGTTCT	CGCATCGATGAAGA
U3S-1-STD	-----TC	-TCTT	GGTTCT	CGCATCGATGAAGA	ACGC	GAGCAATTGCGG	
I2-STD	1	10	20	30	40	50	60
M. zobellii U51433	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. zobellii CBS4821 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
S2S-PDA	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. australis CBS5847 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
N5M-STD	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. noctiluminum DQ002495	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. corniflorae FJ810507	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
C. chrysomelidarum FJ623613	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. zobellii DQ659336	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii CBS8174 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
C. gelsemii DQ988045	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
C. gelsemii DQ988046	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
C. gelsemii DQ988047	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii CBS8978 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
Metschnikowia sp. AY188370	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii CBS5554 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii EF568059	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii CBS8994 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii CBS5834	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii HQ221884	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. reukaufii AY188383	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. cibodasensis AB236924	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. cibodasensis AB236925	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. bicuspidata EF643581	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. bicuspidata U51436	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. bicuspidata var. bicuspidata CBS5575 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. bicuspidata var. chathamia CBS5903 (reversed)	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. bicuspidata DQ534407	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
KK5S-STD	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
M. bicuspidata var. chathamia CBS5980	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
X	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
U5S-PDA	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC
U3S-1-STD	ATACG	TAATAT	GACTT	GCAGA	----CGT	GAATCATT	GAAATTTTGAAC

5.3.3 Agaricomycotina

	1	10	20	30	40	50	60
R. minuta AF190010							
R. slooffiae AF444552	-----	-----	-----	-----	-----	-----	-----
R. slooffiae AF444627	-----	-----	-----	-----	-----	-----	-----
Cy. macerans AF444317	-----	-----	-----	-----	-----	-----	-----
Cy. macerans AF444329	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus AB520409	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus AB520402	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus AB520396	-----	-----	-----	-----	-----	-----	-----
C. sp. AF444448	-----	-----	-----	-----	-----	-----	-----
P4M-STD	-----	-----	-----	-----	-----	-----	-----
T1S-1-PDA	-----	-----	-----	-----	-----	-----	-----
C. macerans EU082232	-----	-----	-----	-----	-----	-----	-----
C. macerans EU082233	-----	-----	-----	-----	-----	-----	-----
C. macerans EU082231	-----	-----	-----	-----	-----	-----	-----
C. macerans AY052490	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus EF504408	-----	-----	-----	-----	-----	-----	-----
Bm. albus AF444664	-----	-----	-----	-----	-----	-----	-----
V5M-PDA	-----	-----	-----	-----	-----	-----	-----
B. unica AF444441	-----	-----	-----	-----	-----	-----	-----
Bm. albus AB093527	-----	-----	-----	-----	-----	-----	-----
Bm. albus CBS7856	TTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT						
C. dimennae AY188365	-----	-----	-----	-----	-----	-----	-----
C. dimennae AF410473	-----	-----	-----	-----	-----	-----	-----
C. dimennae EU266559	TAGCCCGCCGACTCAATCATTATCTTTCCT-CGTAGGTGAACCTGCGGAAGGATCATT						
Uncultured Fungus AM901805	TTTAGAGGAAGTAAAAGTCATAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT						
T1S-3-PDA	-----	-----	-----	-----	-----	-----	-----
Y5S-PDA	-----	-----	-----	-----	-----	-----	-----
Z4S-1-STD	-----	-----	-----	-----	-----	-----	-----
C. oeiensis AY188362	-----	-----	-----	-----	-----	-----	-----
C. magnus AF190009	-----	-----	-----	-----	-----	-----	-----
Y2M-PDA	-----	-----	-----	-----	-----	-----	-----
C. oeiensis AF444349	-----	-----	-----	-----	-----	-----	-----
C. oeiensis AF444364	-----	-----	-----	-----	-----	-----	-----
C. oeiensis EU002866	-----	-----	-----	-----	-----	-----	-----
C. chernovii AF444354	-----	-----	-----	-----	-----	-----	-----
C. chernovii FN400936	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus FM178256	TTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT						
U3S-PDA	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus AJ875389	TTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT						
Uncultured fungus AB520331	-----	-----	-----	-----	-----	-----	-----
C. carnescens AB035050	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus FJ820684	-----	-----	-----	-----	-----	-----	-----
Uncultured fungus AM901777	-----	-----	-----	-----	-----	-----	-----
Z2S-STD	-----	-----	-----	-----	-----	-----	-----
C. carnescens EU149785	-----	-----	-----	-----	-----	-----	-----
C. sp. HM849618	-----	-----	-----	-----	-----	-----	-----
C. carnescens CBS8395	TTTAGAGGAAGTAAAAGTCATAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT						
C. carnescens AB105438	-----	-----	-----	-----	-----	-----	-----
C. victoriae AY188380	-----	-----	-----	-----	-----	-----	-----
C. victoriae AJ581046	-----	-----	-----	-----	-----	-----	-----
C. victoriae AM160647	-----	-----	-----	-----	-----	-----	-----
C. victoriae CBS9265	TTTAGAGGAAGTAAAAGTCATAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT						
C. victoriae HM849622	-----	-----	-----	-----	-----	-----	-----
C. victoriae AF444645	-----	-----	-----	-----	-----	-----	-----
C. victoriae AY040656	-----	-----	-----	-----	-----	-----	-----
C. victoriae AJ581048	-----	-----	-----	-----	-----	-----	-----
L2S-1-PDA	-----	-----	-----	-----	-----	-----	-----
W5S-4-STD	-----	-----	-----	-----	-----	-----	-----
C. sp. HM589279	-----	-----	-----	-----	-----	-----	-----
C. victoriae AY040654	-----	-----	-----	-----	-----	-----	-----
S4S-PDA	-----	-----	-----	-----	-----	-----	-----
C. victoriae CBS9267	TTTAGAGGAAGTAAAAGTCATAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT						

R. minuta	AF190010	ATG---A---ATTTTAG-----G-----ACGTTCTTTT-TAG-----
R. slooffiae	AF444552	ATG-A-----ATTTTAG-----GACGTTCTTTT-----
R. slooffiae	AF444627	ATG-A-----ATTTTAG-----GACGTTCTTTT-----
Cy. macerans	AF444317	AAG-T-----AAACGCCCTC--C-----GGGGCTCTCTT-TATTC--AC-
Cy. macerans	AF444329	AAG-T-----AAACGCCCTC--C-----GGGGCTCTCTT-TATTC--AC-
Uncultured fungus	AB520409	AAG-T-----AAACGCCCTC-----CGGGGCTCTCTT-TATTCAC---
Uncultured fungus	AB520402	AAG-T-----AAACGCCCTC-----CGGGGCTCTCTT-TATTCAC---
Uncultured fungus	AB520396	AAG-T-----AAACGCCCTC-----CGGGGCTCTCTT-TATTCAC---
C. sp.	AF444448	AAG---T-----AAACGCCCTC--C-----GGGGCTCTCTT-TAAT--TCAC-
P4M-STD		AAG-T-----AAACGCCCTC--C-----GGGGCTCTCTT-TATTC--AC-
T1S-1-PDA		AAG-T-----AAACGCCCTC-----CGGGGCTCTCTT-TATTCAC---
C. macerans	EU082232	AAG---T-----AAACGCCCTC--C-----GGGGCTCTCTT-TATTC--AC-
C. macerans	EU082233	AAG---T-----AAACGCCCTC--C-----GGGGCTCTCTT-TATTC--AC-
C. macerans	EU082231	AAG---T-----AAACGCCCTC--C-----GGGGCTCTCTT-TAAT--TCAC-
C. macerans	AY052490	AAG---T-----AAACGCCCTC--C-----GGGGCTCTCTT-TAAT--TCAC-
Uncultured fungus	EF504408	GTG-A-----TTGACCTC-----CGGGCTCTTAA-----
Bm. albus	AF444664	GTG-----ATTGACCTC-----C-----GGGTCTTAAT-
V5M-PDA		GTGA-----TTGACCT-----TCGGGTCTTA-----
B. unica	AF444441	GTG-----ATTGACCT-----T-----C-GGGTCTTAAT-
Bm. albus	AB093527	-----TTAGTGAT-----
Bm. albus	CBS7856	GTG-----ATTGACCTC-----C-----GGGTCTTAAT-
C. dimennae	AY188365	-----CATTAT-----
C. dimennae	AF410473	-----T-----T-GAAT-----
C. dimennae	EU266559	-----T-----T-GAATT-----
Uncultured Fungus	AM901805	TT-----G-----
T1S-3-PDA		-----AGGATCATTAT-----
Y5S-PDA		-----AAGGATCATTAT-----
Z4S-1-STD		-----TCATTAT-----
C. oeiensis	AY188362	ATGAATT---TTACGCCCT---A-----GTCTTAAC-
C. magnus	AF190009	AT---G-----AATT-----T-----AGAT---T-GAACCATAGG-
Y2M-PDA		ATGA-----ATTCAAATC-----GTACTGCTCACGGGTATGT---GG
C. oeiensis	AF444349	ATG---A-----TTATAATCGT-A---CTGTTTCACGCAG-TATGTG-GGGTGGT---
C. oeiensis	AF444364	ATG---A-----TTATAATCGT-A---CTGTTTCACGCAG-TATGTG-GGGTGGT---
C. oeiensis	EU002866	ATG---A-----ATATAAATCGT-A---CTGTTTCACGCAG-TATGTG-GGGTGGT---
C. chernovii	AF444354	TTG-----AATTCAAATCATC-T-----GTGGCTTCGGTCCGGAT-GTGCCAACAG-
C. chernovii	FN400936	TTG-----AATTCAAATCATC-----TGTTGGCTTCGGTCCGGAT-GTGCCAACAG-
Uncultured fungus	FM178256	TTGAATT---CAAATCATCTG-----TGGCTTCGGTCCGGATGTGCCAACAGG
U3S-PDA		TTGAATT---CAAATCATCTG-----TGGCTTCGGTCCGGATGTGCCAACAG-
Uncultured fungus	AJ875389	TTGAATT---CAAATCATCTG-----TGGCTTCGGTCCGGATGTGCCAACAG-
Uncultured fungus	AB520331	TTGAATT---CAAATCATCTG-----TGGCTTCGGTCCGGATGTGCCAACAG-
C. carnescens	AB035050	-----ATAATGCTCTC-----TGGCTTCGGTCAGTT-GAGTT---C-
Uncultured fungus	FJ820684	AT--A-----ATGCTCTC-----TGGCTTCGGTCAGTTGAGTTCAATGAG
Uncultured fungus	AM901777	AT--A-----ATGCTCTC-----TGGCTTCGGTCAGTTGAGTTCAATGAG
Z2S-STD		AT-A-----AATGCTCTC-----TGGCTTCGGTCAGTTGAGTTCAATGAG
C. carnescens	EU149785	AT-----AATGCTCTC-----TGGCTTCGGTCAGCT-GAGT--TCAA-
C. sp.	HM849618	AT-----ATGCTCTC--T-----GGCTTCGGTCAGTT-GAGT--TCAA-
C. carnescens	CBS8395	AT-----AATGCTCTC-----TGGCTTCGGTCAGTT-GAGT--TCAA-
C. carnescens	AB105438	AT-----AATGCTCTC-----TGGCTTCGGTCAGTT-GAGT--TCAA-
C. victorinae	AY188380	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	AJ581046	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	AM160647	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	CBS9265	AT--A-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	HM849622	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	AF444645	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	AY040656	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	AJ581048	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
L2S-1-PDA		AT--A-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
W5S-4-STD		AT-A-----GTGCCCTC-----TGATGCAAATCATT--GGGTT-----
C. sp.	HM589279	AT-----GTGCCCTC-----GATGCAAATCA-TT-GGGTT-----
C. victorinae	AY040654	AT-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----
S4S-PDA		AT-A-----GTGCCCTC-----TGATGCAAATCATT--GGGTT-----
C. victorinae	CBS9267	AT--A-----GTGCCCTC--T-----GATGCAAATCA-TT-GGGTT-----

R. minuta AF190010 --AAGTCCGACC----ATTTCAT-----TTTCTT-----ACACTGT--
 R. slooffiae AF444552 AGAAGTCCGACC----CTTTCA----T-----TTTCTT-----ACACTGTGC
 R. slooffiae AF444627 AGAAGTCCGACC----CTTTCA----T-----TTTCTT-----ACACTGTGC
 Cy. macerans AF444317 ACACCCCTGTGC-A--CTTTGGC-CACCTG--C-----CGCGCT-----TCACTGCGT--
 Cy. macerans AF444329 ACACCCCTGTGC-A--CTTTGGC-CACCTG--C-----CGCGCT-----TA-ACCTGCGTTA
 Uncultured fungus AB520409 ACACCCCTGTGC---ACTTTGGC-CACCTG-----CGCGCT-----TAACTGCGTTA
 Uncultured fungus AB520402 ACACCCCTGTGC---ACTTTGGC-CACCTG-----CGCGCT-----TAACTGCGTTA
 Uncultured fungus AB520396 ACACCCCTGTGC---ACTTTGGC-CACCTG-----CGCGCT-----TAACTGCGTTA
 C. sp. AF444448 ACACCCCTGTGC-A--CTTTGGC-CACCTG-C-----CGCGCT---TTACTG--CGT-T
 P4M-STD ACACCCCTGTGC---ACTTTGGC-CACCTG-----CGCGCT-----TA-ACCTGCGTTA
 T1S-1-PDA ACACCCCTGTGC---ACTTTGGC-CACCTG-----CGCGCT-----TCACTGCGT--
 C. macerans EU082232 ACACCCCTGTGC-A--CTTTGGC-CACCTG-C-----CGCGCT---TAACTG-CGTTAG
 C. macerans EU082233 ACA-CCCTGTGC-A--CTTTGGC-CACCTG-C-----CGCGCT---TAACTG-CGTTAG
 C. macerans EU082231 ACACCCCTGTGC-A--CTTTGGC-CACCTG-C-----CGCGCT---TTACTG-CGTTAG
 C. macerans AY052490 ACACCCCTGTGC-A--CTTTGGC-CACCTG-C-----CGCGCT---TTACTG-CGTTAG
 Uncultured fungus EF504408 -TAACTATAAT-----CTTC-----T-----AATCTT---CTAC-CTCTGT--
 Bm. albus AF444664 AA-----CTA-----T-----T-----AATCTT---CTAC-CTCTGT--
 V5M-PDA ATAATAATAAT-----CTTC-----T-----AATCTT---CTAC-CTCTGT--
 B. unica AF444441 A-----ACTA-----T-----T-----AATCTT---CTAC-CTCTGT--
 Bm. albus AB093527 TGACCTCCGGG---T-CTTAATAACTA-----TAACTCTT---CTAC-CTCTGT--
 Bm. albus CBS7856 AA-----CTA-----T-----T-----AATCTT---CTAC-CTCTGT--
 C. dimennae AY188365 TGAATTCGGCC---TCCTGGCCT-----T-----ATACAT---TAAACACTGT-G
 C. dimennae AF410473 -----TCGGCC---T-TTTGGCCTTA-----TACACATAATATACA--CTGT--
 C. dimennae EU266559 -----CGGCC---TTTGGCCTTA-----T-----ACACATAATATACA--CTGT-G
 Uncultured fungus AM901805 ---AATTCGGCC---TTTGGCCTTA---T-----ACACATA--ATATACACTGT--
 T1S-3-PDA TGAATTCGGCC---TTTGGCCTTA---T-----ACACATA--ATATACACTGT--
 Y5S-PDA TGAATTCGGCC---TTTGGCCTTA---T-----ACACATA--ATATACACTGT--
 Z4S-1-STD TGAATTCGGCC---TTTGGCCTTA---T-----ACACATA--ATATACACTGT--
 C. oeiensis AY188362 TGATAGGGGCTG---GTTC-----T-----ATCCAT---AACAC-CTGT-G
 C. magnus AF190009 CGAAAGCCAGTG---GTCTTCTTTCA---T-----ATCCAT---AACAC-CTGT-G
 Y2M-PDA GGCTCACTGC-----TTGTGACGGCACCATTATATCCAT---AACAC-CTGT--
 C. oeiensis AF444349 -GACTTCGGTC-----CGGCTCATTC---T-----ATCCAT---AACAC-CTGT-G
 C. oeiensis AF444364 -GACTTCGGTC-----CGGCTCATTC---T-----ATCCAT---AACAC-CTGT-G
 C. oeiensis EU002866 -GACTTCGGTC-----CGGCTCATTC---T-----ATCCAT---AACAC-CTGT-G
 C. chernovii AF444354 GTAACTGCTG---T---TGGAATTC-----TATCCAT---AACAC-CTGT--
 C. chernovii FN400936 GTAACTGCTG---T---TGGAATTC-----TATCCAT---AACAC-CTGT--
 Uncultured fungus FM178256 T-AACACTG-----TTGGAATTC-----TATCCAT---AACAC-CTGT--
 U3S-PDA GTAACACTG-----TTGGAATTC---T-----ATCCAT---AACAC-CTGT--
 Uncultured fungus AJ875389 GTAACACTG-----TTGGAATTC---T-----ATCCAT---AACAC-CTGT--
 Uncultured fungus AB520331 GTAACACTG-----TTGGAATTC---T-----ATCCAT---AACAC-CTGT--
 C. carnescent AB035050 AAATGAGTGCCTT-CTCTTCG--GAGTTGGC-----CATCCAT---ACACACCGT--
 Uncultured fungus FJ820684 TGCCTTCT-----CTTCGG---AGTTGGC-----CATCCAT---ACACACCGT--
 Uncultured fungus AM901777 TGCCTTCT-----CTTCGG---AGTTGGC-----CATCCAT---ACACACCGT--
 Z2S-STD TGCCTTCT-----CTTCGG---AGTTGGC-----CATCCAT---ACACACCGT--
 C. carnescent EU149785 TGAGTGCCTTC---T-CTTCG---GAGTTGGC-----CATCCAT---ACACACCGT--
 C. sp. HM849618 TGAGTGCCTTC---T-CTTCG---GAGTTGGC-----CATCCAT---ACACACCGT-G
 C. carnescent CBS8395 TGAGTGCCTTC---T-CTTCG---GAGTTGGC-----CATCCAT---ACACACCGT--
 C. carnescent AB105438 TGAGTGCCTTC---T-CTTCG---GAGTTGGC-----CATCCAT---ACACACCGT--
 C. victoriae AY188380 AGA--TCTGCCC-TT--ATCGCAAGATGAGGG-----CTTCCAT---ATACACCGT-G
 C. victoriae AJ581046 AGA--TCTGCCC-TT--ATCGCAAGATGAGGG-----CTTCCAT---ATACACCGT-G
 C. victoriae AM160647 AGA--TCTGCCC-TT--ATCGCAAGATGAGGG-----CTTCCAT---ATACACCGT-G
 C. victoriae CBS9265 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT--
 C. victoriae HM849622 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT-G
 C. victoriae AF444645 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT-G
 C. victoriae AY040656 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT-G
 C. victoriae AJ581048 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT--
 L2S-1-PDA AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT--
 W5S-4-STD --AGATCTGCTC---TCTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT--
 C. sp. HM589279 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT-G
 C. victoriae AY040654 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT-G
 S4S-PDA AGA--TCTGCTC---TCTTTGCAAGAAGAGGG-----TTTCCAT---ACACACCGT--
 C. victoriae CBS9267 AGA--TCTGCTC---T-CTTCGCAAGAAGAGGG-----TTTCCAT---ACACACCGT--

R. minuta AF190010 -----GCACACACTTCTTTTACA---CACACTTTT-----AACACATTAG--
R. slooffiae AF444552 -A-----CACACT-----TCTTTTTTACACACACTTTT-----AACACCTTAG--
R. slooffiae AF444627 -A-----CACACT-----TCTTTTTTACACACACTTTT-----AACACCTTAG--
Cy. macerans AF444317 T-----AGTAGGTGTGTCTTT-----ATAATTATACCCATATACAC--AAG--
Cy. macerans AF444329 G-----TAG-GTGTGTCTCTTT-----ATTTATACCCA--TATACAC--AAG--
Uncultured fungus AB520409 -----GTAG-GTGTGTCTCTTT--A-----ATT---ATACCCATATACAC--AAG--
Uncultured fungus AB520402 -----GTAG-GTGTGTCTCTTT-----ATTATATACCC--ATATACACAAG--
Uncultured fungus AB520396 -----GTAG-GTGTGTCTCTTT-----ATTATATACCC--ATATACACAAG--
C. sp. AF444448 -----AGTAGGTGTGTCTTTT---TAACATATA---CAC---TATATACACAAG--
P4M-STD --G-----TAG-GTGTGTCTCTTT-----ATTATATACCC--ATATACACAAG--
T1S-1-PDA -----TAGTAGGTGTGTCTTT-A-----TAATTATACCC--ATATACACAAG--
C. macerans EU082232 -----TAG-GTGTGTCTCTTT-----ATTATATACCC--ATATACACAAG--
C. macerans EU082233 -----TAG-GTGTGTCTCTTT-----ATTATATACCC--ATATACACAAG--
C. macerans EU082231 -----TAG-GTGTGTCTTTT---AACTATA---CAC---TATATACACAAG--
C. macerans AY052490 -----TAG-GTGTGTCTTTT---AACTATA---CAC---TATATACACAAG--
Uncultured fungus EF504408 -----GAACCGTTGG--TCTTCGGA---CCGATTCTTATAA---CAAACATCTGTG--
Bm. albus AF444664 -----GAACCGTTGG--TCTTCGGA---CCGATTCTTATAA---CAAACATCTGTG--
V5M-PDA -----GAACCGTTGG--TCTTCGGA---CCGATTCTTATAA---CAAACATCTGTG--
B. unica AF444441 -----GAACCGTTGG--TCTTCGGA---CCGATTCTTATAA---CAAACATCTGTG--
Bm. albus AB093527 -----GAACCGTTGG--TCTTCGGA---CCGATTCTTATAA---CAAACATCTGTG--
Bm. albus CBS7856 -----GAACCGTTGG--TCTTCGGA---CCGATTCTTATAA---CAAACATCTGTG--
C. dimennae AY188365 -----AACCGTG---GCTTCGG---CCCA-----AAC-TTGAAG--
C. dimennae AF410473 -----GAACCGTG---GCTTCGG---CCCA-A-----AC-TTGAAG--
C. dimennae EU266559 -----AACCGTG---GCTTCGG---CCCA-----AAC-TTGAAG--
Uncultured Fungus AM901805 -----GAACCGTG---GCTTCGGC---CCA-----AAC-----TTGAAG--
T1S-3-PDA -----GAACCGTG---GCTTCGG---CCCA-----AAC-----TTGAAG--
Y5S-PDA -----GAACCGTG---GCTTCGGC---CCA-----AAC-----TTGAAG--
Z4S-1-STD -----GAACCGTG---GCTTCGGC---CCA-----AAC-----TTGAAG--
C. oeirensis AY188362 -----CACTGTTGGATGCTTGCA---TCCACTTTTAAAC---TAAACATTATTG--
C. magnus AF190009 -----CACTGTTGGATGCTTGCA---TCCACTTTTAAAC---TAAACATTATTG--
Y2M-PDA -----GCATGTTGGATGCTTGCA---CCACTTTTAAAC---TAAACATTATTG--
C. oeirensis AF444349 -----CACTGTTGGATGCTTGCA---TCCACTTTTAAAC---TAAACATTATTG--
C. oeirensis AF444364 -----CACTGTTGGATGCTTGCA---TCCACTTTTAAAC---TAAACATTATTG--
C. oeirensis EU002866 -----CACTGTTGGATGCTTGCA---TCCACTTTTAAAC---TAAACATTATTG--
C. chernovii AF444354 -----GACTGTTGGATGCTTGCA---CCACTTTTATAC---TAAACATTATTG--
C. chernovii FN400936 -----GACTGTTGGATGCTTGCA---CCACTTTTATAC---TAAACATTATTG--
Uncultured fungus FM178256 -G-----AACTGTTGGATGCTTGCA---CACTTTTATAC---TAAACATTATTG--
U3S-PDA -----GACTGTTGGATGCTTGCA---CCACTTTTATAC---TAAACATTATTG--
Uncultured fungus AJ875389 -----GACTGTTGGATGCTTGCA---CCACTTTTATAC---TAAACATTATTG--
Uncultured fungus AB520331 -----GACTGTTGGATGCTTGCA---CCACTTTTATAC---TAAACATTATTG--
C. carnesens AB035050 -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
Uncultured fungus FJ820684 -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
Uncultured fungus AM901777 -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
Z2S-STD -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
C. carnesens EU149785 -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
C. sp. HM849618 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
C. carnesens CBS8395 -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
C. carnesens AB105438 -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
C. victoriae AY188380 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
C. victoriae AJ581046 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
C. victoriae AM160647 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
C. victoriae CBS9265 G-----AACTGTG---CTTTGG---CCATC-----CACA---AAC-TGTTAG--
C. victoriae HM849622 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
C. victoriae AF444645 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
C. victoriae AY040656 -----AACTGTG---GCTTTGG---CCATC-----AC---AAAC-TGTTAG--
C. victoriae AJ581048 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
L2S-1-PDA -G-----AACTGTG---GCTTCGG---CCATC-----CAC---AAAC-TGTTAG--
W5S-4-STD -----GAAGTGTG---GCTTCGGC---CAT-----CAC---AAAC-TGTTAG--
C. sp. HM589279 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
C. victoriae AY040654 -----AACTGTG---GCTTCGG---CCATC-----AC---AAAC-TGTTAG--
S4S-PDA -----GAAGTGTG---CTTCGG---CCAT-----CAC---AAAC-TGTTAG--
C. victoriae CBS9267 G-----AACTGTG---CTTCGG---CCAT-----CACA---AAC-TGTTAG--

R. minuta AF190010 -TATAAGA-ATG-T--AATAGTCTCTTAATTGAGCATAAACAAAA--ATAAACTTTTCAG
R. slooffiae AF444552 -TATAAGA-ATGTA---ATAGTCTCTTAATTGAGCATAAAATAAAA--ACAAAACCTTTTCAG
R. slooffiae AF444627 -TATAAGA-ATGTA---ATAGTCTCTTAATTGAGCATAAAATAAAA--ACAAAACCTTTTCAG
Cy. macerans AF444317 -TCATTGA-ATG-T-----AAAATCG-T-----TATAAACTA---ATATAACTTTCAA
Cy. macerans AF444329 -TCATTGA-ATG-T-----AAAATCG-T-----TATAAACTA---ATATAACTTTCAA
Uncultured fungus AB520409 -TCATTGA-ATG-T-----AAAATCG-----TTATAAACTA---ATATAACTTTCAA
Uncultured fungus AB520402 -TCATTGA-ATG-T-----AAAATCG-----TTATAAACTA---ATATAACTTTCAA
Uncultured fungus AB520396 -TCATTGA-ATG-T-----AAAATCG-----TTATAAACTA---ATATAACTTTCAA
C. sp. AF444448 -TCATTGA-ATG-T-----AAAATCGT-----TATAAACTA---ATATAACTTTCAA
P4M-STD -TCATTGA-ATG-TA-----AAAATCG--T-----TATAAACTA---ATATAACTTTCAA
T1S-1-PDA -TCATTGA-ATG-TA-----AAAATCG-----TTATAAACTA---TATAACTTTCAA
C. macerans EU082232 -TCATTGA-ATG-T-----AAAATCGT-----TATAAACTA---ATATAACTTTCAA
C. macerans EU082233 -TCATTGA-ATG-T-----AAAATCGT-----TATAAACTA---ATATAACTTTCAA
C. macerans EU082231 -TCATTGA-ATG-T-----AAAATCGT-----TATAAACTA---ATATAACTTTCAA
C. macerans AY052490 -TCATTGA-ATG-T-----AAAATCGT-----TATAAACTA---ATATAACTTTCAA
Uncultured fungus EF504408 -TA-ATGA-ACG-T-----AACCT-----ATATTAATCATA---TAAAACCTTTAA
Bm. albus AF444664 -TA-ATGA-ACG-T-----AACCT-----ATATTAATCAT---ATAAACTTTTAA
V5M-PDA -TA-ATGA-ACG-T-----AACCT-----ATATTAATCATA---TAAAACCTTTAA
B. unica AF444441 -TA-ATGA-ACG-T-----AACCT-----ATATTAATCAT---ATAAACTTTTAA
Bm. albus AB093527 -TA-ATGA-ACG-T-----AACCT-----ATATTAATCAT---ATAAACTTTTAA
Bm. albus CBS7856 -TA-ATGA-ACG-T-----AACCT-----ATATTAATCAT---ATAAACTTTTAA
C. dimennae AY188365 -TCGA-ATG-T-----AATAT--A-----TCAT-AACAAA---ATACAACCTTTAA
C. dimennae AF410473 -TC-TCGA-ATG-T-----AATAT--A-----TCAT-AACAAA---ATACAACCTTTAA
C. dimennae EU266559 -TC-TCGA-ATG-T-----AATAT--A-----TCAT-AACAAA---ATACAACCTTTAA
Uncultured Fungus AM901805 -TC-TCGA-ATG-T-----AATAT-----ATCAT-AACAAA---TACAACCTTTAA
T1S-3-PDA -TC-TCGA-ATG-TA-----AATAT-----ATCAT-AACAAA---ATACAACCTTTAA
Y5S-PDA -TC-TCGA-ATG-T-----AATAT-----ATCAT-AACAAA---TACAACCTTTAA
Z4S-1-STD -TC-TCGA-ATG-T-----AATAT-----ATCAT-AACAAA---TACAACCTTTAA
C. oeiensis AY188362 ---TAACAAATG-T-----AGTCTT-A-----TTAT-AACATA---ATAAACTTTCAA
C. magnus AF190009 ---TAACAAATG-T-----AGTCTT-A-----TTAT-AACATA---ATAAACTTTCAA
Y2M-PDA ---TAACAAATG-T-----AGTCTT-----ATTAT-AACATA---TAAAACCTTTAA
C. oeiensis AF444349 ---TAACAAATG-T-----AGTCTT-A-----TTAT-AACATA---ATAAACTTTCAA
C. oeiensis AF444364 ---TAACAAATG-T-----AGTCTT-A-----TTAT-AACATA---ATAAACTTTCAA
C. oeiensis EU002866 ---TAACAAATG-T-----AGTCTT-A-----TTAT-AACATA---ATAAACTTTCAA
C. chernovii AF444354 ---TAACAAATG-T-----AGTCTT-----ATTAT-AACATA---ATAAACTTTAA
C. chernovii FN400936 ---TAACAAATG-T-----AGTCTT-----ATTAT-AACATA---ATAAACTTTAA
Uncultured fungus FM178256 ---TAACAAATGTG-----GTCTT-----ATTAT-AACATA---ATAAACTTTAA
U3S-PDA ---TAACAAATG-T-----AGTCTT-----ATTAT-AACATA---TAAAACCTTTAA
Uncultured fungus AJ875389 ---TAACAAATG-T-----AGTCTT-----ATTAT-AACATA---ATAAACTTTAA
Uncultured fungus AB520331 ---TAACAAATG-T-----AGTCTT-----ATTAT-AACATA---ATAAACTTTAA
C. carnesens AB035050 -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
Uncultured fungus FJ820684 -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
Uncultured fungus AM901777 -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
Z2S-STD -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
C. carnesens EU149785 -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
C. sp. HM849618 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. carnesens CBS8395 -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
C. carnesens AB105438 -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
C. victorae AY188380 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. victorae AJ581046 -TA-ATGA-ATG-T-----AATAT--C-----AT-GACAAA---ACAAAACCTTTAA
C. victorae AM160647 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. victorae CBS9265 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. victorae HM849622 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. victorae AF444645 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. victorae AY040656 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. victorae AJ581048 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
L2S-1-PDA -TA-ATGA-ATG-TA-----AATAT---C-----AT-AACAAA---ACAAAACCTTTAA
W5S-4-STD -TA-ATGA-ATG-T-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
C. sp. HM589279 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
C. victorae AY040654 -TA-ATGA-ATG-T-----AATAT--C-----AT-AACAAA---ACAAAACCTTTAA
S4S-PDA ---AATGA-ATGT-----AATAT-----CAT-AACAAA---ACAAAACCTTTAA
C. victorae CBS9267 -TA-ATGA-ATG-T-----AATAT---C-----AT-AACAAA---ACAAAACCTTTAA

[illegible]

R. minuta AF190010 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCACTCTTT-GGTATTC
R. slooffiae AF444552 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCACTCTTT-GGTATTC
R. slooffiae AF444627 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCACTCTTT-GGTATTC
Cy. macerans AF444317 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
Cy. macerans AF444329 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
Uncultured fungus AB520409 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
Uncultured fungus AB520402 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
Uncultured fungus AB520396 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
C. sp. AF444448 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
P4M-STD AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
T1S-1-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
C. macerans EU082232 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
C. macerans EU082233 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
C. macerans EU082231 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
C. macerans AY052490 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTT-GGTATTC
Uncultured fungus EF504408 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGC-CTTTTGGTATTC
Bm. albus AF444664 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGC-CTTTTGGTATTC
V5M-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGC-CTTTTGGTATTC
B. unica AF444441 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGC-CTTTTGGTATTC
Bm. albus AB093527 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGC-CTTTTGGTATTC
Bm. albus CBS7856 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGC-CTTTTGGTATTC
C. dimennae AY188365 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTCT-GGTATTC
C. dimennae AF410473 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTCT-GGTATTC
C. dimennae EU266559 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTCT-GGTATTC
Uncultured Fungus AM901805 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTCT-GGTATTC
T1S-3-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTCT-GGTATTC
Y5S-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTCT-GGTATTC
Z4S-1-STD AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTCT-GGTATTC
C. oeirensis AY188362 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
C. magnus AF190009 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
Y2M-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
C. oeirensis AF444349 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
C. oeirensis AF444364 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
C. oeirensis EU002866 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
C. chernovii AF444354 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
C. chernovii FN400936 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
Uncultured fungus FM178256 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
U3S-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
Uncultured fungus AJ875389 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
Uncultured fungus AB520331 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTT-GGTATTC
C. carnescens AB035050 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
Uncultured fungus FJ820684 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
Uncultured fungus AM901777 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
Z2S-STD AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. carnescens EU149785 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. sp. HM849618 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. carnescens CBS8395 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. carnescens AB105438 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae AY188380 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae AJ581046 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae AM160647 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae CBS9265 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae HM849622 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae AF444645 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae AY040656 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae AJ581048 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
L2S-1-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
W5S-4-STD AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. sp. HM589279 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae AY040654 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
S4S-PDA AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC
C. victoriae CBS9267 AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCCCTTT-GGTATTC

R. minuta AF190010 CGAAGAGTATGCTGTTTGGAGTATCATGAAACTCTCAACC---CCCC--TATTTTGTAAAT
R. slooffiae AF444552 CGAAGAGTATGCTGTTTGGAGTATCATGAAACTCTC-AAC---CCCCCTATTTTGTAAATG
R. slooffiae AF444627 CGAAGAGTATGCTGTTTGGAGTATCATGAAACTCTC-AAC---CCCCCTATTTTGTAAATG
Cy. macerans AF444317 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Cy. macerans AF444329 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Uncultured fungus AB520409 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
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Uncultured fungus AB520396 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. sp. AF444448 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
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C. macerans EU082232 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. macerans EU082233 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. macerans EU082231 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. macerans AY052490 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Uncultured fungus EF504408 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Bm. albus AF444664 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
V5M-PDA CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
B. unica AF444441 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Bm. albus AB093527 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Bm. albus CBS7856 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. dimennae AY188365 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. dimennae AF410473 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. dimennae EU266559 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Uncultured Fungus AM901805 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
T1S-3-PDA CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Y5S-PDA CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
Z4S-1-STD CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. oeirensis AY188362 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. magnus AF190009 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
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C. chernovii AF444354 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. chernovii FN400936 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
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Uncultured fungus FJ820684 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
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C. carnesens EU149785 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. sp. HM849618 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. carnesens CBS8395 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. carnesens AB105438 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae AY188380 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae AJ581046 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae AM160647 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae CBS9265 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae HM849622 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae AF444645 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae AY040656 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae AJ581048 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
L2S-1-PDA CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
W5S-4-STD CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. sp. HM589279 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae AY040654 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
S4S-PDA CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA
C. victoriae CBS9267 CGAAGAGCATGCCTGTTTGGAGTATCATGAAACTCTC--AC---CTCCAGCCTTCTTT-AA

R. minuta AF190010 ---GAAATGGGCGTGGGCTTGGATTATGGTTGTCTGTCG--GCGTAATTGC-----CGG
R. slooffiae AF444552 AGATGGGTGT---GGGCTTGGATTATGGTTGTCTGTCG--GCGTAATTGC-----CGG
R. slooffiae AF444627 AGATGGGTGT---GGGCTTGGATTATGGTTGTCTGTCG--GCGTAATTGC-----CGG
Cy. macerans AF444317 TTAGAGGTGTTG--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
Cy. macerans AF444329 TTAGAGGTGTTG--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
Uncultured fungus AB520409 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
Uncultured fungus AB520402 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
Uncultured fungus AB520396 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
C. sp. AF444448 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
P4M-STD TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
T1S-1-PDA TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
C. macerans EU082232 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
C. macerans EU082233 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
C. macerans EU082231 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
C. macerans AY052490 TTAGAGGTGTT--GGGCGTGGACG-TGAGTGC-TGCTGGTGCCC---TGGTTGCATCGG
Uncultured fungus EF504408 TGATCAGTGTT--GGGCTTGGACT-----TGGGTGCTC--GCCAGTTCGCT-----GG
Bm. albus AF444664 TGATCAGTGTT--GGGCTTGGACT-----TGGGTGCTC--TGCCAGTTCGC-----TGG
V5M-PDA TGATCAGTGTT--GGGCTTGGACT-----TGGGTGCTC--GCCAG--GACTTGTCTCTGG
B. unica AF444441 TGATCAGTGTT--GGGCTTGGACT-----TGGGTGCTC--TGCCAG--GACTTGTCTCTGG
Bm. albus AB093527 TGATCAGTGTT--GGGCTTGGACT-----TGGGTGCTC--TGCCAGTTCGC-----TGG
Bm. albus CBS7856 TGATCAGTGTT--GGGCTTGGACT-----TGGGTGCTC--TGCCAGTTCGC-----TGG
C. dimennae AY188365 CC-----GAT--CGG--GTGGACT-----TGGGCGCT--GCCAG-----TGAAATGG
C. dimennae AF410473 CC-----GATC-----GGGTGGATT-----TGGGTGCT--GCCAG--TTACAT-----GG
C. dimennae EU266559 CC-----GAT--CGG--GTGGACT-----TGGGTGCT--GCCAG--TTACAT-----GG
Uncultured Fungus AM901805 CGATC-----GGGTGGATT-----TGGGTGCT--GCCAG--TTACAT-----GG
T1S-3-PDA CGATC-----GGGTGGATT-----TGGGTGCT--GCCAG--TTACAT-----GG
Y5S-PDA CGATC-----GGGTGGATT-----TGGGTGCT--GCCAG--TTACAT-----GG
Z4S-1-STD CGATC-----GGGTGGATT-----TGGGTGCT--GCCAG--TTACAT-----GG
C. oeirensis AY188362 CGGTCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TGAACCGA
C. magnus AF190009 CGATCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TGAACCGA
Y2M-PDA CGATCCCTTGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TGAACCGA
C. oeirensis AF444349 CGGTCCATGCT--TGAGTTTGGATT-----TGGACGTT--TGCCCG--TGA-TGAACCGA
C. oeirensis AF444364 CGGTCCATGCT--TGAGTTTGGATT-----TGGACGTT--TGCCCG--TGA-TGAACCGA
C. oeirensis EU002866 CGGTCCATGCT--TGAGTTTGGATT-----TGGACGTT--TGCCCG--TGA-TGAACCGA
C. chernovii AF444354 CGATCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TAAGCCGA
C. chernovii FN400936 CGATCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TAAGCCGA
Uncultured fungus FM178256 CGATCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TAAGCCGA
U3S-PDA CGATCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TAAGCCGA
Uncultured fungus AJ875389 CGATCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TAAGCCGA
Uncultured fungus AB520331 CGATCCATGCT--TGAGTTTGGATT-----TGGATGTT--TGCCCG--TGA-TAAGCCGA
C. carnescens AB035050 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
Uncultured fungus FJ820684 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
Uncultured fungus AM901777 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
Z2S-STD TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
C. carnescens EU149785 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
C. sp. HM849618 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
C. carnescens CBS8395 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
C. carnescens AB105438 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCCAAA---GG
C. victorinae AY188380 TTGCCTAAG---CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. victorinae AJ581046 TTGCCTAAG---CGGTGGTGATT-----GGGTGTT--TGCC---TTGCTAAA---GG
C. victorinae AM160647 TTGCCTAAG---CGGTGGTGATT-----GGGTGTT--TGCC---TTGCTAAA---GG
C. victorinae CBS9265 TTGCC--TGAGC--GGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. victorinae HM849622 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. victorinae AF444645 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. victorinae AY040656 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. victorinae AJ581048 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
L2S-1-PDA TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
W5S-4-STD TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. sp. HM589279 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. victorinae AY040654 TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
S4S-PDA TTGCC--TGAG--CGGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG
C. victorinae CBS9267 TTGCC--TGAGC--GGTGGTGATT-----GGGTGTT--GCC---TTGCTAAA---GG

R. minuta AF190010 CTCAACTGAAATAC-ACGAGCA-----ACCCCTATT---GAAATAGACGGTTTGACT
R. slooffiae AF444552 CTCAACTGAAATAC-ACGAGCA-----ACCCCTATT---GAAATAACGGTTTGACT
R. slooffiae AF444627 CTCAACTGAAATAC-ACGAGCA-----ACCCCTATT---GAAATAACGGTTTGACT
Cy. macerans AF444317 CTCACCTGAAATATG-TTAGCTG-A-----CTCCTCTA-----GAGGTGGTTCTACT
Cy. macerans AF444329 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCTA-----GAGGTGGTTCTACT
Uncultured fungus AB520409 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
Uncultured fungus AB520402 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
Uncultured fungus AB520396 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
C. sp. AF444448 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
P4M-STD CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
T1S-1-PDA CTCACCTGAAATAT-GTTAGCTG--C-----TCCTCT-----AGAGGTGGTTCTACT
C. macerans EU082232 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
C. macerans EU082233 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
C. macerans EU082231 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
C. macerans AY052490 CTCACCTGAAATAC-ATTAGCTG-A-----ATCCTCT-----AGAGGTGGTTCTACT
Uncultured fungus EF504408 CTCGCCTTAAAGAG-TTAGTGGT---AATAACATC-----CACGGCTA
Bm. albus AF444664 CTCGCCTTAAAGA-GTTAGTGGT---AATAACATC-----CACGGCTA
V5M-PDA CTCGCCTTAAATGAC-TTAGTGGG---AATAGCATC-----CACGGCTA
B. unica AF444441 CTCGCCTTAAATGA-CTTAGTGGG---AATAGCATC-----CACGGCTA
Bm. albus AB093527 CTCGCCTTAAAGA-GTTAGTGGT---AATAACATC-----CACGGCTA
Bm. albus CBS7856 CTCGCCTTAAAGA-GTTAGTGGT---AATAACATC-----CACGGCTA
C. dimennae AY188365 CTCGCCTTAAAGC-ATTAGC--G-----GTTG---T
C. dimennae AF410473 CTCGCCTTAAAGC-ATTAGC--G-----GTTG---T
C. dimennae EU266559 CTCGCCTTAAAGC-ATTAGC--G-----GTTG---T
Uncultured Fungus AM901805 CTCGCCTTAAAGC-ATTAGC--G-----GTTG---T
T1S-3-PDA CTCGCCTTAAAGC-ATTAGC--G-----GTTG---T
Y5S-PDA CTCGCCTTAAAGC-ATTAGC--G-----GTTG---T
Z4S-1-STD CTCGCCTTAAAGC-ATTAGC--G-----GTTG---T
C. oeirensis AY188362 CTCATCTTAAAGT-ATTAGCTGG-----ATCTGTC---TATATGACTGGTTTGACT
C. magnus AF190009 CTCATCTTAAAGT-ATTAGCTTG-----GATCTGTC---TATATGACTGGTTTGACT
Y2M-PDA CTCATCTTAAAGT-ATTAGCTGG-----ATCTGTC---TATATGACTGGTTTGACT
C. oeirensis AF444349 CTCGTCTTAAAGT-ATTAGCTGG-----ATCTGTC---TATATGACTGGTTTGACT
C. oeirensis AF444364 CTCGTCTTAAAGT-ATTAGCTGG-----ATCTGTC---TATATGACTGGTTTGACT
C. oeirensis EU002866 CTCGTCTTAAAGT-ATTAGCTGG-----ATCTGTC---TATATGACTGGTTTGACT
C. chernovii AF444354 CTCATCTTAAAGT-ATTAGCTA-----GATCTGTC---TCTATACTGGTTTGACT
C. chernovii FN400936 CTCATCTTAAAGT-ATTAGCTA-----GATCTGTC---TCTATACTGGTTTGACT
Uncultured fungus FM178256 CTCATCTTAAAGT-ATTAGCTAG-----ATCTGTC---TCTATGACTGGTTTGACT
U3S-PDA CTCATCTTAAAGT-ATTAGCTAG-----ATCTGTC---TCTATGACTGGTTTGACT
Uncultured fungus AJ875389 CTCATCTTAAAGT-ATTAGCTAG-----ATCTGTC---TCTATGACTGGTTTGACT
Uncultured fungus AB520331 CTCATCTTAAAGT-ATTAGCTAG-----ATCTGTC---TCTATGACTGGTTTGACT
C. carnescens AB035050 CTCGCCTTAAAGC-ATAAGC-----ACCT-----TGGA--
Uncultured fungus FJ820684 CTCGCCTTAAAGC-ATAAGC-----CCT-----TGGA--
Uncultured fungus AM901777 CTCGCCTTAAAGC-ATAAGC-----CCT-----TGGA--
Z2S-STD CTCGCCTTAAAGC-ATAAGC-----CCT-----TGGA--
C. carnescens EU149785 CTCGCCTTAAAGC-ATAAGC-----ACCT-----TGGA--
C. sp. HM849618 CTCGCCTTAAAGC-ATAAGC--A-----CCT-----TGGA--
C. carnescens CBS8395 CTCGCCTTAAAGC-ATAAGC-----ACCT-----TGGA--
C. carnescens AB105438 CTCGCCTTAAAGC-ATAAGC-----ACCT-----TGGA--
C. victorinae AY188380 CTCGCCTTAAAGAT-ATAAGC--A-----CCT-----TGGA--
C. victorinae AJ581046 CTCGCCTTAAAGAT-ATAAGC--A-----CCT-----TGGA--
C. victorinae AM160647 CTCGCCTTAAAGAT-ATAAGC--A-----CCT-----TGGA--
C. victorinae CBS9265 CTCGCCTTAAAGAC-ATAAGC--A-----CCT--T-----GGA--
C. victorinae HM849622 CTCGCCTTAAAGAC-ATAAGC--A-----CCT-----TGGA--
C. victorinae AF444645 CTCGCCTTAAAGAC-ATAAGC--A-----CCT-----TGGA--
C. victorinae AY040656 CTCGCCTTAAAGAC-ATAAGC--A-----CCT-----TGGA--
C. victorinae AJ581048 CTCGCCTTAAAGAC-ATAAGC--A-----CCT-----TGGA--
L2S-1-PDA CTCGCCTTAAAGAC-ATAAGC--A-----CCT--T-----GGA--
W5S-4-STD CTCGCCTTAAAGAC-ATAAGC-----CCT-----TGGA--
C. sp. HM589279 CTCGCCTTAAAGAC-ATAAGC--A-----CCT-----TGGA--
C. victorinae AY040654 CTCGCCTTAAAGAC-ATAAGC--A-----CCT-----TGGA--
S4S-PDA CTCGCCTTAAAGAC-ATAAGC-----ACCT-----TGGA--
C. victorinae CBS9267 CTCGCCTTAAAGAC-ATAAGC--A-----CCT--T-----GGA--

R. minuta AF190010 TGCGCTAATAAT-TATTTTCG-----C-----TAAGGA-CGT
R. slooffiae AF444552 TGCGCTAATAA-TTATTTTCG-----C-----TAAGGA-CGC
R. slooffiae AF444627 TGCGCTAATAA-TTATTTTCG-----C-----TAAGGA-CGT
Cy. macerans AF444317 CGACGTGATAA-GATCTCCGTC--G-----AGGACAGTGCAAC-TTGTGTGC-TG-
Cy. macerans AF444329 CGACGTGATAA-GATCTCCGTC--G-----AGGACAGTGCAAC-TTGTGTGC-TG-
Uncultured fungus AB520409 CGACGTGATAAG-ATCTCCGTC-----GAGGACAGTGCAACTTGT--GTGCTG-
Uncultured fungus AB520402 CGACGTGATAAG-ATCTCCGTC-----GAGGACAGTGCAACTTGT--GTGCTG-
Uncultured fungus AB520396 CGACGTGATAAG-ATCTCCGTC-----GAGGACAGTGCAACTTGT--GTGCTG-
C. sp. AF444448 CGACGTGATAA-GATCTCCGTC-G-----AGGACAGTGCAACTT-GTTGTGC-TG-
P4M-STD CGACGTGATAAG-ATCTCCGTC--G-----AGGACAGTGCAAC-TTGTGTGC-TG-
T1S-1-PDA CGACGTGATAA-GATCTCCGTC-----GAGGACAGTGCAAC-TTGTGTGC-TG-
C. macerans EU082232 CGACGTGATAA-GATCTCCGTC-G-----AGGACAGTGCAACTT-GTTGTGC-TG-
C. macerans EU082233 CGACGTGATAA-GATCTCCGTC-G-----AGGACAGTGCAACTT-GTTGTGC-TG-
C. macerans EU082231 CGACGTGATAA-GATCTCCGTC-G-----AGGACAGTGCAACTT-GTTGTGC-TG-
C. macerans AY052490 CGACGTGATAA-GATCTCCGTC-G-----AGGACAGTGCAACTT-GTTGTGC-TG-
Uncultured fungus EF504408 AGACGTAATAAG---TTTCGTC-----T-----GGTCAAGGTG-TGA
Bm. albus AF444664 AGACGTAATAA---GTTTCGTC-----T-----TGGTCAAGGTG-TGA
V5M-PDA AGACGTAATAAG---TTTCGTC-----T-----GGTCAAGGTG-TGA
B. unica AF444441 AGACGTAATAA---GTTTCGTC-----T-----TGGTCAAGGTG-TGA
Bm. albus AB093527 AGACGTAATAA---GTTTCGTC-----T-----TGGTCAAGGTG-TGA
Bm. albus CBS7856 AGACGTAATAA---GTTTCGTC-----T-----TGGTCAAGGTG-TGA
C. dimennae AY188365 TGACGTAATAA---GTTTCGTC-----T-----T-TGT
C. dimennae AF410473 TGACGTAATAA---GTTTCGTC-----T-----TGT
C. dimennae EU266559 TGACGTAATAA---GTTTCGTC-----T-----T-TGT
Uncultured Fungus AM901805 TGACGTAATAAG---TTTCGTC-----T-----GT
T1S-3-PDA TGACGTAATAA---GTTTCGTC-----T-----CGACCGCTCCTAATCTCCTTCGGGATG
Y5S-PDA TGACGTAATAAG---TTTCGTC-----T-----GT
Z4S-1-STD TGACGTAATAAG---TTTCGTC-----T-----CT
C. oeirensis AY188362 TGGCATAATAAGTATTTTGCTG-A-----G-----GACAT-CTTCGGA-TG-
C. magnus AF190009 TGGCATAATAAGTATTTTGCTG-A-----G-----GACAT-CTTCGGA-TG-
Y2M-PDA TGGCATAATAAGTATTTTGCTG-----AGGACA-----TCTTCGGA-TG-
C. oeirensis AF444349 TGGCATAATAAGTATTTTGCTG-A-----G-----GACAT-CTTCGGA-TG-
C. oeirensis AF444364 TGGCATAATAAGTATTTTGCTG-A-----G-----GACAT-CTTCGGA-TG-
C. oeirensis EU002866 TGGCATAATAAGTATTTTGCTGAG-----G-----ACAT-CTTCGGA-TG-
C. chernovii AF444354 TGGCATAATAAGTATTTTGCTG-----A-----GGACAT-CTTCGGA-TG-
C. chernovii FN400936 TGGCATAATAAGTATTTTGCTG-----A-----GGACAT-CTTCGGA-TG-
Uncultured fungus FM178256 TGGCATAATAAGTATTTTGCTG-----AGGACATCTTCGGA-TG-
U3S-PDA TGGCATAATAAGTATTTTGCTG-----AGGACA-----TCTTCGGA-TG-
Uncultured fungus AJ875389 TGGCATAATAAGTATTTTGCTG-----AGGACA-----TCTTCGGA-TG-
Uncultured fungus AB520331 TGGCATAATAAGTATTTTGCTG-----AGGACA-----TCTTCGGA-TG-
C. carnesens AB035050 TG---TAATAC---GTTTCATC-----CTTCT---GGG-TG-
Uncultured fungus FJ820684 TG---TAATACG---TTTCATC-----C-----TTCT---GGGTG-
Uncultured fungus AM901777 TG---TAATACG---TTTCATC-----C-----TTCT---GGGTG-
Z2S-STD TG---TAATACG---TTTCATC-----C-----TTCT---GGGTG-
C. carnesens EU149785 TG---TAATAC---GTTTCATC-----CTTTC---GGG-TG-
C. sp. HM849618 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. carnesens CBS8395 TG---TAATAC---GTTTCATC-----CTTCT---GGG-TG-
C. carnesens AB105438 TG---TAATAC---GTTTCATC-----CTTCT---GGG-TG-
C. victorinae AY188380 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae AJ581046 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae AM160647 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae CBS9265 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae HM849622 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae AF444645 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae AY040656 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae AJ581048 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
L2S-1-PDA TG---TAATACG---TTTCATC---C-----TTCT---GGG-TG-
W5S-4-STD TG---TAATACG---TTTCATC-----C-----TTCT---GGGTG-
C. sp. HM589279 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
C. victorinae AY040654 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-
S4S-PDA TG---TAATAC---GTTTCATC-----C-----TTCT---GGG-TG-
C. victorinae CBS9267 TG---TAATAC---GTTTCATC-C-----TTCT---GGG-TG-

R. minuta AF190010 -----CTTCTTCAAATATAAGAG-----GTGCTTCTAAT
R. slooffiae AF444552 TTTC---TTCAAATATAAGAGGTGCTTCTAATTGCTTC-----
R. slooffiae AF444627 TTTC---TTCAAATATAAGAGGTGCTTCTAATTGCTTC-----
Cy. macerans AF444317 -GCCGCTCCTAGCAGTTGACGTGCTTCTAATTAGCGCAGACTTCGAG--TGC-----TG
Cy. macerans AF444329 -GCCGCCGCTAGCAGTTGAT-ACGCTTCTAATTAGCGCAGACTTCGAG--TGC-----TG
Uncultured fungus AB520409 -GCCGCCGCTAGCAGTTGA-TACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
Uncultured fungus AB520402 -GCCGCCGCTAGCAGTTGA-TACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
Uncultured fungus AB520396 -GCCGCCGCTAGCAGTTGA-TACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
C. sp. AF444448 -GCCGCCGCTAGCTGTTGAT-ACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
P4M-STD -GCCGCCGCTAGCAGTTGAT-ACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
T1S-1-PDA -GCCGCTCCTAGCAGTTGACGTGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
C. macerans EU082232 -GCCGCCGCTAGCAGTTGAT-ACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
C. macerans EU082233 -GCCGCCGCTAGCTGTTGAT-ACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
C. macerans EU082231 -GCCGCCGCTAGCTGTTGAT-ACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
C. macerans AY052490 -GCCGCCGCTAGCTGTTGAT-ACGCTTCTAATTAGCGCAGACTTCGA--GTGC-----TG
Uncultured fungus EF504408 CGAC-----T-----GCT---CATAACCC--GACCGCAA-----G
Bm. albus AF444664 CGAC-----T-----GCT---CATAA--CCCGACCGCAA-----G
V5M-PDA AGCC-----T-----GCT---CATAACCC--GACCGCAA-----G
B. unica AF444441 AGCC-----T-----GCT---CATAA--CCCGACCGCAA-----G
Bm. albus AB093527 CGAC-----T-----GCT---CATAA--CCCGACCGCAA-----G
Bm. albus CBS7856 CGAC-----T-----GCT---CATAA--CCCGACCGCAA-----G
C. dimennae AY188365 CGAC-----C-----CGCT---CCTAATCTCCTTCGGGA---TGTCTCT--G
C. dimennae AF410473 CGAC-----C-----GCT---CCTAATCTCCTTCGGGA---TGTCTCTAGG
C. dimennae EU266559 CGAC-----C-----CGCT---CCTAATCTCCTTCGGGA---TGTCTCTAGG
Uncultured Fungus AM901805 CGAC-----C-----GCT---CCTAATCTCCTTCGGGA---TGTCTCTAGG
T1S-3-PDA CTCTAGGACACTTCATGAT-----
Y5S-PDA CGAC-----C-----GCT---CCTAATCTCCTTCGGGA---TGTCTCTAGG
Z4S-1-STD CGAC-----C-----GCT---CCTAATCTCCTTCGGGA---TGTCTCTAGG
C. oeiensis AY188362 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
C. magnus AF190009 -GCCAGGACCTAGACTACTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
Y2M-PDA -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
C. oeiensis AF444349 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
C. oeiensis AF444364 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
C. oeiensis EU002866 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
C. chernovii AF444354 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
C. chernovii FN400936 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
Uncultured fungus FM178256 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
U3S-PDA -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
Uncultured fungus AJ875389 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
Uncultured fungus AB520331 -GCCAGGACCTAGACTATTGTCTGCT--AACTAAACCATCACTTTAA--GTGCATCCTTG
C. carnescent AB035050 -----GCT---GATAACCCACACA---T-----
Uncultured fungus FJ820684 -G-----CT---GATAACCCACACA-----
Uncultured fungus AM901777 -G-----CT---GATAACCCACACA-----
Z2S-STD -G-----CT---GATAACCCACACA-----
C. carnescent EU149785 -----GCT---GATAACCCACACA---T-----
C. sp. HM849618 -----GCT---GATAACCCACACA-----T-----
C. carnescent CBS8395 -----GCT---GATAACCCACACA---T-----
C. carnescent AB105438 -----GCT---GATAACCCACACA---T-----
C. victoriae AY188380 -----GCT---GATAACCCACACA-----T-----
C. victoriae AJ581046 -----GCT---GATAACCCACACA-----T-----
C. victoriae AM160647 -----GCT---GATAACCCACACA-----T-----
C. victoriae CBS9265 -----GCT---GATAACCCACACA-----T-----
C. victoriae HM849622 -----GCT---GATAACCCACACA-----T-----
C. victoriae AF444645 -----GCT---GATAACCCACACA-----T-----
C. victoriae AY040656 -----GCT---GATAACCCACACA-----T-----
C. victoriae AJ581048 -----GCT---GATAACCCACACA-----T-----
L2S-1-PDA -----GCT---GATAACCCACACA-----T-----
W5S-4-STD -G-----CT---GATAACCCACACA-----
C. sp. HM589279 -----GCT---GATAACCCACACA-----T-----
C. victoriae AY040654 -----GCT---GATAACCCACACA-----T-----
S4S-PDA -G-----CT---GATAACCCACACA-----
C. victoriae CBS9267 -----GCT---GATAACCCACACA-----T-----

R. minuta AF190010 GCGCTTTATAGCAC-----TTTAAGCTTTAGATCTCAAAATCAGTCAGGACTACCCG
R. slooffiae AF444552 -----TAATAGCAT-----TTAAGCTTTAGACCTCAAAATCAGTCAGGACTACCCG
R. slooffiae AF444627 -----TAATAGCAT-----TTAAGCTTTAGACCTCAAAATCAGTCAGGACTACCCG
Cy. macerans AF444317 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Cy. macerans AF444329 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Uncultured fungus AB520409 GCAACTTTTGACA-----ACTTGGC-CTCAAAATCAGGTAGGACTACCCA
Uncultured fungus AB520402 GCAACTTTTGACA-----ACTTGGC-CTCAAAATCAGGTAGGACTACCCA
Uncultured fungus AB520396 GCAACTTTTGACA-----ACTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. sp. AF444448 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
P4M-STD GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
T1S-1-PDA GCAACTTTTGACA-----ACTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. macerans EU082232 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. macerans EU082233 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. macerans EU082231 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. macerans AY052490 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Uncultured fungus EF504408 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Bm. albus AF444664 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
V5M-PDA GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
B. unica AF444441 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Bm. albus AB093527 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Bm. albus CBS7856 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. dimennae AY188365 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. dimennae AF410473 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. dimennae EU266559 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Uncultured Fungus AM901805 GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
T1S-3-PDA GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Y5S-PDA GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
Z4S-1-STD GCAACTTTTGACA-----A-----CTTGGC-CTCAAAATCAGGTAGGACTACCCA
C. oeirensis AY188362 GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
C. magnus AF190009 GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
Y2M-PDA GATGTTACT--AATCGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
C. oeirensis AF444349 GATGTTACT--AATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
C. oeirensis AF444364 GATGTTACT--AATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
C. oeirensis EU002866 GATGTTACT--AATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
C. chernovii AF444354 GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
C. chernovii FN400936 GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
Uncultured fungus FM178256 GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
U3S-PDA GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
Uncultured fungus AJ875389 GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
Uncultured fungus AB520331 GATGTTACT--CATTGTGTAACCTTG-ACATCTGGC-CTCAAAATCAGGTAGGACTACCCG
C. carnescens AB035050 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
Uncultured fungus FJ820684 -----TATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
Uncultured fungus AM901777 -----TATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
Z2S-STD -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. carnescens EU149785 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. sp. HM849618 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. carnescens CBS8395 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. carnescens AB105438 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae AY188380 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae AJ581046 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae AM160647 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae CBS9265 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae HM849622 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae AF444645 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae AY040656 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae AJ581048 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
L2S-1-PDA -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
W5S-4-STD -----TATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. sp. HM589279 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae AY040654 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
S4S-PDA -----TATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG
C. victorinae CBS9267 -----ATT--CAT-----GATCTGGC-CTCAAAATCAGGTAGGCTACCCG

R. minuta AF190010	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAG-----
R. slooffiae AF444552	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
R. slooffiae AF444627	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAG-----
Cy. macerans AF444317	CTGAACCTTAAGCATATCAATAAGTGGAGGA-----
Cy. macerans AF444329	CTGAACCTTAAGCATATCAATAAGTGGAGGA-----
Uncultured fungus AB520409	CTGAACCTTAAGCATATCAATAAGTGGAGGAAAAGAACTAACAAGGA
Uncultured fungus AB520402	CTGAACCTTAAGCATATCAATAAGTGGAGGAAAAGAACTAACAAGGA
Uncultured fungus AB520396	CTGAACCTTAAGCATATCAATAAGTGGAGGAAAAGAACTAACAAGGA
C. sp. AF444448	CTGAACCTTAAGCATATCAATAAGTGGAGGA-----
P4M-STD	CTGAACCTTAA-----
T1S-1-PDA	CTGAACCTTAA-----
C. macerans EU082232	CTGAACCTTAA-----
C. macerans EU082233	C-----
C. macerans EU082231	-----
C. macerans AY052490	CTGAACCTTAAGCATATCAA-----
Uncultured fungus EF504408	CTGAACCTTAAGCA-----
Bm. albus AF444664	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
V5M-PDA	CTGAACCTTAA-----
B. unica AF444441	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
Bm. albus AB093527	CTGAACCTTAAGCATATCAA-----
Bm. albus CBS7856	-----
C. dimennae AY188365	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAACTAACAAGGA
C. dimennae AF410473	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. dimennae EU266559	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAAATATTGAAATT-
Uncultured Fungus AM901805	CTGAACCTTAA-----
T1S-3-PDA	-----
Y5S-PDA	CTGAACCTTAA-----
Z4S-1-STD	CTGAACCTTAA-----
C. oeiensis AY188362	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAACTAACAAGGA
C. magnus AF190009	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
Y2M-PDA	CTGAACCTT-----
C. oeiensis AF444349	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. oeiensis AF444364	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. oeiensis EU002866	CTGAACCTTAA-----
C. chernovii AF444354	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. chernovii FN400936	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGA-----
Uncultured fungus FM178256	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
U3S-PDA	CTGAACCTTAA-----
Uncultured fungus AJ875389	CTGAACCTTAAGCATATCAATAAGCGGAGGAA-----
Uncultured fungus AB520331	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAACTAACAAGGA
C. carnescens AB035050	-----
Uncultured fungus FJ820684	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
Uncultured fungus AM901777	CTGAACCTTAA-----
Z2S-STD	C-----
C. carnescens EU149785	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. sp. HM849618	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. carnescens CBS8395	-----
C. carnescens AB105438	CTGAACCTTAA-----
C. victorinae AY188380	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAACTAAGTAGGA
C. victorinae AJ581046	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. victorinae AM160647	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAACTAAGTAGGA
C. victorinae CBS9265	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAACTAAGTAGGA
C. victorinae HM849622	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. victorinae AF444645	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. victorinae AY040656	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
C. victorinae AJ581048	CCGAACCTTAAGCATATCAATAAGCGGAGGA-----
L2S-1-PDA	CTGAACCTTAA-----
W5S-4-STD	CTGAACCTTAA-----
C. sp. HM589279	CTGAACCTTAAGCATATCAATAAGCCGG-----
C. victorinae AY040654	CTGAACCTTAAGCATATCAATAAGCGGAGGA-----
S4S-PDA	CTGAACCTTAA-----
C. victorinae CBS9267	CTGAACCTTAAGCATATCAATAAGCGGAGGAAAAGAACTAAGTAGGA

5.3.4 Pucciniomycotina

		1	10	20	30	40	50	60
C. chernovii	FN400936	TGCGGAAGGATCATT	-----ATTGAA	-----T	-----TCAA	--A	---TC	-----AT
C. magnus	AF190009	TGCGGAAGGATCATT	-----AATGAA	-----TTTAGATTGA	--AC	CATA	-----GG	
C. oeilensis	AF444364	TGCGGAAGGATCATT	-----AATGAT	-----TATAA	TCGT	--ACTGTT	CACGCAGTA	
	E5S-PDA	-----CATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCC	-----AA
	E3M-STD	-----AGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCC	-----AA
	Fungal sp. GU213437	-----AAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCC	-----AA
R. mucilaginosa	AF444614	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
	Q5S-2-PDA	-----TCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	AF444609	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	AF444503	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	CBS2382	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	FR690147	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	HQ702343	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	FJ515212	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	EU149812	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	EU871492	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
Uncultured fungus	FM875856	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	CBS8618	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
R. mucilaginosa	AF444635	TGCGGAAGGATCATT	-----AGTGAA	-----TA	-----TAGG	--AC	GTCCA	-----A
K. malvinella	AF444498	TGCGGAAGGATCATT	-----AGTGAA	-----ACA	-----TTAG	--AGTGCTC	-----	
K. malvinella	DQ667165	-----GTGAA	-----ACA	-----TTAG	--AGTGCTC	-----		
	K. aeria AM922224	-----GATCATT	-----AGTGAA	-----ACA	-----TAAG	--AGTGCTC	-----	
	K. aeria AF444562	TGCGGAAGGATCATT	-----AGTGAA	-----ACA	-----TAAG	--AGTGCTC	-----	
	K. aeria AF444675	TGCGGAAGGATCATT	-----AGTGAA	-----ACA	-----TAAG	--AGTGCTC	-----	
	H10S-PDA	-----AGGATCATT	-----AGTGAA	-----ACA	-----TAAG	--AGTGCTC	-----	
Basidiomycete	BSU65613	TGCGGAAGGATCATT	-----AATGAA	-----TACAC	--TGG	--AC	GCTC	-----TT
	R. sp. FU238090	TGCGGAAGGATCATT	-----AATGAA	-----TACA	--CTGG	--AC	GCTC	-----TT
	R. sp. FU865356	-----AAGGATCATT	-----AATGAA	-----TACA	--CTGG	--AC	GCTC	-----TT
	P2S-PDA	-----AGGATCATT	-----AATGAA	-----TACAC	--TGG	--AC	GCTCT	-----T
R. oryzicola	AF335160	TGCGGAAGGATCATT	-----AATGAA	-----ATGT	--TAGG	--AC	GCTGT	-----
	R. sp. FJ008055	-----	-----	-----	-----	-----	GCTC	-----TT
S. dacryoidea	AF444571	TGCGGAAGGATCATT	-----AATGAAA	-----TGT	--TAGG	--AC	GCTC	-----TT
	Z4S-1-PDA	-----TCATT	-----AATGAAA	-----TGT	--TAGG	--AC	GCTC	-----TT
S. dacryoidea	AF444597	TGCGGAAGGATCATT	-----AATGAAA	-----TGT	--TAGG	--AC	GCTC	-----TT
S. dacryoidea	AF444500	TGCGGAAGGATCATT	-----AATGAAA	-----TGT	--TAGG	--AC	GCTC	-----TT
S. dacryoidea	AB049027	-----ATT	-----AATGAAA	-----TGT	--TAGG	--AC	GCTC	-----TT
S. dacryoidea	DQ832207	-----ATGAAA	-----TGT	--TAGG	--AC	GCTC	-----TT	
	R. minuta AB078490	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	TCTCT	-----T
	R. minuta AB078484	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	TCTCT	-----T
	R. minuta AB038117	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	TCTCT	-----T
	B4M-STD	-----AGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	TCTCT	-----TT
	R. minuta AB078501	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	TCTCT	-----T
	R. minuta AF190010	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----T
	R. minuta AB078493	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----T
	R. minuta AB078497	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----T
	I1-STD	-----TCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
	R. sp. AF444619	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	FJ515215	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	AB025994	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
	J3S-STD	-----TCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	FJ807685	-----AAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	AF444589	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	AB078491	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	AB052212	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	AF444627	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	AF444552	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	AB078495	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT
R. slooffiae	CBS8411	TGCGGAAGGATCATT	-----AATGAA	-----TTT	--TAGG	--AC	GTTCT	-----TT

C. chernovii FN400936 CT--GTGGCT--TCG-GT-----CCGGATGTGCCA--ACAGG-----TA--ACACTG
 C. magnus AF190009 CG--AAAGCC--AGTGGT-----TCTTCT-----T--TCAT--ATCCATA--ACACCT
 C. oeiensis AF444364 TG--TGGGTGGTGACTT-----CGGTCC--CGC--TCATTTCATATCCATA--ACACCT
 E5S-PDA CT--TAACCT--TGGAGT-----CCGAAC--TC--TCACCT--TT--CTA--ACCCT-
 E3M-STD CT--TAACCT--TGGAGT-----CCGAAC--TC--TCACCT--TT--CTA--ACCCT-
 Fungal sp. GU213437 CT--TAACCT--TGGAGT-----CCGAAC--TC--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso AF444614 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 Q5S-2-PDA CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso AF444609 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso AF444503 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso CBS2382 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso FR690147 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso HQ702343 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso FJ515212 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso EU149812 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso EU871492 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 Uncultured fungus FM875856 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso CBS8618 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 R. mucilaginoso AF444635 CT--TAACCT--TGGAGT-----CCGAACCT--C--TCACCT--TT--CTA--ACCCT-
 K. malvinella AF444498 TTTCAT-T-----GAGGC-----TCG-----TT--TAACCT--ATCCATTACACTTT-
 K. malvinella DQ667165 TTTCAT-T-----GAGGC-----TCG-----TT--TAACCT--ATCCATTACACTTT-
 K. aeria AM922224 TTTCAT-T-----GAGGC-----TCG-----TT--TAACCT--ATCCATTACACTTT-
 K. aeria AF444562 TT--TAT-----TGAGGC-----TCG-----TT--TAACCT--ATCCATTACACTTT-
 K. aeria AF444675 TTTCAT-T-----GAGGC-----TCG-----TT--TAACCT--ATCCATTACACTTT-
 H10S-PDA TT--TAT-----TGAGGC-----TCG-----TT--TAACCT--ATCCATTACACTTT-
 Basidiomycete BSU65613 TT--TA-----GAGGT-----CCGACC--CT--TCA--TTACCTT-CACACT-
 R. sp. FU238090 TT--TA-----GAGGT-----CCGACC--TTTCAT--TACCTT-CACACT-
 R. sp. FU865356 TT--TA-----GAGGT-----CCGACC--TTTCAT--TACCTT-CACACT-
 P2S-PDA TT--TA-----GAGGT-----CCGACC--T--TCA--TTACCTT-CACACT-
 R. oryzicola AY335160 TT--TA-----GAGGT-----CCGACC--CTT--TTA--TTACCTTTCACACT-
 R. sp. FU008055 TT--TA-----GAGGT-----CCGACC--ACTCATT--TTACCTTTCACACT-
 S. dacryoidea AF444571 TT--TA-----GAGGT-----CCGACC--ACTCAT--TTACCTTTCACACT-
 Z4S-1-PDA TT--TA-----GAGGT-----CCGACC--ACTCATT--TTACCTTTCACACT-
 S. dacryoidea AF444597 TT--TA-----GAGGT-----CCGACC--ACTCAT--TTACCTTTCACACT-
 S. dacryoidea AF444500 TT--TA-----GAGGT-----CCGACC--ACTCATT--TTACCTTTCACACT-
 S. dacryoidea AB049027 TT--TA-----GAGGT-----CCGACC--ACTCATT--TTACCTTTCACACT-
 S. dacryoidea DQ832207 TT--TA-----GAGGT-----CCGACC--ACTCAT--TTACCTTTCACACT-
 R. minuta AB078490 TT--TA-----GAGGT-----CCGACC--TT--TCA--TTTCCTT--ACACT-
 R. minuta AB078484 TT--TA-----GAGGT-----CCGACC--TT--TCA--TTTCCTT--ACACT-
 R. minuta AB038117 TT--TA-----GAGGT-----CCGACC--CT--TCA--TTTCCTT--ACACT-
 B4M-STD TT--TA-----GAGGT-----CCGACC--ACT--TCA--TTTCCTT--ACACT-
 R. minuta AB078501 TT--TA-----GAGGT-----CCGACC--CT--TCA--TTTCCTT--ACACT-
 R. minuta AF190010 TT--TA-----GAAGT-----CCGACC--TT--TCATT--TT--CTT--ACACT-
 R. minuta AB078493 TT--TA-----GAAGT-----CCGACC--ATT--TCATT--TT--CTT--ACACT-
 R. minuta AB078497 TT--TA-----GAAGT-----CCGACC--TT--TCATT--TT--CTT--ACACT-
 I1-STD TT--TA-----GAAGT-----CCGACC--CTT--TCATT--TT--CTT--ACACT-
 R. sp. AF444619 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae FJ515215 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae AB025994 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 J3S-STD TT--TA-----GAAGT-----CCGACC--CTT--TCATT--TT--CTT--ACACT-
 R. slooffiae FJ807685 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae AF444589 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae AB078491 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae AB052212 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae AF444627 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae AF444552 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae AB078495 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-
 R. slooffiae CBS8411 TT--TA-----GAAGT-----CCGACC--CTTTCATT--TT--CTT--ACACT-

C. chernovii FN400936 TTGTA-----ATTCTAT-CCATAA---CACCTGTG-AACTGTTG----GATGC
C. magnus AF190009 GTG-CAC-----TGTTGGGATGC-----TTGCAATC-----
C. oeiensis AF444364 GTG-CAC-----TGTTGGGATGC-----TTGCAATC-----
E5S-PDA GTG-CAC-T-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
E3M-STD GTG-CAC-T-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
Fungal sp. GU213437 GTG-CAC-T-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso AF444614 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
Q5S-2-PDA GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso AF444609 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso AF444503 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso CBS2382 GTG-CAT-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso FR690147 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso HQ702343 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso FJ515212 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso EU149812 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso EU871492 GTG-CAC-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
Uncultured fungus FM875856 GTG-CAT-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso CBS8618 GTG-CAT-----TGTTTGGGATAGT--AACTCTCGCAAGAGAGC----GAACT
R. mucilaginoso AF444635 GTG-CA--T-----TTGAAACATT---ACT-TGGTAACCTAG-----GGCTT
K. malvinella AF444498 GTG-CA--T-----TTGAAACATT---ACT-TGGTAACCTAG-----GGCTT
K. malvinella DQ667165 GTG-CATTTGA-AACATTACTT--GGATGCTTTGGGCTTCGGTCCTCTG-----TGT
K. aeria AM922224 GTG-CATTTGAAACATTACTT--GGATGCTTTGGGCTTCGGTCCTCTG-----TGT
K. aeria AF444562 GTG-CATTTGAAACATTACTT--GGATGCTTTGGGCTTCGGTCCTCTG-----TGT
K. aeria AF444675 GTG-CATTTGAAACATTACTT--GGATGCTTTGGGCTTCGGTCCTCTG-----TGT
H10S-PDA GTG-CAC-----ACACTTCATTTTACAC--CCATTTTAAAC-----ACT
Basidiomycete BSU65613 GTG-CAC-----ACACTTCATTTTACAC--CCATTTTAAAC-----ACT
R. sp. FU238090 GTG-CACA-----CACTTCATTTTACAC--CCATTTTAAAC-----ACT
R. sp. FU865356 GTG-CACA-----CACTTCATTTTACAC--CCATTTTAAAC-----ACT
P2S-PDA GTG-CAC-----ACACTTCATTTTACACC--CATTTT--AAAC-----ACT
R. oryzicola AF335160 GTG-CAC-----ATCACTACTTTTACACC--CATTTT--AAAC-----ACT
R. sp. FU008055 GTG-CACA-----TCACTACTTTTACAC--CCATTTTAAAC-----ACA
S. dacryoidea AF444571 GTG-CACA-----TCACTACTTTTACAC--CCATTTTAAAC-----ACT
Z4S-1-PDA GTG-CACA-----TCACTACTTTTACAC--CCATTTTAAAC-----ACT
S. dacryoidea AF444597 GTG-CACA-----TCACTACTTTTACACC--CATTTT--AAAC-----ACT
S. dacryoidea AF444500 GTG-CACA-----TCACTACTTTTACACC--CATTTT--AAAC-----ACT
S. dacryoidea AB049027 GTG-CACA-----TCACTACTTTTACACC--CATTTT--AAAC-----ACT
S. dacryoidea DQ832207 GTG-CACA-----TCACTACTTTTACACC--CATTTT--AAAC-----ACT
R. minuta AB078490 GTG-CAC-----ACACTTCATTTTACACA--TTTT--AAC-----ACT
R. minuta AB078484 GTG-CAC-----ACACTTCATTTTACACA--TTTT--AAC-----ACT
R. minuta AB038117 GTG-CAC-----ACACTTCATTTTACACA--TTTT--AAC-----ACT
B4M-STD GTG-CAC-----ATACTTCATTTTACAC--ATTTT--AAC-----ACA
R. minuta AB078501 GTG-CAC-----ATACTTCATTTTACAC--TTTT--AAC-----ACA
R. minuta AF190010 GTG-CAC-----ACACTTCATTTTACACA--CACTTTT--AAC-----ACA
R. minuta AB078493 GTG-CAC-----ACACTTCATTTTACACA--CACTTTT--AAC-----ACA
R. minuta AB078497 GTG-CAC-----ACACTTCATTTTACACA--CACTTTT--AAC-----ACA
I1-STD GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. sp. AF444619 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae FJ515215 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae AB025994 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
J3S-STD GTG-CAC-----ACACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae FJ807685 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae AF444589 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae AB078491 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae AB052212 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae AF444627 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae AF444552 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae AB078495 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC
R. slooffiae CBS8411 GTG-CACA-----CACTTCATTTTACACA--CACTTTT--AAC-----ACC

C. chernovii FN400936 TTGCATCCACT--TTT-----AT--AC-----TAAACATTATTGTAACAAATG-----
C. magnus AF190009 -----CACT--TTT-----AA--AC-----TAAACATTATTGTAACAAATG-----
C. oesirensis AF444364 -----CACT--TTT-----AA--AC-----TAAACATTATTGTAACAAATG-----
E5S-PDA CC-TATTCAC--TAT-----AA--AC-----ACAA-----AGT-CTATGAATG----TA
E3M-STD CC-TATTCAC--TAT-----AA--AC-----ACAA-----AGT-CTATGAATG----TA
Fungal sp. GU213437 CC-TATTCAC--TAT-----AA--AC-----ACAA-----AGT-CTATGAATG----TA
R. mucilaginoso AF444614 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
Q5S-2-PDA CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso AF444609 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso AF444503 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso CBS2382 CC-TATTCAC--TAT-----AAACAC-----ACAA-----AGT-CTATGAATG----TA
R. mucilaginoso FR690147 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso HQ702343 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso FJ515212 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso EU149812 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso EU871492 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
Uncultured fungus FM875856 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso CBS8618 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
R. mucilaginoso AF444635 CC-TATTCAC--TAT-----AAACAC-----AA-----AGT-CTATGAATG----TA
K. malvinella AF444498 CGGTCCTCTGT--TATGCTAGCAAGTACTTTACATAACCCCATGCTTTACATGAGATGA
K. malvinella DQ667165 CGGTCCTCTGT--TATGCTAGCAAGTACTTTACATAACCCCATGCTTTACATGAGATGA
K. aerea AM922224 TGCTATCAAGT---AT-----CTTTAC-----ACAACCCCATGCTTTACATGAGATGA
K. aerea AF444562 TGCTATCAAGT---AT-----CTTTAC-----ACAACCCCATGCTTTACATGAGATGA
K. aerea AF444675 TGCTATCAAGT---AT-----CTTTAC-----ACAACCCCATGCTTTACATGAGATGA
H10S-PDA TGCTATCAAGT---AT-----CTTTAC-----ACAACCCCATGCTTTACATGAGATGA
Basidiomycete BSU65613 AT-----AGT---AT-----AAGAA--GTAC---CAGT-CTCTTAAT-----
R. sp. FU238090 TT-----AGT---AT-----AAGAA--GTAC---CAGT-CTCTTAAT-----
R. sp. FU865356 AC-----AGT---AT-----AAGAA--CTAC---CAGT-CTCTTAAT-----
P2S-PDA AT-----AGT---AT-----AAGAA--GTACC---AGT-CTCTTAAT-----
R. oryzicola AF335160 ---TATAAAGT--CATT-----AGAAT-----GTAAA--CAGT-CTCTTAAT-----
R. sp. FU008055 TA-----AAAGT---CT-----AAGAA--GTAAA--CAGT-CTCTTAAG-----
S. dacryoidea AF444571 ---ATAAAGT---CT-----AAGAA--GTAAA--CAGT-CTCTTAAC-----
Z4S-1-PDA TT--AACAAGT---CT-----AAGAA--GTAAAC--TAGT-CTCTTAAC-----
S. dacryoidea AF444597 TT-TAACAAGT---CT-----AAGAA--GTAAAACCAGT-CTCTTAAC-----
S. dacryoidea AF444500 TT-TAACAAGT---CT-----AAGAA--GTAAAACCAGT-CTCTTAAC-----
S. dacryoidea AB049027 TT-TAACAAGT---CT-----AAGAA--GTAAAACCAGT-CTCTTAAC-----
S. dacryoidea DQ832207 TT-TAACAAGT---CT-----AAGAA--GTAAAACCAGT-CTCTTAAC-----
R. minuta AB078490 AT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
R. minuta AB078484 AT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
R. minuta AB038117 TT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
B4M-STD TT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
R. minuta AB078501 TT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
R. minuta AF190010 TT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
R. minuta AB078493 TT-----AGT---ATA-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. minuta AB078497 TT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
I1-STD TT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
R. sp. AF444619 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae FJ515215 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae AB025994 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
J3S-STD TT-----AGT---AT-----AAGAA--GTAAC---AGT-CTCTTAAT-----
R. slooffiae FJ807685 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae AF444589 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae AB078491 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae AB052212 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae AF444627 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae AF444552 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae AB078495 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----
R. slooffiae CBS8411 TT-----AGT---AT-----AAGAA--GTAAC---TAGT-CTCTTAAT-----

C. chernovii FN400936 TAGTCTTATTATAACA-----TAATAA--AACTTTTACAACCGGATCTCTTGGCTCTC
 C. magnus AF190009 TAGTCTTATTATAACA-----TAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 C. oeiensis AF444364 TAGTCTTATTATAACA-----TAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 E5S-PDA TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 E3M-STD TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 Fungal sp. GU213437 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso AF444614 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 Q5S-2-PDA TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso AF444609 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso AF444503 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso CBS2382 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso FR690147 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso HQ702343 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso FJ515212 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso EU149812 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso EU871492 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 Uncultured fungus FM875856 TTAATTTT-ATAACA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso CBS8618 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. mucilaginoso AF444635 TTAATTTT-ATAACA-----AAATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 K. malvinella AF444498 TGATGTTAC-ATAATTGAAATGAAAGAAACAACCTTCAGCAACCGGATCTCTTGGCTCTC
 K. malvinella DQ667165 TGATGTTAC-ATAATTGAAATGAAAGAAACAACCTTCAGCAACCGGATCTCTTGGCTCTC
 K. aeria AM922224 TGATGTTAC-ATAATTGAAATGAAAGAAACAACCTTCAGCAACCGGATCTCTTGGCTCTC
 K. aeria AF444562 TGATGTTAC-ATAATTGAAATGAAAGAAACAACCTTCAGCAACCGGATCTCTTGGCTCTC
 K. aeria AF444675 TGATGTTAC-ATAATTGAAATGAAAGAAACAACCTTCAGCAACCGGATCTCTTGGCTCTC
 H10S-PDA TGAGCATAA-ATATAT-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 Basidiomycete BSU65613 TGAGCATAA-ATATAT-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. sp. FU238090 TGAGCATAA-ATATAT-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. sp. FU865356 TGAGCATAA-ATATAT-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 P2S-PDA TGAGCATAA-ATATAT-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. oryzicola AY335160 TGAGCATAAACTATA-----ACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. sp. FU008055 TGAGCATAA-ACAT-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 S. dacryoidea AF444571 TGAGCATAA-ACAT-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 Z4S-1-PDA TGAGCATAA-ACAT-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 S. dacryoidea AF444597 TGAGCATAA-ACAT-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 S. dacryoidea AF444500 TGAGCATAA-ACAT-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 S. dacryoidea AB049027 TGAGCATAA-ACAT-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 S. dacryoidea DQ832207 TGAGCATAA-ACAT-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. minuta AB078490 TGAGCATAA-ATAA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. minuta AB078484 TGAGCATAA-ATAA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. minuta AB038117 TGAGCATAA-ATAA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 B4M-STD TGAGCATAA-ATAA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. minuta AB078501 TGAGCATAA-ATAA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. minuta AF190010 TGAGCATAA-ACAA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. minuta AB078493 TGAGCATAA-ACAA-A-----AATAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. minuta AB078497 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 I1-STD TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. sp. AF444619 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae FU515215 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae AB025994 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 J3S-STD TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae FJ807685 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae AF444589 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae AB078491 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae AB052212 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae AF444627 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae AF444552 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae AB078495 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC
 R. slooffiae CBS8411 TGAGCATAA-ATAA-----AAACAA--AACTTTCAACAACCGGATCTCTTGGCTCTC

[illegible]

C. chernovii FN400936 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
C. magnus AF190009 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
C. oeiensis AF444364 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
E58-PDA CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
E3M-STD CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
Fungal sp. GU213437 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso AF444614 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
Q58-2-PDA CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso AF444609 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso AF444503 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso CBS2382 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso FR690147 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso HQ702343 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso FJ515212 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso EU149812 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso EU871492 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
Uncultured fungus FM875856 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso CBS8618 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. mucilaginoso AF444635 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
K. malvinella AF444498 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
K. malvinella DQ667165 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
K. aerea AM922224 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
K. aerea AF444562 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
K. aerea AF444675 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
H108-PDA CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
Basidiomycete BSU65613 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. sp. FU238090 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. sp. FU865356 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
P28-PDA CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. oryzicola AF335160 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. sp. FU008055 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
S. dacryoidea AF444571 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
Z4S-1-PDA CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
S. dacryoidea AF444597 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
S. dacryoidea AF444500 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
S. dacryoidea AB049027 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
S. dacryoidea DQ832207 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. minuta AB078490 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. minuta AB078484 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. minuta AB038117 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
B4M-STD CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. minuta AB078501 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. minuta AF190010 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. minuta AB078493 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. minuta AB078497 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
I1-STD CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. sp. AF444619 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae FJ515215 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae AB025994 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
J3S-STD CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae FJ807685 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae AF444589 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae AB078491 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae AB052212 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae AF444627 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae AF444552 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae AB078495 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT
R. slooffiae CBS8411 CATCGAATCTTTGAACGCACCTTGCCTCCTTGG-TATTCC---GAGGAGCATGCCTGTT

C. chernovii FN400936 TGAGTGTGCATGAA-ACCTCTCAA-CCCAAGT---TTTGGATTTCGATCCATGCT---TG
 C. magnus AF190009 TGAGTGTGCATGAA-ACCTCTCAA-CCCAAGT---TTTGGATTTCGATCCATGCT---TG
 C. oeiensis AF444364 TGAGTGTGCATGAA-ACCTCTCAA-CCCAAGT---TTTGGATTTCGATCCATGCT---TG
 E5S-PDA TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGCGGT-GT-
 E3M-STD TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 Fungal sp. GU213437 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso AF444614 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 Q5S-2-PDA TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso AF444609 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso AF444503 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso CBS2382 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso FR690147 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso HQ702343 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso FJ515212 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso EU149812 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso EU871492 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 Uncultured fungus FM875856 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso CBS8618 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 R. mucilaginoso AF444635 TGAGTGTGCATGAATACT-TCAA--CCCTCCTCT-TTCTTAA-TGA-TTGAAGAGGT-GT-
 K. malvinella AF444498 TGAGTGTGCGGAAC-CTCTCAAC-CCCGCCAAAGCGCTTAC-TGACTTTGGTTGTT--TG
 K. malvinella DQ667165 TGAGTGTGCGGAAC-CTCTCAAC-CCCGCCAAAGCGCTTAC-TGACTTTGGTTGTT--TG
 K. aeria AM922224 TGAGTGTGCGGAAC-CTCTCAACCCCGCCCAAG--GCTTAATTGACTTGCGGTTGT-CTG
 K. aeria AF444562 TGAGTGTGCGGAAC-CTCTCAACCCCGCCCAAG--GCTTAATTGACTTGCGGTTGT-CTG
 K. aeria AF444675 TGAGTGTGCGGAAC-CTCTCAACCCCGCCCAAG--GCTTAATTGACTTGCGGTTGT-CTG
 H10S-PDA TGAGTGTGCGGAAC-CTCTCAACCCCGCCCAAG--GCTTAATTGACTTGCGGTTGT-CTG
 Basidiomycete BSU65613 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-CGA---GATAGGC--GTG
 R. sp. FU238090 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 R. sp. FU865356 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 P2S-PDA TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 R. oryzicola AF335160 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 R. sp. FU008055 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 S. dacryoidea AF444571 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 Z4S-1-PDA TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 S. dacryoidea AF444597 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 S. dacryoidea AF444500 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 S. dacryoidea AB049027 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 S. dacryoidea DQ832207 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTGT-TTTGTAA-TGA---GATAGGC--GTG
 R. minuta AB078490 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---GATAAGT--GCG
 R. minuta AB078484 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---GATAAGT--GCG
 R. minuta AB038117 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 B4M-STD TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. minuta AB078501 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. minuta AF190010 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. minuta AB078493 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. minuta AB078497 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 I1-STD TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. sp. AF444619 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae FU515215 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae AB025994 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 J3S-STD TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae FJ807685 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae AF444589 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae AB078491 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae AB052212 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae AF444627 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae AF444552 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae AB078495 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG
 R. slooffiae CBS8411 TGAGTGTGCATGAA-ACCTCTCAA--CCCCCCTAT-TTTGTAA-TGA---AATGGGC--GTG

C. chernovii FN400936 AGTTTGGATT-TGGATGTTTGCCCG-----GTGATAAGCC-GACTCATCTTAAAAGTATT
 C. magnus AF190009 AGTTTGGATT-TGGATGTTTGCCCG-----TGATGAACCGACTCATCTTAAAAGTATT
 C. oeiensis AF444364 AGTTTGGATT-TGGACGTTTGCCCG-----TGATGAACCGACTCGTCTTAAAAGTATT
 E5S-PDA ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 E3M-STD ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 Fungal sp. GU213437 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso AF444614 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 Q5S-2-PDA ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso AF444609 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso AF444503 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso CBS2382 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso FR690147 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso HQ702343 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso FJ515212 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso EU149812 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso EU714192 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 Uncultured fungus FM875856 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso CBS8618 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 R. mucilaginoso AF444635 ---TTGGTTTCTGAGCG-CTGCTGG---CCTTTACGGTCTAG-CTCGTTCGTAATGCATT
 K. malvinella AF444498 GGCTTGGATCATGGTCTCTTGTGCTTACCTTTCGGGGTTTGGACTGGACTGAAATACAAC
 K. malvinella DQ667165 GGCTTGGATCATGGTCTCTTGTGCTTACCTTTCGGGGTTTGGACTGGACTGAAATACAAC
 K. aeria AM922224 GGCTTGGATCATGGTCTCTTGTGCTTACCTTTCGGGGTTTGGACTGGACTGAAATACAAC
 K. aeria AF444562 GGCTTGGATCATGGTCTCTTGTGCTTACCTTTCGGGGTTTGGACTGGACTGAAATACAAC
 K. aeria AF444675 GGCTTGGATCATGGTCTCTTGTGCTTACCTTTCGGGGTTTGGACTGGACTGAAATACAAC
 H10S-PDA GGCTTGGATCATGGTCTCTTGTGCTTACCTTTCGGGGTTTGGACTGGACTGAAATACAAC
 Basidiomycete BSU65613 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AAAGTC--GGCTCAACTGAAATACAG
 R. sp. FU238090 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AAAGTC--GGCTCAGCTGAAATACAG
 R. sp. FU865356 GGCTTGGATTATGGCTGCCTGTGCTGG---CGT--AAAGTC--GGCTCAGCTGAAATACAG
 P2S-PDA GGCTTGGATTATGGCTGTCTGTGCTGG---CGT--AAAGTC--GGCTCAGCTGAAATACAG
 R. oryzicola AF335160 GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 R. sp. FU008055 GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 S. dacryoidea AF444571 GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 Z4S-1-PDA GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 S. dacryoidea AF444597 GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 S. dacryoidea AF444500 GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 S. dacryoidea AB049027 GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 S. dacryoidea DQ832207 GGCTTGGATTATGGCTG-CTGCCGG---CCTTCATTAGTCGACTCGGCTGAAATACAG
 R. minuta AB078490 GGCTTGGATTATGGCTG-CTGTCGG---CGT--AATTGCCGG-CTCAGCTGAAATACAG
 R. minuta AB078484 GGCTTGGATTATGGCTG-CTGTCGG---CGT--AATTGCCGG-CTCAGCTGAAATACAG
 R. minuta AB038117 GGCTTGGATTATGGTTGT-TGTGCG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 B4M-STD GGCTTGGATTATGGTTGT-TGTGCG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. minuta AB078501 GGCTTGGATTATGGTTGT-TGTGCG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. minuta AF190010 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. minuta AB078493 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. minuta AB078497 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 I1-STD GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. sp. AF444619 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae FU515215 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae AB025994 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 J3S-STD GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae FJ807685 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae AF444589 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae AB078491 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae AB052212 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae AF444627 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae AF444552 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae AB078495 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG
 R. slooffiae CBS8411 GGCTTGGATTATGGTTGTCTGTGCTGG---CGT--AATTGCCGG-CTCAACTGAAATACAG

C. chernovii FN400936 AGCTAGATCTGTCTC-----TATGACTGGTTGA--CTT--GGCAT-----
 C. magnus AF190009 AGCTTGGATCTGTCT-----ATATGACTGGTTGA--CTT--GGCA-----T
 C. oeiensis AF444364 AGCTGGATCTGTCT-----ATATGACTGGTTGA--CTT--GGCA-----T
 E5S-PDA AGC---ATCCGCAATC-G-----AACTT--CGGATTGA--CTT--GGCG-----T
 E3M-STD AGC---ATCCGCAATC-G-----AACTT--CGGATTGA--CTT--GGCG-----T
 Fungal sp. GU213437 AGC---ATCCGCAATC-G-----AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso AF444614 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 Q5S-2-PDA AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso AF444609 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso AF444503 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso CBS2382 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso FR690147 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso HQ702343 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso FJ515212 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso EU149812 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso EU871492 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 Uncultured fungus FM875856 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso CBS8618 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 R. mucilaginoso AF444635 AGC---ATCCGCAATC-----G---AACTT--CGGATTGA--CTT--GGCG-----T
 K. malvinella AF444498 AAGTTGAATGGTT-----A-----CATTTCAGCTTGAC-CT---GATG-----T
 K. malvinella DQ667165 AAGTTGAATGGTT-----ACATTTCAGCTTGAC--CTGATGTTGTAACT
 K. aerea AM922224 AAGTTGAATGGTTTCC---A-----TTTGCAGCTTGAC--CTGATGTTGTAACT
 K. aerea AF444562 AAGTTGAATGGTTTCC-----ATTTGCAGCTTGAC-CTG---ATG-----T
 K. aerea AF444675 AAGTTGAATGGTTTCC---A-----TTTGCAGCTTGAC-CT---GATG-----T
 H10S-PDA AAGTTGAATGGTTTCC-----ATTTGCAGCTTGAC-CTG---ATG-----T
 Basidiomycete BSU65613 AGC---AACCCATTT-----GAAATAGACGGTTTGACTC-----GGCGT-----
 R. sp. FU238090 AGC---AACCCATTT-----G---AAATAGACGGTTTGACTC-----GGCG-----T
 R. sp. FU865356 AGC---AACCCATTT-----G---AAATAGACGGTTTGACTC-----GGCG-----T
 P2S-PDA AGC---AACCCATTT-----G---AAATAGACGGTTTGACTC-----GGCG-----T
 R. oryzicola AY335160 AGCTGCCCCGGTGTCTCT-TTCGAAGAAACAAACGGCTTGACTC-----GGCGT-----
 R. sp. FU008055 AGCT---ACCCCGATTCTTTCTTAAGAAATAGACGGTTTGACTC-----GGCG-----T
 S. dacryoidea AF444571 AGCT---ACCCCGATTCTTATTAA-AGAAACAAACGGTTTGACTC-----GGCG-----T
 Z4S-1-PDA AGCT---ACCCCGATTCTGTATTAG-AGAAACAAACGGTTTGACTC-----GGCG-----T
 S. dacryoidea AF444597 AGCT---ACCCCGATTCTTATTAG-AGAAACAAACGGTTTGACTC-----GGCG-----T
 S. dacryoidea AF444500 AGCT---ACCCCGATTCTTATTAG-AGAAACAAACGGTTTGACTC-----GGCG-----T
 S. dacryoidea AB049027 AGCT---ACCCCGATTCTTATTAG-AGAAACAAACGGTTTGACTC-----GGCG-----T
 S. dacryoidea DQ832207 AGCT---ACCCCGATTCTTATTAG-AGAAACAAACGGTTTGACTC-----GGCG-----T
 R. minuta AB078490 AGC---AACCCATTT-----G---AAATAACGGTTTGACTC-----GGCG-----T
 R. minuta AB078484 AGC---AACCCATTT-----G---AAATAACGGTTTGACTC-----GGCG-----T
 R. minuta AB038117 AGC---AACCCCTTT-----G---AAATAGACGGTTTGACTC-----GGCG-----T
 B4M-STD AGC---AACCCCTTT-----GAAATAGACGGTTTGACTC-----GGCGT-----
 R. minuta AB078501 AGC---AACCCCTTT-----G---AAATAGACGGTTTGACTC-----GGCG-----T
 R. minuta AF190010 AGC---AACCTATT-----G---AAATAGACGGTTTGA--CTT--GGCG-----T
 R. minuta AB078493 AGC---AACCTATT-----GAAATAGACGGTTTGA--CTT--GGCGT-----
 R. minuta AB078497 AGC---AACCTATT-----G---AAATAGACGGTTTGA--CTT--GGCG-----T
 I1-STD AGC---AACCTACT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. sp. AF444619 AGC---AACCTACT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae FJ515215 AGC---AACCTACT-----G---AAACAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae AB025994 AGC---AACCTACT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 J3S-STD AGC---AACCTATT-----G-----AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae FJ807685 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae AF444589 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae AB078491 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae AB052212 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae AF444627 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae AF444552 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae AB078495 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T
 R. slooffiae CBS8411 AGC---AACCTATT-----G---AAATAACGGTTTGA--CTT--GGCG-----T

C. chernovii FN400936 AATAAGT-----ATTTT-GC-T-GAGGA-----C-----ATCTTCG
C. magnus AF190009 AATAAGT-----ATTTT-GC-T-GAGGA-----C-----ATCTTCG
C. oeiensis AF444364 AATAAGT-----ATTTT-GC-T-GAGGA-----CATCTTCG
E5S-PDA AATAGACT-----ATTTC--GC-T-GAGGA-----ATT--CTAGTCTTCG
E3M-STD AATAGACT-----ATTTC--GC-T-GAGGA-----ATT--CTAGTCTTCG
Fungal sp. GU213437 AATAGACT-----ATTTC--GC-T-GAGGA-----ATT--CTAGTCTTCG
R. mucilaginoso AF444614 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
Q5S-2-PDA AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso AF444609 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso AF444503 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso CBS2382 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso FR690147 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso HQ702343 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso FJ515212 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso EU149812 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso EU871492 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
Uncultured fungus FM875856 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso CBS8618 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
R. mucilaginoso AF444635 AATAGACT-----ATTTC--GC-T-GAGGA-----A-----TT--CTAGTCTTCG
K. malvinella AF444498 TGTAAGT-----ACT---CATCGGGA---T-----G---CAATGC---
K. malvinella DQ667165 ACTCATCGGGGATGCAATGCAGC-TAAAGGA-----ACTTTAACAACCCCTT--
K. aerea AM922224 ACTCATCGGGGATGCAATGAAGC-TAAAGGAACCTTAACAG-----
K. aerea AF444562 TGTAAGT-----ACT-CATC---GGGGA-----T---GCAAT---G
K. aerea AF444675 TGTAAGT-----ACT---CATCGGGA-----T---GCAAT---G
H10S-PDA TGTAAGT-----ACT-CATC---GGGGA-----T---GCAAT---G
Basidiomycete BSU65613 AATAATT-----ATTTC-GC-T-GAGGA-----C-----GCTCTTCT--
R. sp. FU238090 AATAATT-----ATTTC-GC-T-GAGGAC-----G-----TCTTCTT--
R. sp. FU865356 AATAATT-----ATTTC-GC-T-GAGGAC-----G-----TCTTCTT--
P2S-PDA AATAATT-----ATTTC-GC-T-GAGGA-----C-----CGTCTTCT
R. oryzicola AY335160 AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TT--ACATTTCTAT
R. sp. FU008055 AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TCACATTTCT
S. dacryoidea AF444571 AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TTACATTTTAA
Z4S-1-PDA AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TTACATTTCTAAG
S. dacryoidea AF444597 AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TTACATTTCTAAG
S. dacryoidea AF444500 AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TTACATTTCTAAG
S. dacryoidea AB049027 AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TTACATTTCTAAG
S. dacryoidea DQ832207 AATAACAT-----ATTTC-GC-T-GAGGAC-----G-----TTACATTTCTAAG
R. minuta AB078490 AATAATT-----ATTTC-GC-T-GAGGAC-----G-----TTTTCTTCA
R. minuta AB078484 AATAATT-----ATTTC-GC-T-GAGGAC-----G-----TTTTCTTCA
R. minuta AB038117 AATAATT-----ATTTC-GC-T-GAGGAC-----G-----TCTTCTTCA
B4M-STD AATAATT-----ATTTC-GC-T-GAGGA-----C-----GTCTTCTTC-
R. minuta AB078501 AATAATT-----ATTTC-GC-T-GAGGAC-----G-----TCTTCTTCA
R. minuta AF190010 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TCTTCTTC-
R. minuta AB078493 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TCTTCTTC-
R. minuta AB078497 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TCTTCTTC-
I1-STD AATAATT-----ATTTC-GC-T-GAGGA-----C-----GTTTTCTTCA
R. sp. AF444619 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTCA
R. slooffiae FU515215 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTCA
R. slooffiae AB025994 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTCA
J3S-STD AATAATT-----ATTTC-GC-T-AAGGA-----C-----GTTTTCTTC-
R. slooffiae FJ807685 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTC-
R. slooffiae AF444589 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTC-
R. slooffiae AB078491 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTC-
R. slooffiae AB052212 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTC-
R. slooffiae AF444627 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----TTTTCTTC-
R. slooffiae AF444552 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----CTTCTTTC-
R. slooffiae AB078495 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----CTTCTTTC-
R. slooffiae CBS8411 AATAATT-----ATTTC-GC-T-AAGGAC-----G-----CTTCTTTC-

C. chernovii FN400936 GAT---GGCC-----AGGACCTTGACTATTGTCTGCTAACTAAACCATTAC
 C. magnus AF190009 G---ATGGCC-----AGGACCTAGACTACTGTCTGCTAACTAAACCATCAC
 C. oeiensis AF444364 G---ATGGCC-----AGGACCTAGACTATTGTCTGCTAACTAAACCATCAC
 E5S-PDA GATTAGAGCC-----GGGTTG--GGTTAAAGGAAGTT-----TC-----
 E3M-STD GACTAGAGCC-----GGGTTG--GGTTAAAGGAAGCT-----TC-----
 Fungal sp. GU213437 GACTAGAGCC-----GGGTTG--GGTTAAAGGAAGCT-----TC-----
 R. mucilaginosa AF444614 GACTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 Q5S-2-PDA GACTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa AF444609 GACTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa AF444503 GATTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa CBS2382 GACTAGAGCC-----G-----GGTTGAGGTGTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa FR690147 GACTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa HQ702343 GACTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa FJ515212 GACTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa EU149812 GATTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa EU871492 GATTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 Uncultured fungus FM875856 GACTAGAGCC-----GGGTTG--GGTTAAAGGAAGCT-----TC-----
 R. mucilaginosa CBS8618 GATTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 R. mucilaginosa AF444635 GATTAGAGCC-----G-----GGTTG--GGTTAAAGGAAGCT-----TC-T-----
 K. malvinella AF444498 -----AGC-----T-----AAAGGAAGCT-----T-----
 K. malvinella DQ667165 --TTAAATGGTACCTAGTACATTT-----
 K. aeria AM922224 -----AAGC-----T-----AAAGGAAGCT-----T-----
 K. aeria AF444562 ---GAAGC-----T-----AAAGGAAGCT-----T-----
 K. aeria AF444675 -----AAGC-----T-----AAAGGAAGCT-----T-----
 H10S-PDA ---TAAAGTC-----AGTGGTTGCTT-----C-----
 Basidiomycete BSU65613 ---TAAAGTC-----AGTGG--TGCT-----TC-----
 R. sp. FU238090 ---TAAAGTC-----AGTGG--TGCT-----TC-----
 R. sp. FU865356 ---TAAAGTC-----A-----GTGG--TGCT-----TC-T-----
 P2S-PDA GTTAAAGATTA-----C-----AATGGTTG--TGCT-----TC--T-----
 R. oryzicola AY335160 TAATACACAC-----A-----AAGAATCTTAGTGG--TGCT-----TC-----
 R. sp. FU008055 G--TAAACTA-----G-----AATCTTAGTGG--TGCT-----TC-----
 S. dacryoidea AF444571 TAA-AAAGAA-----TCCTTAGTGG--TGCT-----TC-----
 Z4S-1-PDA TTATAAAGAA-----TCCTTAGTGG--TGCT-----TC-----
 S. dacryoidea AF444597 TTATAAAGAA-----TCCTTAGTGG--TGCT-----TC-----
 S. dacryoidea AF444500 TTATAAAGAA-----TCCTTAGTGG--TGCT-----TC-----
 S. dacryoidea AB049027 TTATAAAGAA-----TCCTTAGTGG--TGCT-----TC-----
 S. dacryoidea DQ832207 ---AAAG-----T-----A-----AGAGG--TGCT-----TC-T-----
 R. minuta AB078490 ---AAAG-----T-----A-----AGAGG--TGCT-----TC-T-----
 R. minuta AB078484 ---AAAG-----T-----A-----AGCGG--TGCT-----TC-T-----
 R. minuta AB038117 ---AAAAGT-----A-----AGCGG--TGCTT-----C-----
 B4M-STD ---AAAG-----T-----A-----AGCGG--TGCT-----TC-T-----
 R. minuta AB078501 ---AAATA-----T-----A-----AGAGG--TGCT-----TC-T-----
 R. minuta AF190010 ---AAATA-----T-----A-----AGAGG--TGCT-----TC--T-----
 R. minuta AB078493 ---AAATA-----T-----A-----AGAGG--TGCT-----TC-----
 R. minuta AB078497 ---ACTATA-----GAGG--TGCT-----TC-----
 I1-STD ---ATTATA-A-----GAGG--TGCT-----TC-----
 R. sp. AF444619 ---ATTATA-A-----GAGG--TGCT-----TC-----
 R. slooffiae FJ515215 ---ATTATA-A-----GAGG--TGCT-----TC-----
 R. slooffiae AB025994 ---AAATAT-----A-----AGAGG--TGCT-----TC-----
 J3S-STD ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae FJ807685 ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae AF444589 ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae AB078491 ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae AB052212 ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae AF444627 ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae AF444552 ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae AB078495 ---AAATA-----TAAGAGG--TGCT-----TC-----
 R. slooffiae CBS8411 ---AAATA-----TAAGAGG--TGCT-----TC-----

C. chernovii FN400936 TTTAA---GTGCATCTTTGGATGTTACTCATTGTA---TA-ACCTTGA-CATCTGGCCTC
 C. magnus AF190009 TTTAA---GTGCATCTTTGGATGTTACTCATTGTG---TA-ACCTTGA-CATCTGGCCTC
 C. oeiensis AF444364 TTTAA---GTGCATCTTTGGATGTTACTAATTGTG---TA-ACCTTGA-CATCTGGCCTC
 E5S-PDA --TAAT--CAGAATGTCT-----ACATTTTA--AG----ATTA-GA-----TCTC
 E3M-STD --TAAT--CAGAATGTCT-----ACATTTTA--AG----ATTA-GA-----TCTC
 Fungal sp. GU213437 --TAAT--CAGAATGTCT-----ACATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso AF444614 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 Q5S-2-PDA --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso AF444609 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso AF444503 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso CBS2382 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso FR690147 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso HQ702343 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso FJ515212 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso EU149812 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso EU871492 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 Uncultured fungus FM875856 --TAATC--AGAATGTCT-----ACATTTTA--AG----ATTA-GA-----TCTC
 R. mucilaginoso CBS8618 --AAT--CAGAATGTCT--A-----CATTTT-----
 R. mucilaginoso AF444635 --AAT--CAGAATGTCT--A-----CATTTTA--AG----ATTA-GA-----TCTC
 K. malvinella AF444498 --AACACC-CTTTTAA-A-----TGGTACCTAGTACATTATGA-----CCTC
 K. malvinella DQ667165 -----
 K. aerea AM922224 --AA---CAGAACCCCT-----AAATGGTACCTAGTACATTATGA-----CCTC
 K. aerea AF444562 --AA---CAGAACCCCTTA-----AATGGTACCTAGTACATTATGA-----CCTC
 K. aerea AF444675 --AA---CAGAACCCCTTGAATGGTACCTAGTAC--A-----TTATGA-----CCTC
 H10S-PDA --TAAT---GCGTATTATA-----CATCATA--AG--CCTTTGA-GAC-----CCTC
 Basidiomycete BSU65613 --TAAT---GCGTATCAT-----ACACTTTT--AG---CTTTA-GA-----CCTC
 R. sp. FU238090 --TAAT---GCGTATCAT-----ACACTTTT--AG---CTTTA-GA-----CCTC
 R. sp. FU865356 --TAAT---GCGTATCAT-----ACACTTTT--AG---CTTTA-GA-----CCTC
 P2S-PDA --AAT---GCGTATCAT-A-----CACTTTT--AG---CTTTA-GA-----CCTC
 R. oryzicola AF335160 --AAT---GCGTCTGTTTCA--GTCAGACACCTTA--AGC---TTTA-GA-----CCTC
 R. sp. FU008055 --TAAT---GCGTCTGTTTGTAGTCAGACACCTTA--AG---CTTTA-GA-----CCTC
 S. dacryoidea AF444571 --TAAT---GCGTCTGTTTCA--GTCAGACACCTTA--AG---CTTTA-GA-----CCTC
 Z4S-1-PDA --TAAT---GCGTCTGTTTCA--GTCAGACACCTTA--AG---CTTTA-GA-----CCTC
 S. dacryoidea AF444597 --TAAT---GCGTCTGTTTCA--GTCAGACACCTTA--AG---CTTTA-GA-----CCTC
 S. dacryoidea AF444500 --TAAT---GCGTCTGTTTCA--GTCAGACACCTTA--AG---CTTTA-GA-----CCTC
 S. dacryoidea AB049027 --TAAT---GCGTCTGTTTCA--GTCAGACACCTTA--AG---CTTTA-GA-----CCTC
 S. dacryoidea DQ832207 --TAAT---GCGTCTGTTTCA--GTCAGACACCTTA--AG---CTT-----
 R. minuta AB078490 --AAT---GCGCTTTTAA--A-----GCAACTTA--AG---CTTTA-GA-----CCTC
 R. minuta AB078484 --AAT---GCGCTTTTAA--A-----GCAACTTA--AG---CTTTA-GA-----CCTC
 R. minuta AB038117 --AAT---GCGCTTTTAA--A-----GCATCTTA--AG---CTTTA-GA-----CCTC
 B4M-STD --TAAT---GCGCTTTTAA--A-----GCATCTTA--AG-C--TTTA-GA-----CCTC
 R. minuta AB078501 --AAT---GCGCTTTTAA--A-----GCATCTTA--AG---CTTTA-GA-----CCTC
 R. minuta AF190010 --AAT---GCGCTT-TAT--A-----GCACTTTA--AG---CTTTA-GA-----TCTC
 R. minuta AB078493 --AAT---GCGCTT-TAT--A-----GCACTTTA--AGC---TTTA-GA-----TCTC
 R. minuta AB078497 --AAT---GCGCTT-TAT--A-----GCACTTTA--AG---CTTTA-GA-----TCTC
 I1-STD --TAAT--TCGCTTCTAAT-----AGCAT-TTA--AG-C--TTTA-GA-----CCTC
 R. sp. AF444619 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae FJ515215 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae AB025994 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 J3S-STD --TAAT--TCGCTTCTAAT-----AGCAT-TTA--AG-C--TTTA-GA-----CCTC
 R. slooffiae FJ807685 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae AF444589 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae AB078491 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae AB052212 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae AF444627 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae AF444552 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae AB078495 --TAATT--CGCTTCTAAT-----AGCAT-TTA--AG---CTTTA-GA-----CCTC
 R. slooffiae CBS8411 --TAATT--CGCTTCTAAT-----AGCA--TTA--AG---CTTA-GA-----CCT-

C. chernovii	FN400936	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
C. magnus	AF190009	AAATCAAGTAGGACTACCCGCTGAACCTTAAGCA
C. osirensis	AF444364	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
	E5S-PDA	AAATCAGGTAGGACTACCCGCTGAACCTTAA---
	E3M-STD	AAATCAGGTAGGACTACCCGCTGAACCTTAA---
Fungal sp.	GU213437	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	AF444614	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
	Q5S-2-PDA	AAATCAGGTAGGACTACCCGCTGAACCTTAA---
R. mucilaginoso	AF444609	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	AF444503	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	CBS2382	AAATCAGTAA-----
R. mucilaginoso	FR690147	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	HQ702343	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	FJ515212	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	EU149812	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	EU871492	AAATCAGGTAGGACTACCCGCTGAACCTTAA---
Uncultured fungus	FM875856	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. mucilaginoso	CBS8618	-----
R. mucilaginoso	AF444635	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
K. malvinella	AF444498	AAATCAAGTAGGACTACCCGCTGAACCTTAAGCA
K. malvinella	DQ667165	-----
	K. aerea	AM922224
	K. aerea	AF444562
	K. aerea	AF444675
	H10S-PDA	AAATCAAGTAGGACTACCCGCTGAACCTTAA---
Basidiomycete	BSU65613	AAATCGGTAGGACTACCCGCTGAACCTT-----
R. sp.	FJ238090	AAATCAGGTAGGACTACCCGCTGAACCTTAAGCA
R. sp.	FJ865356	AAATCAGGTAGGACTACCCGCTGAACCTTAA---
	P2S-PDA	AAATCAGGTAGGACTACCCGCTG-----
R. oryzae	AY335160	AAATCAGTCAGGACTACCCGCTG-----
R. sp.	FJ008055	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
S. dactyloidea	AF444571	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
	Z4S-1-PDA	AAATCAGTC-----
S. dactyloidea	AF444597	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
S. dactyloidea	AF444500	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
S. dactyloidea	AB049027	-----
S. dactyloidea	DQ832207	-----
	R. minuta	AB078490
	R. minuta	AB078484
	R. minuta	AB038117
	B4M-STD	AAATCAGTCAGGACTACCCGCTGAACCTTAA---
	R. minuta	AB078501
	R. minuta	AF190010
	R. minuta	AB078493
	R. minuta	AB078497
	I1-STD	AAATCAGTCAGGACTACCCGCTGAACCTTAA---
	R. sp.	AF444619
R. slooffiae	FJ515215	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
R. slooffiae	AB025994	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
	J3S-STD	AAATCAGTCAGGACTACCCGCTGAACCTTAA---
R. slooffiae	FJ807685	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
R. slooffiae	AF444589	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
R. slooffiae	AB078491	AAATCA-----
R. slooffiae	AB052212	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
R. slooffiae	AF444627	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
R. slooffiae	AF444552	AAATCAGTCAGGACTACCCGCTGAACCTTAAGCA
R. slooffiae	AB078495	AAATCA-----
R. slooffiae	CBS8411	-----

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