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(54) **Title**: BROAD RANGE PCR-BASED COMPOSITIONS AND METHODS FOR THE DETECTION AND IDENTIFICATION OF FUNGAL PATHOGENS

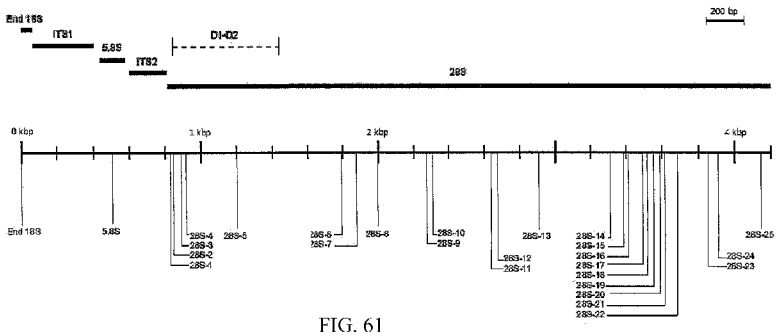

FIG. 61

(57) **Abstract**: Disclosed herein are methods for detecting a fungal pathogen in a patient sample, involving isolating the sample, carrying out a PCR reaction on the sample to generate an amplicon that includes a region of the fungal 28S ribosomal RNA gene, and detecting the PCR amplicon. Also disclosed are sequences of primers for specifically detecting a broad range of fungal pathogens in the presence of human ribosomal DNA. In certain embodiments, the amplicon is detected by sequencing or by two-dimensional melt-curve analysis. In yet other embodiments, more than one fungal pathogen is detected in a sample using the methods disclosed herein.

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BROAD RANGE PCR-BASED COMPOSITIONS AND METHODS FOR THE DETECTION AND IDENTIFICATION OF FUNGAL PATHOGENS

GOVERNMENT SPONSORED RESEARCH OR DEVELOPMENT

[001] This disclosure was made in part in the course of research sponsored by the National Institute of Health, grant number R01 AI054703. The U.S. government may have certain rights in this disclosure.

CROSS REFERENCE TO RELATED APPLICATIONS

[002] This application claims the benefit of U.S. Provisional Patent Application No. 61/118,230, filed November 26, 2008, and which provisional patent application is incorporated by reference in its entirety herein.

BACKGROUND OF THE DISCLOSURE

Technical Field

[003] The present disclosure is directed, generally, to the detection of fungal pathogens in a patient sample. More specifically, disclosed herein are methods for detecting and/or identifying a fungal pathogen in a patient sample, involving isolating the sample, optionally extracting DNA from the sample, carrying out a PCR reaction on the sample to generate an amplicon that includes a region of the fungal ribosomal RNA (rRNA) gene, such as an internal transcribed spacer 1 (ITS-1) region and/or a 28S rRNA gene region, and detecting the PCR amplicon. The present disclosure also provides primers and primer sets for specifically detecting a broad range of fungal pathogens in the presence of human ribosomal DNA (rDNA). In certain embodiments of the present disclosure, the PCR amplicon is further characterized by sequencing or by using two-dimensional melt-curve analysis. In yet other embodiments, more than one fungal pathogen is detected in a sample using the methods disclosed herein. The present disclosure also provides methods for identifying alternative primers that are useful for detecting fungal pathogens, and for detecting fungal pathogens in the presence of non-fungal DNA.

Description of the Related Art

[004] Fungal infections remain a major cause of morbidity and mortality in immunocompromised patients, such as those undergoing cancer chemotherapy, solid organ

transplants, or hematopoietic cell transplants. The rapid detection and accurate identification of fungal pathogens can be critical for initiating treatment in the earliest stages of infection and for guiding antifungal therapy. Cultivation and histological analysis often have poor diagnostic sensitivity, and histopathological findings frequently do not distinguish among fungal species [McLintock and Jones (2004) *Br. J. Haematol.* 126:289-97; Reichenberger *et al.* (1999) *Bone Marrow Transplant* 24:1195-9]. Moreover, some molecular diagnostic tests such as the galactomannan antigen assay detect only pathogens from the Aspergillus genus, and the beta-glucan antigen assay does not detect fungi in the Zygomycete or Basidiomycete taxa [Kedzierska *et al.* (2007) *Eur. J. Clin. Microbiol. Infect. Dis.* 26:755-66; McLintock and Jones (2004) *Br. J. Haematol.* 126:289-97; Ostrosky-Zeichner *et al.* (2005) *Clin. Infect. Dis.* 41:654-9; Yeo and Wong (2002) *Clin. Microbiol. Rev.* 15:465-84]. Such shortcomings may lead to more empiric antifungal therapy because a fungal infection is not completely excluded with negative results from either of these antigen assays. In addition, the spectrum of fungal infections is likely to change with increasing use of antifungal medications for prophylaxis. The next generation of diagnostic tests must be capable of detecting these emerging pathogens. Finally, pathogenic fungi within the same genus may have different antifungal susceptibility profiles, such as *Candida albicans* and *Candida krusei*.

[005] PCR assays for the detection of fungal pathogens are an appealing approach due to their potential for rapid, sensitive, and accurate diagnosis of fungal infections. Ribosomal RNA genes are particularly attractive targets because they are present in multiple copies per genome, have conserved regions for designing broad-range primers, and more variable regions for identifying fungi. Most studies have focused on 18S rRNA genes [Einsele *et al.* (1997) *J. Clin. Microbiol.* 35:1353-60], internal transcribed spacers (ITS1 and ITS2) [Bergman *et al.* (2007) *Eur. J. Clin. Microbiol. Infect. Dis.* 26:813-8; Chen *et al.* (2001) *J Clin Microbiol* 38:2302-10; Iwen *et al.* (2002) *Med. Mycol.* 40:87-109; Turenne *et al.* (1999) *J. Clin. Microbiol.* 37:1846-51] and the 5′ end of the 28S rRNA gene (D1–D2 hypervariable region) [(Hinrikson *et al.*(2005) *J. Clin. Microbiol.* 43:2092-103; Kurtzman and Robnett (1997) *J. Clin. Microbiol.* 35:1216-23; Rakeman *et al.* (2005) *J. Clin. Microbiol.* 43:3324-33; Sandhu *et al.* (1995) *J. Clin. Microbiol.* 33:2913-9; Vollmer *et al.* (2008) *J. Clin. Microbiol.* 46:1919-26)] for developing broad– range PCR assays targeting human fungal pathogens.

[006] While certain PCR primers and methods have been developed based on amplification of fungal ITS and D1-D2 regions within the rRNA operon, there are critical limitations of these primers and the approach. First, these PCR primers have not been designed to prevent the interaction with human DNA. The amplification of human DNA in a patient sample substantially diminishes the utility of such PCR primers thereby compromising the sensitivity and/or specificity of methods for the detection of a fungal pathogen in a human sample. Many of these fungal primers have a high degree of sequence similarity (or are exact matches) with human rRNA genes. Second, there can be intraspecies variability for the ITS regions which could lead to inconclusive species identification in the absence of more complete ITS sequence information in public databases [(Chen *et al.* (2000) *J Clin Microbiol* 38:2302-10; O'Donnell *et al.* (1998) *Mycologia* 90:465– 493; Rakeman *et al.* (2005) *J. Clin. Microbiol.* 43:3324-33)]. Third, variability in ITS sequence length could result in inconsistent analytical sensitivity of the fungal PCR assay. For instance, an ITS assay may produce a 200 bp amplicon from one fungus, and a 600 bp amplicon from a second fungus. The detection assay thresholds for these two fungi are not likely to be the same.

[007] What is critically needed in the art are compositions and methods for achieving the rapid detection and identification of a broad-range of fungal pathogens in patient samples without interference from or interaction with human DNA.

SUMMARY OF THE DISCLOSURE

[008] The present disclosure achieves these and other related needs by providing compositions and methods for detecting fungal pathogens in patient samples. In certain aspects, the methods include the steps of (a) isolating a patient sample, (b) carrying out a PCR reaction on the patient sample to generate a PCR amplicon that comprises a region of a fungal ribosomal RNA (rRNA) gene, wherein the PCR reaction uses a primer set including a forward primer and a reverse primer wherein at least one of the forward primer and the reverse primer is complementary to the fungal rRNA gene, and (c) detecting the PCR amplicon.

[009] In certain embodiments of the methods disclosed herein, the region of the fungal rRNA gene includes an internal transcribed spacer 1 (ITS-1) region. In other

embodiments, the fungal rRNA gene region includes a 28S rRNA gene. In still further embodiments of the methods disclosed herein, the region of the fungal 28S rRNA gene detected by PCR includes a sequence that is 3' to a D1-D2 highly variable region of the fungal 28S rRNA gene.

[0010] The methods for detecting a fungal pathogen may further involve the step of sequencing the PCR amplicon generated by the PCR reaction, such as a quantitative PCR reaction. Typically, the PCR amplicon is between 50 and 1000 base pairs or between 75 and 400 base pairs.

[0011] The forward primer used in the presently disclosed methods may be complementary to a fungal 18S rRNA gene and the reverse primer may be complementary to a fungal 28S rRNA gene. For example, the forward primer may comprise the nucleotide sequence 5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1). In other aspects, the forward primer may be complementary to a fungal 5.8S rRNA gene and the reverse primer may be complementary to a fungal 28S rRNA gene. For example, the forward primer may comprise the nucleotide sequence 5'- GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2).

[0012] In still further aspects, the forward primer and the reverse primer may both be complementary to a fungal 28S rRNA gene. For example, the forward primer may selected from the group consisting of:

5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1),
5'-GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2),
5'-TACCCGCTGAACTTAAGCATA-3' (SEQ ID NO: 3),
5'-GCATATCAATAAGCGGAGGAAA-3' (SEQ ID NO: 4),
5'-AGTARCGGCGAGTGAAGCGG-3' (SEQ ID NO: 5),
5'-AGCTCAAATTTGAAASCTGG-3' (SEQ ID NO: 6),
5'-CTTCCCTTTCAACAATTTCACRT-3' (SEQ ID NO: 7),
5'-AGGTAAAGCGAATGATTAG-3' (SEQ ID NO: 8),
5'-CTTGTTRCTTARTTGAACGTG-3' (SEQ ID NO: 9),
5'-ACCACAAAAGGTGTTAGTWCATC-3' (SEQ ID NO: 10),
5'-GAAGTGGGGAAAGGTTCC-3' (SEQ ID NO: 11),
5'-GACATGGGTTAGTCGATCCTA-3' (SEQ ID NO: 12),
5'-TCGTACTCATAACCGCAGC-3' (SEQ ID NO: 13),
5'-GTTGATAGAAYAATGTAGATAAGG-3' (SEQ ID NO: 14),
5'-CAAGGGGAATCTGACTGTC-3' (SEQ ID NO: 15),
5'-TTTACTTAWTCAATGAAG CGG-3' (SEQ ID NO: 16),
5'-CCGGGTTGAWGACATTGTCA-3' (SEQ ID NO: 17),

5'-GCTGGGGCGGCACATCTGTT-3' (SEQ ID NO: 18),
5'-GAACAAAAGGGTAAAAGTCCC-3' (SEQ ID NO: 19),
5'-TTTGATTTTCAGTGTGAATACAAACCA-3' (SEQ ID NO: 20),
5'-ATGAAAGTGTGGCCTATCG-3' (SEQ ID NO: 21),
5'-GAGGCTAGAGGTGCCAGAA-3' (SEQ ID NO: 22),
5'-AGGGATAACTGGCTTGTGGC-3' (SEQ ID NO: 23),
5'-ACCGAAGCAGAATTCGGTAAG-3' (SEQ ID NO: 24),
5'-GATAAT TGGTWTTTGCGGCTG-3' (SEQ ID NO: 25),
5'-GCTGAACGCCTCTAAGTCAGA-3' (SEQ ID NO: 26), and
5'-TCGTARCAACAAGGCTACT-3' (SEQ ID NO: 27)

and the reverse primer may be selected from the group consisting of:

5'-GAAACCTTGTTACGACTTTTAC-3' (SEQ ID NO: 28),
5'-GTTCAAAGAYTCGATGATTCAC-3' (SEQ ID NO: 29),
5'-TATGCTTAAGTTCAGCGGGTA-3' (SEQ ID NO: 30),
5'-TTTCCTCCGCTTATTGATATGC-3' (SEQ ID NO: 31),
5'-CCGCTTCACTCGCCGYTACT-3' (SEQ ID NO: 32),
5'-CCAGSTTTCAAATTTGAGCT-3' (SEQ ID NO: 33),
5'-AYGTGAAATTGTTGAAAGGGAAG-3' (SEQ ID NO: 34),
5'-CTAATCATTCGCTTTACCTC-3' (SEQ ID NO: 35),
5'-CACGTTCAAYTAAGYAACAAG-3' (SEQ ID NO: 36),
5'-GATGWACTAACACCTTTTGTGGT-3' (SEQ ID NO: 37),
5'-GGAACCTTTCCCCACTTC-3' (SEQ ID NO: 38),
5'-TAGGATCGACTAACCCATGTC-3' (SEQ ID NO: 39),
5'-GCTGCGGTTATGAGTACGA-3' (SEQ ID NO: 40),
5'-CCTTATCTACATTRTTCTATCAAC-3' (SEQ ID NO: 41),
5'-GACAGTCAGATTCCCCTTG-3' (SEQ ID NO: 42),
5'-CCGCTTCATTGAWTAAGTAAA-3' (SEQ ID NO: 43),
5'-TGACAATGTCWTCAACCCGG-3' (SEQ ID NO: 44),
5'-AACAGATGTGCCGCCCCAGC-3' (SEQ ID NO: 45),
5'-GGGACTTTTACCCTTTTGTTC-3' (SEQ ID NO: 46),
5'-TGGTTTGTATTCACACTGAAAATCAAA-3' (SEQ ID NO: 47),
5'-CGATAGGCCACACTTTCAT-3' (SEQ ID NO: 48),
5'-TTCTGGCACCTCTAGCCTC-3' (SEQ ID NO: 49),
5'-GCCACAAGCCAGTTATCCCT-3' (SEQ ID NO: 50),
5'-CTTACCGAATTCTGCTTCGGT-3' (SEQ ID NO: 51),
5'-CAGCCGCAAAWACCAATTATC-3' (SEQ ID NO: 52),
5'-TCTGACTTAGAGGCGTTCAGC-3' (SEQ ID NO: 53),
5'-AGTAGCCTTGTTGYTACGA-3' (SEQ ID NO: 54), and
5'- CCTTATCTACATTATTCTATGGAC-3' (SEQ ID NO 108).

[0013] Within certain embodiments disclosed herein, the methods employ primer sets that include a forward and reverse primer pair wherein the primer sets may be selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 31), (SEQ ID NO: 2 and SEQ ID NO: 32), (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 1 and SEQ ID

NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54) or may be selected from the group consisting of (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54) or may be selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), and (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108).

[0014] Within other embodiments disclosed herein, primer sets are provided for detecting a fungal pathogen in a patient sample. Primer sets include a forward and reverse primer pair/set as exemplified by the primer sets selected from the group consisting of (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

[0015] In other aspects disclosed herein, methods for detecting a fungal pathogen in a patient sample are provided, wherein the fungal pathogen is selected from the group consisting of *Absidia corymbifera; Cunninghamella bertholletiae; Fusarium solani; Mucor racemosus; Paecilomyces variotii; Penicillium chrysogenum; Rhizomucor miehei ; Rhodotorula glutinis ; Scedosporium apiospermum; Antrodia vaillantii; Aspergillus fumigatus; Aspergillus niger; Aspergillus oryzae; Aspergillus terreus; Batrachochytrium dendrobatidis; Botrytis cinerea; Candida albicans; Candida dublineinsis; Candida glabrata; Candida gulliermundei; Candida kefyr; Candida krusei; Candida lipolytica; Candida lusitaniae; Candida parapsilosis; Candida tropicalis; Chaetomium globosum; Coccidioides immitis; Coccidioides posadasii; Cryptococcus neoformans; Fusarium graminearum; Fusarium oxysporum; Histoplasma capsulatum; Hypocrea jecorina; Lodderomyces elongisporus; Magnaporthe grisea; Metarhizium anisopliae; Microsporum gypseum; Mucor racemosus; Neurospora crassa; Paracoccidioides brasiliens; Pneumocystis carinii; Penicillium verrucosum; Pichia stipitis; Rhizomucor miehei; Rhizopus oryzae;*

Saccharomyces cerevisiae; Schizosaccharomyces japonicus; Schizosaccharomyces pombe; Sclerotinia sclerotiorum; Stagonospora nodorum; Umbilicaria esculenta; and *Uncinocarpus reesii*. Thus, the methods provided herein may be suitably adapted for detecting a fungal pathogen that causes a fungal infection selected from the group consisting of aspergillosis, candidiasis, zygomycosis, scedosporiosis, fusariosis, cryptococcosis, histoplasmosis, coccidioidomycosis, and blastomycosis.

[0016] Primers disclosed herein were designed to be used in PCR-based methods for detecting fungal DNA in a patient sample. Thus, these primers specifically bind to a fungal DNA but not to DNA in a patient sample. Thus, each primer of the primer set specifically binds only to a fungal DNA in the presence of a non-fungal DNA, such as mammalian DNA, typically human DNA. As demonstrated herein, primers of the present disclosure permit the amplification of fungal DNA in a patient sample where the non-fungal DNA is present in greater than 1,000,000-fold, 5,000,000-fold, or 30,000,000-fold mass excess over the amount of fungal DNA.

[0017] Within other embodiments, the present disclosure provides primer sets for detecting a fungal DNA, wherein the primer sets include a forward primer and a reverse primer, wherein at least one of the forward primer and the reverse primer is complementary to a region in the 18S rRNA gene, 5.8S rRNA gene, and/or to a 28S rRNA gene. Typically, the forward primer and/or the reverse primer of the primer set is complementary to a sequence that is 3' to a D1-D2 highly variable region in the fungal 28S ribosomal rRNA gene. In yet other embodiments, the forward primer of the primer set is complementary to a fungal 18S rRNA gene and the reverse primer is complementary to a fungal 28S rRNA gene. An exemplary forward primer suitable for use in such primer sets includes the nucleotide sequence 5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1). In other embodiments, the forward primer of the primer set is complementary to a fungal 5.8S rRNA gene and the reverse primer is complementary to a fungal 28S rRNA gene. An exemplary forward primer suitable for use in such primer sets includes the nucleotide sequence 5'- GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2).

[0018] In certain aspects, the forward primer and the reverse primer of the primer set are both complementary to a fungal 28S rRNA gene and include the forward and reverse

primers described above, including SEQ ID NOs: 1-27 and SEQ ID NOs: 28-54, respectively.

[0019] Exemplary primer sets include a forward and reverse primer pair/set and may be selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 31), (SEQ ID NO: 2 and SEQ ID NO: 32), (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54). Preferably, the forward and reverse primer pair of the primer set is selected from the group consisting of (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54). More preferably, the forward and reverse primer set is selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), and (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108).

[0020] In certain aspects, the forward primer of the primer set has the sequence set forth in SEQ ID NO: 1 and the reverse primer has the sequence set forth in SEQ ID NO: 30. In other aspects, the forward primer has the sequence set forth in SEQ ID NO: 12 and the reverse primer has the sequence set forth in SEQ ID NO: 41. In some aspects, a second reverse primer with the sequence set forth in SEQ ID NO 108 may be included in a forward and reverse primer set also comprising a forward primer (SEQ ID NO: 12) and a reverse primer (SEQ ID NO: 41), and may be included and/or added at a concentration equivalent to 5-10% (e.g. 9%) of the reverse primer concentration.

[0021] Another embodiment of the present disclosure provides methods for determining the identity of a fungal species in a patient sample. Such methods include the steps of: (a) isolating a patient sample; (b) carrying out a first PCR reaction to generate a first PCR amplicon, wherein the first PCR reaction includes a first primer set capable of amplifying a region in a fungal ribosomal RNA (rRNA) gene having an internal transcribed spacer 2

(ITS-2) sequence; (c) carrying out a second PCR reaction to generate a second PCR amplicon, wherein the second PCR reaction has a second primer set capable of amplifying a region in a fungal ribosomal 28-S rRNA gene; and (d) determining the melting temperature of the first PCR amplicon and of the second PCR amplicon, wherein the identity of the fungal species is determined by comparing the melting point of the first PCR amplicon and of the second PCR amplicon to known standards.

[0022] In certain aspects of these methods, the first and second PCR reactions are quantitative PCR (qPCR) reactions. In other aspects, the first primer set includes a forward primer sequence as set forth in SEQ ID NO: 2 and a reverse primer sequence as set forth in SEQ ID NO: 30, and the second primer set includes a forward primer sequence as set forth in SEQ ID NO: 12 and a reverse primer sequence as set forth in SEQ ID NO: 41. In some aspects, the second primer set further includes a second reverse primer sequence as set forth in SEQ ID NO: 108. The second reverse primer sequence may be included in or added to the second primer set at a concentration of 5-10% (e.g. 9%) of the reverse primer sequence concentration.

[0023] Also disclosed herein are methods for identifying a primer set capable of detecting a fungal pathogen in a sample, wherein the method includes the steps of: (a) obtaining the nucleic acid sequence of at least the 28S region of a fungal rRNA operon, (b) designing a forward primer capable of hybridizing with the nucleic acid sequence at a specific site in said 28S region, (c) designing a reverse primer capable of hybridizing with the nucleic acid sequence at a region in the sequence that is 3' to the region to which the forward primer is capable of hybridizing, and (d) determining whether the forward primer and the reverse primer are capable of generating a PCR amplicon that is useful for identifying fungal DNA in a PCR reaction containing a specific fungal DNA.

[0024] Certain embodiments of these methods further include the step of resolving the PCR amplicon on an agarose gel to determine the analytical sensitivity of the forward primer and the reverse primer. The agarose gel may be stained with ethidium bromide and the PCR amplicon may be visualized by ultraviolet light.

[0025] Other embodiments of these methods further include the step of determining the cross-reactivity of the forward primer and reverse primer with non-fungal DNA. In certain aspects, the non-fungal DNA is mammalian DNA, such as human DNA.

[0026] Yet other embodiments of these methods further include the step of determining the species resolution of the forward primer and the reverse primer, wherein the forward primer and the reverse primer are a primer set. The ability of the primer set to resolve a species may be determined by the following steps: (a) sequencing the PCR amplicon, (b) comparing the sequence of the PCR amplicon with a sequence of a second PCR amplicon generated using the forward and reverse primers in a PCR reaction containing DNA from a different fungal species, and (c) repeating steps (a) and (b) using fungal DNA from at least 30 different fungal species to determine sequences of amplicons for at least 31 different fungal species, and (d) comparing the sequences of each amplicon. The sequences of each amplicon may be compared to each other by generating a multiple sequence alignment of the sequences.

[0027] Still further embodiments of these methods include the step of generating a distance matrix for each amplicon from the multiple sequence alignment. The distance matrix may be compared to the distance matrix of each other amplicon, and the comparison used to determine which of the primer sets are capable of resolving a fungal species. In certain aspects, the distance matrix is generated using the Tajima-Nei algorithm.

[0028] These and other embodiments, features and advantages of the disclosure will become apparent from the detailed description and the appended claims set forth herein below.

BRIEF DESCRIPTION OF THE FIGURES AND SEQUENCE IDENTIFIERS

[0029] Figure 1 is a matrix of all possible amplicon lengths from unique combinations of 27 broad-range fungal primers. Shaded regions indicate amplicons with lengths between 75 to 400 bp, selected for further analysis.

[0030] Figure 2A is a map of fungal rRNA from the 3' end of 18S to the 3' end of 28S rRNA gene based on *Saccharomyces cerevisae*.

[0031] Figure 2B is a schematic map showing the general location of the 27 broad-range fungal primers along the region spanning from the 3' end of the 18S gene to the 5' end of the 28S gene.

[0032] Figure 3 is a schematic diagram of the approach used for the development of broad-range PCR assays.

[0033] Figure 4A is table showing PCR amplification results for 11 PCR primer pairs on 27 different fungal species or on 1 μg human DNA.

[0034] Figure 4B is an exemplary image of PCR products run on a 1.5% agarose gel, wherein a band having a high intensity is scored as '+++', medium intensity '++', low intensity '+', or no amplification '-'.

[0035] Figure 5A is a distance matrix of nucleotide differences based on the ITS1(18SF-5.8SR) amplicon of 28 human fungal pathogens.

[0036] Figure 5B is a distance matrix of nucleotide differences based on the ITS2(5.8SF-1R) amplicon of 30 human fungal pathogens.

[0037] Figure 5C is a distance matrix of nucleotide differences based on the 28S (10F-12R) amplicon of 30 human fungal pathogens.

[0038] Figure 5D is a distance matrix of nucleotide differences based on the 28S (12F-13R) amplicon of 30 human fungal pathogens.

[0039] Figure 5E is a distance matrix of nucleotide differences based on the 28S (15F-22R) amplicon of 30 human fungal pathogens.

[0040] Figure 5F is a distance matrix of nucleotide differences based on the 28S (18F-22R) amplicon of 30 human fungal pathogens.

[0041] Figure 5G is a distance matrix of nucleotide differences based on the 28S (18F-23R) amplicon of 30 human fungal pathogens.

[0042] Figure 5H is a distance matrix of nucleotide differences based on the 28S (23F-25R) amplicon of 26 human fungal pathogens.

[0043] Figure 6 displays the ability of the 28S(10F-12R) amplicon to distinguish between 51 different fungal species spanning 30 genera as a phylogenetic tree which was constructed based on the neighbor joining tree building method and distances estimated using Tajima-Nei algorithm.

[0044] Figure 7 displays the ability of the ITS2(5.8SF-1R) amplicon to distinguish between 51 different fungal species spanning 30 genera as a phylogenetic tree which was constructed based on the neighbor joining tree building method and distances estimated using Tajima-Nei algorithm.

[0045] Figure 8 is a partial rRNA nucleic acid sequence of *Absidia corymbifera* strain (SEQ ID NO: 55).

[0046] Figure 9 is a partial rRNA nucleic acid sequence of *Cunninghamella bertholletiae* strain ATCC # 42115 (SEQ ID NO: 56).

[0047] Figure 10 is a partial rRNA nucleic acid sequence of *Fusarium solani* strain, ATCC # 56480 (SEQ ID NO: 57).

[0048] Figure 11 is a partial rRNA nucleic acid sequence of *Mucor racemosus* strain, ATCC # 42647, (SEQ ID NO: 58).

[0049] Figure 12 is a partial rRNA nucleic acid sequence of *Paecilomyces variotii* strain, ATCC # 10865, (SEQ ID NO: 59).

[0050] Figure 13 is a partial rRNA nucleic acid sequence of *Penicillium chrysogenum* strain, ATCC # 10108, (SEQ ID NO: 60).

[0051] Figure 14 is a partial rRNA nucleic acid sequence of *Rhizomucor miehei* strain, ATCC # 46345, (SEQ ID NO: 61).

[0052] Figure 15 is a partial rRNA nucleic acid sequence of *Rhodotorula glutinis* strain, ATCC # 16726, (SEQ ID NO: 62).

[0053] Figure 16 is a partial rRNA nucleic acid sequence of *Scedosporium apiospermum* strain, ATCC # 28206, (SEQ ID NO: 63).

[0054] Figure 17 is a partial rRNA nucleic acid sequence of *Antrodia vaillantii* strain (SEQ ID NO: 64).

[0055] Figure 18 is a partial rRNA nucleic acid sequence of *Aspergillus fumigatus* strain (SEQ ID NO: 65).

[0056] Figure 19 is a partial rRNA nucleic acid sequence of *Aspergillus niger* strain (SEQ ID NO: 66).

[0057] Figure 20 is a partial rRNA nucleic acid sequence of *Aspergillus oryzae* strain (SEQ ID NO: 67).

[0058] Figure 21 is a partial rRNA nucleic acid sequence of *Aspergillus terreus* strain (SEQ ID NO: 68).

[0059] Figure 22 is a partial rRNA nucleic acid sequence of *Batrachochytrium dendrobatidis* strain (SEQ ID NO: 69).

[0060] Figure 23 is a partial rRNA nucleic acid sequence of *Botrytis cinerea* strain (SEQ ID NO: 70).

[0061] Figure 24 is a partial rRNA nucleic acid sequence of *Candida albicans* strain (SEQ ID NO: 71).

[0062] Figure 25 is a partial rRNA nucleic acid sequence of *Candida dublineinsis* strain (SEQ ID NO: 72).

[0063] Figure 26 is a partial rRNA nucleic acid sequence of *Candida glabrata* strain (SEQ ID NO: 73).

[0064] Figure 27 is a partial rRNA nucleic acid sequence of *Candida gulliermundei* strain (SEQ ID NO: 74).

[0065] Figure 28 is a partial rRNA nucleic acid sequence of *Candida kefyr* strain (SEQ ID NO: 75).

[0066] Figure 29 is a partial rRNA nucleic acid sequence of *Candida krusei* strain (SEQ ID NO: 76).

[0067] Figure 30 is a partial rRNA nucleic acid sequence of *Candida lipolytica* strain (SEQ ID NO: 77).

[0068] Figure 31 is a partial rRNA nucleic acid sequence of *Candida lusitaniae* strain (SEQ ID NO: 78).

[0069] Figure 32 is a partial rRNA nucleic acid sequence of *Candida parapsilosis* strain (SEQ ID NO: 79).

[0070] Figure 33 is a partial rRNA nucleic acid sequence of *Candida tropicalis* strain (SEQ ID NO: 80).

[0071] Figure 34 is a partial rRNA nucleic acid sequence of *Chaetomium globosum* strain (SEQ ID NO: 81).

[0072] Figure 35 is a partial rRNA nucleic acid sequence of *Coccidioides immitis* strain (SEQ ID NO: 82).

[0073] Figure 36 is a partial rRNA nucleic acid sequence of *Coccidioides posadasii* strain (SEQ ID NO: 83).

[0074] Figure 37 is a partial rRNA nucleic acid sequence of *Cryptococcus neoformans* strain (SEQ ID NO: 84).

[0075] Figure 38 is a partial rRNA nucleic acid sequence of *Fusarium graminearum* strain (SEQ ID NO: 85).

[0076] Figure 39 is a partial rRNA nucleic acid sequence of *Fusarium oxysporum* strain (SEQ ID NO: 86).

[0077] Figure 40 is a partial rRNA nucleic acid sequence of *Histoplasma capsulatum* strain (SEQ ID NO: 87).

[0078] Figure 41 is a partial rRNA nucleic acid sequence of *Hypocrea jecorina* strain (SEQ ID NO: 88).

[0079] Figure 42 is a partial rRNA nucleic acid sequence of *Lodderomyces elongisporus* strain (SEQ ID NO: 89).

[0080] Figure 43 is a partial rRNA nucleic acid sequence of *Magnaporthe grisea* strain (SEQ ID NO: 90).

[0081] Figure 44 is a partial rRNA nucleic acid sequence of *Metarhizium anisopliae* strain (SEQ ID NO: 91).

[0082] Figure 45 is a partial rRNA nucleic acid sequence of *Microsporum gypseum* strain (SEQ ID NO: 92).

[0083] Figure 46 is a partial rRNA nucleic acid sequence of *Mucor racemosus* strain (SEQ ID NO: 93).

[0084] Figure 47 is a partial rRNA nucleic acid sequence of *Neurospora crassa* strain (SEQ ID NO: 94).

[0085] Figure 48 is a partial rRNA nucleic acid sequence of *Paracoccidioides brasiliens* strain (SEQ ID NO: 95).

[0086] Figure 49 is a partial rRNA nucleic acid sequence of *Pneumocystis carinii* strain (SEQ ID NO: 96).

[0087] Figure 50 is a partial rRNA nucleic acid sequence of *Penicillium verrucosum* strain (SEQ ID NO: 97).

[0088] Figure 51 is a partial rRNA nucleic acid sequence of *Pichia stipitis* strain (SEQ ID NO: 98).

[0089] Figure 52 is a partial rRNA nucleic acid sequence of *Rhizomucor miehei* strain (SEQ ID NO: 99).

[0090] Figure 53 is a partial rRNA nucleic acid sequence of *Rhizopus oryzae* strain (SEQ ID NO: 100).

[0091] Figure 54 is a partial rRNA nucleic acid sequence of *Saccharomyces cerevisiae* strain (SEQ ID NO: 101).

[0092] Figure 55 is a partial rRNA nucleic acid sequence of *Schizosaccharomyces japonicus* strain (SEQ ID NO: 102).

[0093] Figure 56 is a partial rRNA nucleic acid sequence of *Schizosaccharomyces pombe* strain (SEQ ID NO: 103).

[0094] Figure 57 is a partial rRNA nucleic acid sequence of *Sclerotinia sclerotiorum* strain (SEQ ID NO: 104).

[0095] Figure 58 is a partial rRNA nucleic acid sequence of *Stagonospora nodorum* strain (SEQ ID NO: 105).

[0096] Figure 59 is a partial rRNA nucleic acid sequence of *Umbilicaria esculenta* strain (SEQ ID NO: 106).

[0097] Figure 60 is a partial rRNA nucleic acid sequence of *Uncinocarpus reesii* strain (SEQ ID NO: 107).

[0098] Figure 61 illustrates a map of a fungal 28S rRNA gene and corresponding positions of twenty-seven broad-range fungal PCR primers for sequencing and PCR assay development.

[0099] Figure 62 illustrates a two-dimensional melt curve plot based on the broad-range fungal qPCR assays ITS2(5.8SF-1R) and 28S(10F-12R) allowing rapid identification of species.

[00100] Figure 63 illustrates melt temperature curves of pathogenic fungi amplified from blood, representing the 10-12 amplicon on the fungal 28S rRNA gene.

DETAILED DESCRIPTION OF THE DISCLOSURE

[00101] The present disclosure is based on the unexpected discovery that a specific fungal pathogen in a patient sample may be rapidly identified using broad-range PCR primers that specifically amplify fungal DNA including a portion of the rRNA gene, including a portion of an internal transcribed spacer 1 (ITS-1) region and/or a portion of a 28S rRNA gene. Methods using the primers and primer sets provided herein uniquely identify and differentiate among at least 27 different species of fungal pathogens, even in the presence of human DNA. Thus, the present methods are useful in a clinical setting for the rapid identification of one or more fungal pathogen(s) in a patient sample.

[00102] The primers, primer sets, and methods provided herein have both excellent analytical sensitivity and species level resolution which helps to overcome the potential shortcomings of the ITS regions. For PCR assays that use amplicon length or melting temperature of the amplicons to distinguish between species, a single amplicon approach may be insufficient, therefore use of more than one PCR target may be optimal. As described herein, the exemplary combination of ITS2(5.8SF–1R) and 28S(10F– 12R) amplicons provides effective analytical sensitivity and potential for fungal species resolution.

[00103] To create a database of fungal sequences including the ITS1, 5.8S, ITS2 and 28S rRNA genes, 9 clinically and phylogentically relevant fungal pathogens were sequenced and sequences from fungal genomic databases or the GenBank® genetic sequence database (herein, "GenBank®") for 41 fungal species were derived, resulting in an alignment of a total of 50 fungal sequences spanning 30 genera. In the nearly 3900 bp region from the 3 end of 18S to the 3 end of 28S rRNA genes, 27 broad-range PCR primers were designed. Sixty two amplicons between the sizes of 75 to 400 bp were selected for screening, with amplicon sizes minimized to enhance analytical sensitivity. Optimal PCR assays were selected based on their ability to detect phylogentically diverse fungi and amplify small quantities of fungal DNA in the presence of large quantities of human DNA. The analysis of this region of the rRNA operon showed that there is nearly 2800 bp of sequence beyond the D1-D2 region which is useful for the development of broad-range fungal PCR assays. As described herein, the 28S rRNA gene beyond the D1-D2 region was found to be useful for the design of broad-range fungal PCR assays with good species-level resolution and the

potential to detect the equivalent of a single fungal genome (30 fg) in a background of 1 μg of human DNA, representing a 30,000,000 fold excess of non-fungal DNA.

[00104] The present disclosure will be best understood by reference to the following definitions:

Definitions

[00105] An "individual" or "subject", "mammal", "patient" or "animal", as used herein, refers to vertebrates that support a fungal infection, including, but not limited to, birds (such as water fowl and chickens) and members of the mammalian species, such as canine, feline, lupine, mustela, rodent (racine, and murine, etc.), equine, bovine, ovine, caprine, porcine species, and primates, the latter including humans.

[00106] As used herein, the term "isolated" means that the referenced material is removed from its native environment, *e.g.*, a cell or fungus. Thus, an isolated biological material can be free of some or all cellular components, *i.e.*, components of the cells in which the native material occurs naturally (*e.g.*, cytoplasmic or membrane component). A material shall be deemed isolated if it is present in a cell extract or supernatant. In the case of nucleic acid molecules, an isolated nucleic acid includes a PCR product, an isolated mRNA, a cDNA, or a restriction fragment. In another embodiment, an isolated nucleic acid is preferably excised from the chromosome in which it may be found, and more preferably is no longer joined or proximal to non-coding regions (but may be joined to its native regulatory regions or portions thereof), or to other genes, located upstream or downstream of the gene contained by the isolated nucleic acid molecule when found in the chromosome. In yet another embodiment, the isolated nucleic acid lacks one or more introns. Isolated nucleic acid molecules include sequences inserted into plasmids, cosmids, artificial chromosomes, and the like, *i.e.*, when it forms part of a chimeric recombinant nucleic acid construct. Thus, in a specific embodiment, a recombinant nucleic acid is an isolated nucleic acid. An isolated protein may be associated with other proteins or nucleic acids, or both, with which it associates in the cell, or with cellular membranes if it is a membrane-associated protein. An isolated organelle, cell, or tissue is removed from the anatomical site in which it is found in an organism. An isolated material may be, but need not be, purified.

[00107] The term "purified" as used herein refers to material that has been isolated under conditions that reduce or eliminate the presence of unrelated materials, *i.e.* contaminants, including native materials from which the material is obtained. For example, a purified fungal DNA is preferably substantially free of cell or culture components, including tissue culture components, contaminants, and the like. As used herein, the term "substantially free" is used operationally, in the context of analytical testing of the material. Preferably, purified material substantially free of contaminants is at least 50% pure; more preferably, at least 90% pure, and more preferably still at least 99% pure. Purity can be evaluated by chromatography, gel electrophoresis, immunoassay, composition analysis, biological assay, and other methods known in the art.

[00108] As used herein, the terms "include" and "comprise" are used synonymously. It should be understood that the terms "a" and "an" as used herein refer to "one or more" of the enumerated components. The use of the alternative (*e.g.*, "or") should be understood to mean either one, both, or any combination thereof of the alternatives.

[00109] In the present description, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. Also, any number range recited herein relating to any physical feature, such as polymer subunits, size or thickness, are to be understood to include any integer within the recited range, unless otherwise indicated. As used herein, "about" or "consisting essentially of" mean $\pm$ 20% of the indicated range, value, or structure, unless otherwise indicated.

[00110] In a specific embodiment, the term "about" or "approximately" means within a statistically meaningful range of a value. Such a range can be within an order of magnitude, preferably within 50%, more preferably within 20%, more preferably still within 10%, and even more preferably within 5% of a given value or range. The allowable variation encompassed by the term "about" or "approximately" depends on the particular system under study, and can be readily appreciated by one of ordinary skill in the art.

[00111] The term "contig" as used herein, refers to one of a set of overlapping clones that represent a continuous region of DNA. However, in certain embodiments, "contig"

also refers to a contiguous sequence constructed from many clone sequences or PCR products, and herein, is used synonymously with the term "sequence."

[00112] "Endpoint PCR" is understood to mean a semi-quantitative approach to measuring relative amounts of template (DNA) in a sample involving the measurement of the amount of PCR product present at the end of a PCR reaction. In certain embodiments of the present disclosure, end-point PCR is performed by resolving the PCR amplicon on an agarose gel and staining the gel with an "intercalating" dye, such as, for example, ethidium bromide. Ethidium bromide binds between the bases of the DNA helix. When it is inserted into the DNA, it becomes much more fluorescent when exposed to ultraviolet light as compared to ethidium bromide just in solution. This characteristic of ethidium bromide permits semi-quantitative measurements of the amount of DNA in the PCR product by measuring the degree of fluorescence of the PCR product in the gel.

[00113] The term "sample" as used in the present disclosure can be any tissue, fluid, or other source of DNA from a patient or mammal.

[00114] Techniques to isolate and modify specific nucleic acids and proteins are well known to those of skill in the art. In accordance with the present disclosure there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition (Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, 1989) ("Sambrook *et al.*, 1989"); DNA Cloning: A Practical Approach, Volumes I and II (D.N. Glover ed. 1985); Oligonucleotide Synthesis (M.J. Gait ed. 1984); Nucleic Acid Hybridization (B.D. Hames & S.J. Higgins eds. (1985)); Transcription And Translation (B.D. Hames & S.J. Higgins, eds. (1984)); Animal Cell Culture (R.I. Freshney, ed. (1986)); Immobilized Cells And Enzymes (IRL Press, (1986)); Perbal, "A Practical Guide To Molecular Cloning" (Ausubel, F.M. *et al.* eds., (1984)). Current Protocols in Molecular Biology (John Wiley & Sons, Inc., 1994). These techniques include site directed mutagenesis employing oligonucleotides with altered nucleotides for generating PCR products with mutations (*e.g.*, the "Quikchange" kit manufactured by Stratagene).

[00115] DNA typing (or "genotyping") involves the analysis of alleles of genomic DNA with characteristics of interest, commonly referred to as "markers." Most typing methods in use today are specifically designed to detect and analyze differences in the length and/or sequence of one or more regions of DNA markers known to appear in at least two different forms in a population. Such length and/or sequence variation is referred to as "polymorphism." Any region (*i.e.*, "locus") of DNA in which such a variation occurs is referred to as a "polymorphic locus."

[00116] The terms "nucleic acid" and "oligonucleotide," as used herein, refer to polydeoxyribonucleotides (containing 2-deoxy-D-ribose), to polyribonucleotides (containing D-ribose), and to any other type of polynucleotide which is an N glycoside of a purine or pyrimidine base. There is no intended distinction in length between the terms "nucleic acid" and "oligonucleotide", and these terms will be used interchangeably. These terms refer only to the primary structure of the molecule. Thus, these terms include double- and single-stranded DNA, as well as double- and single-stranded RNA. For use in the present disclosure, an oligonucleotide also can comprise non-purine or non-pyrimidine nucleotide analogs. The length of a nucleic acid sequence is referred to as the number of "base pairs (bp)" present in the double-stranded nucleic acid sequence.

[00117] The nucleic acid molecules of sequences disclosed herein are written according to The International Union of Pure and Applied Chemistry (IUPAC) DNA codes. Specifically, "A" is Adenine, "C" is Cytosine, "G" is Guanine, "T" is Thymine, "U" is Uracil, "R" is any Purine (A or G), "Y" is any Pyrimidine (C, T, or U), "M" is C or A, "K" is T, U, or G, "W" is T, U, or A, "S" is C or G, "B" is C, T, U, or G (not A), "D" is A, T, U, or G (not C), "H" is A, T, U, or C (not G), "V" is A, C, or G (not T, not U), and "N" is any base (A, C, G, T, or U).

[00118] In certain embodiments, the amount of fungal DNA present in a sample is described in terms of the "fold-excess" of human or non-fungal DNA over the amount of fungal DNA present in the same sample. For example, if 1 μg of human genomic DNA is present in a sample that has 0.001 μg of fungal DNA, then the human DNA is understood to be in 1000-fold excess of the fungal DNA.

[00119] Oligonucleotides can be prepared by any suitable method, including direct chemical synthesis by a method such as the phosphotriester method of Narang *et al.* (1979) *Meth. Enzymol.* 68:90-99; the phosphodiester method of Brown *et al.*, (1979) *Meth. Enzymol.* 68:109-151; the diethylphosphoramidite method of Beaucage *et al.* (1981) *Tetrahedron Lett.* 22:1859-1862; and the solid support method of U.S. Pat. No. 4,458,066, each incorporated herein by reference. A review of synthesis methods of conjugates of oligonucleotides and modified nucleotides is provided in Goodchild (1990) *Bioconjugate Chemistry* 1(3):165-187, incorporated herein by reference.

[00120] The term "primer," as used herein, refers to an oligonucleotide capable of acting as a point of initiation of DNA synthesis under conditions in which synthesis of a primer extension product complementary to a nucleic acid strand is induced, *i.e.*, either in the presence of four different nucleoside triphosphates and an agent for extension (*e.g.*, a DNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. A primer is preferably a single-stranded DNA. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 6 to 50 nucleotides, preferably from 15-35 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template nucleic acid, but must be sufficiently complementary to hybridize with the template. The design of suitable primers for the amplification of a given target sequence is well known in the art and described in the literature cited herein. As used herein, a "forward primer" is understood to mean a primer that is capable of hybridizing to a region of DNA along the 5' (coding) strand of DNA. A "reverse" primer is understood to mean a primer that is capable of hybridizing to a region of DNA along the 3' (non-coding) strand of DNA.

[00121] Primers can incorporate additional features which allow for the detection or immobilization of the primer but do not alter the basic property of the primer, that of acting as a point of initiation of DNA synthesis. For example, primers may contain an additional nucleic acid sequence at the 5' end which does not hybridize to the target nucleic acid, but which facilitates cloning of the amplified product. The region of the primer which is sufficiently complementary to the template to hybridize is referred to herein as the hybridizing region.

[00122] A "primer set" or "primer pair" refers to a specific combination of a forward primer and one or more reverse primers. Some "primer sets" or "primer pairs" may include, for example, one forward primer and two reverse primers (*e.g.*, a primer set comprising SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108). The "primer set" or "primer pair" may be used in a PCR reaction to generate a specific PCR product or amplicon.

[00123] The term "amplicon" as used herein, refers to the DNA sequence generated by a PCR or qPCR reaction. "Amplicon" may further be used synonymously with the term "PCR product."

[00124] In certain embodiments, the term "primer" is also intended to encompass the oligonucleotides used in ligation-mediated amplification processes, in which one oligonucleotide is "extended" by ligation to a second oligonucleotide which hybridizes at an adjacent position. Thus, the term "primer extension", as used herein, refers to both the polymerization of individual nucleoside triphosphates using the primer as a point of initiation of DNA synthesis and to the ligation of two oligonucleotides to form an extended product.

[00125] The terms "target, "target sequence", "target region", and "target nucleic acid," as used herein, are synonymous and refer to a region or subsequence of a nucleic acid which is to be amplified or detected.

[00126] The term "hybridization," as used herein, refers to the formation of a duplex structure by two single-stranded nucleic acids due to complementary base pairing. Hybridization can occur between fully complementary nucleic acid strands or between "substantially complementary" nucleic acid strands that contain minor regions of mismatch. Conditions under which only fully complementary nucleic acid strands will hybridize are referred to as "stringent hybridization conditions" or "sequence-specific hybridization conditions". Stable duplexes of substantially complementary sequences can be achieved under less stringent hybridization conditions; the degree of mismatch tolerated can be controlled by suitable adjustment of the hybridization conditions. Those skilled in the art of nucleic acid technology can determine duplex stability empirically considering a number of variables including, for example, the length and base pair composition of the

oligonucleotides, ionic strength, and incidence of mismatched base pairs, following the guidance provided by the art (see, *e.g.*, Sambrook *et al.*, (1989) Molecular Cloning--A Laboratory Manual (Cold Spring Harbor Laboratory, Cold Spring Harbor, New York); and Wetmur (1991) *Critical Review in Biochem. and Mol. Biol.* 26(3/4):227-259; both incorporated herein by reference).

[00127] The term "amplification reaction" refers to any chemical reaction, including an enzymatic reaction, which results in increased copies of a template nucleic acid sequence or results in transcription of a template nucleic acid. Amplification reactions include reverse transcription and the polymerase chain reaction (PCR), including Real Time PCR (see U.S. Pat. Nos. 4,683,195 and 4,683,202; PCR Protocols: A Guide to Methods and Applications (Innis *et al.*, eds, 1990)). Exemplary "amplification reactions conditions" or "amplification conditions" typically comprise either two or three step cycles. Two step cycles have a denaturation step followed by a hybridization/elongation step. Three step cycles comprise a denaturation step followed by a hybridization step followed by a separate elongation step.

[00128] Polymerase chain reaction (PCR) is a method that allows exponential amplification of short DNA sequences (usually 100 to 600 bases) within a longer double stranded DNA molecule. PCR entails the use of a pair of primers, each about 20 nucleotides in length, that are complementary to a defined sequence on each of the two strands of the DNA. These primers are extended by a DNA polymerase so that a copy is made of the designated sequence. After making this copy, the same primers can be used again, not only to make another copy of the input DNA strand but also of the short copy made in the first round of synthesis. This leads to logarithmic amplification. Since it is necessary to raise the temperature to separate the two strands of the double strand DNA in each round of the amplification process, a major step forward was the discovery of a thermo-stable DNA polymerase (Taq polymerase) that was isolated from *Thermus aquaticus*, a bacterium that grows in hot pools; as a result it is not necessary to add new polymerase in every round of amplification. After several (often about 40) rounds of amplification, the PCR product is analyzed on an agarose gel and is abundant enough to be detected with an ethidium bromide stain.

[00129] In other embodiments, real-time PCR, also called quantitative real time PCR, quantitative PCR (Q-PCR/qPCR), or kinetic polymerase chain reaction, is a laboratory technique based on PCR, which is used to amplify and simultaneously quantify a targeted DNA molecule. qPCR enables both detection and quantification (as absolute number of copies or relative amount when normalized to DNA input or additional normalizing genes) of a specific sequence in a DNA sample. For example, in the embodiments disclosed herein, qPCR may be used to quantify the amount of fungal DNA in a patient sample. The procedure follows the general principle of PCR; its key feature is that the amplified DNA is quantified as it accumulates in the reaction in real time after each amplification cycle. Two common methods of quantification are the use of fluorescent dyes that intercalate with double-stranded DNA, and modified DNA oligonucleotide probes that fluoresce upon binding to complementary DNA (such as with molecular beacons) or with completion of each PCR cycle (such as with dual labeled probes rendered more fluorescent with the 5' exonuclease activity of polymerase enzymes).

[00130] As used herein, a "polymerase" refers to an enzyme that catalyzes the polymerization of nucleotides. Generally, the enzyme will initiate synthesis at the 3'-end of the primer annealed to a nucleic acid template sequence. "DNA polymerase" catalyzes the polymerization of deoxyribonucleotides. Known DNA polymerases include, for example, *Pyrococcus furiosus* (Pfu) DNA polymerase (Lundberg *et al.*, (1991) *Gene* 108:1), *E. coli* DNA polymerase I (Lecomte and Doubleday (1983) *Nucleic Acids Res.* 11:7505), T7 DNA polymerase (Nordstrom *et al.* (1981) *J. Biol. Chem.* 256:3112), *Thermus thermophilus* (Tth) DNA polymerase (Myers and Gelfand (1991) *Biochemistry* 30:7661), *Bacillus stearothermophilus* DNA polymerase (Stenesh and McGowan (1977) *Biochim Biophys Acta* 475:32), *Thermococcus litoralis* (Tli) DNA polymerase (also referred to as Vent DNA polymerase, Cariello *et al.* (1991) *Nucleic Acids Res* 19:4193), *Thermotoga maritima* (Tma) DNA polymerase (Diaz and Sabino (1998) *Braz J. Med. Res* 31:1239), *Thermus aquaticus* (Taq) DNA polymerase (Chien *et al.*, (1976) *J. Bacteoriol* 127:1550), *Pyrococcus kodakaraensis* KOD DNA polymerase (Takagi *et al.* (1997) *Appl. Environ. Microbiol.* 63:4504), JDF-3 DNA polymerase (Patent application WO 0132887), and *Pyrococcus* GB-D (PGB-D) DNA polymerase (Juncosa-Ginesta *et al.* (1994) *Biotechniques* 16:820). The polymerase activity of any of the above enzymes can be determined by means well known in the art.

[00131] As used herein, a primer is "specific," for a target sequence if, when used in an amplification reaction under sufficiently stringent conditions, the primer hybridizes primarily only to the target nucleic acid. Typically, a primer is specific for a target sequence if the primer-target duplex stability is greater than the stability of a duplex formed between the primer and any other sequence found in the sample. One of skill in the art will recognize that various factors, such as salt conditions as well as base composition of the primer and the location of the mismatches, will affect the specificity of the primer, and that routine experimental confirmation of the primer specificity will be needed in most cases. Hybridization conditions can be chosen under which the primer can form stable duplexes only with a target sequence. Thus, the use of target-specific primers under suitably stringent amplification conditions enables the specific amplification of those target sequences which contain the target primer binding sites. The use of sequence-specific amplification conditions enables the specific amplification of those target sequences which contain the exactly complementary primer binding sites.

[00132] As used herein, "complementary" refers to a nucleic acid molecule that can form hydrogen bond(s) with another nucleic acid molecule by either traditional Watson-Crick base pairing or other non-traditional types of pairing (*e.g.*, Hoogsteen or reversed Hoogsteen hydrogen bonding) between complementary nucleosides or nucleotides.

[00133] It is understood in the art that a nucleic acid molecule need not be 100% complementary to a target nucleic acid sequence to be specifically hybridizable. That is, two or more nucleic acid molecules may be less than fully complementary and is indicated by a percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds with a second nucleic acid molecule. For example, if a first nucleic acid molecule has 10 nucleotides and a second nucleic acid molecule has 10 nucleotides, then base pairing of 5, 6, 7, 8, 9, or 10 nucleotides between the first and second nucleic acid molecules represents 50%, 60%, 70%, 80%, 90%, and 100% complementarity, respectively. "Perfectly" or "fully" complementary nucleic acid molecules means those in which all the contiguous residues of a first nucleic acid molecule will hydrogen bond with the same number of contiguous residues in a second nucleic acid molecule, wherein the nucleic acid molecules either both have the same number of nucleotides (*i.e.*, have the same length) or the two molecules have different lengths.

[00134] The term "non-specific amplification," as used herein, refers to the amplification of nucleic acid sequences other than the target sequence which results from primers hybridizing to sequences other than the target sequence and then serving as a substrate for primer extension. The hybridization of a primer to a non-target sequence is referred to as "non-specific hybridization" and is apt to occur especially during the lower temperature, reduced stringency, pre-amplification conditions.

[00135] The term "primer dimer," as used herein, refers to a template-independent non-specific amplification product, which is believed to result from primer extensions wherein another primer serves as a template. Although primer dimers frequently appear to be a concatamer of two primers, *i.e.*, a dimer, concatamers of more than two primers also occur. The term "primer dimer" is used herein generically to encompass a template-independent non-specific amplification product.

[00136] The term "reaction mixture," as used herein, refers to a solution containing reagents necessary to carry out a given reaction. An "amplification reaction mixture", which refers to a solution containing reagents necessary to carry out an amplification reaction, typically contains oligonucleotide primers and a DNA polymerase or ligase in a suitable buffer. A "PCR reaction mixture" typically contains oligonucleotide primers, a DNA polymerase (most typically a thermostable DNA polymerase), dNTPs, and a divalent metal cation in a suitable buffer. A reaction mixture is referred to as complete if it contains all reagents necessary to enable the reaction, and incomplete if it contains only a subset of the necessary reagents. It will be understood by one of skill in the art that reaction components are routinely stored as separate solutions, each containing a subset of the total components, for reasons of convenience, storage stability, or to allow for application-dependent adjustment of the component concentrations, and that reaction components are combined prior to the reaction to create a complete reaction mixture. Furthermore, it will be understood by one of skill in the art that reaction components are packaged separately for commercialization and that useful commercial kits may contain any subset of the reaction components which includes the blocked primers of the disclosure.

[00137] For the purposes of this disclosure, the term "activated," as used herein, refers to a primer or other oligonucleotide that is capable of participating in a reaction with DNA

polymerase or DNA ligase. A primer or other oligonucleotide becomes activated when it hybridizes to a substantially complementary nucleic acid sequence and is chemically modified so that it can interact with a DNA polymerase or a DNA ligase. For example, when the oligonucleotide is a primer, and the primer is hybridized to a template, a 3'-blocking group can be removed from the primer by, for example, a cleaving enzyme such that DNA polymerase can bind to the 3' end of the primer and promote primer extension.

[00138] The term "fluorescent generation probe" refers either to a) an oligonucleotide having an attached fluorophore and quencher, and optionally a minor groove binder or to b) a DNA binding reagent such as Sybr® g reen dye.

[00139] The terms "fluorescent label" or "fluorophore" refers to compounds with a fluorescent emission maximum between about 350 and 900 nm. A wide variety of fluorophores can be used, including but not limited to: 5-FAM (also called 5-carboxyfluorescein; also called Spiro(isobenzofuran-1(3H), 9'-(9H)xanthene)-5-carboxylic acid,3',6'-dihydroxy-3-oxo-6-carboxyfluorescein); 5-Hexachloro-Fluorescein ([4,7,2',4',5',7'-hexachloro-(3',6'-dipivaloyl-fluoresceinyl)-6-carboxyli- c acid]); 6-Hexachloro-Fluorescein ([4,7,2',4',5',7'-hexachloro-(3',6'-dipivaloylfluoresceinyl)-5-carboxylic acid]); 5-Tetrachloro-Fluorescein ([4,7,2',7'-tetra-chloro-(3',6'-dipivaloylfluoresceinyl)-5-carboxylic acid]); 6-Tetrachloro-Fluorescein ([4,7,2',7'-tetrachloro-(3',6'-dipivaloylfluoresceinyl)-6-carboxylic acid]); 5-TAMRA (5-carboxytetramethylrhodamine; Xanthylium, 9-(2,4-dicarboxyphenyl)-3,6-bis(dimethyl-amino); 6-TAMRA (6-carboxytetramethylrhodamine; Xanthylium, 9-(2,5-dicarboxyphenyl)-3,6-bis(dimethylamino); EDANS (5-((2-aminoethyl)amino)naphthalene-1-sulfonic acid); 1,5-IAEDANS (5-((((2-iodoacetyl)amino)ethyl)amino)naphthalene-1-sulfonic acid); DABCYL (4-((4-(dimethylamino)phenyl)azo)benzoic acid) Cy5 (Indodicarbocyanine-5) Cy3 (Indo-dicarbocyanine-3); and BODIPY FL (2,6-dibromo-4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-pr- oprionic acid), Quasar-670 (Biosearch Technologies), CalOrange (Biosearch Technologies), Rox, as well as suitable derivatives thereof.

[00140] The term "ligation" as used herein refers to the covalent joining of two polynucleotide ends. In various embodiments, ligation involves the covalent joining of a 3' end of a first polynucleotide (the acceptor) to a 5' end of a second polynucleotide (the

donor). Ligation results in a phosphodiester bond being formed between the polynucleotide ends. In various embodiments, ligation may be mediated by any enzyme, chemical, or process that results in a covalent joining of the polynucleotide ends. In certain embodiments, ligation is mediated by a ligase enzyme.

[00141] As used herein, "ligase" refers to an enzyme that is capable of covalently linking the 3' hydroxyl group of a nucleotide to the 5' phosphate group of a second nucleotide. Examples of ligases include *E. coli* DNA ligase, T4 DNA ligase, etc.

[00142] The ligation reaction can be employed in DNA amplification methods such as the "ligase chain reaction" (LCR), also referred to as the "ligase amplification reaction" (LAR), see Barany (1991) *Proc. Natl. Acad. Sci. U.S.A.* 88:189; and Wu and Wallace (1989) *Genomics* 4:560, incorporated herein by reference. In LCR, four oligonucleotides, two adjacent oligonucleotides which uniquely hybridize to one strand of the target DNA, and a complementary set of adjacent oligonucleotides, that hybridize to the opposite strand are mixed and DNA ligase is added to the mixture. Provided that there is complete complementarity at the junction, ligase will covalently link each set of hybridized molecules. Importantly, in LCR, two probes are ligated together only when they base-pair with sequences in the target sample, without gaps or mismatches. Repeated cycles of denaturation, hybridization and ligation amplify a short segment of DNA. LCR has also been used in combination with PCR to achieve enhanced detection of single-base changes, see Segev PCT Pub. No. WO/9001069.

[00143] As used herein, the term "conserved region" or "conserved sequence" refers to a nucleic acid sequence in a region of a gene that is the same or highly similar across different species. For example, a sequence or region of a gene that is conserved may have the same nucleic acid sequence in several types of fungal species, or, in some cases, may have the same or highly similar sequence across different taxonomic phyla (*e.g.*, a human DNA sequence and a fungal DNA sequence in a highly conserved region of a gene may be the same or highly similar). Conversely, a "highly variable" or "hypervariable" region or sequence of gene is not conserved across species or phyla, and will have many nucleotides differences in the hypervariable region in the gene from each species.

Methods for Identifying Fungal Pathogens

[00144] As described above, fungal infections remain a major cause of morbidity and mortality in immunocompromised patients. Cultivation-based methods have poor diagnostic sensitivity for many fungal infections, which has led to the adoption of other diagnostic approaches such as detection of fungal antigens. However, antigen-based assays such as the galactomannan and glucan assays do not detect all fungal species. Thus, there is a need in the art (1), for reliable methods for the detection of fungal pathogen, especially in the context of human DNA (in samples from infected patients, human and fungal DNA are mixed together), and (2), for reliable methods for accurately and rapidly distinguishing among different species of fungi.

[00145] Thus, disclosed herein are methods for detecting a fungal pathogen in a patient sample. The methods disclosed herein target the fungal rRNA operon, which is a continuous sequence made of the 18S, ITS1, 5.8S, ITS2, and 28S subunit regions [Iwen *et al.* (2002) *Med. Mycol.* 40:87-109]. Because certain aspects of the operon are highly conserved among a broad range of fungi, while other regions, such as the D1-D2 hypervariable region are not conserved among species, the DNA sequences of the operon can be targeted by broad range PCR assays for the identification of fungal infection and for the determination of the specific fungal species. The human rRNA operon is also a continuous sequence made of the 18S, ITS1, 5.8S, ITS2, and 28S subunit regions, and has considerable sequence homology with the fungal rRNA operon. Thus, a critical aspect of the present disclosure provides methods and PCR primers which do not cross-react with human DNA. The present disclosure provides PCR primers which amplify regions that are 3' to the D1-D2 hypervariable region specifically because they are discovered to have less cross-reactivity to human DNA. This is especially critical for the identification of fungal DNA in patient samples, which also contain human DNA.

[00146] "Broad-range" PCR primers as disclosed herein may be understood to be primers that hybridize with conserved regions of fungal DNA, and thus are useful in PCR assays that detect the presence of a wide range of fungal pathogens.

[00147] In certain aspects of the disclosure, the method includes the steps of (a) isolating a patient sample, (b) carrying out a PCR reaction on the patient sample to generate a PCR amplicon that includes a region of a fungal 28S ribosomal RNA (rRNA) gene, wherein the

PCR reaction uses a primer set having a forward primer and a reverse primer wherein at least one of the forward primer and the reverse primer is complementary to the fungal 28S rRNA gene, and (c) detecting the PCR amplicon. The patient sample may be, for example, a blood sample, a sputum sample, a lung lavage fluid sample, or a tissue biopsy sample. Any fluid, tissue, or other source of DNA from a patient may constitute a sample in the present disclosure.

[00148] The PCR reaction carried out on the patient sample may be performed according to any of the methods known in the art. The purpose of the PCR reaction is to amplify a target sequence within a fungal DNA sequence, thereby generating a PCR amplicon. Preferably, the region amplified by the PCR reaction is in the 28S region of the fungal rRNA gene. More preferably, the region of the fungal 28S rRNA gene detected by PCR includes a sequence that is 3' to a D1-D2 highly variable region of the fungal 28S rRNA gene. The PCR assays of the present disclosure target this region, achieving resolution among different species of fungi without cross-reacting with or being inhibited by the presence of human DNA.

[00149] In certain embodiments, PCR reactions are used to detect fungal DNA in a sample. In other embodiments, qPCR reactions are used to detect fungal DNA in a sample. In yet other embodiments, alternative methods other than PCR, such as ligase chain reaction, may be used to detect the presence of fungal DNA in a sample. Alternatively, Nucleic Acid Sequence Based Amplification (NASBA) could be used to amplify fungal rRNA directly from tissues using these primers. Any method suitable for amplifying a region of the target fungal gene (rDNA) or rRNA is contemplated in the present disclosure.

[00150] In certain aspects of the present disclosure, the methods for detecting a fungal pathogen disclosed herein further involve the step of sequencing the PCR amplicon derived from sequencing. In some aspects, the PCR amplicon is between 50 and 1000 base pairs, and preferably, between 75 and 400 base pairs. Smaller amplicon sizes are desirable, since they are easier to sequence and useful for qPCR reactions. However, it is also important that the amplicon be large enough to facilitate accurate species identification, *e.g.*, enhance resolution among different fungal species.

[00151] Sequencing of the PCR amplicon may be carried out according to any methods known in the art suitable for determining the sequence of a PCR amplicon. The sequences of the PCR amplicons disclosed in the present invention are unique to each type of fungal pathogen, thereby allowing identification of the specific type of fungal DNA in a sample.

[00152] In certain embodiments, methods for the detection of fungal DNA involving the step of carrying out a PCR reaction on a patient sample are provided, wherein each primer of the primer set in the PCR reaction specifically binds only to a fungal DNA. Preferably, each primer of the primer set specifically binds only to a fungal DNA in the presence of a non-fungal DNA. In some embodiments, the non-fungal DNA is mammalian DNA. In other embodiments, the mammalian DNA is human DNA. In yet other embodiments, the non-fungal DNA is in greater than 1,000,000-fold, 5,000,000-fold, or 30,000,000-fold mass excess of the fungal DNA.

[00153] In some aspects, methods for detecting a fungal pathogen are provided, wherein the fungal pathogen causes a fungal infection selected from the group consisting of aspergillosis, candidiasis, zygomycosis, scedosporiosis, fusariosis, cryptococcosis, histoplasmosis, coccidioidomycosis, and blastomycosis.

Primer Sequences for Identifying Fungal DNA

[00154] In certain embodiments of the present disclosure, specific sequences of the forward and reverse primers of the PCR reaction for identifying fungal DNA are disclosed. In certain embodiments, the forward primer of the PCR reaction is complementary to a fungal 18S rRNA gene and the reverse primer is complementary to a fungal 28S rRNA gene. In still other embodiments, the forward primer comprises the nucleotide sequence 5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1). In yet other embodiments, the forward primer is complementary to a fungal 5.8S rRNA gene and the reverse primer is complementary to a fungal 28S rRNA gene. In still other embodiments, the forward primer includes the nucleotide sequence 5'- GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2). In certain other aspects of the present disclosure, the forward primer and the reverse primer of the PCR reaction for detecting fungal DNA in a patient sample are both complementary to a fungal 28S rRNA gene.

[00155] In certain embodiments disclosed herein, a primer set for detecting a fungal DNA by PCR is provided, wherein the primer set includes a forward primer and a reverse primer wherein at least one of the forward primer and the reverse primer is complementary to a fungal 28S ribosomal RNA (rRNA) gene. In certain embodiments, the forward primer or the reverse primer of the primer set is complementary to a sequence that is 3' to a D1-D2 highly variable region in the fungal 28S ribosomal rRNA gene. In yet other embodiments, the forward primer of the primer set is complementary to a fungal 18S rRNA gene and the reverse primer is complementary to a fungal 28S rRNA gene. In other embodiments, the forward primer and the reverse primer of the primer set are both complementary to a fungal 28S rRNA gene.

[00156] In other aspects of the present disclosure, the forward primer of the PCR reaction or of the primer set for detecting fungal DNA in a sample may have one of the following sequences:

5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1),
5'-GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2),
5'-TACCCGCTGAACTTAAGCATA-3' (SEQ ID NO: 3),
5'-GCATATCAATAAGCGGAGGAAA-3' (SEQ ID NO: 4),
5'-AGTARCGGCGAGTGAAGCGG-3' (SEQ ID NO: 5),
5'-AGCTCAAATTTGAAASCTGG-3' (SEQ ID NO: 6),
5'-CTTCCCTTTCAACAATTTCACRT-3' (SEQ ID NO: 7),
5'-AGGTAAAGCGAATGATTAG-3' (SEQ ID NO: 8),
5'-CTTGTTRCTTARTTGAACGTG-3' (SEQ ID NO: 9),
5'-ACCACAAAAGGTGTTAGTWCATC-3' (SEQ ID NO: 10),
5'-GAAGTGGGGAAAGGTTCC-3' (SEQ ID NO: 11),
5'-GACATGGGTTAGTCGATCCTA-3' (SEQ ID NO: 12),
5'-TCGTACTCATAACCGCAGC-3' (SEQ ID NO: 13),
5'-GTTGATAGAAYAATGTAGATAAGG-3' (SEQ ID NO: 14),
5'-CAAGGGGAATCTGACTGTC-3' (SEQ ID NO: 15),
5'-TTTACTTAWTCAATGAAG CGG-3' (SEQ ID NO: 16),
5'-CCGGGTTGAWGACATTGTCA-3' (SEQ ID NO: 17),
5'-GCTGGGGCGGCACATCTGTT-3' (SEQ ID NO: 18),
5'-GAACAAAAGGGTAAAAGTCCC-3' (SEQ ID NO: 19),
5'-TTTGATTTTCAGTGTGAATACAAACCA-3' (SEQ ID NO: 20),
5'-ATGAAAGTGTGGCCTATCG-3' (SEQ ID NO: 21),
5'-GAGGCTAGAGGTGCCAGAA-3' (SEQ ID NO: 22),
5'-AGGGATAACTGGCTTGTGGC-3' (SEQ ID NO: 23),
5'-ACCGAAGCAGAATTCGGTAAG-3' (SEQ ID NO: 24),
5'-GATAAT TGGTWTTTGCGGCTG-3' (SEQ ID NO: 25),
5'-GCTGAACGCCTCTAAGTCAGA-3' (SEQ ID NO: 26), and
5'-TCGTARCAACAAGGCTACT-3' (SEQ ID NO: 27).

In yet other aspects of the present disclosure, the reverse primer of the PCR reaction or of the primer set for detecting fungal DNA may include one of the following sequences:

5'-GAAACCTTGTTACGACTTTTAC-3' (SEQ ID NO: 28),
5'-GTTCAAAGAYTCGATGATTCAC-3' (SEQ ID NO: 29),
5'-TATGCTTAAGTTCAGCGGGTA-3' (SEQ ID NO: 30),
5'-TTTCCTCCGCTTATTGATATGC-3' (SEQ ID NO: 31),
5'-CCGCTTCACTCGCCGYTACT-3' (SEQ ID NO: 32),
5'-CCAGSTTTCAAATTTGAGCT-3' (SEQ ID NO: 33),
5'-AYGTGAAATTGTTGAAAGGGAAG-3' (SEQ ID NO: 34),
5'-CTAATCATTCGCTTTACCTC-3' (SEQ ID NO: 35),
5'-CACGTTCAAYTAAGYAACAAG-3' (SEQ ID NO: 36),
5'-GATGWACTAACACCTTTTGTGGT-3' (SEQ ID NO: 37),
5'-GGAACCTTTCCCCACTTC-3' (SEQ ID NO: 38),
5'-TAGGATCGACTAACCCATGTC-3' (SEQ ID NO: 39),
5'-GCTGCGGTTATGAGTACGA-3' (SEQ ID NO: 40),
5'-CCTTATCTACATTRTTCTATCAAC-3' (SEQ ID NO: 41),
5'-GACAGTCAGATTCCCCTTG-3' (SEQ ID NO: 42),
5'-CCGCTTCATTGAWTAAGTAAA-3' (SEQ ID NO: 43),
5'-TGACAATGTCWTCAACCCGG-3' (SEQ ID NO: 44),
5'-AACAGATGTGCCGCCCCAGC-3' (SEQ ID NO: 45),
5'-GGGACTTTTACCCTTTTGTTC-3' (SEQ ID NO: 46),
5'-TGGTTTGTATTCACACTGAAAATCAAA-3' (SEQ ID NO: 47),
5'-CGATAGGCCACACTTTCAT-3' (SEQ ID NO: 48),
5'-TTCTGGCACCTCTAGCCTC-3' (SEQ ID NO: 49),
5'-GCCACAAGCCAGTTATCCCT-3' (SEQ ID NO: 50),
5'-CTTACCGAATTCTGCTTCGGT-3' (SEQ ID NO: 51),
5'-CAGCCGCAAAWACCAATTATC-3' (SEQ ID NO: 52),
5'-TCTGACTTAGAGGCGTTCAGC-3' (SEQ ID NO: 53),
5'-AGTAGCCTTGTTGYTACGA-3' (SEQ ID NO: 54), and
5'- CCTTATCTACATTATTCTATGGAC-3' (SEQ ID NO: 108).

[00157] In certain embodiments disclosed herein, the PCR reaction for detecting fungal DNA includes a forward and reverse primer pair (or primer set) selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 31), (SEQ ID NO: 2 and SEQ ID NO: 32), (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54). More preferably, the primer set includes a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51),

(SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54), and still more preferably, the primer set includes a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), and (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108).

[00158] In certain aspects, the primer set includes a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

[00159] It is to be understood in the present disclosure that any of the primer sequences disclosed herein may be modified without departing from the intended scope of the disclosure. Specifically, nucleotide substitutions, deletions and/or additions may be introduced into any of the primer sequences disclosed herein without altering the ability of the primers to identify fungal DNA. Moreover, it is to be understood that the lengths of the primers may be shorter or longer than the sequences disclosed herein.

[00160] In certain embodiments of the present disclosure, methods and primer sets for detecting fungal DNA are provided which detect DNA from a fungal species such as, but not limited to *Absidia corymbifera; Cunninghamella bertholletiae; Fusarium solani; Mucor racemosus; Paecilomyces variotii; Penicillium chrysogenum; Rhizomucor miehei; Rhodotorula glutinis; Scedosporium apiospermum; Antrodia vaillantii; Aspergillus fumigatus; Aspergillus niger; Aspergillus oryzae; Aspergillus terreus; Batrachochytrium dendrobatidis; Botrytis cinerea; Candida albicans; Candida dublineinsis; Candida glabrata; Candida gulliermundei; Candida kefyr; Candida krusei; Candida lipolytica; Candida lusitaniae; Candida parapsilosis; Candida tropicalis; Chaetomium globosum; Coccidioides immitis; Coccidioides posadasii; Cryptococcus neoformans; Fusarium graminearum; Fusarium oxysporum; Histoplasma capsulatum; Hypocrea jecorina; Lodderomyces elongisporus; Magnaporthe grisea; Metarhizium anisopliae; Microsporum gypseum; Mucor racemosus; Neurospora crassa; Paracoccidioides brasiliens; Pneumocystis carinii; Penicillium verrucosum; Pichia stipitis; Rhizomucor miehei; Rhizopus oryzae;*

Saccharomyces cerevisiae; Schizosaccharomyces japonicus; Schizosaccharomyces pombe; Sclerotinia sclerotiorum; Stagonospora nodorum; Umbilicaria esculenta; or *Uncinocarpus reesii*.

[00161] In certain embodiments, the methods described herein may be used to detect DNA from other known fungi not specifically disclosed herein and from newly identified fungal species. In other words, the methods provided herein are useful for detecting a broad range of fungal DNA, and are not limited to the specific examples of fungal species disclosed herein.

Methods for Identifying Alternative Primers for Identifying Fungal DNA

[00162] Also disclosed herein are methods for identifying a primer set capable of detecting a fungal pathogen in a sample, the method including the steps of: (a) obtaining the DNA sequence of at least the 28S region of a fungal rRNA operon, (b) designing a forward primer capable of hybridizing with the DNA sequence, (c) designing a reverse primer capable of hybridizing with the DNA sequence at a region in the DNA that is 3' to the region to which the forward primer is capable of hybridizing, (d) testing whether the forward and reverse primers are capable of generating a PCR amplicon that is useful for identifying fungal DNA using a PCR reaction containing fungal DNA.

[00163] In certain embodiments, the method also includes the steps of testing the forward and reverse primers in a PCR reaction containing fungal DNA and human DNA. In yet other embodiments, the method includes running the PCR amplicon on an agarose gel and determining the product size. In still other embodiments, the method includes sequencing the PCR amplicon.

[00164] In yet other embodiments, the analytical sensitivity and cross-reactivity (*i.e.*, degree of species resolution) of a specific primer set may be determined by testing the specific primer set on a panel of individual samples, each sample containing genomic DNA isolated from a single, distinct fungal species. An amplicon is generated by each PCR reaction containing the isolated genomic fungal DNA. Each amplicon is then sequenced and the sequences of each amplicon are compared. In certain embodiments, the sequence of each amplicon is compared using multiple sequence alignment, for example using the

Clustal W algorithm. The Clustal W algorithm aligns two or more sequences simultaneously, such that regions of identical and similar residues are aligned. Clustal W does a pairwise comparison of every sequence first and then starts the multiple alignment with the pair of sequences that is most similar. Sequences are added one by one to the alignment based on their similarities to the starting pair. The software for using Clustal W alignment is freely available on the World Wide Web at the European Bioinformatics Institute website (http://www.ebi.ac.uk/Tools/clustalw2/index.html). Any algorithm suitable for comparing multiple sequences may be used, such as, e.g., the Needleman-Wunsch algorithm or the Smith-Waterman algorithm. The number of nucleotide differences among each amplicon is determined and assembled in a distance matrix, such as for example, using Microsoft Excel. The distance matrix is generated using Accelrys Gene® software (Accelrys, Inc., San Diego, CA). If species resolution within a genus or between any two species is desired, the comparison of distance matrix data can help select which amplicon (primer pair) would provide the most species resolution.

[00165] In other embodiments, phylogenetic trees may be assembled based on the Neighbor-Joining tree building method and distances estimated from the Tajima-Nei or absolute difference algorithms also using the Accelrys Gene® software (Accelrys, Inc.) or other similar tools. The Neighbor-Joining tree building method is described in detail in Saitou and Nei (1987) *Mol. Biol. Evol.* 4:406-25, and the Tajima-Nei algorithm is described in detail in Tajima and Nei (1984) *Mol. Biol. Evol.* 1:269-85, both incorporated herein by reference in their entireties. A phylogenetic tree compares the distance between two species, usually interpreted as evolutionary distance, as determined by the number of varying nucleotide positions in a sequence such as a specific PCR product generated by broad-range fungal PCR. Other examples of algorithms that may be used to construct phylogenetic trees include maximum likelihood, minimum evolution, and parsimony. Other distance-based methods include unweighted pair-group method using arithmetic averages, BIONJ, and the Weighbor algorithm or "weighted NJ". These algorithms and methods are well known in the art and are described in detail in Hollich, V. et al. (2005) Molecular Biology and Evolution; 22(11):2257-2264, which is herein incorporated by reference in its entirety.

[00166] In still other embodiments, the distance matrices and phylogenetic trees are used to determine which PCR primer sets generate amplicons that permit the highest degree of species resolution. The primers that give the highest degree of resolution among distinct fungal species are selected for further use.

Two-dimensional Melt-Curve Analysis for the Identification of Fungal DNA

[00167] In certain embodiments, methods are provided for both the detection of fungal DNA in a patient sample, and further, for determining which type of fungal infection is present using two-dimensional melt curve analysis.

[00168] In the two-dimensional melt curve analysis, a melting profile of a PCR amplicon can be characterized by measuring fluorescence of a DNA binding dye. Specifically, each double-stranded DNA has its own specific melting temperature (Tm), which is defined as the temperature at which 50% of the DNA becomes single stranded. These melting temperatures are primarily determined by dsDNA length, degree of GC content (Tm is higher in GC-rich fragments), and degree of complementarity between strands (*e.g.*, especially important in heteroduplexes consisting of a probe and a single-stranded target DNA sequence). With the use of DNA-binding dyes such as SYBR® Green I, a melt-curve profile can be generated. A thermal cycler system records the total fluorescence generated by the fluorescent DNA binding dye binding to double-stranded DNA as temperature changes, and plots the fluorescence in real time as a function of temperature. The first derivative of this plot, dF/dT, is the rate of change of fluorescence in the reaction, and a significant change in fluorescence accompanies the melting of the double-stranded PCR products. A plot of -dF/dT vs. temperature will display these changes in fluorescence as distinct peaks. The melting temperature (Tm) of each product is defined as the temperature at which the corresponding peak maximum occurs. Importantly, each unique amplicon will have a unique Tm that distinguishes it from each different amplicon.

[00169] The present disclosure provides methods for characterizing the melting profiles of amplicons generated from known fungi, and further, for using this information to infer the identity of a fungus from an unknown sample. Moreover, using information from more than one amplicon, as disclosed in the present invention, further increases species resolution. Specifically, in certain embodiments, a first amplicon is generated in the ITS2 region of the rRNA operon, and a second amplicon is generated in the 28S region. The Tm

is determined for each amplicon, and the combination of the two Tm uniquely identifies a fungal species.

[00170] In certain embodiments disclosed herein, a method for determining the identity of a fungal species in a patient sample is provided, wherein the method includes the steps of: isolating the patient sample; carrying out a first PCR reaction to generate a first PCR amplicon, wherein the first PCR reaction includes a first primer set capable of amplifying a region in a fungal ribosomal RNA (rRNA) gene having an internal transcribed spacer 2 (ITS-2) sequence; carrying out a second PCR reaction to generate a second PCR amplicon, wherein the second PCR reaction has a second primer set capable of amplifying a region in a fungal ribosomal 28-S rRNA gene; and determining the melting temperature of the first PCR amplicon and of the second PCR amplicon, wherein the identity of the fungal species is determined by comparing the melting point of the first PCR amplicon and of the second PCR amplicon to known standards.

[00171] This method has the advantage that the melt curve analysis can be carried out very quickly, without the need for sequencing the PCR amplicon, at the end of each PCR reaction.

[00172] In certain aspects disclosed herein, the first and second PCR reactions carried out for determining the identity of a fungal species in a patient sample are each quantitative PCR (qPCR) reactions. In other aspects, the first primer set includes a forward primer sequence as set forth in SEQ ID NO: 2 and a reverse primer sequence as set forth in SEQ ID NO: 30, and the second primer set includes a forward primer sequence as set forth in SEQ ID NO: 12 and a reverse primer sequence as set forth in SEQ ID NO: 41. In some aspects, the second primer set includes a forward primer sequence as set forth in SEQ ID NO: 12, a first reverse primer sequence as set forth in SEQ ID NO: 41, and a second primer sequence as set forth in SEQ ID NO: 108.

[00173] In certain embodiments, the two-dimensional melt curve analysis is useful for resolving multiple fungal infections in a single patient sample. For example, if DNA is present from two fungal species, then one primer set, targeted, for example, to the ITS2 region, will generate two distinct amplicons with distinct melting curves. Then, a second primer set, targeted, for example, to the 28S region in a separate PCR reaction, will

amplify two distinct amplicons with two distinct melting temperatures. Since each fungal species has a unique combination of melting temperatures for each amplicon, these melting temperatures can be combined to determine which fungal species are present. Certain fungal species are more likely to be present in a co-infection, and this information can also be used to determine the two types of fungal species present in the sample. This method is highly useful in the clinical setting because it can be performed rapidly. According to conventional methods, the individual PCR products would have to be cloned before sequencing in order to resolve multiple fungal species.

[00174] In still other embodiments, when two or more fungal infections are present, the two-dimensional melt curve analysis may be used to narrow down the list of possible fungi. Thereafter, a taxon-specific PCR reaction may be performed to confirm the suspected type of fungal infections. These taxon specific PCR reactions amplify regions of fungal DNA that are unique to a specific fungal species.

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[00175] All U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications, non-patent publications, figures, tables, and websites referred to in this specification are expressly incorporated herein by reference, in their entirety.

EXAMPLES

[00176] The above disclosure generally describes the present disclosure, which is further exemplified by the following examples. These specific examples are described solely for purposes of illustration, and are not intended to limit the scope of this disclosure. Although specific targets, terms, and values have been employed herein, such targets, terms, and values will likewise be understood as exemplary and non-limiting to the scope of this disclosure.

EXAMPLE 1
Materials and Methods used in Examples 2 - 6

[00177] This Example discloses the materials and methods used in Examples 2 through 6 of the present disclosure.

Microorganisms

[00178] Table 1 lists 9 clinically or phylogenetically relevant fungal pathogens subjected to sequencing of their ITS, 5.8S, and 28S rRNA genes. Table 2 lists 43 fungi of which the same gene sequences were obtained from publicly available genomic databases or GenBank® . Genomic DNA of the following organisms was used for analytical sensitivity testing to screen broad– range fungal primers: *Aspergillus candidus* (ATCC # 20022), *Aspergillus flavus* (ATCC # MYA-3631), *Aspergillus fumigatus* (ATCC # MYA- 1163), *Aspergillus oryzae* (ATCC # 20719), *Aspergillus terreus* (ATCC # 10070), *Aspergillus ustus* (ATCC # 20063), *Candida albicans* (ATCC # 90028), *Candida dubliniensis* (ATCC # MYA-580), *Candida glabrata* (ATCC # 90876), *Candida guilliermondii* (ATCC # 90877), *Candida kefyr* (ATCC # 28838), *Candida krusei* (clinical isolate), *Candida lusitaniae* (ATCC # 42720), *Candida parapsilosis*, *Candida tropicalis* (clinical isolate), *Rhizopus oryzae* (ATCC # 10260), *Saccharomyces cerevisiae* (Novagen, Madison, WI), and *Cryptococcus neoformans* (ATCC # 28958D-5). In addition, the genomic DNA of 9 organisms listed in Table 1 was tested.

TABLE 1
Fungal Pathogens in which rRNA Gene Sequence was Obtained De novo

SEQ ID NO	Fungal Pathogen	ATCC #	GenBank® Accession #	Length (bp)	Figure
55	*Absidia corymbifera*	14058	FJ345350	3733	8
56	*Cunninghamella bertholletiae*	42115	FJ345351	4035	9
57	*Fusarium solani*	56480	FJ345352	3830	10
58	*Mucor racemosus*	42647	FJ345353	3999	11
59	*Paecilomyces variotii*	10865	FJ345354	3972	12
60	*Penicillium chrysogenum*	10108	FJ345355	3916	13
61	*Rhizomucor miehei*	46345	FJ345356	3983	14
62	*Rhodotorula glutinis*	16726	FJ345357	3971	15
63	*Scedosporium apiospermum*	28206	FJ345358	4907	16

TABLE 2

Fungi in which rRNA Gene Sequence was Derived from Publicly Available Genomes or Larger Sequences Found in GenBank®

SEQ ID NO	Microorganism	Source of rRNA gene sequence	Strain	Figure
64	*Antrodia vaillantii*	GenBank® Accession # AM286436	Isolate 240	17
65	*Aspergillus fumigatus*	Broad Institute[1]	Af293	18
66	*Aspergillus niger*	GenBank® Accession # NW_001594105	CBS 513.88	19
67	*Aspergillus oryzae*	GenBank® Accession # NW_001884680	RIB40	20
68	*Aspergillus terreus*	Broad Institute	NIH 2624	21
69	*Batrachochytrium dendrobatidis*	Broad Institute	JEL423	22
70	*Botrytis cinerea*	Broad Institute	B05.10	23
71	*Candida albicans*	Broad Institute	SC5314	24
72	*Candida dublineinsis*	Sanger Institute[2]	CD36	25
73	*Candida glabrata*	GenBank® Accession # AY198398	CBS 138	26
74	*Candida gulliermundei*	Broad Institute	ATCC 6260	27
75	*Candida kefyr*	GenBank® Accession # AF543841	IFO1777	28
76	*Candida krusei*	GenBank® Accession # EF550222 and # AB369918	NRRL Y-5396 *(28S rRNA gene subunit)* and IFM 47973 *(ITS1, 5.8S, ITS2 gene subunit)*	29
77	*Candida lipolytica*	GenBank® Accession # AJ616903 and # DQ680839	E122 *(28S rRNA gene subunit) and* HN2.4 *(ITS1, 5.8S, ITS2 gene subunit)*	30
78	*Candida lusitaniae*	Broad Institute	ATCC 42720	31
79	*Candida parapsilosis*			32
80	*Candida tropicalis*	Broad Institute	MYA-3404	33
81	*Chaetomium globosum*	Broad Institute	CBS 148.51	34
82	*Coccidioides immitis*	Broad Institute	RMSCC 2394	35
83	*Coccidioides posadasii*	Broad Institute	RMSCC 1040	36
84	*Cryptococcus neoformans*	GenBank® Accession # AE017342	JEC21	37
85	*Fusarium graminearum*	Broad Institute	PH-1 (NRRL 31084)	38
86	*Fusarium oxysporum*	Broad Institute	FGSC 4286 (NRRL 34936)	39
87	*Histoplasma capsulatum*	Broad Institute	NAm1	40
88	*Hypocrea jecorina*	GenBank® Accession # AF510497	ATCC 13631	41
89	*Lodderomyces elongisporus*	Broad Institute	NRLL YB-4239	42
90	*Magnaporthe grisea*	GenBank® Accession # DQ493955	70-15	43
91	*Metarhizium anisopliae*	GenBank® Accession # AF218207	Isolate ME1	44
92	*Microsporum gypseum*	Broad Institute	CBS 118893	45

SEQ ID NO	Microorganism	Source of rRNA gene sequence	Strain	Figure
93	*Mucor racemosus*	GenBank® Accession # AJ271061	ATCC 1216B	46
94	*Neurospora crassa*	Broad Institute	N150	47
95	*Paracoccidioides brasiliens*	Broad Institute	Pb03	48
96	*Pneumocystis carinii*	GenBank® A ccession # M86760	—	49
97	*Penicillium verrucosum*	GenBank® A ccession # AF510496	WA30 (ATCC 62396)	50
98	*Pichia stipitis*	GenBank® A ccession # CP000497	CBS 6054	51
99	*Rhizomucor miehei*	GenBank® A ccession # AF205941	ATCC 26282	52
100	*Rhizopus oryzae*	Broad Institute	99-880 (FGSC 9543)	53
101	*Saccharomyces cerevisiae*	GenBank® Accession # Z73326	—	54
102	*Schizosaccharomyces japonicus*	Broad Institute	yFS275	55
103	*Schizosaccharomyces pombe*	Broad Institute	972h–	56
104	*Sclerotinia sclerotiorum*	Broad Institute	ATCC 18683	57
105	*Stagonospora nodorum*	Broad Institute	SN15	58
106	*Umbilicaria esculenta*	GenBank® A ccession # EU534208	Isolate F3	59
107	*Uncinocarpus reesii*	Broad Institute	1704	60

1 – http ://www.broad.mit.edu/annotation/fgi/
2 – http ://www.sanger.ac.uk/Projects/Fungi/

Obtaining rRNA gene sequences from fungal genomic databases

[00179] The fungal rRNA operon is a continuous sequence made of the 18S, ITS1, 5.8S, ITS2, and 28S subunit regions [Iwen *et al.* (2002) *Med. Mycol.* 40:87-109]. For most fungi whose genomes are publicly available, the rRNA gene sequences were obtained using the following protocol: the 18S subunit and/or ITS1/5.8S/ITS2 subunit sequence of a specific fungus was first obtained through GenBank®, from the Sanger Institute Website (http://www.sanger.ac.uk/Projects/Fungi/), or from the Broad Institute Website (http://www.broad.mit.edu/annotation/fgi/). The sequences of the fungal species listed in Table 2 are shown in Figures 17 – 61. This section of the sequence was then used to perform a BLASTn search within its genome. Six kilobase pairs (kbp) of sequence was obtained on either side of the match in the genome. This large contig was trimmed to obtain the complete rRNA gene sequence using a combination of sequence analysis tools in Accelrys Gene® software (Accelrys, San Diego, CA). Well defined rRNA gene sequence of *S. cerevisiae* and *C. albicans*, and other smaller sequence subunits (ITS1/5.8S/ITS2 region and D1-D2 region of the 28S) of each fungus, if available through GenBank® were also used to map and confirm the derived complete rRNA gene sequence.

Primers for sequencing and broad- range fungal assays

[00180] Primers which could be used for either sequencing or broad- range PCR were designed based on the multiple sequence alignment of about 40 fungal rRNA operons. Maximizing nucleotide differences with the human rRNA gene sequence was an important criterion in designing primers. Primers that met this criterion are listed in Tables 3 and 4 (forward and reverse complement orientations, respectively), and the location of these primers is displayed on a map of the rRNA gene operon in Figure 2B. In addition to these primers, during the initial stages of sequencing, primers from the website of the Vilgalys Lab at Duke University [Vilgalys, Conserved primer sequences for PCR amplification and sequencing from nuclear ribosomal RNA (URL: http://www.biology.duke.edu/fungi/mycolab/primers.htm)] were used. Most of these primers had significant homology with human rRNA gene sequences and therefore were not considered further for broad-ra nge PCR development. The primers of the Vilgalys lab are mapped for comparison to the distinct primers provided by the present disclosure (Figure 2C). In addition, Figure 2C contains several widely used broad-range fungal primers from the literature which target the ITS, 5.8S and D1-D2 region of the 28S. Most of thes primers have significant homology with human rRNA gene sequences and thus cross-react with human DNA making them unappealing for diagnostics in human samples.

Sequencing of ribosomal RNA operons

(i) PCR amplification

[00181] Each 50 µl PCR reaction contained 1.5 U of PfuTurbo® Hotstart Polymerase, 1X PfuTurbo® 10X PCR Buffer (Stratagene, La Jolla, CA), 0.8 mM of GeneAmp® dNTP Blend (Applied Biosystems, Foster City, CA), 0.4 µM each of forward and reverse primers selected from Table 3 and Table 4, respectively, and 20 ng of extracted fungal genomic DNA. The volume was brought up to 50 µl with DNA-grade water that was filtered through an Amicon Ultra-15 30 kDa centrifugal filter unit (Millipore Corporation, Billerica, MA) and UV-irradiated at 240 mJ/cm^2 (Spectrolinker™, Westbury, NY).

[00182] PCR cycling conditions consisted of a pre-melt time of 2 min at 95°C, followed by 30 cycles of 95°C for 30 sec (melt), a temperature between 50°C to 58°C for 30 sec (annealing), 72°C for 2 min (extension), and ending with a hold at 72°C for 10 min. The

annealing temperature was selected to be lower than the lowest melting temperature of the two primers chosen for the PCR reaction.

[00183] PCR products were visualized on 1.5% agarose gels with ethidium bromide staining. (See a representative example in Figure 2B). Products with visible bands that came within approximately 200 bp of the expected amplicon size according to the primer map (Figure 2A) were considered positives. Products with one distinct band were sequenced.

ii) Sequencing of amplicon

[00184] PCR products were cleaned with Montage-PCR Filters (Millipore Corporation, Billerica, MA), eluted with 30 µl of DNA-grade water, and frozen at -20℃ until use. Sequencing was performed with Big Dye® terminators and an Applied Biosystems capillary sequencer. In addition to the primers used to amplify the original PCR product, 1 to 2 other primers that were expected to be contained in the amplicon were also used to sequence each product.

Broad- range PCR amplicon selection and screening criteria

[00185] A matrix of all possible amplicon lengths from the 27 broad- range primers was generated in Microsoft Excel (Figure 1). For the data shown in Figure 1, the primer start and end positions are based on *S. cerevisae* from the 3' end of the 18S to the 3' end of the 28S rRNA gene. This 4230 bp segment of the *S. cerevisae* rRNA gene begins with ---GGTCATTTAGAGGAACTAAA--- and ends with ---GTTTTTTATTTCTTTCTAAG---. Out of a total of 351 possible amplicons using all possible combinations of these primers, 62 amplicons were chosen for screening based on an amplicon size ranging from 75 to 400 bp. The general screening strategy is shown in Figure 3. Endpoint PCR was used to assess successful amplification of each fungal target, the impact of human genomic DNA on fungal amplification, and the cross-reactivity of human DNA in the fungal PCR assays. In addition, the ability of each amplicon to identify and differentiate fungal species was analyzed using distance matrices.

(i) Endpoint PCR.

[00186] Each 50 µl PCR reaction contained 1X Buffer A, 3 mM of $MgCl_2$, 1 mM of GeneAmp® dNTP Blend (12.5mM with dUTP), 2.2U of AmpliTaq Gold® DNA Polymerase, 0.05U AmpErase® Uracil N-glycosylase (all from Applied Biosystems, Foster City, CA), 0.6 µM each of forward and reverse primer,and 0.002% of Triton-X 100. The primer sequences are shown in Figure 4A. PCR cycling conditions consisted of a Uracil N-glycosylase activation for 2 min at 50°C, pre-melt for 10 min at 95°C, then 40 cycles of 15 sec at 95°C (melt), 30 sec at 55°C (anneal), 40 sec at 72° C (extend), and finished with a 7 min hold at 72° C.

(ii) Analytical sensitivity and cross-reactivity testing

[00187] The analytical sensitivity for amplicon screening was assessed by testing extracted fungal genomic DNA. Genomic DNA was extracted based on a previously described protocol [Khot *et al.* (2008) *BMC Infect. Dis.* 8:73]. An optimized version of the MasterPure™ Yeast DNA Purification Kit (Epicentre® Biotechnologies, Madison, WI) was used for fungal DNA extraction. The 100% isopropanol, 70% ethanol and DNA grade water used for extraction were filtered in an Amicon Ultra-15 centrifugal filter unit with a molecular weight cut-off of 30 kDa (Millipore Corporation, Billerica, MA). Yeast Cell Lysis™ solution and MPC Protein Precipitation Reagent™ were UV irradiated at 240 mJ/cm^2 with pelleted fungal samples approximately 15 cm from the bulbs (Spectrolinker™, Westbury, NY). The silicon carbide sharps were washed 10 times in DNA free water and baked at 180°C for 48 h. DNA-free microcentrifuge tubes were used with DNA extraction (Eppendorf Biopur tubes, Eppendorf AG, Hamburg, Germany). Sham digest controls consisting of DNA-free water were processed with every extraction run serving as negative controls to monitor for contamination. Two milliliter sterile screw-cap tubes were loaded with silicon carbide sharps of sizes 0.1 mm and 1 mm (BioSpec Products, Inc., Bartlesville, OK) at a 1:1 ratio up to a volume equivalent to 250 l. Yeast Cell Lysis™ solution at a volume of 550 l and BAL pellet at 100 – 400 l, or 200 l of water as digest control, were added to the tube. The contents of the tube were homogenized in a FastPrep® -24 System (MP Biomedicals, Solon, OH) at 5 m/sec for 60 sec. Each tube was incubated at 65°C for 45 min then kept on ice for 5 min. MPC Protein Precipitation Reagent™ was added at a volume of 325 l for pellet processing. The tubes were vortexed for 10 sec and centrifuged at 11,000 rcf for 10 min. The resulting supernatant was transferred to a new

microcentrifuge tube containing an equal volume of 100% isopropanol pre-cooled to -20°C. The contents of the tube were mixed thoroughly by inversion and incubated at -20°C for 1 hour. Precipitated DNA was pelleted by centrifugation at 11,000 rcf for 10 min. This supernatant was removed and discarded. The pellet containing DNA was resuspended in 0.5 ml of pre-cooled (-20°C) 70% ethanol and vortexed. The tube was then centrifuged at 11,000 rcf for 5 min. This supernatant was removed to a level just short of disturbing the pellet. The remaining volume of ethanol was allowed to evaporate by air drying for 5 min within the laminar flow hood. The pellet was resuspended in 100 1 of 0.1% Triton-X prewarmed to 65°C then incubated at room temperature for one minute with periodic gentle vortexing. The DNA was either used immediately for qPCR, stored at -20°C overnight or at -80°C for longer periods. If PCR inhibition was detected in the extracted samples, they were reprocessed from the protein precipitation step onwards.

[00188] Cross-reactivity of the primers was assessed in the presence of human genomic DNA (Roche Applied Sciences, Indianapolis, IN). A preliminary screen of all 62 amplicons involved amplification of 1000 pg, 10 pg and 30 fg of *C. albicans* genomic DNA, and 30 fg of *C. albicans* genomic DNA in the presence of 100 ng of human genomic DNA. The final screen involved analytical sensitivity testing with 30 fg of genomic DNA from 27 different fungal species spanning 15 genera. Cross-reactivity testing was assessed using 10 fg of *A. fumigatus* genomic DNA in the presence of 1 µg of human genomic DNA.

(iii) Data analysis

[00189] Multiple sequence alignment based on the Clustal W algorithm, distance matrices and phylogenetic trees based on the Neighbor–J oining tree building method [Saitou and Nei (1987) *Mol. Biol. Evol.* 4:406-25] and distances estimated from the Tajima-Nei [Tajima and Nei (1984) *Mol. Biol. Evol.* 1:269-85] or absolute differences algorithms were generated using Accelrys Gene® software. The distance matrices and phylogenetic trees were used to assess the potential of amplicons to resolve species identity.

EXAMPLE 2
Generation of New Fungal Ribosomal rRNA Gene Sequences

[00190] This Example discloses novel sequences of fungal rRNA genes of phylogenetically and clinically relevant fungal species.

[00191] Sequence information for several medically important fungi is not available in public databases, limiting one's ability to design broad range fungal PCR assays. To address this limitation, rRNA genes from 9 phylogenetically and clinically relevant fungal species were sequenced. Seven (7) of these fungal species were missing rRNA sequences from the 3' end of 18S rRNA gene to the 3' end of 28S rRNA gene. Table 1, shown in Example 1, above, lists these organisms with their American Type Culture Collection (ATCC) numbers, GenBank® accession numbers for sequences deposited from this study, and their sequence lengths. The full-length sequences of these organisms are shown in Figures 8 - 16. In some cases, the sequences disclosed herein may be up to 90 bp short of the true end of the 28S rRNA gene since a conserved primer (28S- 25) at the 3' end of the gene was used for both PCR and sequencing. Overlapping reads were generated from all amplicons using multiple sequencing primers. Accelrys Gene® software was used to assemble smaller amplicons into the larger sequence. The sequencing of Zygomycetes like *Rhizomucor miehei*, *Cunninghamella bertholletiae* and *Mucor racemosus* was relatively complicated due to significant divergence of these species from other fungi. Several custom primers had to be used to successfully complete sequencing for these species. In addition, *Scedosporium apiospermum* posed a significant sequencing challenge due to the presence of inserts in the rRNA operon, resulting in multiple bands on agarose gel electrophoresis of PCR products.

EXAMPLE 3
Selection of Broad Range Fungal rRNA Gene Primers

[00192] This Example discloses primer sequences for PCR-based amplification of the fungal rRNA operon of 50 unique fungal species and the method used to design these primer sequences.

[00193] A multiple sequence alignment was created using the 52 fungal rRNA gene sequences presented in Tables 1 and 2, which represent 30 genera. The phylogenetic position of these fungi based on the alignment was used to further verify the identity of the fungal sequences. Twenty seven (27) broad-range fungal primers (Tables 3 and 4) were designed by manually reviewing the alignment to select areas of sequence conservation among fungi that had multiple nucleotide differences with the human rRNA operon. Table 3 lists the forward orientation of the primer sequences (SEQ ID NOs: 1-27) and Table 4

lists the reverse complement of the primer sequences (SEQ ID NOs: 28-54), shown in Table 3. Ten (10) primers, including End18S Forward and Reverse (SEQ ID NOs: 1 and 28), 5.8S Forward and Reverse (SEQ ID NOs: 2 and 29), 28S– 2 Forward and Reverse (SEQ ID NOs: 4 and 31), 28S–5 Forward and Reverse (SEQ ID NOs: 7 and 34), and 28S– 24 Forward and Reverse (SEQ ID NOs: 26 and 53) overlap either completely or partially with those found in the literature, and most lie in the region spanning the 3′ end of 18S rRNA gene, the 5.8S rRNA gene, and the 5′ end of 28S rRNA gene [(Chen *et al. J Clin Microbiol* 38:2302-10; Hinrikson *et al.* (2005) *J. Clin. Microbiol.* 43:2092-103; Kurtzman and Robnett (1997) *J. Clin. Microbiol.* 35:1216-23; Sandhu *et al.* (1995) *J. Clin. Microbiol.* 33:2913-9; Turenne *et al.* (1999) *J. Clin. Microbiol.* 37:1846-51; Vollmer *et al.* (2008) *J. Clin. Microbiol.* 46:1919-26)]. Twenty-two (22) primers from the 5' end of the 28S rRNA gene up to its 3′ end are newly described in the present disclosure. The positions of these primers are shown on the rRNA gene map (Figure 2B). The broad-range primers disclosed herein were used for de novo sequencing of fungal rRNA genes. In addition, all primers listed in Table 3 and Table 4 were chosen as candidates for the development of broad-range fungal PCR assays applicable to human tissue samples. In Table 3, the number of base pair mismatches with human fungal rDNA is shown.

TABLE 3
Broad– range Fungal rRNA Gene Forward Primer Sequences

SEQ ID NO:	Primer Name	Primer sequence (5' – 3 ')	# bp mismatches with human rDNA
SEQ. ID NO: 1	End18S	GTAAAAGTCGTAACAAGGTTTC	7
SEQ. ID NO: 2	5.8S	GTGAATCATCGARTCTTTGAAC	9
SEQ. ID NO: 3	28S–1	TACCCGCTGAACTTAAGCATA	2
SEQ. ID NO: 4	28S–2	GCATATCAATAAGCGGAGGAAA	3
SEQ. ID NO: 5	28S–3	AGTARCGGCGAGTGAAGCGG	2
SEQ. ID NO: 6	28S–4	AGCTCAAATTTGAAASCTGG	6
SEQ. ID NO: 7	28S–5	CTTCCCTTTCAACAATTTCACRT	6
SEQ. ID NO: 8	28S–6	GAGGTAAAGCGAATGATTAG	2
SEQ. ID NO: 9	28S–7	CTTGTTRCTTARTTGAACGTG	8
SEQ. ID NO: 10	28S–8	ACCACAAAAGGTGTTAGTWCATC	5
SEQ. ID NO: 11	28S–9	GAAGTGGGGAAAGGTTCC	2
SEQ. ID NO: 12	28S–10	GACATGGGTTAGTCGATCCTA	4
SEQ. ID NO: 13	28S–11	TCGTACTCATAACCGCAGC	3

SEQ ID NO:	Primer Name	Primer sequence (5' – 3 ')	# bp mismatches with human rDNA
SEQ. ID NO: 14	28S–12	GTTGATAGAAYAATGTAGATAAGG	5
SEQ. ID NO: 15	28S–13	CAAGGGGAATCTGACTGTC	3
SEQ. ID NO: 16	28S–14	TTTACTTAWTCAATGAAGCGG	6
SEQ. ID NO: 17	28S–15	CCGGGTTGAWGACATTGTCA	7
SEQ. ID NO: 18	28S–16	GCTGGGGCGGCACATCTGTT	4
SEQ. ID NO: 19	28S–17	GAACAAAAGGGTAAAAGTCCC	5
SEQ. ID NO: 20	28S–18	TTTGATTTTCAGTGTGAATACAAACCA	5
SEQ. ID NO: 21	28S–19	ATGAAAGTGTGGCCTATCG	5
SEQ. ID NO: 22	28S–20	GAGGCTAGAGGTGCCAGAA	5
SEQ. ID NO: 23	28S–21	AGGGATAACTGGCTTGTGGC	0
SEQ. ID NO: 24	28S–22	ACCGAAGCAGAATTCGGTAAG	5
SEQ. ID NO: 25	28S–23	GATAATTGGTWTTTGCGGCTG	7
SEQ. ID NO: 26	28S–24	GCTGAACGCCTCTAAGTCAGA	1
SEQ. ID NO: 27	28S–25	TCGTARCAACAAGGCTACT	7

TABLE 4

Broad– range Fungal rRNA Gene Reverse Primers

SEQ ID NO:	Reverse Primer Name	Primer Sequence (5' – 3 ')
SEQ ID NO: 28	End18S	GAAACCTTGTTACGACTTTTA
SEQ ID NO: 29	5.8S	GTTCAAAGAYTCGATGATTCAC
SEQ ID NO: 30	28S–1	TATGCTTAAGTTCAGCGGGTA
SEQ ID NO: 31	28S–2	TTTCCTCCGCTTATTGATATGC
SEQ ID NO: 32	28S–3	CCGCTTCACTCGCCGYTACT
SEQ ID NO: 33	28S–4	CCAGSTTTCAAATTTGAGCT
SEQ ID NO: 34	28S–5	AYGTGAAATTGTTGAAAGGGAAG
SEQ ID NO: 35	28S–6	CTAATCATTCGCTTTACCTC
SEQ ID NO: 36	28S–7	CACGTTCAAYTAAGYAACAAG
SEQ ID NO: 37	28S–8	GATGWACTAACACCTTTTGTGGT
SEQ ID NO: 38	28S–9	GGAACCTTTCCCCACTTC
SEQ ID NO: 39	28S–10	TAGGATCGACTAACCCATGTC
SEQ ID NO: 40	28S–11	GCTGCGGTTATGAGTACGA
SEQ ID NO: 41	28S–12	CCTTATCTACATTRTTCTATCAAC
SEQ ID NO: 42	28S–13	GACAGTCAGATTCCCCTTG
SEQ ID NO: 43	28S–14	CCGCTTCATTGAWTAAGTAAA

SEQ ID NO: 44	28S-15	TGACAATGTCWTCAACCCGG
SEQ ID NO: 45	28S-16	AACAGATGTGCCGCCCCAGC
SEQ ID NO: 46	28S-17	GGGACTTTTACCCTTTTGTTC
SEQ ID NO: 47	28S-18	TGGTTTGTATTCACACTGAAAATCAAA
SEQ ID NO: 48	28S-19	CGATAGGCCACACTTTCAT
SEQ ID NO: 49	28S-20	TTCTGGCACCTCTAGCCTC
SEQ ID NO: 50	28S-21	GCCACAAGCCAGTTATCCCT
SEQ ID NO: 51	28S-22	CTTACCGAATTCTGCTTCGGT
SEQ ID NO: 52	28S-23	CAGCCGCAAAWACCAATTATC
SEQ ID NO: 53	28S-24	TCTGACTTAGAGGCGTTCAGC
SEQ ID NO: 54	28S-25	AGTAGCCTTGTTGYTACGA
SEQ ID NO: 108	12R-opt1	CCTTATCTACATTATTCTATGGAC

EXAMPLE 4

Screening of PCR Amplicons Based on Analytical Sensitivity and Cross-reactivity

[00194] The following Example describes the development of broad-range PCR primers and methods for characterizing the primers.

[00195] Based on the 27 broad-range primers designed in this study, a total of 351 unique amplicons could be generated of various sizes (Figure 1). To develop broad-range PCR assays with maximum sensitivity, amplicons in the range of 75 to 400 bp were selected for screening. A preliminary screen of 62 such amplicons eliminated 51 primer combinations due to amplification of human genomic DNA and/or the inability to amplify 30 fg of *C. albicans* DNA in the presence of 100 ng of human genomic DNA. The remaining 11 amplicons were subjected to extensive screening using analytical sensitivity testing with 30 fg fungal genomic DNA from 27 fungi spanning 15 genera (Figure 4A). The top 11 amplicons, and the primers used to generate the amplicons are shown in Table 5, below. None of these top 11 broad-r ange fungal rRNA gene amplicons generated a product with 1 μg human genomic DNA or were inhibited from amplifying 10 fg of *A. fumigatus* DNA in the presence of 1 μg of human genomic DNA (Figure 4A). Five amplicons, ITS2(5.8SF-1 R), 28S(9F- 12R), 28S(10F- 12R), 28S(18F- 22R) and 28S(18F- 23R) detected the widest range of fungi. The ITS2(5.8SF-1 R) amplicon detected all tested fungi, but had some weak detections as evidenced by relatively faint gel bands. The 28S(10F- 12R) amplicon strongly detected 26 out of the 27 fungi, but could

not detect *Rhodotorula glutinis* at the 30 fg level. In most cases where amplification was either unsuccessful or weak (Figure 4A), there was a mismatch between the sequence of the specific organism and the primer. An exemplary image of a 1.5% agarose gel, on which the PCR products were resolved, is shown in Figure 4B. As indicated in Figure 4B, a band having high intensity was scored as '+++', medium intensity as '++', low intensity as '+', or no amplification as '-'.

TABLE 5
Primer Pairs Used to Generate Top 11 Amplicons

Amplicon	Forward Primer	Reverse Primer
ITS1(End18SF-5.8SR)	GTAAAAGTCGTAACAAGGTTTC (SEQ ID NO: 1)	GTTCAAAGAYTCGATGATTCAC (SEQ ID NO: 29)
ITS2(5.8SF-1R)	GTGAATCATCGARTCTTTGAAC (SEQ ID NO: 2)	TATGCTTAAGTTCAGCGGGTA (SEQ ID NO: 30)
ITS2(5.8SF-2R)	GTGAATCATCGARTCTTTGAAC (SEQ ID NO: 2)	TTTCCTCCGCTTATTGATATGC (SEQ ID NO: 31)
ITS2(5.8SF-3R)	GTGAATCATCGARTCTTTGAAC (SEQ ID NO: 2)	CCGCTTCACTCGCCGYTACT (SEQ ID NO: 32)
28S(9F-12R)	GAAGTGGGGAAAGGTTCC (SEQ ID NO: 11)	CCTTATCTACATTRTTCTATCAAC (SEQ ID NO: 41)
28S(10F-12R)	GACATGGGTTAGTCGATCCTA (SEQ ID NO: 12)	CCTTATCTACATTRTTCTATCAAC (SEQ ID NO: 41) CCTTATCTACATTATTCTATGGAC (SEQ ID NO: 108)
28S(12F-13R)	GTTGATAGAAYAATGTAGATAAGG (SEQ ID NO: 14)	GACAGTCAGATTCCCCTTG (SEQ ID NO: 42)
28S(15F-22R)	CCGGGTTGAWGACATTGTCA (SEQ ID NO: 17)	CTTACCGAATTCTGCTTCGGT (SEQ ID NO: 51)
28S(18F-22R)	TTTGATTTTCAGTGTGAATACAAACCA (SEQ ID NO: 20)	CTTACCGAATTCTGCTTCGGT (SEQ ID NO: 51)
28S(18F-23R)	TTTGATTTTCAGTGTGAATACAAACCA (SEQ ID NO: 20)	CAGCCGCAAAWACCAATTATC (SEQ ID NO: 52)
28S(23F-25R)	AGGGATAACTGGCTTGTGGC (SEQ ID NO: 25)	AGTAGCCTTGTTGYTACGA (SEQ ID NO: 54)

EXAMPLE 5
Assessment of the Potential for Species Resolution Among Amplicons

[00196] The following Example discloses the generation of distance matrices and phylogenetic trees for characterization of the ability of the top eleven (11) amplicons (primer pairs) of the present disclosure to resolves fungal species identity.

[00197] Distances matrices and phylogenetic trees generated from sequence alignments of amplicons for a specific set of PCR primers display the nucleotide differences between fungi and depict the species resolution of amplicons. Such analyses have been used to distinguish species within the *Candida* and *Aspergillus* genus using the D1-D2 region of the 28S rRNA gene and also compare the D1-D2, ITS1 and ITS2 regions for their potential to

resolve species of medically important fungi [(Chen, *et al.* J Clin Microbiol 38:2302-10; Henry, *et al.* (2000) J. Clin. Microbiol. 38:1510-5; Hinrikson, *et al.* (2005) Med. Mycol. 43 Suppl. 1:S129-37; Hinrikson, *et al.*(2005) J. Clin. Microbiol. 43:2092-103; Kurtzman and Robnett (1997) J. Clin. Microbiol. 35:1216-23; Rakeman, *et al.* (2005). J. Clin. Microbiol. 43:3324-33)]. The parameter in Figure 4A and Table 6, which represents the sum of all elements of the distance matrix provides a global measure of nucleotide differences between fungal sequences for a specific amplicon.

[00198] To evaluate the potential for species identification using the top 11 PCR amplicons, distance matrices were generated from the multiple sequence alignment of 50 fungi for each amplicon. The sequences of the forward and reverse primer were excluded from the analysis. Distance matrices for 3 amplicons ITS2(5.8SF- 2R), ITS2(5.8SF-3R) and 28S(9F-1 2R) were not estimated due to significant sequence overlap with another amplicon that showed greater breadth of analytical sensitivity.

[00199] The distance matrices based on the absolute difference algorithm for the remaining top 8 amplicons are shown in Figure 5A - 5H, which show the amplicons ITS1 (end18SF-5.8SR), ITS2(5.8SF-1R), 28S(10F-12R), 28S(12F-13R), 28S(15F-22R), 28S(18F-22R), 28S(18F-23R), and 28S(23F-25R), respectively. The sum of all the elements in the distance matrix resulted in a numerical quantity that reflected the magnitude of species resolution for each amplicon. For distances estimated using the Tajima-Nei algorithm, larger values reflect more nucleotide differences among fungi and therefore greater phylogenetic resolution for species identification. For example, the amplicon ITS2(5.8SF- 1R) overlapping the ITS2 region, for which the distance matrix is shown in Figure 5B, was expected to have the highest level of sequence variation and had a distance matrix sum of 1055.8 (Figure 4A and Table 6, below), whereas the amplicon 28S(18F-22R) which covers a highly conserved region of the 28S rRNA gene (distance matrix shown in Figure 5F) had a distance matrix sum of only 74.5 (Figure 4A and Table 6, below). A similar and more intuitive trend emerged when the sum of the distance matrix was estimated based on the absolute differences algorithm, which calculates the total number of base differences between fungal sequences in an alignment. In this case the ITS2(5.8SF-1R) amplicon overlapping the ITS2 region also had the highest nucleotide differences with a sum of 113,388, while the 28S(18F-2 2R) amplicon showed the lowest sum of nucleotide

differences at 9,629 (Figure 4A and Table 6, below). Therefore, based on genetic distances, the ITS2(5.8SF–1R) amplicon had the highest level of species resolution. Among the top 5 amplicons ranked in terms of breadth of fungi detected, 28S(10F– 12R) also manifested a high degree of species resolution as evidenced by its distance matrix in Figure 5C.

Table 6
Distance Matrix Sums and Amplicon Lengths of Top 11 Amplicons

	ITS1(End1 8SF-5.8SR)	ITS2 (5.8SF-1R)	ITS2 (5.8SF-2R)	ITS2 (5.8SF-3R)	28S (9F-12R)	28S (10F-12R)	28S (12F-13R)	28S (15F-22R)	28S (18F-22R)	28S (18F-23R)	28S (23F-25R)
Sum of distance matrix based on Tajima-Nei algorithm & Neighbor Joining tree building method	642.5	1055.8	ND	ND	ND	310.8	470.6	67.5	74.5	117.3	358.3.
Sum of distance matrix based on absolute nucleotide differences and Neighbor Joining tree building method	97914	113388	ND	ND	ND	82452	61321	17522	9629	28716	66445
Amplicon length ± standard deviation of 50 fungal species representing 30 genera	297±70	254±42	ND	ND	ND	339±7	200±25	299±67	157±67	318±80	263±10

[00200] Combining information from the amplicon matrix (Figure 1), primer map (Figure 2), sensitivity data (Figure 4A) and distance matrices (Figures 5A-5H) provides useful data for selecting broad range fungal PCR assays. Based on the ability to detect the widest range of fungi and simultaneously resolve species identity, the ITS2(5.8SF–1 R), and 28S(10F–1 2R) amplicons emerged as top assays for broad– range fungal PCR.

[00201] Conventional endpoint PCR with gel electrophoresis was used to assess amplification. Quantitative PCR can also be used as an indicator of amplification efficiency, but analysis of PCR products by gel electrophoresis provides data on amplicon size, the generation of non-specific amplification products, and product throughput (band intensity). The present invention discloses primers that are primarily specific for the 28S region. However, also contemplated are primers in the 18S rRNA gene that are useful

when used in conjunction with primers described in the present disclosure. The method and compositions provided by the present disclosure are useful for targeting regions beyond the D1-D2 region for the identification of novel fungi. Since primers were designed at highly conserved regions, the specificity of the primers is highly unlikely to be affected by the presence of any polymorphic positions at primer site or within the amplicons disclosed in the present description.

[00202] An alternative approach for analyzing the species resolution of amplicons uses phylogenetic trees based on the Neighbor–J oining tree building method and Tajima-Nei algorithm for calculation of distances. Figures 6 and 7 are phylogenetic trees for amplicons ITS2(5.8SF– 1R) and 28S(10F– 12R), respectively. Note that the ITS2(5.8SF–1R) amplicon is highly polymorphic and lacks the property of a molecular clock, making it unreliable for inferring evolutionary relationships. The trees demonstrate that closely related fungi are resolved using the proposed amplicon sequences.

EXAMPLE 6

Identification of Fungal Species Using Two-dimensional Melt Curve Analysis

[00203] The following example discloses methods for the identification of DNA from one or more fungal pathogens in a patient sample using two-dimensional melt-curve analysis.

[00204] To develop better broad range fungal PCR assays for application to human tissues, an extensive analysis of fungal rRNA gene sequences was performed, focusing on ~3950 bp of sequence from the 3 end of the 18S rRNA gene to the 3 end of the 28S gene. *See* Khot et al. (2009) *Appl Environ Microbiol* 75(6): 1559-1565, incorporated herein by reference. Sequence data was generated *de novo* for numerous fungal species and collected data from databases and genome projects. The focus was on selecting primers with broadly conserved sequences among fungi while having significant sequence dissimilarity with human rRNA genes. Out of 62 amplicons analyzed, two successfully amplified 30 fg of fungal DNA from 25 of 26 fungi and provided the most phylogenetic information for species identification based on distance matrices. The primers for these top two PCR assays, called ITS2(5.8SF–1R) a nd 28S(10F– 12R), are located illustrated in Fig. 61.

[00205] Figure 61 illustrates a map of a fungal 28S rRNA gene and corresponding positions of twenty-seven broad-range fungal PCR primers for sequencing and PCR assay development. Figure 61A shows a map of fungal rRNA from the 3 end of 18S to 3 end of 28S rRNA gene based on *Saccharomyces cerevisiae*. Figure 61B illustrates the positions of 27 newly designed broad- range fungal primers based on differences with human rRNA gene designed for this. *See* Khot *et al.* (2009) *Appl Environ Microbiol* 75(6): 1559-1565. The combination of primers 10F and 12R at50 pmol/PCR each did not amplify *Rhodotorula glutinis* (even at 1000 pg). The inclusion of a second reverse primer (12R-opt1; SEQ ID NO: 57) in the 28S(10F-12R) assay at 9% of total reverse primer concentration resulted in successful amplification of 30 fg of fungal DNA from Rhodotorula glutinis. The 28S(10F- 12R) assay included primer 10F (SEQ ID NO: 108) at 50 pmol/PCR, primer 12R (SEQ ID NO: 56) at 50 pmol/PCR, and primer 12R-opt1 (SEQ ID NO: 57) at 5 pmol/PCR. 12R-opt1 lacks degeneracies and differs from 12R by three bases.

[00206] Figure 62 illustrates a two-dimensional melt curve plot based on the broad-range fungal qPCR assays ITS2(5.8SF-1R) and 28S(10F-12R) allowing rapid identification of species. Different PCR products can be differentiated from each other based on the characteristic temperature at which they "melt" in going from a double-stranded to single-stranded confirmation. For instance, amplicons which are longer and have higher GC content have higher melting temperatures. The melting profile of an amplicon can be determined by adding a fluorescent double-stranded DNA binding dye to the PCR and measuring fluorescence as the temperature changes. As an amplicon melts, the fluorescence decreases. Assessing the melting temperature of a single broad-range fungal amplicon provides useful information about the possible identity of the fungus, but even more accurate information is gleaned using data from several different broad range fungal PCR assays—a approach called two dimensional (2D) melt curve analysis. *See* Gigli et al. (2003) *Nucleic Acids Res.* 31(22): e136, incorporated herein by reference.

[00207] An approach was developed using the top two broad- range PCR amplicons described above. This strategy allows for the rapid preliminary identification of fungi which may be very clinically useful. The ITS2(5.8SF-1R) and 28S(10F-1 2R) PCR assays were transformed into a qPCR format using a double stranded DNA binding dye (EvaGreen™, Biotium Inc., Hayward, CA). Fig. 62 shows the ability of the two amplicons

to identify 25 fungal species based on their melting temperatures. Nucleotide sequencing can be used to resolve the identity of fungi for which the 2D melt temperature analysis provides ambiguous results.

[00208] To test the diagnostic ability of the top two broad- range qPCR assays and the feasibility of using a 2D melt curve approach, these assays were applied to 26 BAL samples which were previously tested with our Aspergillus 18S rRNA gene qPCR. Of these 26 BAL samples, half were positive with culture for fungus and/or with the Aspergillus 18S assay and the other half were not. The 28S(10F-1 2R) qPCR assay was positive for 13 of 13 and the ITS2(5.8SF- 1R) qPCR assay for 10 of 13 of those BALs that were positive with culture and/or with the Aspergillus 18S assay. Sequencing of all these amplicons confirmed the identities predicted by the 2D melt curve approach. These preliminary data suggest that broad range fungal PCR with rapid melt curve analysis can be useful for identifying fungal pathogens, though additional testing is necessary to assess the sensitivity and specificity of this approach.

[00209] Figure 63 illustrates melt temperature curves of pathogenic fungi amplified from blood, representing the 10-12 amplicon on the fungal 28S rRNA gene. The ability to distinguish between fungal amplification products in broad-range PCR was demonstrated using one dimensional melt curve analysis as displayed in Figure 63. Genomic DNA from 4 different fungal species was added to blood. The PCR targeted the same segment of the fungal rRNA operon (28S rRNA 10F-12R), wherein the PCR product was detected using a double stranded DNA binding dye. Amplicon melt analysis was performed after PCR, demonstrating characteristic peaks corresponding to the melting temperature of the different amplicons. The melt temperature at which ds DNA binding dye dissociates from the amplicon with loss of fluorescence depends on amplicon length and base composition. For instance, the *Candida albicans* PCR product has a melting temperature of 87 degrees in this assay. The use of more than one broad range PCR target allows the melt temperature peaks to be plotted on a graph resulting in two dimensional melt curve analysis with even greater ability to resolve fungi. See Fig. 62 for an example of this approach.

[00210] All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the

disclosure has been descried in each of its various embodiments, it is expected that certain modifications thereto may be undertaken and effected by the person skilled in the art without departing from the true spirit and scope of the disclosure, as set forth in the previous description and as further embodied in the following claims. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the scope of the disclosure as defined by the appended claims.

[00211] The present disclosure is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the methods and compositions disclosed herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims. It is further to be understood that all values are approximate, and are provided for description. All patents and patent applications cited herein are hereby incorporated herein by reference in their entireties.

WHAT IS CLAIMED IS:

1. A method for detecting a fungal pathogen in a patient sample, said method comprising the steps of:

(a) isolating a patient sample,

(b) carrying out a PCR reaction on said patient sample to generate a PCR amplicon that comprises a region of a fungal ribosomal RNA (rRNA) gene, wherein said PCR reaction uses a primer set comprising a forward primer and a reverse primer and wherein at least one of said forward primer and said reverse primer is complementary to said fungal rRNA gene, and

(c) detecting said PCR amplicon.

2. The method of claim 1 further comprising the step of extracting DNA from said isolated patient sample.

3. The method of claim 1 wherein said PCR amplicon comprises a region of a fungal internal transcribed spacer 1 (ITS-1) region and wherein at least one of said forward and said reverse primer is complementary to said fungal ITS-1 region.

4. The method of claim 1 wherein said PCR amplicon comprises a region of a fungal 28S rRNA gene and wherein at least one of said forward and said reverse primer is complementary to said fungal 28S rRNA gene.

5. The method of claim 4 wherein said region of a fungal 28S rRNA gene comprises a sequence that is 3' to a D1-D2 highly variable region.

6. The method of claim 1, further comprising the step of sequencing said PCR amplicon.

7. The method of claim 1 wherein said PCR amplicon is between 50 and 1000 base pairs.

8. The method of claim 7 wherein said PCR amplicon is between 75 and 400 base pairs.

9. The method of claim 1 wherein said PCR reaction is a quantitative PCR reaction.

10. The method of claim 1 wherein said forward primer is complementary to a fungal 18S rRNA gene and said reverse primer is complementary to a fungal 28S rRNA gene.

11. The method of claim 10 wherein said forward primer comprises the nucleotide sequence 5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1).

12. The method of claim 1 wherein said forward primer is complementary to a fungal 5.8S rRNA gene and said reverse primer is complementary to a fungal 28S rRNA gene.

13. The method of claim 12 wherein said forward primer comprises the nucleotide sequence 5'- GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2).

14. The method of claim 1 wherein said forward primer and said reverse primer are both complementary to a fungal 28S rRNA gene.

15. The method of claim 1 wherein said forward primer is selected from the group consisting of:

5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1),
5'-GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2),
5'-TACCCGCTGAACTTAAGCATA-3' (SEQ ID NO: 3),
5'-GCATATCAATAAGCGGAGGAAA-3' (SEQ ID NO: 4),
5'-AGTARCGGCGAGTGAAGCGG-3' (SEQ ID NO: 5),
5'-AGCTCAAATTTGAAASCTGG-3' (SEQ ID NO: 6),
5'-CTTCCCTTTCAACAATTTCACRT-3' (SEQ ID NO: 7),
5'-AGGTAAAGCGAATGATTAG-3' (SEQ ID NO: 8),
5'-CTTGTTRCTTARTTGAACGTG-3' (SEQ ID NO: 9),
5'-ACCACAAAAGGTGTTAGTWCATC-3' (SEQ ID NO: 10),
5'-GAAGTGGGGAAAGGTTCC-3' (SEQ ID NO: 11),
5'-GACATGGGTTAGTCGATCCTA-3' (SEQ ID NO: 12),
5'-TCGTACTCATAACCGCAGC-3' (SEQ ID NO: 13),

5'-GTTGATAGAAYAATGTAGATAAGG-3' (SEQ ID NO: 14),
5'-CAAGGGGAATCTGACTGTC-3' (SEQ ID NO: 15),
5'-TTTACTTAWTCAATGAAG CGG-3' (SEQ ID NO: 16),
5'-CCGGGTTGAWGACATTGTCA-3' (SEQ ID NO: 17),
5'-GCTGGGGCGGCACATCTGTT-3' (SEQ ID NO: 18),
5'-GAACAAAAGGGTAAAAGTCCC-3' (SEQ ID NO: 19),
5'-TTTGATTTTCAGTGTGAATACAAACCA-3' (SEQ ID NO: 20),
5'-ATGAAAGTGTGGCCTATCG-3' (SEQ ID NO: 21),
5'-GAGGCTAGAGGTGCCAGAA-3' (SEQ ID NO: 22),
5'-AGGGATAACTGGCTTGTGGC-3' (SEQ ID NO: 23),
5'-ACCGAAGCAGAATTCGGTAAG-3' (SEQ ID NO: 24),
5'-GATAAT TGGTWTTTGCGGCTG-3' (SEQ ID NO: 25),
5'-GCTGAACGCCTCTAAGTCAGA-3' (SEQ ID NO: 26), and
5'-TCGTARCAACAAGGCTACT-3' (SEQ ID NO: 27).

16. The method of claim 1 wherein said reverse primer is selected from the group consisting of:

5'-GAAACCTTGTTACGACTTTTAC-3' (SEQ ID NO: 28),
5'-GTTCAAAGAYTCGATGATTCAC-3' (SEQ ID NO: 29),
5'-TATGCTTAAGTTCAGCGGGTA-3' (SEQ ID NO: 30),
5'-TTTCCTCCGCTTATTGATATGC-3' (SEQ ID NO: 31),
5'-CCGCTTCACTCGCCGYTACT-3' (SEQ ID NO: 32),
5'-CCAGSTTTCAAATTTGAGCT-3' (SEQ ID NO: 33),
5'-AYGTGAAATTGTTGAAAGGGAAG-3' (SEQ ID NO: 34),
5'-CTAATCATTCGCTTTACCTC-3' (SEQ ID NO: 35),
5'-CACGTTCAAYTAAGYAACAAG-3' (SEQ ID NO: 36),
5'-GATGWACTAACACCTTTTGTGGT-3' (SEQ ID NO: 37),
5'-GGAACCTTTCCCCACTTC-3' (SEQ ID NO: 38),
5'-TAGGATCGACTAACCCATGTC-3' (SEQ ID NO: 39),
5'-GCTGCGGTTATGAGTACGA-3' (SEQ ID NO: 40),
5'-CCTTATCTACATTRTTCTATCAAC-3' (SEQ ID NO: 41),
5'-GACAGTCAGATTCCCCTTG-3' (SEQ ID NO: 42),
5'-CCGCTTCATTGAWTAAGTAAA-3' (SEQ ID NO: 43),
5'-TGACAATGTCWTCAACCCGG-3' (SEQ ID NO: 44),

5'-AACAGATGTGCCGCCCCAGC-3' (SEQ ID NO: 45),
5'-GGGACTTTTACCCTTTTGTTC-3' (SEQ ID NO: 46),
5'-TGGTTTGTATTCACACTGAAAATCAAA-3' (SEQ ID NO: 47),
5'-CGATAGGCCACACTTTCAT-3' (SEQ ID NO: 48),
5'-TTCTGGCACCTCTAGCCTC-3' (SEQ ID NO: 49),
5'-GCCACAAGCCAGTTATCCCT-3' (SEQ ID NO: 50),
5'-CTTACCGAATTCTGCTTCGGT-3' (SEQ ID NO: 51),
5'-CAGCCGCAAAWACCAATTATC-3' (SEQ ID NO: 52),
5'-TCTGACTTAGAGGCGTTCAGC-3' (SEQ ID NO: 53),
5'-AGTAGCCTTGTTGYTACGA-3' (SEQ ID NO: 54), and
5'- CCTTATCTACATTATTCTATGGAC-3' (SEQ ID NO: 108).

17. The method of claim 1 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 31), (SEQ ID NO: 2 and SEQ ID NO: 32), (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

18. The method of claim 1 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

19. The method of claim 17 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

20. The method of claim 19 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), and (SEQ ID NO: 12 and SEQ ID NO: 41).

21. The method of claim 1 wherein said fungal pathogen is selected from the group consisting of *Absidia corymbifera; Cunninghamella bertholletiae; Fusarium solani; Mucor racemosus; Paecilomyces variotii; Penicillium chrysogenum; Rhizomucor miehei; Rhodotorula glutinis; Scedosporium apiospermum; Antrodia vaillantii; Aspergillus fumigatus; Aspergillus niger; Aspergillus oryzae; Aspergillus terreus; Batrachochytrium dendrobatidis; Botrytis cinerea; Candida albicans; Candida dublineinsis; Candida glabrata; Candida gulliermundei; Candida kefyr; Candida krusei; Candida lipolytica; Candida lusitaniae; Candida parapsilosis; Candida tropicalis; Chaetomium globosum; Coccidioides immitis; Coccidioides posadasii; Cryptococcus neoformans; Fusarium graminearum; Fusarium oxysporum; Histoplasma capsulatum; Hypocrea jecorina; Lodderomyces elongisporus; Magnaporthe grisea; Metarhizium anisopliae; Microsporum gypseum; Mucor racemosus; Neurospora crassa; Paracoccidioides brasiliens; Pneumocystis carinii; Penicillium verrucosum; Pichia stipitis; Rhizomucor miehei; Rhizopus oryzae; Saccharomyces cerevisiae; Schizosaccharomyces japonicus; Schizosaccharomyces pombe; Sclerotinia sclerotiorum; Stagonospora nodorum; Umbilicaria esculenta;* and *Uncinocarpus reesii*.

22. The method of claim 1 wherein each primer of the primer set specifically binds only to a fungal DNA.

23. The method of claim 1 wherein each primer of the primer set specifically binds only to a fungal DNA in the presence of a non-fungal DNA.

24. The method of claim 23 wherein the non-fungal DNA is mammalian DNA.

25. The method of claim 24 wherein the mammalian DNA is human DNA.

26. The method of claim 23 wherein the non-fungal DNA is in greater than 1,000,000-fold mass excess of the fungal DNA.

27. The method of claim 23 wherein the non-fungal DNA is in greater than 5,000,000-fold excess of the fungal DNA.

28. The method of claim 23 wherein the non-fungal DNA is in greater than 30,000,000-fold excess of the fungal DNA.

29. The method of claim 1 wherein said patient sample is selected from the group consisting of a blood sample, a sputum sample, a lung lavage fluid sample, and a tissue biopsy sample.

30. The method of claim 29 wherein said blood sample is selected from the group consisting of whole blood, plasma, serum, and a white blood cell fraction.

31. The method of claim 1 wherein said fungal pathogen causes a fungal infection selected from the group consisting of aspergillosis, candidiasis, zygomycosis, scedosporiosis, fusariosis, cryptococcosis, histoplasmosis, coccidioidomycosis, and blastomycosis.

32. A primer set for detecting a fungal DNA, said primer set comprising a forward primer and a reverse primer wherein at least one of said forward primer and said reverse primer is complementary to a fungal 28S ribosomal RNA (rRNA) gene.

33. The primer set of claim 32 wherein at least one of said forward primer and said reverse primer is complementary to a sequence that is 3' to a D1-D2 highly variable region in said fungal 28S ribosomal rRNA gene.

34. The primer set of claim 32 wherein said forward primer is complementary to a fungal 18S rRNA gene and said reverse primer is complementary to a fungal 28S rRNA gene.

35. The primer set of claim 34 wherein said forward primer comprises the nucleotide sequence 5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1).

36. The primer set of claim 32 wherein said forward primer is complementary to a fungal 5.8S rRNA gene and said reverse primer is complementary to a fungal 28S rRNA gene.

37. The primer set of claim 36 wherein said forward primer comprises the nucleotide sequence 5'- GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2).

38. The primer set of claim 32 wherein said forward primer and said reverse primer are both complementary to a fungal 28S rRNA gene.

39. The primer set of claim 32 wherein said forward primer is selected from the group consisting of:

5'-GTAAAAGTCGTAACAAGGTTTC-3' (SEQ ID NO: 1),
5'-GTGAATCATCGARTCTTTGAAC-3' (SEQ ID NO: 2),
5'-TACCCGCTGAACTTAAGCATA-3' (SEQ ID NO: 3),
5'-GCATATCAATAAGCGGAGGAAA-3' (SEQ ID NO: 4),
5'-AGTARCGGCGAGTGAAGCGG-3' (SEQ ID NO: 5),
5'-AGCTCAAATTTGAAASCTGG-3' (SEQ ID NO: 6),
5'-CTTCCCTTTCAACAATTTCACRT-3' (SEQ ID NO: 7),
5'-GAGGTAAAGCGAATGATTAG-3' (SEQ ID NO: 8),
5'-CTTGTTRCTTARTTGAACGTG-3' (SEQ ID NO: 9),
5'-ACCACAAAAGGTGTTAGTWCATC-3' (SEQ ID NO: 10),
5'-GAAGTGGGGAAAGGTTCC-3' (SEQ ID NO: 11),
5'-GACATGGGTTAGTCGATCCTA-3' (SEQ ID NO: 12),
5'-TCGTACTCATAACCGCAGC-3' (SEQ ID NO: 13),
5'-GTTGATAGAAYAATGTAGATAAGG-3' (SEQ ID NO: 14),
5'-CAAGGGGAATCTGACTGTC-3' (SEQ ID NO: 15),
5'-TTTACTTAWTCAATGAAG CGG-3' (SEQ ID NO: 16),
5'-CCGGGTTGAWGACATTGTCA-3' (SEQ ID NO: 17),
5'-GCTGGGGCGGCACATCTGTT-3' (SEQ ID NO: 18),
5'-GAACAAAAGGGTAAAAGTCCC-3' (SEQ ID NO: 19),
5'-TTTGATTTTCAGTGTGAATACAAACCA-3' (SEQ ID NO: 20),
5'-ATGAAAGTGTGGCCTATCG-3' (SEQ ID NO: 21),
5'-GAGGCTAGAGGTGCCAGAA-3' (SEQ ID NO: 22),
5'-AGGGATAACTGGCTTGTGGC-3' (SEQ ID NO: 23),
5'-ACCGAAGCAGAATTCGGTAAG-3' (SEQ ID NO: 24),
5'-GATAAT TGGTWTTTGCGGCTG-3' (SEQ ID NO: 25),
5'-GCTGAACGCCTCTAAGTCAGA-3' (SEQ ID NO: 26), and

5'-TCGTARCAACAAGGCTACT-3' (SEQ ID NO: 27).

40. The primer set of claim 32 wherein said reverse primer is selected from the group consisting of:

5'-GAAACCTTGTTACGACTTTTAC-3' (SEQ ID NO: 28),
5'-GTTCAAAGAYTCGATGATTCAC-3' (SEQ ID NO: 29),
5'-TATGCTTAAGTTCAGCGGGTA-3' (SEQ ID NO: 30),
5'-TTTCCTCCGCTTATTGATATGC-3' (SEQ ID NO: 31),
5'-CCGCTTCACTCGCCGYTACT-3' (SEQ ID NO: 32),
5'-CCAGSTTTCAAATTTGAGCT-3' (SEQ ID NO: 33),
5'-AYGTGAAATTGTTGAAAGGGAAG-3' (SEQ ID NO: 34),
5'-CTAATCATTCGCTTTACCTC-3' (SEQ ID NO: 35),
5'-CACGTTCAAYTAAGYAACAAG -3' (SEQ ID NO: 36),
5'-GATGWACTAACACCTTTTGTGGT-3' (SEQ ID NO: 37),
5'-GGAACCTTTCCCCACTTC-3' (SEQ ID NO: 38),
5'-TAGGATCGACTAACCCATGTC-3' (SEQ ID NO: 39),
5'-GCTGCGGTTATGAGTACGA-3' (SEQ ID NO: 40),
5'-CCTTATCTACATTRTTCTATCAAC-3' (SEQ ID NO: 41),
5'-GACAGTCAGATTCCCCTTG-3' (SEQ ID NO: 42),
5'-CCGCTTCATTGAWTAAGTAAA-3' (SEQ ID NO: 43),
5'-TGACAATGTCWTCAACCCGG-3' (SEQ ID NO: 44),
5'-AACAGATGTGCCGCCCCAGC-3' (SEQ ID NO: 45),
5'-GGGACTTTTACCCTTTTGTTC-3' (SEQ ID NO: 46),
5'-TGGTTTGTATTCACACTGAAAATCAAA-3' (SEQ ID NO: 47),
5'-CGATAGGCCACACTTTCAT-3' (SEQ ID NO: 48),
5'-TTCTGGCACCTCTAGCCTC-3' (SEQ ID NO: 49),
5'-GCCACAAGCCAGTTATCCCT-3' (SEQ ID NO: 50),
5'-CTTACCGAATTCTGCTTCGGT-3' (SEQ ID NO: 51),
5'-CAGCCGCAAAWACCAATTATC-3' (SEQ ID NO: 52),
5'-TCTGACTTAGAGGCGTTCAGC-3' (SEQ ID NO: 53),
5'-AGTAGCCTTGTTGYTACGA-3' (SEQ ID NO: 54), and
5'- CCTTATCTACATTATTCTATGGAC-3' (SEQ ID NO: 108).

41. The primer set of claim 32 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 31), (SEQ ID NO: 2 and SEQ ID NO: 32), (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

42. The primer set of claim 32 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 1 and SEQ ID NO: 29), (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

43. The primer set of claim 32 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 11 and SEQ ID NO: 41), (SEQ ID NO: 12 and SEQ ID NO: 41), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), (SEQ ID NO: 14 and SEQ ID NO: 42), (SEQ ID NO: 17 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 51), (SEQ ID NO: 20 and SEQ ID NO: 52), and (SEQ ID NO: 25 and SEQ ID NO: 54).

44. The primer set of claim 32 wherein said primer set comprises a forward and reverse primer pair selected from the group consisting of (SEQ ID NO: 2 and SEQ ID NO: 30), (SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108), and (SEQ ID NO: 12 and SEQ ID NO: 41).

45. The primer set of claim 32 wherein said fungal DNA is from a fungal species selected from the group consisting of *Absidia corymbifera; Cunninghamella bertholletiae; Fusarium solani; Mucor racemosus; Paecilomyces variotii; Penicillium chrysogenum; Rhizomucor miehei; Rhodotorula glutinis; Scedosporium apiospermum; Antrodia vaillantii; Aspergillus fumigatus; Aspergillus niger; Aspergillus oryzae; Aspergillus terreus; Batrachochytrium dendrobatidis; Botrytis cinerea; Candida albicans; Candida dublineinsis;*

Candida glabrata; Candida gulliermundei; Candida kefyr; Candida krusei; Candida lipolytica; Candida lusitaniae; Candida parapsilosis; Candida tropicalis; Chaetomium globosum; Coccidioides immitis; Coccidioides posadasii; Cryptococcus neoformans; Fusarium graminearum; Fusarium oxysporum; Histoplasma capsulatum; Hypocrea jecorina; Lodderomyces elongisporus; Magnaporthe grisea; Metarhizium anisopliae; Microsporum gypseum; Mucor racemosus; Neurospora crassa; Paracoccidioides brasiliens; Pneumocystis carinii; Penicillium verrucosum; Pichia stipitis; Rhizomucor miehei; Rhizopus oryzae; Saccharomyces cerevisiae; Schizosaccharomyces japonicus; Schizosaccharomyces pombe; Sclerotinia sclerotiorum; Stagonospora nodorum; Umbilicaria esculenta; and *Uncinocarpus reesii*.

46. The primer set of claim 32 wherein said forward primer has the sequence set forth in SEQ ID NO: 1 and wherein said reverse primer has the sequence set forth in SEQ ID NO: 30.

47. The primer set of claim 32 wherein said forward primer has the sequence set forth in SEQ ID NO: 12 and wherein said reverse primer has the sequence set forth in SEQ ID NO: 41.

48. The primer set of claim 32 wherein said primer set comprises an additional reverse primer, the primer set consisting of SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108.

49. A method for determining the identity of a fungal species in a patient sample, said method comprising the steps of:

(a) isolating a patient sample;

(b) carrying out a first PCR reaction to generate a first PCR amplicon, wherein said first PCR reaction comprises a first primer set capable of amplifying a region in a fungal ribosomal RNA (rRNA) gene comprising an internal transcribed spacer 2 (ITS-2) sequence;

(c) carrying out a second PCR reaction to generate a second PCR amplicon, wherein said second PCR reaction comprises a second primer set capable of amplifying a region in a fungal ribosomal 28S rRNA gene; and

(d) determining the melting temperature of said first PCR amplicon and of said second PCR amplicon, wherein the identity of said fungal species is determined by comparing the melting point of said first PCR amplicon and of said second PCR amplicon to known standards using a dye that binds to double stranded DNA and fluoresces preferentially in that state.

50. The method of claim 49 further comprising the step of extracting DNA from said isolated patient sample.

51. The method of claim 49 wherein said first PCR reaction and said second PCR reaction are each quantitative PCR (qPCR) reactions.

52. The method of claim 49 wherein said first primer set comprises a forward primer sequence as set forth in SEQ ID NO: 2 and a reverse primer sequence as set forth in SEQ ID NO: 30 and wherein said second primer set comprises a forward primer sequence as set forth in SEQ ID NO: 12 and a reverse primer sequence as set forth in SEQ ID NO: 41.

53. A method for identifying a primer set capable of detecting a fungal pathogen in a sample, said method comprising the steps of: (a) obtaining the nucleic acid sequence of at least the 28S region of a fungal rRNA operon, (b) designing a forward primer capable of hybridizing with said nucleic acid sequence at a specific site in said 28S region, (c) designing a reverse primer capable of hybridizing with said nucleic acid sequence at a region in said sequence that is 3' to the region to which the forward primer is capable of hybridizing, and (d) determining whether said forward primer and said reverse primer are capable of generating a PCR amplicon that is useful for identifying fungal DNA in a PCR reaction containing a specific fungal DNA.

54. The method of claim 53 wherein the method further comprises the step of resolving said PCR amplicon on an agarose gel to determine the analytical sensitivity of said forward primer and said reverse primer.

55. The method of claim 54 wherein said agarose gel is stained with ethidium bromide and said PCR amplicon is visualized by ultraviolet light.

56. The method of claim 53 wherein the method further comprises the step of determining the cross-reactivity of said forward primer and said reverse primer with non-fungal DNA.

57. The method of claim 56 wherein the non-fungal DNA is mammalian DNA.

58. The method of claim 57 wherein the mammalian DNA is human DNA.

59. The method of claim 53 wherein the method further comprises the step of determining the species resolution of said forward primer and said reverse primer, wherein said forward primer and said reverse primer comprise a primer set.

60. The method of claim 59 wherein an ability of said primer set to resolve a species is determined by a method comprising the following steps: (a) sequencing said PCR amplicon, (b) comparing the sequence of said PCR amplicon with a sequence of a second PCR amplicon generated using said forward and reverse primers in a PCR reaction containing DNA from a different fungal species, and (c) repeating steps (a) and (b) using fungal DNA from at least 30 different fungal species to determine sequences of amplicons for at least 31 different fungal species, and (d) comparing the sequences of each amplicon.

61. The method of claim 60 wherein the sequences of each amplicon are compared to each other by generating a multiple sequence alignment of said sequences.

62. The method of claim 61 wherein the method further comprises the step of generating a distance matrix for each amplicon from said multiple sequence alignment.

63. The method of claim 62 wherein the distance matrix of each amplicon is compared to the distance matrix of each other amplicon, and wherein the comparison is used to determine which of said primer sets are capable of resolving a fungal species.

64. The method of claim 62 wherein the distance matrix is generated using the Tajima-Nei algorithm.

65. The method of claim 61, further comprising the step of assembling a phylogenetic tree.

66. The method of claim 65 wherein said phylogenetic tree is assembled using the Neighbor-Joining tree building method.

67. The method of claim 53 wherein said sample comprises 1,000,000-fold mass excess of non-fungal DNA to fungal DNA.

68. The method of claim 1 wherein said primer set further comprises a second reverse primer, the primer set consisting of SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 108.

Primer	End18S	5.8S	28S-1	28S-2	28S-3	28S-4	28S-5	28S-6	28S-7	28S-8	28S-9	28S-10	28S-11	28S-12	28S-13	28S-14	28S-15	28S-16	28S-17	28S-18	28S-19	28S-20	28S-21	28S-22	28S-23	28S-24	28S-25
start →	16	511	841	857	901	925	1218	1807	1885	2009	2296	2330	2647	2691	2929	3324	3398	3429	3506	3533	3559	3600	3628	3708	3861	3925	4160
end →	37	532	861	878	920	944	1240	1826	1905	2036	2313	2350	2665	2714	2952	3344	3417	3450	3526	3559	3577	3618	3648	3728	3881	3945	4178
Primer	**start ↓**	**end ↓**																									
End18S	16	37	0																								
5.8S	511	532	516	0																							
28S-1	841	861	845	350	0																						
28S-2	857	878	862	367	37	0																					
28S-3	901	920	904	409	79	63	0																				
28S-4	925	944	928	433	103	87	43	0																			
28S-5	1218	1240	1224	729	399	383	339	315	0																		
28S-6	1807	1826	1810	1315	985	969	925	901	608	0																	
28S-7	1885	1905	1889	1394	1064	1048	1004	980	687	98	0																
28S-8	2009	2036	2020	1525	1195	1179	1135	1111	818	229	151	0															
28S-9	2296	2313	2297	1802	1472	1456	1412	1388	1095	506	428	304	0														
28S-10	2330	2350	2334	1839	1509	1493	1449	1425	1132	543	465	341	54	0													
28S-11	2647	2665	2649	2154	1824	1808	1764	1740	1447	858	780	656	369	335	0												
28S-12	2691	2714	2698	2203	1873	1857	1813	1789	1496	907	829	705	418	384	67	0											
28S-13	2929	2952	2936	2441	2111	2095	2051	2027	1734	1145	1067	943	656	622	305	261	0										
28S-14	3324	3344	3328	2833	2503	2487	2443	2419	2126	1537	1459	1335	1048	1014	697	653	415	0									
28S-15	3398	3417	3401	2906	2576	2560	2516	2492	2199	1610	1532	1408	1121	1087	770	726	488	93	0								
28S-16	3429	3450	3434	2939	2609	2593	2549	2525	2232	1643	1565	1441	1154	1120	803	759	521	126	52	0							
28S-17	3506	3526	3510	3015	2685	2669	2625	2601	2308	1719	1641	1517	1230	1196	879	835	597	202	128	97	0						
28S-18	3533	3559	3543	3048	2718	2702	2658	2634	2341	1752	1674	1550	1263	1229	912	868	630	235	161	130	53	0					
28S-19	3559	3577	3561	3066	2736	2720	2676	2652	2359	1770	1692	1568	1281	1247	930	886	648	253	179	148	71	44	0				
28S-20	3600	3618	3602	3107	2777	2761	2717	2693	2400	1811	1733	1609	1322	1288	971	927	689	294	220	189	112	85	59	0			
28S-21	3628	3648	3632	3137	2807	2791	2747	2723	2430	1841	1763	1639	1352	1318	1001	957	719	324	250	219	142	115	89	48	0		
28S-22	3708	3728	3712	3217	2887	2871	2827	2803	2510	1921	1843	1719	1432	1398	1081	1037	799	404	330	299	222	195	169	128	100	0	
28S-23	3861	3881	3865	3370	3040	3024	2980	2956	2663	2074	1996	1872	1585	1551	1234	1190	952	557	483	452	375	348	322	281	253	173	0
28S-24	3925	3945	3929	3434	3104	3088	3044	3020	2727	2138	2060	1936	1649	1615	1298	1254	1016	621	547	516	439	412	386	345	317	237	84
28S-25	4160	4178	4162	3667	3337	3321	3277	3253	2960	2371	2293	2169	1882	1848	1531	1487	1249	854	780	749	672	645	619	578	550	470	317

FIG. 1

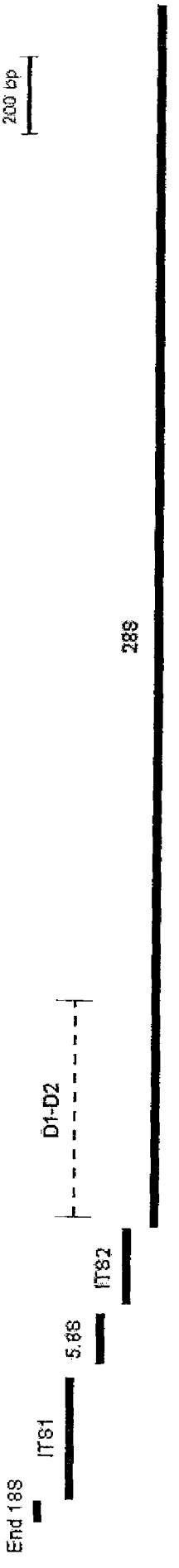

FIG. 2A

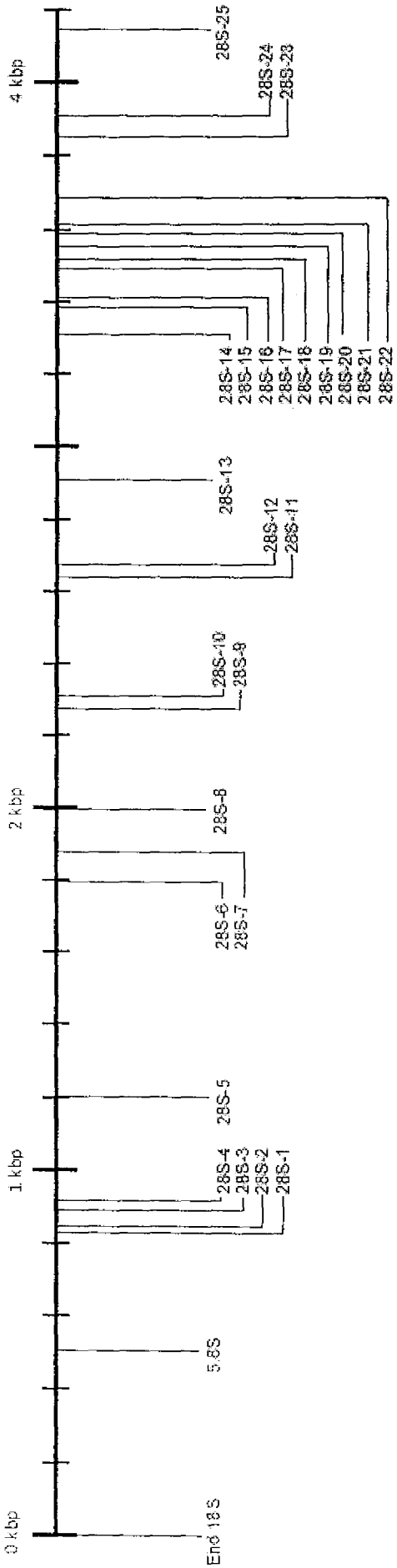
4 kbp
2 kbp
1 kbp
0 kbp
End 18S
5.8S
28S-1
28S-2
28S-3
28S-4
28S-5
28S-6
28S-7
28S-8
28S-9
28S-10
28S-11
28S-12
28S-13
28S-14
28S-15
28S-16
28S-17
28S-18
28S-19
28S-20
28S-21
28S-22
28S-23
28S-24
28S-25

FIG. 2B

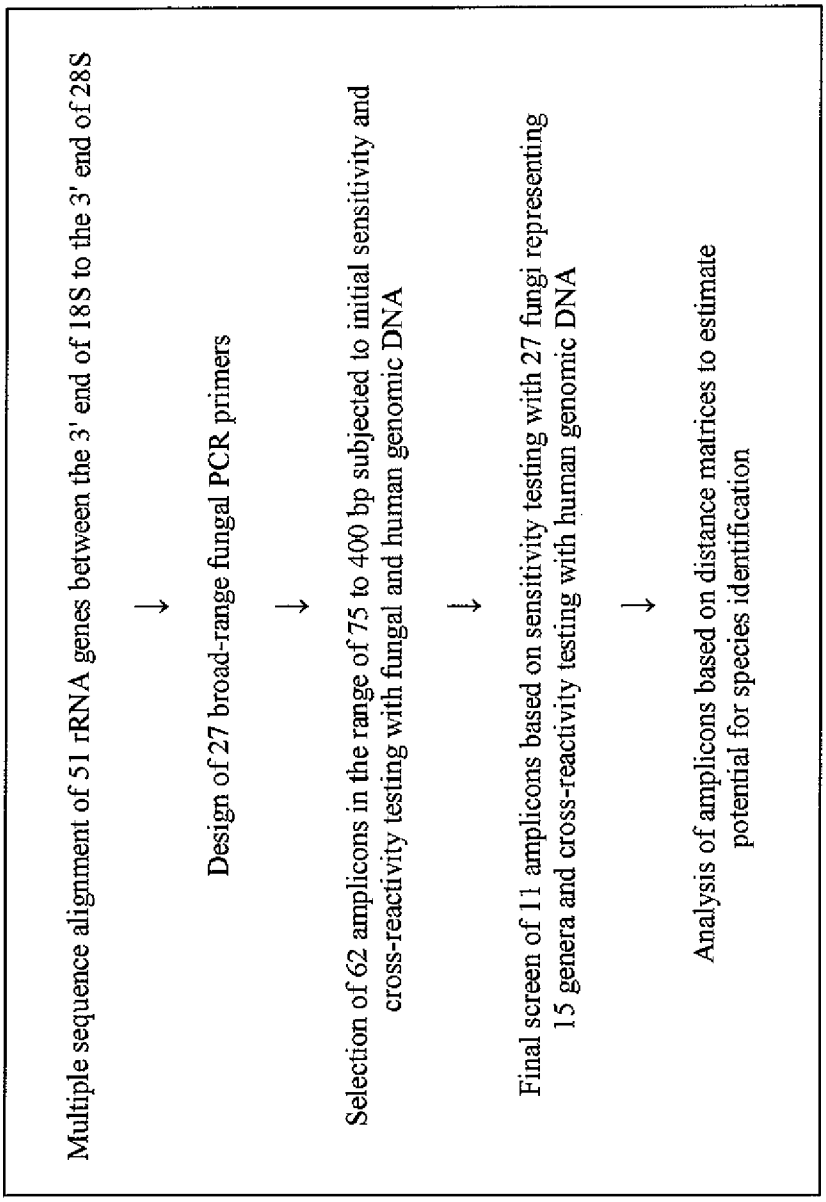
Development of broad-range PCR assays.
Multiple sequence alignment of 51 rRNA genes between the 3' end of 18S to the 3' end of 28S
Design of 27 broad-range fungal PCR primers
Selection of 62 amplicons in the range of 75 to 400 bp subjected to initial sensitivity and cross-reactivity testing with fungal and human genomic DNA
Final screen of 11 amplicons based on sensitivity testing with 27 fungi representing 15 genera and cross-reactivity testing with human genomic DNA
Analysis of amplicons based on distance matrices to estimate potential for species identification

FIG. 3

FIG. 4A

	End18SF — 5.8SR	5.8SF — 28S-1R	5.8SF — 28S-2R	5.8SF — 28S-3R	28S (9F — 12R)	28S (10F — 12R)	28S (12F — 13R)	28S (15F — 22R)	28S (18F — 22R)	28S (18F — 23R)	28S (23F — 25R)
Absidia corymbifera	–[a]	+	–	–	+++	+++	+++	–	++	+++	+
Aspergillus candidus	+++	+++	+	+	+++	+++	+++	+++	+++	+++	+
Aspergillus flavus	+++	+++	+++	+++	+++	+++	++	+++	+++	+++	++
Aspergillus fumigatus	+++	+++	+++	+++	+++	+++	++	+++	+++	+++	+
Aspergillus oryzae	+++	+++	+++	+++	+++	+++	++	+++	+++	+++	++
Aspergillus terreus	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	++
Aspergillus ustus	+++	+++	+++	+++	+++	+++	++	+++	+++	+++	++
Candida albicans	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Candida dubliensis	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Candida glabrata	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Candida guilliermondii	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Candida kefyr	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Candida krusei	+++	+++	+++	+++	+++	+++	++	+++	+++	+++	+++
Candida lusitaniae	+++	+++	+++	+++	+++	+++	+	+++	+++	++	–
Candida tropicalis	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Cryptococcus neoformans	+++	+++	+	++	+++	+++	++	+++	+++	++	–
Cunninghamella berthollotiae	–	++	++	+	+++	+++	+++	–	++	+++	–
Fusarium solani	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	++
Mucor racemosus	+++	++	++	+++	+++	+++	+++	–	+++	+++	+
Paecilomyces variotii	–	+++	+++	+++	+++	+++	++	+++	+++	+++	+
Penicillium notatum	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Rhizomucor miehei	–	++	+	–	+	+++	+	–	++	+++	+
Rhizopus oryzae	+++	+++	+++	+++	+++	+++	+++	–	–	+++	++
Rhodotorula glutinis	+++	+++	+++	+++	–	–	+++	+++	+++	–	+++
Saccharomyces cerevisiae	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
Scedosporium apiospermum	++	+++	+++	+++	+++	+++	++	+++	+++	+++	+
Trichosporon cutaneum	+	+++	++	+	++	+++	+	++	+++	+++	+
Sum of +++	21	23	20	21	24	26	16	21	23	24	10
Sum of ++	1	3	3	1	1	0	8	1	3	2	6
Sum of +	1	1	3	3	1	0	3	0	0	0	8
Sum of –	4	0	1	2	1	1	0	5	1	1	3
Effect of 1 μg human DNA[b]	none	none	none	none	none	none	none	none	none	none	none
Sum[c] of distance matrix[d]	670.9	1057.2	ND	ND	ND	321.3	486.8	69.4	72.7	118.2	418[h]
Sum of distance matrix[e]	106027	117468	ND	ND	ND	84495	63155	17988	9406	28943	75324[g]
Amplicon length[f]	297 ± 70	254 ± 42	ND	ND	ND	339 ± 7	200 ± 25	299 ± 67	157 ± 67	318 ± 80	263 ± 10[g]

a — PCR yield reflected by intensity level of product bands on a 1.5% agarose gel. '+++', '++', '+' indicate decreasing intensity levels and '–' represents no amplification.

b — Cross–reactivity evaluated based on the ability to amplify 10 fg of *A. fumigatus* DNA in the presence of 1 μg of human genomic DNA.

c — The sum of distance matrix was estimated from amplicons of 51 fungal species representing 30 genera. A higher value indicates greater sequence diversity among fungi for the selected amplicon.

d — Distances based on Tajima-Nei algorithm and Neighbor Joining tree building method.

e — Distances based on absolute nucleotide differences and Neighbor Joining tree building method.

f — Mean amplicon lengths ± standard deviation of 51 fungal species representing 30 genera.

g — Distances and amplicon length estimated for 49 sequences due to unavailability of sequence data for some.

ND — Distances not estimated because the amplicon overlaps significantly with another in the Table which has a greater breadth of fungi detected.

FIG. 4A (CONT.)

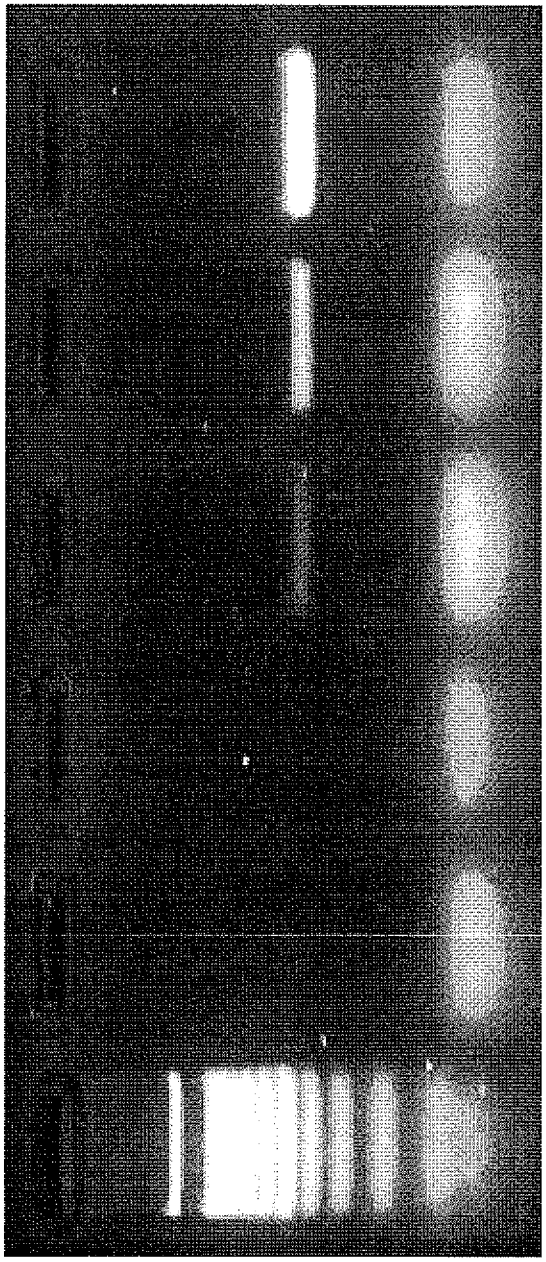

FIG. 4B

FIG. 5A

ITS1(End18SF-5.8SR)	A. fumigatus	A. niger	A. oryzae	A. terreus	C. albicans	C. dubliniensis	C. glabrata	C. guilliermondii	C. kefyr	C. krusei	C. lusitaniae	C. parapsilosis	C. tropicalis	C. immitis	C. posadasi	C. neoformans	C. bertholletiae	F. oxysporum	F. solani	H. capsulatum	M. racemosus	P. variotii	P. brasiliensis	P. chrysogenum	R. miehei	R. oryzae	R. glutinis	S. cerevisiae
Aspergillus niger	26																											
Aspergillus oryzae	39	33																										
Aspergillus terreus	27	16	36																									
Candida albicans	63	67	73	70																								
Candida dubliniensis	64	66	71	69	10																							
Candida glabrata	138	141	141	138	100	100																						
Candida guilliermondii	93	96	94	93	69	70	128																					
Candida kefyr	105	107	109	105	69	66	65	85																				
Candida krusei	74	73	69	75	61	60	73	77	67																			
Candida lusitaniae	58	61	60	63	36	37	43	41	32	39																		
Candida parapsilosis	77	76	79	79	67	67	113	68	84	66	43																	
Candida tropicalis	68	67	66	70	53	53	104	75	73	61	38	68																
Coccidioides immitis	56	67	59	63	71	68	164	93	114	77	60	81	69															
Coccidioides posadasi	54	65	58	63	71	68	166	92	115	76	60	80	71	4														
Cryptococcus neoformans	71	76	77	73	77	70	110	69	75	63	46	61	64	71	72													
Cunninghamella bertholletiae	127	127	124	130	128	123	162	121	130	105	81	110	113	135	133	109												
Fusarium oxysporum	56	60	63	61	65	62	112	77	84	59	51	68	70	58	57	71	125											
Fusarium solani	52	56	57	59	70	69	116	84	93	69	56	77	75	60	59	74	130	25										
Histoplasma capsulatum	48	50	54	54	72	73	163	100	112	75	65	82	73	66	66	73	130	62	64									
Mucor racemosus	114	117	109	115	91	90	168	88	107	83	60	90	87	122	124	58	132	98	103	126								
Paecilomyces variotti	34	39	41	42	67	67	140	98	104	77	59	81	72	54	53	78	132	59	56	51	120							
Paracoccidioides brasiliensis	52	58	61	55	70	71	151	95	111	73	63	73	67	66	66	70	131	66	66	40	124	58						
Penicillium chrysogenum	27	37	33	41	65	62	125	90	98	70	55	76	61	48	47	70	122	60	53	50	110	32	55					
Rhizomucor miehei	112	115	112	112	90	90	164	93	113	91	75	91	100	122	123	62	129	101	112	123	93	121	119	112				
Rhizopus oryzae	113	118	112	114	86	86	163	102	121	82	61	90	83	128	127	70	127	95	101	121	94	123	114	106	103			
Rhodotorula glutinis	83	87	88	87	70	67	123	81	87	67	49	87	73	87	90	47	123	80	80	89	81	89	85	77	74	91		
Saccharomyces cerevisiae	139	144	145	143	99	99	129	119	62	68	38	120	102	152	155	111	157	118	122	149	146	140	146	129	153	157	118	
Scedosporium apiospermum	69	69	71	67	66	63	102	63	63	51	41	56	59	67	69	28	104	61	62	75	56	77	73	66	55	63	41	94

FIG. 5B

ITS2(5.8SF-1R)	A. corymbifera	A. fumigatus	A. niger	A. oryzae	A. terreus	C. albicans	C. dubliniensis	C. glabrata	C. guilliermondii	C. kefyr	C. krusei	C. lusitaniae	C. parapsilosis	C. tropicalis	C. immitis	C. posadasi	C. neoformans	C. bertholletiae	F. oxysporum	F. solani	H. capsulatum	M. racemosus	P. variotii	P. brasiliensis	P. chrysogenum	P. carinii	R. miehei	R. oryzae	R. glutinis	S. cerevisiae
Aspergillus fumigatus	155																													
Aspergillus niger	157	18																												
Aspergillus oryzae	153	17	16																											
Aspergillus terreus	161	16	22	17																										
Candida albicans	137	75	75	79	79																									
Candida dubliniensis	132	78	79	85	82	30																								
Candida glabrata	189	111	108	108	118	105	110																							
Candida guilliermondii	160	106	110	112	112	55	63	123																						
Candida kefyr	213	116	115	118	123	110	114	89	135																					
Candida krusei	139	82	83	80	89	85	87	109	109	117																				
Candida lusitaniae	95	47	45	48	49	55	57	69	68	71	58																			
Candida parapsilosis	128	74	71	73	75	64	63	91	78	92	73	72																		
Candida tropicalis	125	72	72	79	77	39	38	90	38	98	80	50	51																	
Coccidioides immitis	141	48	51	50	44	70	74	116	112	115	90	47	77	69																
Coccidioides posadasi	141	48	53	50	44	71	76	115	111	112	90	47	77	68	2															
Cryptococcus neoformans	153	107	106	104	116	103	113	123	130	133	83	71	87	94	109	108														
Cunninghamella bertholletiae	117	127	128	126	133	103	102	138	127	145	109	80	99	89	116	118	119													
Fusarium oxysporum	144	69	70	71	78	74	78	108	98	101	87	42	64	65	76	75	94	114												
Fusarium solani	146	76	76	76	84	83	89	120	110	118	88	53	74	72	83	82	105	129	33											
Histoplasma capsulatum	160	34	38	36	41	80	83	119	111	129	85	48	74	77	44	46	107	131	75	83										
Mucor racemosus	107	99	100	98	108	92	95	122	109	131	92	73	82	79	89	90	99	97	96	108	101									
Paecilomyces variotti	158	28	32	34	32	87	91	113	118	116	89	45	75	83	55	55	115	127	79	85	40	100								
Paracoccidioides brasiliensis	185	38	41	38	40	80	84	132	111	143	83	39	69	78	49	48	105	143	79	79	24	114	39							
Penicillium chrysogenum	148	74	77	79	81	16	44	115	72	117	90	67	82	50	75	76	114	114	72	90	83	97	87	85						
Pneumocystis carinii	151	102	101	106	108	93	95	77	106	83	98	61	79	81	97	96	98	113	90	101	106	100	103	123	103					
Rhizomucor miehei	200	144	142	142	154	119	122	177	147	189	134	82	71	102	129	130	140	151	126	138	139	125	138	162	138	144				
Rhizopus oryzae	134	110	113	109	120	110	105	125	115	129	111	77	89	97	111	108	113	113	101	120	113	98	108	130	118	107	138			
Rhodotorula glutinis	162	103	100	99	109	98	101	137	117	137	98	72	99	83	98	96	109	132	96	106	102	101	97	121	105	111	160	94		
Saccharomyces cerevisiae	170	120	119	118	125	96	97	107	117	120	109	68	86	82	111	110	124	139	113	129	122	124	121	137	106	100	175	90	98	
Scedosporium apiospermum	172	77	79	81	85	108	112	137	137	144	105	63	91	95	83	83	121	145	63	64	85	128	90	83	115	119	165	139	127	153

FIG. 5C

28S(10F-12R)	A. corymbifera	A. fumigatus	A. niger	A. oryzae	A. terreus	C. albicans	C. dubliniensis	C. glabrata	C. guilliermondii	C. kefyr	C. krusei	C. lusitaniae	C. parapsilosis	C. tropicalis	C. immitis	C. posadasi	C. neoformans	C. bertholletiae	F. oxysporum	F. solani	H. capsulatum	M. racemosus	P. variotii	P. brasiliensis	P. chrysogenum	P. carinii	R. miehei	R. oryzae	R. glutinis	S. cerevisiae
Aspergillus fumigatus	94																													
Aspergillus niger	92	9																												
Aspergillus oryzae	92	2	9																											
Aspergillus terreus	94	4	9	4																										
Candida albicans	93	64	65	63	60																									
Candida dubliniensis	94	64	65	63	60	1																								
Candida glabrata	102	59	62	58	55	26	26																							
Candida guilliermondii	89	65	66	64	61	12	13	29																						
Candida kefyr	97	57	60	56	55	27	27	19	27																					
Candida krusei	99	56	59	55	53	33	33	41	38	41																				
Candida lusitaniae	103	60	62	60	61	48	48	59	55	60	42																			
Candida parapsilosis	94	64	65	63	60	4	3	28	13	27	36	51																		
Candida tropicalis	93	68	69	67	64	11	10	34	16	31	42	56	8																	
Coccidioides immitis	93	16	17	16	12	64	63	58	64	57	57	64	63	63																
Coccidioides posadasi	93	16	17	16	12	64	63	58	64	57	57	64	63	63	0															
Cryptococcus neoformans	89	71	72	70	73	75	74	69	66	67	78	86	73	72	71	71														
Cunninghamella bertholletiae	114	110	105	110	108	111	110	117	106	117	116	117	108	105	107	107	107													
Fusarium oxysporum	88	40	44	39	39	70	70	62	66	60	64	74	68	72	43	43	75	111												
Fusarium solani	88	38	41	37	37	73	73	65	69	63	62	73	72	76	40	40	75	112	8											
Histoplasma capsulatum	94	12	14	11	13	66	65	60	67	58	59	63	65	69	14	14	71	114	41	41										
Mucor racemosus	78	89	88	88	89	89	88	93	84	91	95	101	87	86	90	90	84	86	81	83	86									
Paecilomyces variotii	95	15	16	15	13	65	64	59	65	58	59	66	64	69	11	11	73	113	45	43	9	86								
Paracoccidioides brasiliensis	91	14	13	12	14	62	61	56	64	53	56	64	61	65	13	13	72	109	41	38	7	83	10							
Penicillium chrysogenum	95	8	13	7	8	60	60	60	61	57	53	59	60	64	20	20	73	111	44	42	16	90	19	17						
Pneumocystis carinii	90	58	61	56	56	52	53	50	47	52	59	75	54	58	61	61	53	114	65	63	58	85	59	56	57					
Rhizomucor miehei	84	86	88	86	86	97	97	102	93	100	106	111	95	95	81	81	96	109	88	94	87	94	86	84	83	86				
Rhizopus oryzae	63	77	75	75	76	77	76	82	75	80	82	91	76	77	72	72	76	90	71	73	77	33	75	70	77	74	78			
Rhodotorula glutinis	100	81	86	79	81	78	79	74	78	82	85	91	80	85	85	85	71	124	87	90	81	101	84	80	78	65	101	92		
Saccharomyces cerevisiae	100	60	63	59	56	24	24	11	25	15	47	60	26	28	57	57	65	120	64	67	61	95	60	57	62	49	99	82	80	
Scedosporium apiospermum	98	48	45	46	46	78	78	72	76	68	68	79	77	81	47	47	82	121	30	30	46	95	48	43	49	67	101	86	94	75

FIG. 5D

28S(12F-13R)	A. conymbifera	A. fumigatus	A. niger	A. oryzae	A. terreus	C. albicans	C. dubliniensis	C. glabrata	C. guilliermondi	C. kefyr	C. krusei	C. lusitaniae	C. parapsilosis	C. tropicalis	C. immitis	C. posadasi	C. neoformans	C. bertholletiae	F. oxysporum	F. solani	H. capsulatum	M. racemosus	P. vanottii	P. brasiliensis	P. chrysogenum	P. carinii	R. miehei	R. oryzae	R. glutinis	S. cerevisiae
Aspergillus fumigatus	55																													
Aspergillus niger	56	4																												
Aspergillus oryzae	56	5	1																											
Aspergillus terreus	57	7	7	6																										
Candida albicans	54	53	53	52	51																									
Candida dubliniensis	55	51	51	50	49	12																								
Candida glabrata	56	63	62	61	61	44	39																							
Candida guilliermondii	60	55	53	52	54	26	27	48																						
Candida kefyr	52	65	64	63	63	44	40	21	48																					
Candida krusei	52	51	50	49	47	48	45	48	50	45																				
Candida lusitaniae	27	41	41	41	43	29	27	29	37	30	23																			
Candida parapsilosis	54	53	53	52	51	24	20	47	32	47	50	29																		
Candida tropicalis	55	49	49	48	47	14	10	40	28	37	46	29	24																	
Coccidioides immitis	55	17	17	18	17	53	53	60	56	64	48	41	55	51																
Coccidioides posadasi	55	17	17	18	17	53	53	60	56	64	48	41	55	51	0															
Cryptococcus neoformans	59	53	53	52	51	64	61	69	63	74	58	37	59	65	47	47														
Cunninghamella bertholletiae	62	75	75	74	76	67	68	70	68	70	61	41	68	69	71	71	59													
Fusarium oxysporum	54	29	29	28	29	53	52	58	59	65	44	40	58	53	25	25	45	71												
Fusarium solani	56	28	29	28	28	57	56	59	60	63	43	41	62	53	30	30	50	71	12											
Histoplasma capsulatum	52	24	25	24	24	58	55	61	59	65	46	39	58	55	17	17	46	74	24	29										
Mucor racemosus	58	68	69	69	70	62	62	69	62	71	60	43	62	61	66	66	59	65	68	68										
Paecilomyces variotti	55	19	17	16	19	45	46	58	50	58	51	42	47	44	16	16	44	71	27	32	22	62								
Paracoccidioides brasiliensis	51	22	23	22	20	55	55	60	57	64	47	40	58	53	15	15	46	73	23	27	6	67	18							
Penicillium chrysogenum	54	13	10	9	12	52	50	60	54	62	47	40	52	46	17	17	52	70	30	31	24	65	19	22						
Pneumocystis carinii	59	55	54	53	55	60	55	64	53	69	61	48	55	59	51	51	43	69	49	53	52	58	45	52	52					
Rhizomucor miehei	45	36	36	35	37	39	35	43	36	46	42	29	34	35	39	39	36	41	39	37	39	40	37	40	37	24				
Rhizopus oryzae	57	66	65	65	62	61	62	67	63	71	53	42	62	61	63	63	59	53	63	65	64	32	59	61	64	62	43			
Rhodotorula glutinis	64	54	55	56	57	72	68	74	73	77	53	41	70	70	49	49	56	81	52	53	48	79	51	47	56	73	46	79		
Saccharomyces cerevisiae	50	64	62	61	62	45	39	19	49	14	44	24	47	40	61	61	72	69	62	63	64	68	58	63	59	69	43	67	74	
Scedosporium apiospermum	58	34	35	34	32	68	66	67	63	69	52	45	69	66	28	28	50	73	23	25	26	67	32	24	33	48	39	66	59	68

FIG. 5E

28S(15F-22R)	*A. corymbifera*	*A. fumigatus*	*A. niger*	*A. oryzae*	*A. terreus*	*C. albicans*	*C. dubliniensis*	*C. glabrata*	*C. guilliermondii*	*C. kefyr*	*C. krusei*	*C. lusitaniae*	*C. parapsilosis*	*C. tropicalis*	*C. immitis*	*C. posadasi*	*C. neoformans*	*C. bertholletiae*	*F. oxysporum*	*F. solani*	*H. capsulatum*	*M. racemosus*	*P. variotii*	*P. brasiliensis*	*P. chrysogenum*	*P. carinii*	*R. miehei*	*R. oryzae*	*R. glutinis*	*S. cerevisiae*
Aspergillus fumigatus	18																													
Aspergillus niger	18	0																												
Aspergillus oryzae	18	0	0																											
Aspergillus terreus	18	0	0	0																										
Candida albicans	17	6	6	6	6																									
Candida dubliniensis	17	6	6	6	6	0																								
Candida glabrata	18	7	7	7	7	1	1																							
Candida guilliermondii	17	6	6	6	6	0	0	1																						
Candida kefyr	18	9	9	9	9	3	3	2	3																					
Candida krusei	19	8	8	8	8	2	2	1	2	3																				
Candida lusitaniae	20	9	9	9	9	3	3	2	3	4	3																			
Candida parapsilosis	17	6	6	6	6	0	0	1	0	3	2	3																		
Candida tropicalis	20	9	9	9	9	4	3	4	4	6	5	6	4																	
Coccidioides immitis	17	1	1	1	1	5	5	6	5	8	7	8	5	8																
Coccidioides posadasi	17	1	1	1	1	5	5	6	5	8	7	8	5	8	0															
Cryptococcus neoformans	18	6	6	6	6	7	7	8	7	10	9	10	7	10	5	5														
Cunninghamella bertholletiae	10	22	22	22	22	23	23	24	23	24	25	24	23	26	21	21	24													
Fusarium oxysporum	20	5	5	5	5	9	9	10	9	12	11	10	9	12	4	4	9	22												
Fusarium solani	11	3	3	3	3	7	7	7	7	9	8	7	7	7	3	3	5	10	0											
Histoplasma capsulatum	17	1	1	1	1	5	5	6	5	8	7	8	5	8	0	0	5	21	4	3										
Mucor racemosus	16	15	15	15	15	15	15	16	15	16	17	18	15	18	14	14	16	16	17	8	14									
Paecilomyces variotti	20	5	5	5	5	9	9	10	9	12	11	12	9	12	4	4	9	24	8	4	4	18								
Paracoccidioides brasiliensis	17	1	1	1	1	5	5	6	5	8	7	8	5	8	0	0	5	21	4	3	0	14	4							
Penicillium chrysogenum	17	1	1	1	1	6	6	7	6	9	8	9	6	9	2	2	5	21	6	3	2	15	6	2						
Pneumocystis carinii	27	18	18	18	18	20	20	21	20	20	22	21	20	23	17	17	19	29	19	8	17	20	21	17	18					
Rhizomucor miehei	24	32	32	32	32	31	31	32	31	31	33	30	31	34	31	31	33	25	32	19	31	26	32	31	32	34				
Rhizopus oryzae	16	13	13	13	13	13	13	14	13	14	15	16	13	16	12	12	14	18	15	8	12	2	16	12	13	20	28			
Rhodotorula glutinis	13	7	7	7	7	8	8	9	8	11	10	11	8	11	6	6	7	21	10	4	6	13	10	6	6	18	29	13		
Saccharomyces cerevisiae	20	9	9	9	9	3	3	2	3	4	3	0	3	6	8	8	10	24	10	7	8	18	12	8	9	21	30	16	11	
Scedosporium apiospermum	56	45	44	44	44	46	46	45	46	47	45	45	46	49	43	43	44	60	43	41	43	55	47	43	45	58	69	53	47	45

FIG. 5F

28S(18F-22R)	A. corymbifera	A. fumigatus	A. niger	A. oryzae	A. terreus	C. albicans	C. dubliniensis	C. glabrata	C. guilliermondii	C. kefyr	C. krusei	C. lusitaniae	C. parapsilosis	C. tropicalis	C. immitis	C. posadasi	C. neoformans	C. bertholletiae	F. oxysporum	F. solani	H. capsulatum	M. racemosus	P. variotii	P. brasiliensis	P. chrysogenum	P. carinii	R. miehei	R. oryzae	R. glutinis	S. cerevisiae
Aspergillus fumigatus	9																													
Aspergillus niger	9	0																												
Aspergillus oryzae	9	0	0																											
Aspergillus terreus	9	0	0	0																										
Candida albicans	9	4	4	4	4																									
Candida dubliniensis	9	4	4	4	4	0																								
Candida glabrata	9	4	4	4	4	0	0																							
Candida guilliermondii	9	4	4	4	4	0	0	0																						
Candida kefyr	9	6	6	6	6	2	2	2	2																					
Candida krusei	9	6	6	6	6	2	2	2	2	0																				
Candida lusitaniae	9	4	4	4	4	0	0	0	0	2	2																			
Candida parapsilosis	9	4	4	4	4	0	0	0	0	2	2	0																		
Candida tropicalis	9	4	4	4	4	0	0	0	0	2	2	0	0																	
Coccidioides immitis	9	0	0	0	0	4	4	4	4	6	6	4	4	4																
Coccidioides posadasi	9	0	0	0	0	4	4	4	4	6	6	4	4	4	0															
Cryptococcus neoformans	9	2	2	2	2	4	4	4	4	6	6	4	4	4	2	2														
Cunninghamella bertholletiae	3	8	8	8	8	10	10	10	10	10	10	10	10	10	8	8	10													
Fusarium oxysporum	11	3	3	3	3	7	7	7	7	9	9	7	7	7	3	3	5	10												
Fusarium solani	11	3	3	3	3	7	7	7	7	9	9	7	7	7	3	3	5	10	0											
Histoplasma capsulatum	9	0	0	0	0	4	4	4	4	6	6	4	4	4	0	0	2	8	3	3										
Mucor racemosus	7	6	6	6	6	8	8	8	8	8	8	8	8	8	6	6	8	6	8	8	6									
Paecilomyces variotti	10	1	1	1	1	5	5	5	5	7	7	5	5	5	1	1	3	9	4	4	1	7								
Paracoccidioides brasiliensis	9	0	0	0	0	4	4	4	4	6	6	4	4	4	0	0	2	8	3	3	0	6	1							
Penicillium chrysogenum	9	0	0	0	0	4	4	4	4	6	6	4	4	4	0	0	2	8	3	3	0	6	1	0						
Pneumocystis carinii	12	5	5	5	5	9	9	9	9	8	8	9	9	9	5	5	7	11	8	8	5	8	6	5	5					
Rhizomucor miehei	13	17	17	17	17	18	18	18	18	17	17	18	18	18	17	17	17	13	19	19	17	16	18	17	17	18				
Rhizopus oryzae	7	6	6	6	6	8	8	8	8	8	8	8	8	8	6	6	8	6	8	8	6	0	7	6	6	8	16			
Rhodotorula glutinis	10	3	3	3	3	5	5	5	5	7	7	5	5	5	3	3	3	11	4	4	3	9	4	3	3	8	19	9		
Saccharomyces cerevisiae	9	4	4	4	4	0	0	0	0	2	2	0	0	0	4	4	4	10	7	7	4	8	5	4	4	9	18	8	5	
Scedosporium apiospermum	35	32	32	32	32	35	35	35	36	34	34	35	35	35	32	32	32	35	30	30	32	39	31	32	32	34	37	32	33	35

FIG. 5G

28S(18F-23R)	A. corymbifera	A. fumigatus	A. niger	A. oryzae	A. terreus	C. albicans	C. dubliniensis	C. glabrata	C. guilliermondii	C. kefyr	C. krusei	C. lusitaniae	C. parapsilosis	C. tropicalis	C. immitis	C. posadasi	C. neoformans	C. bertholletiae	F. oxysporum	F. solani	H. capsulatum	M. racemosus	P. variotii	P. brasiliensis	P. chrysogenum	P. carinii	R. miehei	R. oryzae	R. glutinis	S. cerevisiae
Aspergillus fumigatus	23																													
Aspergillus niger	23	0																												
Aspergillus oryzae	23	0	0																											
Aspergillus terreus	23	0	0	0																										
Candida albicans	18	13	13	13	13																									
Candida dubliniensis	18	13	13	13	13	0																								
Candida glabrata	21	14	14	14	14	3	3																							
Candida guilliermondii	19	14	14	14	14	1	1	2																						
Candida kefyr	21	18	18	18	18	5	5	4	4																					
Candida krusei	17	14	14	14	14	3	3	6	4	4																				
Candida lusitaniae	19	15	15	15	15	4	4	6	4	8	5																			
Candida parapsilosis	18	13	13	13	13	0	0	3	1	5	3	4																		
Candida tropicalis	17	12	12	12	12	1	1	4	2	6	2	3	1																	
Coccidioides immitis	23	1	1	1	1	13	13	14	14	18	14	15	13	12																
Coccidioides posadasi	23	0	0	0	0	13	13	14	14	18	14	15	13	12	1															
Cryptococcus neoformans	23	17	17	17	17	15	15	15	14	16	16	14	15	14	16	17														
Cunninghamella bertholletiae	8	22	22	22	22	18	18	21	19	21	19	22	18	19	23	22	25													
Fusarium oxysporum	26	11	11	11	11	13	13	14	14	18	16	16	13	14	12	11	15	25												
Fusarium solani	27	8	8	8	8	16	16	17	17	21	17	17	16	15	9	8	16	28	3											
Histoplasma capsulatum	23	0	0	0	0	13	13	14	14	18	14	15	13	12	1	0	17	22	11	8										
Mucor racemosus	12	22	22	22	22	17	17	20	18	20	18	20	17	18	22	22	22	10	23	26	22									
Paecilomyces variotti	24	1	1	1	1	14	14	15	15	19	15	16	14	13	2	1	18	23	12	9	1	23								
Paracoccidioides brasiliensis	21	1	1	1	1	12	12	13	13	17	13	14	12	11	1	1	16	20	11	8	1	20	2							
Penicillium chrysogenum	16	8	8	8	8	6	6	9	7	11	7	7	6	5	7	8	13	16	12	13	8	15	9	8						
Pneumocystis carinii	27	13	13	13	13	14	14	17	15	16	14	18	14	15	13	13	21	25	15	14	13	23	14	13	13					
Rhizomucor miehei	11	21	21	21	21	19	19	22	20	22	18	22	19	18	21	21	25	17	25	26	21	19	22	20	17	24				
Rhizopus oryzae	13	23	23	23	23	18	18	21	19	21	19	21	18	19	23	23	25	13	24	27	23	5	24	21	16	24	20			
Rhodotorula glutinis	26	12	12	12	12	10	10	11	9	13	13	13	10	11	11	12	14	22	16	15	12	22	13	12	10	15	26	25		
Saccharomyces cerevisiae	21	14	14	14	14	3	3	0	2	4	6	6	3	4	14	14	15	21	14	17	14	20	15	13	9	17	22	21	11	
Scedosporium apiospermum	51	40	40	40	40	45	45	46	47	49	45	47	45	44	40	40	45	53	35	32	40	53	39	40	44	43	51	54	45	46

FIG. 5H

28S(23F-25R)	A. fumigatus	A. niger	A. oryzae	A. terreus	C. albicans	C. dubliniensis	C. glabrata	C. guilliermondii	C. kefyr	C. krusei	C. lusitaniae	C. parapsilosis	C. tropicalis	C. immitis	C. posadasi	C. neoformans	F. oxysporum	F. solani	H. capsulatum	M. racemosus	P. variotti	P. brasiliensis	P. chrysogenum	P. carinii	R. oryzae	S. cerevisiae
Aspergillus niger	11																									
Aspergillus oryzae	10	8																								
Aspergillus terreus	8	12	10																							
Candida albicans	65	64	64	61																						
Candida dubliniensis	65	64	64	60	1																					
Candida glabrata	62	61	60	58	21	19																				
Candida guilliermondii	73	72	71	68	21	19	31																			
Candida kefyr	70	67	68	64	27	24	20	32																		
Candida krusei	66	68	63	64	35	33	39	38	40																	
Candida lusitaniae	65	69	67	66	37	38	48	45	56	49																
Candida parapsilosis	71	68	70	66	7	6	24	22	28	40	42															
Candida tropicalis	66	65	65	62	7	6	25	22	30	38	40	12														
Coccidioides immitis	24	27	25	21	61	62	64	67	68	68	63	68	63													
Coccidioides posadasi	25	28	26	22	60	61	63	66	67	67	62	67	62	1												
Cryptococcus neoformans	88	88	89	84	71	71	72	68	74	77	79	73	73	80	79											
Fusarium oxysporum	70	73	73	71	69	68	73	73	76	73	77	71	70	76	75	91										
Fusarium solani	69	72	72	70	68	67	72	74	76	72	74	70	71	75	74	91	4									
Histoplasma capsulatum	21	27	24	21	66	66	64	72	71	64	68	72	68	20	21	82	74	73								
Mucor racemosus	108	109	108	108	94	94	100	94	95	92	94	93	94	106	105	96	104	102	106							
Paecilomyces variotti	8	14	14	11	61	61	58	69	66	66	62	67	62	21	22	84	68	67	18	109						
Paracoccidioides brasiliensis	18	22	19	17	59	60	60	66	66	59	63	66	62	11	12	82	70	69	9	106	16					
Penicillium chrysogenum	13	15	15	12	62	62	61	70	67	69	65	68	63	21	22	82	69	68	22	108	5	19				
Pneumocystis carinii	90	88	90	86	63	62	70	68	69	73	74	61	62	83	82	76	73	75	88	91	90	86	88			
Rhizopus oryzae	101	103	99	99	87	86	91	89	91	87	85	88	86	98	97	85	99	99	95	30	101	98	100	83		
Saccharomyces cerevisiae	67	64	65	63	30	27	15	34	19	43	54	31	28	67	66	75	72	73	71	101	63	63	66	68	96	
Scedosporium apiospermum	57	60	61	61	68	69	67	75	73	67	73	67	71	69	68	89	33	35	66	99	61	62	62	70	95	76

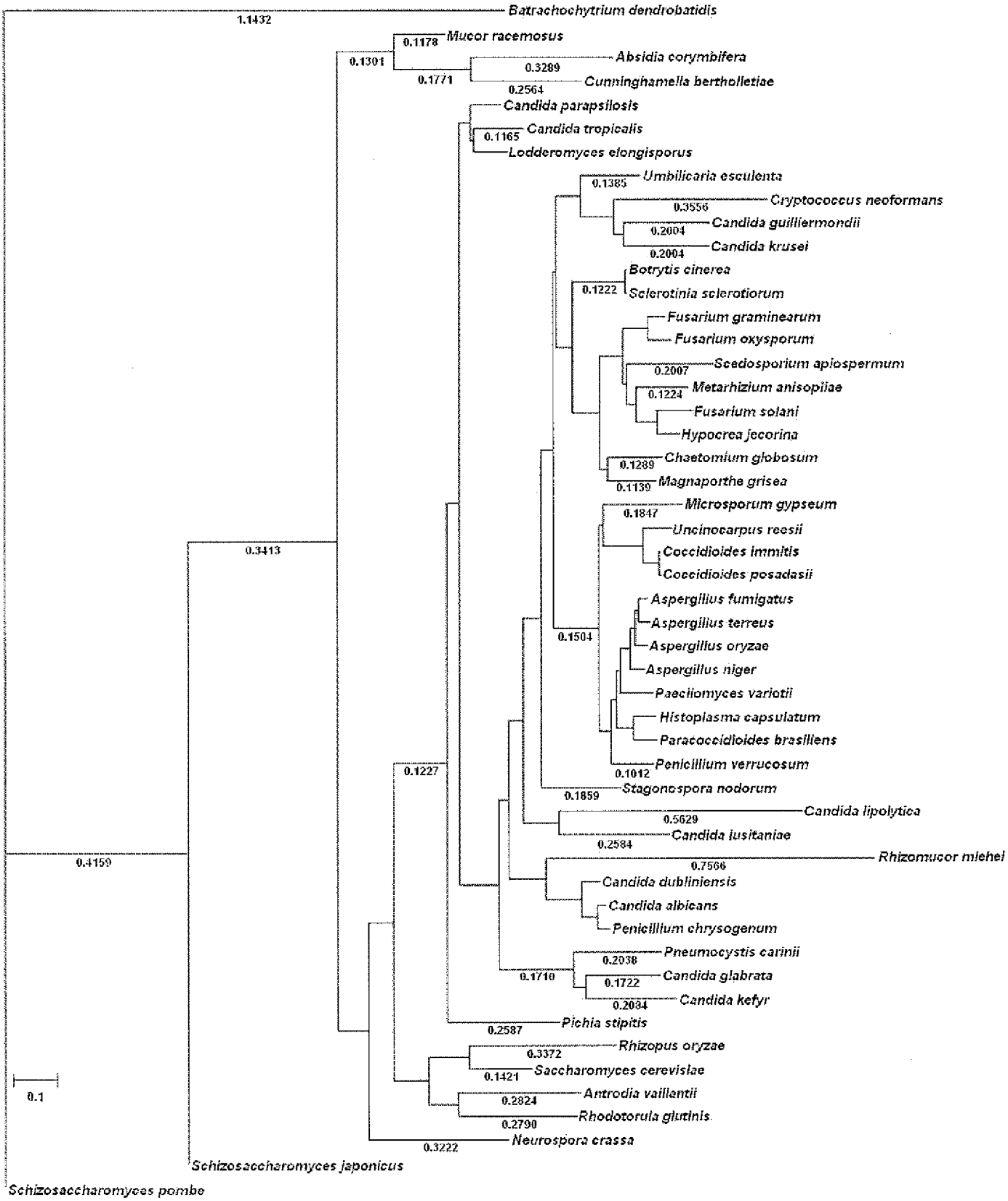
Batrachochytrium dendrobatidis
1.1432
Mucor racemosus
0.1178
Absidia corymbifera
0.1301
0.3289
Cunninghamella bertholletiae
0.1771
0.2564
Candida parapsilosis
Candida tropicalis
0.1165
Lodderomyces elongisporus
Umbilicaria esculenta
0.1385
Cryptococcus neoformans
0.3556
Candida guilliermondii
0.2004
Candida krusei
0.2004
Botrytis cinerea
0.1222
Sclerotinia sclerotiorum
Fusarium graminearum
Fusarium oxysporum
Scedosporium apiospermum
0.2007
Metarhizium anisopliae
0.1224
Fusarium solani
Hypocrea jecorina
Chaetomium globosum
0.1289
Magnaporthe grisea
0.1139
Microsporum gypseum
0.1847
Uncinocarpus reesii
Coccidioides immitis
Coccidioides posadasii
0.3413
Aspergillus fumigatus
Aspergillus terreus
Aspergillus oryzae
Aspergillus niger
0.1504
Paeciliomyces variotii
Histoplasma capsulatum
Paracoccidioides brasiliens
Penicillium verrucosum
0.1012
0.1227
Stagonospora nodorum
0.1859
Candida lipolytica
0.5629
Candida lusitaniae
0.2584
0.4159
Rhizomucor miehei
0.7566
Candida dubliniensis
Candida albicans
Penicillium chrysogenum
Pneumocystis carinii
0.2038
0.1710
Candida glabrata
0.1722
Candida kefyr
0.2084
Pichia stipitis
0.2587
Rhizopus oryzae
0.3372
Saccharomyces cerevisiae
0.1421
Antrodia vaillantii
0.2824
Rhodotorula glutinis
0.2790
Neurospora crassa
0.3222
0.1
Schizosaccharomyces japonicus
Schizosaccharomyces pombe

FIG. 6

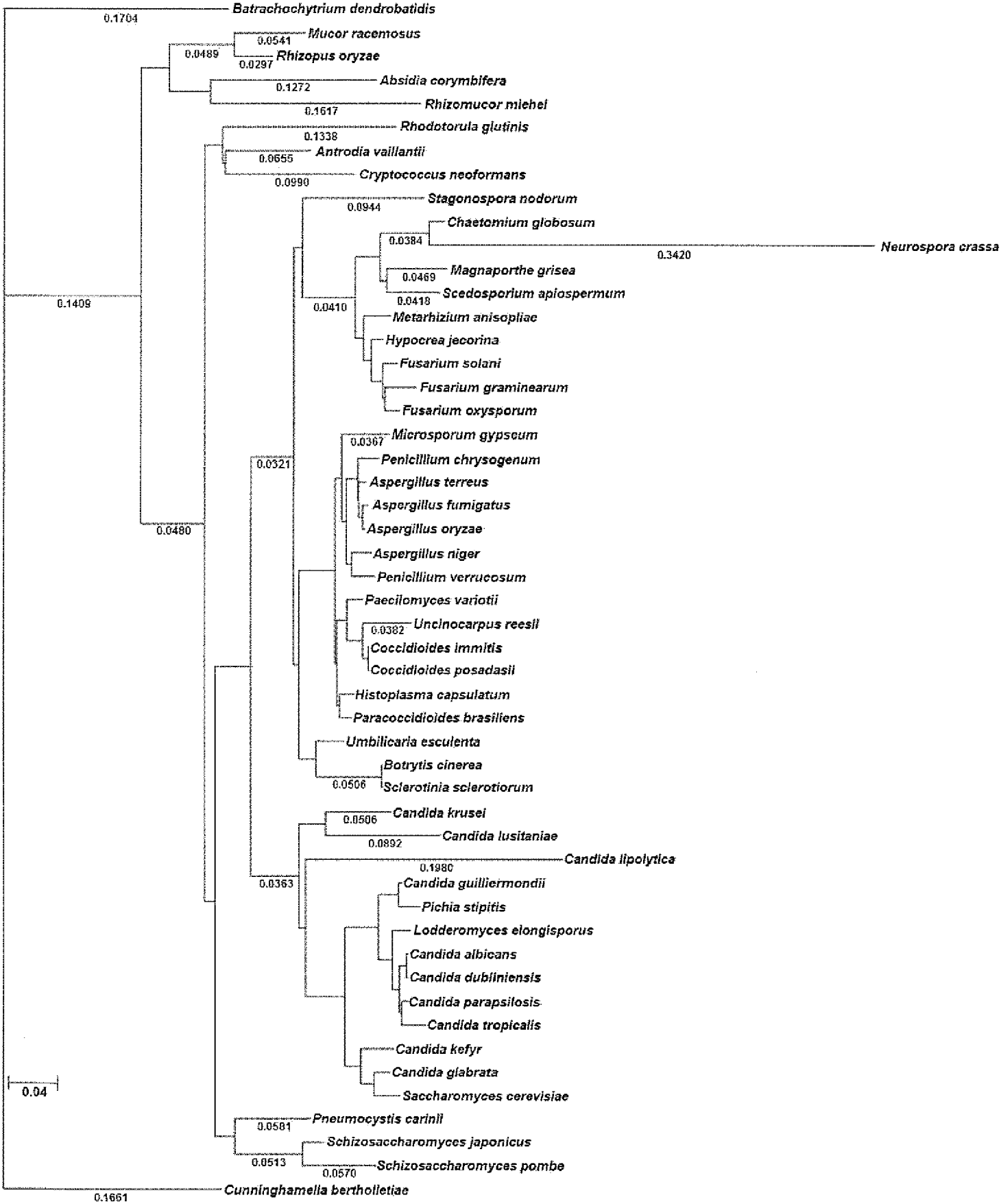
Batrachochytrium dendrobatidis
0.1704
Mucor racemosus
0.0541
0.0489
Rhizopus oryzae
0.0297
Absidia corymbifera
0.1272
Rhizomucor miehei
0.1617
Rhodotorula glutinis
0.1338
Antrodia vaillantii
0.0655
Cryptococcus neoformans
0.0990
Stagonospora nodorum
0.0944
Chaetomium globosum
0.0384
Neurospora crassa
0.3420
Magnaporthe grisea
0.0469
Scedosporium apiospermum
0.0418
0.0410
Metarhizium anisopliae
Hypocrea jecorina
Fusarium solani
Fusarium graminearum
Fusarium oxysporum
0.1409
Microsporum gypseum
0.0367
0.0321
Penicillium chrysogenum
Aspergillus terreus
Aspergillus fumigatus
Aspergillus oryzae
0.0480
Aspergillus niger
Penicillium verrucosum
Paecilomyces variotii
Uncinocarpus reesii
0.0382
Coccidioides immitis
Coccidioides posadasii
Histoplasma capsulatum
Paracoccidioides brasiliens
Umbilicaria esculenta
Botrytis cinerea
0.0506
Sclerotinia sclerotiorum
Candida krusei
0.0506
Candida lusitaniae
0.0892
Candida lipolytica
0.1980
0.0363
Candida guilliermondii
Pichia stipitis
Lodderomyces elongisporus
Candida albicans
Candida dubliniensis
Candida parapsilosis
Candida tropicalis
Candida kefyr
Candida glabrata
Saccharomyces cerevisiae
0.04
Pneumocystis carinii
0.0581
Schizosaccharomyces japonicus
0.0513
Schizosaccharomyces pombe
0.0570
Cunninghamella bertholletiae
0.1661

FIG. 7

Figure 8

Absidia corymbifera rRNA gene (SEQ ID NO: 55)

ATTAACTATCCCCAAAGGTGTTTATTCTTCTCGTGCTAAACCATGATGTACGAAAAAGTTAGTTGTTAACTTAAAAACA
ACTCTTGGCAATGGATCTCTTGGTTCTCGCATCGATGAAGAGCGTAGCAAAGTGCGATAATTATTGCGACTTGCATTCA
TAGCGAATCATCGAGTTCTCGAACGCATCTTGCGCCTAGTAGTCAATCTACTAGGCACAGTTGTTTCAGTATCTGCAAC
TACCAATCAGTTCAACTTGGTTCTTTGAACCTAAGCGAGCTGGAAATGGGCTTGTGTTGATGGCATTCAGTTGCTGTCA
TGGCCTTAAATACATTTAGTCCTAGGCAATTGGCTTTAGTCATTTGCCGGATGTAGACTCTAGAGTGCCTGAAGAGCA
ACGACTTGGTTAGTGAGTTCATAATTCCAAGTCAATCAGTCTCTTCTTGAACTAGGTCTTAATCTTTACGGACTAGTGA
GAGGATCTAACTTGGGTCTTCTCTTGAACAAACTCACATCTAGATCTGAAATCAACTGAGATCACCCGCTGAACTTAA
GCATATCAATAAGCGGAGGAAAAGAAAATAACCATGGATTCCCCTAGTAACGGCGAGTGAAGAGGGAAAAGCTCAAA
GTTGGAACCTGGCTGCCCTAGGCAGTCCGGATTGTAAACTAAAGAGCGTGATTCCAGGCAAGCCGGTTGACCAAGTCC
TTTGGAATGAGGCGCCACTGAGGGTGAGAGCCCCGTAAGTCGACTGAGCATTTGTCTTTTGTGTTTCGCGTTCAAAGA
GTCAGGTTGTTTGGGAATGCAGCCTAAAGCTGGTGGTAAATCCCACCTAAAGCTAAATACAGGCGAGAGACCGATAG
CGAACAAGTACCGTGAGGGAAAGATGAAAAGAACTTTGAAAAGAGAGTTAAACAGTATGTGAAATTGCCAAGAGGGA
AGCATTTGGAGTTAGATTGACTAGGAGTTAATCAGCTTGGTCTTTGGACTGGGTGTACTTGACTTCTTACAGTCTGCCA
ATAGCAGTTAGTCCTAGTGGAAAAAACCAGAGGGAAGGTAGTCCTTCGGGATGTTTATAGACCTTTGGAAAATACACT
GGGATTGACTGAGGAATGCAGTAGATGCCACTAAGGCTTCGTCTAGTGGGTGCTAGGCAAAGGTACTTGGTATTTTCA
GCTTGCTGATGTGCTAGGTTACTCGAGTCTAGTCGCCTACTAGAACTGTAATCTACTTTGGTTATTGGCTTAATGACTC
TAAATGGCCCGTCTTGAAACACGGACCAAGGAGTCCACCACAGGTGCGAGTATTAGGGTGGCAAACCCATAATGCGC
AATGAAAGTGACACTTTAAGCTACCAAGGTTCCTTCGGGGGCCTGCAGTAGCCTCAGGCATGGACGTTTTATACTGAA
ATGACCTAGAGAAAGCACTTGTGATGGGACCCGAAAGATGGTGAACTATGCTTGAGTAGGATGAAGCCAGAGGAAAC
TCTGGTGGAGGTCCGAAGCGGTTCTGACGTGCAAATCGATCGTCAAACTTGAGCATAGGGGCGAAAGACTAATCGAA
CCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAACTCAAAGGCAGTTTTACGTGGTAAAGCGAA
TGATTAGAGGCCTTGGGGACGAAATGTCCTTAACCTATTCTCAAACTTTAAATATGTAAGATGTCCTTCTTTCTTAGTT
GAAGTTGGACCATCGAATGTCGAGTTTCTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAAC
GCAAAGTTAAAGCGCCGGAATACTCGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGG
CCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCT
TAAGCGAGTTGCTTATACTTTGCCCATAGGGTAAAAGCGATGCTCTATGGAGTAGGCAGGCGTGGAGGTCTAGTTGCG
AAGCTCTGACCGTAAGGTTGAGTGGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAGTGAGAACC
TTGAAGACTGAAGTGGAGAAGGGTTCCTCGAGAACATTAGTTGGTCGAGGGTTAGTCGATCCTAAGAGATAGGGAAGT
TCCGTTTTATCAAAGTGCTCAATTTACTTGGGCCGCCTATCGAAAGGGAAACTGGTTAAAATTCCAGTACTGGGACAC
AGGTCTTTTGCGGCAACGCAAATGAACTTGGCGACGCTGGCATGGATCCCGAGAAGAGTTCTCTTTTCTTTTTAACAGT
TTATCTTTGACCATGAAATCAGTTTATCTGGAGAAATGGTTAAAGTGCTGGAAGAGTCCTACACTTTTAGTAGGATTCG
GTGCATCCATTACAGTCCTTGAAAAGCCAGGGGAAACTTATAGACTTTGTGCCTAGTCGTACCCATAACCGCAGCAGG
TCTCCTAGGTGTTAAGCCTCTAGTTGATGGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGA
TAAGGATTGGCTCTAAGGGCTGGGTAGATTTGAGCCTAGGTCTTCGGTGAGTTGGGACTTGGTGCTGGGGCTTTCGGG
CTCTGGTGCTAGGATCTAGCTTGCCACTTGGCCTAGGAAGTTCGGTCTACAATTAACAGCCAACTTAGAACTGGTACG
GACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGTCAGAAAGTGATTTTGACGCAATGTGATTTCT
GCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAA
GGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATC
TAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTT
TGCATTGTGAAAAGACATAGAGGGTGTAGCATATGAGGGAGACTTCGGTCGCCAGTGAAATACCTCAACCTCTATTGT
TTTTTTACTTAAATATTCAAGTGGGACTGGGTAGCAATACCTATGTTCTAGTATTAAGCCTACATTGTTAGGTGACCCA
CGATATTGACATTGTCAAGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACAATAACGCAGGTGTCCTAAGGGGG
ACTCAGTGAGAACAGAAATCTCACGTAGAGCAAAAGGGCAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAA
CCATGAAAGTGTGGCCTATCGATCCTTTAGTTSCTYRGRATTTRAGSCTAGAGGTGCCAGAAAAGTTACCACAGGGATA
ACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACTGAAG
CAGAATTCAGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTA
GTTTTACCCTACTGATGGAATTGGTGTCTCAACAGTAATTGAAGTTAGTACGAGAGGAACCCTTCATTCAGATAATTG
GTATTTGCGCCTGGTTGAAAGGCCAATGGCGCGAAGCTACCATCTGCTGGATAATGGCTGA

Figure 9

Cunninghamella bertholletiae rRNA gene (SEQ ID NO: 56)

CGATTGAATGGTCATAGTGAGCATGTGGGATCTTTGAAGGCTGGTTGGCAACAACCGGCTTTTGAGGAGAACTATGGC
AAACTAGATTATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACATATTG
GGTCAAAAGAATAGTTTGAAAAAGGCTATTTTTTTTTGACTTAAAAAACTTATCCACAGTGTGGGAAATGTCTTCTAAC
GCTTGTGCCTGGTTCAGTCTAGTGCTGCCACTTGAGTTTATCCTTAGATCAAGGGATCTTTGGGTAGTTGTTCATTATTT
TCTCTCTCTTTTTAGGGGGGGGGAGATTAATGATGGGCACCTCTTGTAAAGGGGATAAGATTACTTTTATTATACTAAA
TTTTACTGAACTGATAGACCATAAATCTATGGTTGTTTTTTATTATAATTAAAAAAAAAAAAACAACTTTCAGCAATGGA
TCTCTCGGCTTTCGTATCGATGAAGAACGCAGCAAATCGCGATATGTAATGTGATCTGCCTATAGTGAATCATCAAAT
CTTTGAACGCATCTTGCACCTTATGGTATTCCATAAGGTACGTCTGTTTCAGTACCACTAATAAATCTCTCTCTATCCTT
GATGATAGAAAAAAAGAGATAAATTATTACTGGTCCTGGTGATTCTTTTTTTTTTTTTTATTAAAAAGAACCACTCTCG
GCCTAAATATAAGGCTCGACTTTTTTTTACCAGATCTTGCATCTAGTAAAAACCTAGTCGGCTTTAATAGATTTTTATT
TTCTATTAAGTTTATAGCCATTCTTATATTTTTTAAAATCTTGGCCTGAAATCAGATGGGACTACCCGCTGAACTTAAG
CATATCAATAAGCGGAGGAAAAGAAAATAACAATGATTCCCCTAGTARCGGCGAGTGAAGAGGGAAAAGCTCAAAGT
TGGAACCTGGTAGGCATAGCTTACCCGGATTGTAAACTAAAGTTTTCGAGTCGTTTAGTCAGCCAGGTAAATAAGTCC
TCTGGAAAGGGGCGACATAGAGGGTGAAATCCCCGTCTTTGGCCTGAGTTTTGATTAGGCGTTTGGCTTGGAAACGAA
GAGTCAGGTTGTTTGGGAATGCAGCCTAAAATGGGAGGTAAATCTCTCCTAAAGCTAAATATTGACGAAAGACCGATA
GCGAACAAGTACCGTGAGGGAAAGATGAAAAGCACTTTGAAAAGAGGGTCAAAAAGTACGTGAAATTGCTGAAAGGG
AACCGTATGAAATCAGATCTACTGGTAGGTAATCAATCTTTCCTTTGGGAAGGATGCACTTGCCTACTATGTATGCCAG
CGACATTTTGGTTGGGAGGAAAAAAATAAAGGAAATGTAGCTTAGGTTTCGGCTTAGGTGTTATAGTCCTTTATAAAA
TACTCTCGGCTGGAATGAGGAACGCAGCAAACCGTAAGGCGAAGATTTCAGGCGCTTAGAGGGAATAATTAGAGAAT
TTCTGCTTCGGGTGGTGCTTTGATTATTACCTTTAACACGCTTGGAGTTCTTTTAATTTGCTTAGGTTGTTGGCTTAATG
ATTTTATATGACCCGTCTTGAAACACGGACCAAGGAGTCCACCATAGGCGCGAGTCTTTGGGTGTAAAAACCCATGGG
CGGAAGGAAATTGACTAAGATACCAAGGCGCAAGCTGGCAGTATCCCCCGGCGTAGACGTTTTTATACTGAAATGACT
GAGGGCAAGCGCTTATGATGGGACCCGAAAGATGGTGAACTATACTTGAATAGGGTAAAGCCAGAGGAAACTCTGGT
GGAAGCTCGCAGCGATTCTGACGTGCAAATCGATCGTCAAATTTGAGTATAGGGGCGAAAGACTAATCGAACCATCTA
GTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTAGGCAGTTTTATGAGGTAAAGCGAATGATTAG
AGGCCTAGGGGGCTTATTGCCCTTTACCTATTCTCAAACTTTAAATATGTAAGACGTTTGGCTTGCTTAATTGAAGTCA
AACATATGAATGCAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGTAAAGT
TAAGGTGCCCAAATTCACGCTCATCAGACACCAGAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGA
AGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTTAAGCGT
GATACCTATACTTTACCGTCAAAGTAAAAGCGAAGCTTTGACGAGTAGGCAGGCGTGGAGGTTTTGTATAGAAGCCTT
GGGCGTGAGCTCGGGTGAAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCTAATGAGAATTTTGAAGA
CTGAAGTGGAGAAAGGTTCCTAGAGAACAGTAGTTGGTCTAGGGTTAGTCGCTCCTAAGGCACAGGGAAGTTCTGTCA
AATGCAGATCCATTTTATGGGTCCAGGTGCCGAAAGGGAAACTGGTTAATATTCCAGTACTAGGATAGGGGGTTCTAA
TATGGTAACATAACGGATCTTGGGGACATTGGTATGAAGCCCAGAAAGAGTTAACTTTTCTTTCTTACGGTCTCTTAAG
TTGATATTCCTTGGAAACGGTTTAGCCGGAGCAAAGGTGTATCGGCCGGTAAAGCATGATTTTTTATGATCATGTCTGG
AGCCTTCATAACGATCCTTGAAAACCCAAGGGACATATATGGCCTTCCTACCTAGGCGTACTCATAACCGCAGCAGGT
CTCCAAGGTTAACAGCCTCTAGTTGATAGAATAATGTAGGTAAGGGAAGTCGGCAAATTAGATCCGTAACTTCGGGAT
AAGGATTGGCTCTAAGGGTTAGGTAGGAAACGTATTAGATGGATGAAGAGGTGAGTCTGGAGAAGGCTGGTTGGGGC
AACCTGACTGGCTTTTTTTGGGCAATCCTCTTGTACCGTCTAATGGCGGCCTACAATAATAACCACTTAGAACTGGTAC
GGACAAAGGGAATCTGACTGTCTAATTAAAACATAGCATTGTGATAGTCAGAAAGTGATTTTGACACAATGTGATTTC
TGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTA
AGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTA
TCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAG
TTTGACATTGTGAAAAGACATAGAGGGTGTAGAATAAGTGGGAGCTCCGGCGCCAGTGAAATACCACTACCTCTATTG
TTTTTTTACTTAGATAATTATAAGGGATTAGGTGGCAACACCTACTTTCTAGACAGAATCCACTTCGTGTGGAGACCCT
CGTTATTGACATTGTCAAGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACAATAACGCAGGTGTCCTAAGGGGG
GCTCAGCGAGACGAGAAATTTCGCGTAGAGTAAAAGGGCAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAA
CCATGAAAGTGTGGCCTATCGATCCTTTAGTTGCTAAAGATTTTAGCCTAGAGGTGCCAGAAAAGTTACCACAGGGAT
AACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACTGAA
GCAGAATTCAGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTT
AGTTTTACCCTACTGATGTTAATGGGTATCGTAACAGTAATTGAAGTTAGTACGAGAGGAACCCTTCATTCAGATAATT
GGTATTTGCGGCTGGTTGTCCAGCCAATGCCGCGAAGCTACCGT

Figure 10

Fusarium solani rRNA gene (SEQ ID NO: 57)

TAAGAGGAAGTAAAAGTCGTAACAAGGTTTCGTTGGTGAACCAGCGGAGGGATCATTACCGAGTTATACAACTCATCA
ACCCTGTGAACATACCTATAACGTTGCCTCGGCGGGAACAGACGGCCCCGTAACACGGGCCGCCCCCGCCAGAGGACC
CCCTAACTCTGTTTCTATAATGTTTCTTCTGAGTAAACAAGCAAATAAATTAAAACTTTCAACAACGGATCTCTTGGCTC
TGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAAC
GCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCCCCCGGGCCTGGCGT
TGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAAATACAGTGGCGGTCCCGCCGCAGCTTCCATTGC
GTAGTAGCTAACACCTCGCAACTGGAGAGCGGCGCGGCCACGCCGTAAAACACCCAACTTCTGAATGTTGACCTCGAA
TCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCCAGTAAC
GGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCTCTCGGGCCCGAGTTGTAATTTGTAGAGGATGCTTTTGGT
GAGGTGCCTTCCGAGTTCCCTGGAACGGGACGCCATAGAGGGTGAGAGCCCCGTCTGGTTGGACACCGATCCTCTGTA
AAGCTTCTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCTAAATGGGAGGTATATGTCTTCTAAAGCTAAATACCGGC
CAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGAACTTTGAAAAGAGAGTTAAAAAGTACGTGAAA
TTGTTGAAAGGGAAGCGCTTGTGACCAGACTTGGGCTTGGTTGATCATCCGGGGTTCTCCCCGGTGCACTCTTCCGGCT
CAGGCCAGCATCAGTTCGCCCTGGGGGATAAAGGCTTCGGGAATGTGGCTCTCTCCGGGGAGTGTTATAGCCCGCTGCG
TAATACCCTGTGGCGGACTGAGGTTCGCGCATTCGCAAGGATGCTGGCGTAATGGTCATCAGTGACCCGTCTTGAAACA
CGGACCAAGGAGTCGTCTTCGTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGAAATGAAAGTGAACGCAGGTGAGA
GCTTCGGCGCATCATCGACCGATCCTGATGTTATCGGATGGATTTGAGTAAGAGCATACGGGGCCGGACCCGAAAGAA
GGTGAACTATGCCTGTGTAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGAT
CGTCAAACATGGGCATGGGGGCGAAAGACTAATCGAACCTTCTAGTAGCTGGTTTCCGCCGAAGTTTCCCTCAGGATAG
CAGTGTTGAACTCAGTTTTATGAGGTAAAGCGAATGATTAGGGACTCGGGGGCGCTATTTAGCCTTCATCCATTCTCAA
ACTTTAAATATGTAAGAAGCCCTTGTTGCTTAATTGAACGTGGGCATTCGAATGAATCAACACTAGTGGGCCATTTTTG
GTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCAGAGTAGACGCTCATCAGACACCACAA
AAGGTGTTAGTACATCTTGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGACTGTGTAACAACTCACCT
GCCGAATGTACTAGCCCTGAAAATGGATGGCGCTCAAGCGTCTCACCCATACCTCGCCCTCAGGGTAGAAACGATGCC
CTGAGGAGTAGGCGGACGTGGAGGTCAGTGACGAAGCCTAGGGCGTGAGCCCGGGTTGAACGGCCTCTAGTGCAGATC
TTGGTGGTAGTAGCAAATACTTCAATGAGAACTTGAAGGACCGAAGTGGGGAAAGGTTCCATGTGAACAGCGGTTGGA
CATGGGTTAGTCGATCCTAAGCCATAGGGAAGTTCCGTTTCAAAGGCGCACTATGCGCCGTCNTGGCGAAAGGGGAGC
CGGTCAATATTCCGGCACCTGGATGTGGGTTTTGCGCGGCAACGCAACTGAACGCGGAGACGACGGCGGGGGCCCCGG
GCAGAGTTCTCTTTTCTTCTTAACAGTCTCTCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAATGGCTGGAAGAGC
CCAGCACCTCTGCTGGGTCCGGTGCGCTCTCGACGTCCCTTGAAAATCCGCGGGAAGAAATAATTCTCACGCCAGGTCG
TACTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTGGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAA
TAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGCACGCAGGGCCTTGGGCGGACGCCATGGGGGCAGG
CTGCTTCTAGCCGGGCAACCGGCCGGCGGCGGCCAGCACCCGTGCGCTGATGCCCTTGGCAGGCTTCGGCCGTCCGGC
GTGCGGTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGG
CCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGTAATTCAACCAAGCGCGG
GTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGAT
TAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGG
AAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGAGGTGTAGAATAGGTGGGAGCTTCG
GCGCGGTGAAATACCACTACTCCTATTGTTTTTTTACTTATTCAATGAAGCGGGGCTGGATTTTCGTCCAACTTCTGGTT
TTAAGGTCCTTCGCGGGCCGACCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAC
CATAACGCAGGTGTCCTAAGGGGGTCTCATGGAGAACAGAAATCTCCAGTAGAGCAAAAGGGCAAAAGTCCCCTTGAT
TTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGACATTTGAGGCTAGAGGT
GCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTGATCCTTCGATG
TCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGT
TTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCTCGCCGCAATGGTAATTCAGCTTAGTACGAGAGGAA
CCGCTGATTCAGATAATTGGTTTTTGCGGCTGTCCGACCGGGCAGTGCCGCGAAGCTACCATCTGCTGGATAATGGCTG
AACGCCTCTAAGTCAGAATCCATGCCAGAACGCGGTGATACCGCCCGCACGTACAGATGGACAAGAATAGGCTTCGGC
TTAGCGTCTTAGCAGGCGATTCTTCCGCGGCGCACGAAGCGCGTCGTGGTATTTCGCGTATTGTAATTTCAACACGAGC
GGGGTCAAATCCTTTGCAGACGACTTAGCTGTGCGAAACGGTCCTGTAAGCAGTAGAGTAGCCTG

Figure 11

Mucor racemosus rRNA gene (SEQ ID NO: 58)

TAGGTGAACCTGCGGAAGGATCATTAAATAATCAATAATCTTGGCTTGTCCATTATTATCTATTTACTGTGAACTGTATT
ATTATTTGACATTTGAGGGATGTTCCAATGTTATAAGGATAGACATTGGAAATGTTAACCGAGTCATAATCAGGTTTAG
GCCTGGTATCCTATTATTATTTACCAAATGAATTCAGAATTAATATTGTAACATAGACCTAAAAAATCTATAAAACAAC
TTTTAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCAAAGTGCGATAACTAGTGTGAATTGCATATTCA
GTGAATCATCGAGTCTTTGAACGCAACTTGCGCTCATTGGTATTCCAATGAGCACGCCTGTTTCAGTATCAAAACAAAC
CCTCTATCCAACTTTTGTTGTATAGGATTATTGGGGGCCTCTCGATCTGTATAGATCTTGAAATCCCTGAAATTTACTAA
GGCCTGAACTTGTTTAAATGCCTGAACTTTTTTTTAATATAAAGGAAAGCTCTTGTAATTGACTTTGATGGGGCCTCCCA
AATAAATCTTTTTTAAATTTGATCTGAAATCAGGCGGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAA
GAAAATAACAATGATTTCCCTAGTAACGGCGAGTGAAGAGGAAAGAGCTCAAAGTTGGAACCTGTTTGGCTTAGCTAA
ACCGGATTGTAAACTGTAGAAACATTTTCCAGATACACTAGACAAAAAAGTCCTTTGGAACAGGGCATCATAGAGGGT
GAGAATCCCGTCTTTGGTCTAAGTAGTTGTCTATTGTGATATGTTTTCAAAGAGTCAGGTTGTTTGGGAATGCAGCCTAA
ATTGGGTGGTAAATCTCACCTAAAGCTAAATATTTGCGAGAGACCGATAGCGAACAAGTACCGTGAGGGAAAGATGAA
AAGAACTTTGAAAAGAGAGTTAAACAGTATGTGAAATTGTTAAAAGGGAACCGTTTGGAGCCAGATTGGCTTGATTGT
AATCAACCTAGAATTCGTTTTGGGTGCACTTGCAGTCTATGCCTGCCAACGACAGTTTGATTTGGAGGAAAAAATTAAT
AGGAATGTGGCCTTTCGAGGTGTTATAGCCTATTATCATACTCTGGATTGGACTGAGGAACGCAGCGAATGCCTTTAGG
CAAGATTGCTGGGCGCTTTCCCTAATAAATGTTAGAATTTCTGCTTCGGGTGGTGCTAATGTTTAAAGGAGGAACCCGC
TTAGTATATTTTTTATTCGCTTAGGTTTGTTGGCTTAATGACTCTAAATGACCCGTCTTGAAACACGGACCAAGGAGTCC
ACCATAAGTGCAAGTATTTGGGTGCCAAACCCATATGCGTAAGGAAACTGATTGATACGAAATCGCGAGATGGCAGTA
TCACCCGGCGCTGACGTTTTATACTGAATTGACCGAGGTAAAGCACTTATGATGGGACCCGAAAGATGGTGAACTATGC
CTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGATTCTGACGTGCAAATCGATCGTCAAATTTGG
GTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAAAAACTTAA
AAGCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGACGAAATGTCCTTAACCTATTCTCAACTTTAAATAT
GTAAGACGACCTGTTTGCTTAATTGAAGCAGGTCATTGAATGTGAGTTTTTAGTGGGCCATTTTTGGTAAGCAGAACTG
GCGATGCGGGATGAACCGAACGGAAAGTTAAGGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGTTCA
TCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCTGCCGAATGAACTAG
CCCTGAAAATGGATGGCGCTTAAGCGTGTTACCCATACTTTCCCGTTATTGTAAAAGCGAAGCAATAACGAGTAGGCAG
GCGTGGAGGTTTTTATAAACTGTTAAGAAGCTCTTGGTGTGAACCGGAGTGAAACAGCCTCTAGTGCAGATCTTGGTGG
TAGTAGCCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGAGAAGGTTCCTGGAGAACATTATTTGGTCCCGGGG
TAGTCGATCCTAGAGGTAGGGAAGTTCCGTTATTTCAAAGTGATCAATTTTGATCCGCCTATCGAAAGGGAAACAGTTT
AATATTACTGTACTAGGACGAGGATTTTCTGCGGCAACGCAAATGAACTTGGAGACATCAGTGTGGGTCCCGGGAAGA
GTTATCTTTTCTTTTTAACAACTTTGTTGTAGACCTTGAAATCTGTTTAGCAGGAGAAAAGGTTTACCGGTTGGTAGAGC
ATAGTACTTTTTGCTATGTCCGGTGCATTCACAACGATCCTTGAAAATCCAAGGGAAAGAATAATTTTCTCGCCTAGTC
GTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAA
ATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGTAGATATGGACTTTTGGTATGGTTGATTTCTAGGC
GATTTCAAATGATTTCGGTTGTTTGATTTTGCTCGGAGATCTTCGTTAACCAAGAGAGCCCAGTTTACGTTTAACAACCA
ACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTG
ACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTA
ACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACT
GTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTG
AGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGAGGGTGTAGCATAAGTGGGAGCTTCGGCGCCAGTGAAATACC
ACTACCTTTATCGTTTTTTTACTTAAATAATTAAGTGGGATTGAGTCGCAAGACTCACCTTCTAGTATTAAGCATCTTCG
GATGTGACCCACGTTATTGACATTGTCAAGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGT
CCTAAGGGGGACTCAACGAGAACAGAAATCTCGTGTAGAATAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGT
GAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGAATCTCAAGATTTGAGGCTAGAGGTGCCAGAAAAGTTAC
CACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATC
ATACTGAAGCAGAATTCAGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGA
GACAGGTTAGTTTTACCCTACTGATGGTATTGGTATCGTAACAGTAATTGAAGTTAGTACGAGAGGAACCCTTCATTCA
GATAATTGGTATTTGCGGCTGGTTGAAAGGCCAATGCCGCGAAGCTACCATCTGCTGGATAATGGCTGAACGCCTCTAA
GTCAGAATCCATGCTGAAAACGATACTACTGTGTTTTGATTGTACCAGATGAGTACTAATAAAGCTTCGGCTTGAAAAC
CTTTACTTGTGAGCTAGGCTTGGTAACGGAAATGTTGCTAGGTCTACTTGCTAATGATAATGCTAATACATCAAAATGA
TAAATCGCATGCAGACGACATGAAATGGACGGGGTATTGTAAGTACTAGAGTAGCCTG

Figure 12

Paecilomyces variotii rRNA gene (SEQ ID NO: 59)

CGATTGAATGGCTCAGTGAGGCCTTCGGACTGGCTCAGGGGGGTTGGCAACGACCGCCCAGAGCCGGAAAGTTGGTCA
AACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGA
GGGTCCCTCGGGGCCCAACCTCCCATCCGTGTTGTCCTGACACCTGTTGCTTCGGCGGGCCCGCCGTGGTTCACGCCCC
GGCCGCCGGGGGGTTCACGCCCCCGGGCCCGCGCCCGCCGAAGACCCCTGGAACGCTGCCTGGAAGGTTGCCGTCTGA
GTATACAATCAATCAATTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGAT
AAGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGCATTCCGGGGGGCAT
GCCTGTCCGAGCGTCATTGCTAACCCTCCAGCCCGGCTGGTGTGTTGGGCCGCCGTCCCCCCTCCCCGGGGGACGGGCC
CGAAAGGCAGCGGCGGCGTCGCGTCCGGTCCTCGAGCGTATGGGGCTCTGTCACACGCTTCAGTAGAACCGGCCGGCT
TGCTGGCCATCACCTATATTTTTCTCTTAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA
AGCGGAGGAAAAGAAACCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAATTTGAAATCTGG
CCCCTCCGGGGTCCGAGTTGTAATTTGCAGAGGATGCTTCGGGCGCGGTCCCCGTCTAAGTACCCTGGAACGGGTCGTC
ATAGAGGGTGAGAATCCCGTCTGGGACGGGTGGCCGTGTCCGTGTGAAGCTCCTTCGACGAGTCGAGTTGTTTGGGAAT
GCAGCTCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCG
AAAGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCGACCAGACTC
GCCCGCGGGGGTTCAGCCGGTACTCGTACCGGTGTACTCCCCCGGGGGCGGGCCAGCGTCGGTTTGGGCGGTCGGTCA
AAGGCCTCCGGAATGTGTCGCCCCCCGGGGCGTCTTATAGCCGGAGGTGCAATGCGGCCAGCCTGGACCGAGGAACGC
GCTTCGGCTCGGACGCTGGCGTAATGGTCGTAAGCGGCCCGTCTTGAAACACGGACCAAGGAGTCTAACATCTACGCG
AGTGTTCGGGTGTCAAACCCGTCCGCGCAGTGAAAGCGAACGGAGGTGGGAACCCCCCCCGGGGTGCACCATCGACCG
ATCCTGATGTCTTCGGATGGATTTGAGTAAGAGCGTAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGG
GCGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGG
CGAAAGACTAATCGAACCATCTGGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGTTTTCAGTTTTAT
GAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGCC
CTTGTTGCTTAGTTGAACGTGGGCATTTGAATGTATCGTTACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCG
GGATGAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACA
GCCCGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACGGGCCGAATGAACTAGCCCTGAAA
ATGGATGGCGCTCAAGCGTGCTACCCATACCTCGCCGTCGGGGTAGAAACGATGCCCCGACGAGTAGGCAGGCGTGGA
GGTCCGTGACGAAGCCTTGGGAGTGATCCCGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTC
AAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGA
CATAGGGAAATTCCGTTTGAAAGCGCGCCCTCGTGCGCCGTTCGTCGAAAGGGAAGCCGGTTAATATTCCGGCACCTGG
ATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCGGGGGTCCTGGGAAGAGTTCTCTTTTCTTCTTGA
CGGCCTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTCCATGGCCGGCAGAGCCCCGCACCTTTGCGGGGTCCGG
TGCACTCCCGACGACCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCT
CCAAGGTGAAAAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAA
GGATTGGCTCTAAGGATCGGGTACGTTGGGCCTTGGGGGGAAGCCCCCGGAGCAGGAGGGCACTAGCCGGGCAACCG
GCCGGCGCCCTCCAGCATCGGGCGGTGGACGCCCTTGGCAGGCCTCGGCCGTCCGGCGTACGCTTAACGATCAACTTA
GAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCA
ATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTAT
GACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCC
TATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTT
GACTCTAGTTTGACATTGTGAAAAGACATATGGGGGTGTAGAATAGGTGGGAGCTCCGGCGCCAGTGAAATACCACTAC
CTTTATCGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTCACCGCCCAACTTCTGGCGTTAAGGTCCTTCGCGGGC
CGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCATAACGCAGGTGTCCT
AAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGA
ATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCAC
AGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATA
CCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGAC
AGGTTAGTTTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTTAGTACGAGAGGAACCGTTGATTCAGATAA
TTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGCCGGATTATGGCTGAACGCCTCTAAGTCAG
AATCCGTGCCGGAACGCGGCGATTTCGCCCCGCACGTCGTAGTTGGATACGAATAGGCCTTCGGGCCATGCACCTCAGC
AGGCTGGCGACGGCCCCCGGGGAGAAACCCCCGGGGGCTGGCTGGCGGATTGCAATGTCACCTCGCGCGGGGATAGAT
CCTCTGCAGACGACTGAAGTGACCAAGCGGGTCGTGTAAGCGGTCAAGTACT

Figure 13

Penicillium chrysogenum rRNA gene (SEQ ID NO: 60)

GACCCCCCAGAGCCGARAACTTGGTCAAACTCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA
ACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTATTTTACCTTGTTGCTTCGG
CGGGCCCGCCTTAACTGGCCGCCGGGGGGCTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCT
GAAGATTGTAGTCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGA
ACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTG
GTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATC
AATACGACTTGGGTTTGCTTGAAAGACGGTAGTGGTAAGGCGGGATCGCTTTGACAATGGCTTAGGTCTAACCAAAAA
CATTGCTTGCGGCGGTAACGTCCACCACGTATATCTTCAAACTTTGACCTCAAATCAGGTAGGACTACCCGCTGAACTT
AAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAA
ATTTGAAATCTGGCGTCTTTGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGCCCGGCTCTTGTCTATGTTCCCT
GGAACGGGACGTCATAGAGGGTGAGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGACGAGTC
GAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATATTGGCCGGAGACCGATAGCGCAC
AAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGAAAGGGAAGCGC
TTGCGACCAGACTCGCTCGCGGGGTTCAGCCGGCATTCGTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTG
GGCGGTCGGTCAAAGGCCCTCGGAAGGTAACGCCCCTAGGGGCGTCTTATAGCCGAGGGTGCAATGCGACCTGCCTAG
ACCGAGGAACGCGCTTCGGCTCGGACGCTGGCATAATGGTCGTAAACGACCCGTCTTGAAACACGGACCAAGGAGTCT
AACATCTACGCGAGTGTTCGGGTGTCAACCCGTGCGCGAAGTGAAAGCGAACGGAGGTGGGAACCCTCACGGGTGCAC
CATCGACCGATCCTGAAGTCTTCGGATGGATTTGAGTAAGAGCGTAGCTGTTGGGACCCGAAAGATGGTGAACTATGC
CTGAATAGGGCGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGG
GTATAGGGGCGAAAGACTAATCGAACCATCTGGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGCGA
ATTCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATA
TGTAAGAAGCCCTTGTTGCTTAATTGAACGTGGGCATTAGAATGATGCGTTACTAGTGGGCCATTTTTGGTAAGCAGAA
CTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGT
TCATCTAGACAGCCCGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACGGGCCGAATGAAC
TAGCCCTGAAAATGGATGGCGCTTAAGCGTGTTACCCATACCTCGCCGTCAGGGTAGAAACGATGCCCTGACGAGTAG
GCAGGCGTGGGGGTCCGTGACGAAGCCTTGGGAGTGATCCCGGGTCGAACGGCCCCTAGTGCAGATCTTGGTGGTAGT
AGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGT
CGATCCTAAGGCATAGGGAAGTTCCGTTTGAAAGGCGCCCTCGTGCGCCGTGTGCCCGAAAGGGAAGCCGGTTAACATT
CCGGCACCTAGATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCGGGGGTCCTGGGAAGAGTTCTC
TTTTCTTCTTGACAGCCTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTCTATGGCTGGCAGAGCGCCGCACTTTT
GCGGCGTCCGGTGCGCCCCCGACGACCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCTAGGTCGTACTCATAAC
CGCAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAGTCGGCAAAATGGATCCGTAA
CTTCGGGATAAGGATTGGCTCTAAGGGTCGGGCTCGCTGGGCCTTGGGGGGAACCTCCTGGAGCAGTAGGGCACTAGC
CGGGCAACCGGCCGGCGCCCCGCAGCACCGGGTTGGGGACGCCCTTGGCAGGCTTCGGCCGTCCGGCGGGCGATTAAC
GACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGG
TGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGG
GAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTC
CCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAGGGGAACGGGCCTGGCAGAATCAGCGGGGAAAGAAGACCC
TGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATATGGGGTGTAGAATAGGTGGGAGCTCCGGCGCCAGTGAA
ATACCACTACCTTTATCGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTCACCGCCCATCTTCTAGCGTTAAGGTC
CTTCGCGGGCCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACAACAACG
CAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATT
TTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAA
AAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTCGATGTCGGCTCT
TCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCG
TCGTGAGACAGGTTAGTTTTACCCTACTGATGAAGGTTGTCGCAACAGTAATTGAACTTAGTACGAGAGGAACCGTTCA
TTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGCCGGATTATGGCTGAACGCCT
CTAAGTCAGAATCCGTGCCGGAACGCGGCGATTTCGCCCCGCACGTCGTAGTTGGATACGAATAGGCCTTCGGGCCAT
GCACCTCAGCAGGCTGGCGACGGCTCCCGGGGAGAAACCCTCGGGAGCTGGCTAGCGGATTGTAATGTCACCTCGCGC
GGGGATAGATCCTCTGCAGACGACTGAAGTGACCAAGCGGGTCGTGTAAGCGGTCAAGTAGCCTTGTTGCTAC

Figure 14

Rhizomucor miehei rRNA gene (SEQ ID NO: 61)

GGTCCGAAGCTTTAGCCGAACTATGGCAAACTTCTCCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTG
AACCTGCGGAAGACATTAAAAAAGTTGATATCATGGTGACCCCTTTACGGGGGTGAGCCATGATTTCTTCTCCCTTTTT
GTGCAATGTTTGAGGGATTGCTCCAGATCTCTCTTTCCTTTTTTTTACGTATTGATTTGACTGAACATTTTTGTTTTAAA
ATGAAAAAAAGTTTTGAAGCCAATCAATTGGTTCAAGACAAATCAAATTTTGAAACAACTTTAAGCAATGGATCACTT
GGTTCTCGCATCGATGAAGAGCGTAGCAAATTGCGAAAAGTAATGCGATCTGCAGCCTTTGCGAATCATCGAATTCTC
GAACGCATCTTGCACCCTTTGGTTCATCCATTGGGTACGTCTAGTTCAGTATCTTTTTGAAACCCTAAAGATTCAATTT
TGTTGTTGAATCTTTGGATTTGCGGTGCTGATGGGGGGGAGGACAAAGCAAATCTTTTGTGTTCCCCCGTTCAAGCTAC
TCGAACAGTTTTTGAGTTTTTGGCCTTTTTAGATTGGTGAACATTCTTGAAGGGCTTACTTTGATATCTAAAATTTTCGA
ATTTTGGGTTATCATTGCTTTGAGAAAACCCCATCTAAAAGCAAAAACTCTATATAAACTTTTTTTTTTTTTCATTCATG
GATCTGAACTTAGACGGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAAATAACAATGATACC
CTTAGTAGCGGCGAGCGAAGTGGGTAAAGCTCAAGTTTAAAACCTGTTTGTCATAGACAAACCGGATTGTAAACTATG
GACATGTTATCCAGGCTCTTTGGACCTTCAAGTCCTTTGGAATAAGGCTTCACAGAGGGTGACAATCCCGTAGAGGGT
CTTGAACAGAGTCTATTGCGATGCATGCTCCAAGAGTCAGGTTGTTTGGGAATGCAGCCTAAAGTGGGAGGTAAATCC
CTCCTAAAGCTAAATATTGGCGAGAAACCGATAGCAAACAAGTACCGTGAGGGAAAGTTGAAAAGGACTTTGAAAAG
AGAGTCAAAAGTACGTGAAATTGCTTAAAGGGAAGCGTTTGGAGCTAGTTTGGCTAGTCTGTTATCAGCCTGAGCTTC
GGCTTTGGTGTACTATCAGGCTATTTTTGCCGGCCAACTCTCAGGATTGAAAGGAAAGCTTGGTGCTTTGGAGTCTAAA
GAGACCCTCGCGGAAGCCTCTGGTGGAGCGTGGTCTGCCCTTGGCCCTTTTGAGCCTATAGTTGGCTTAATGGCTCTAA
ACGGCCCGTCTTGAAACACGGACCAAGGAGTCCACCACTGTTGCGAGTGTTTGGGTGGCAAACCCATACGCGAAATG
AAAGTGAAAGCTATGAAATCCGCAAGGATGGCAATAGCGTCCGGCCTTTAGGACCGAGACAAAGCAATAGTGATGGG
ACCCGAAAGATGGTGAACTATGCTTGAGTAGAGTGAAGCCAGAAGAAATTCTGGTGGAAGCTCGTAACGGTTCTGAC
GTGCAAATCGATCGTCGAACTTGAGCATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTT
TCCCTCAGGATAGCAGAAGCTTATAGGCAGTTTTATGTGGTAAAGCGAATGATTAGAGGTCTTGGGGACGCAATGTCC
TTAACCTATTCTCAAACTTTAAATATGTAAGACGTTCTTGCTGCTTGAATTATGAGCTTGAACCGTCGAATGCTGAGCT
TCTAGTGGGCCGTTCTTGGTAAGCAGGACTGGCGATGCGGGATGAACCGAACGCAAAGATAAGGCGTCAAAGAACAC
GCTCATCAGACACCACAAAAGGTGTTGGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGG
AGTGTGTAACAACTCACCTGCCGAATGAACCAGCCCTGAAAATTAATGACGCTGAAGCGTGTCGCCTATACTTTGCCG
TCAAAGTTTAAGCGAAGCTTTGACGAGTAGGCAGGCGTGGAGGTTATGAGCATCGAAGCCTTTGGCGTGAGCCTAGGT
GGAGCAGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGATCTTTGAAGACTGAAGTGGAGAAGGG
TTCCTCGAGAACATTGGTTGGTCGAGGGTTAGTCGATCCTAAGAGATAGGGTAGTTCCGTTTTACCAAATGGTCCTTTG
GACCATCCTATCGAAAGGGAAGCTGGTTAATATTCCAGCACCAAGACATGGATTCTATGCGGCAACGCAGATGAACAT
AGGGACATTGGCATGGATCCTGGGAAGAGTTCTCTTTTCTTTTTGACAGCGTTTTCTTAAGCCATGAAATCGGTCTAAC
CGGTGCAATGTTTGCTTAAGAGCTGTTAGAGTACCGCAATTTTTGTGGTATCCAGAGCATTCATGACGATCCTTGAAAA
CCTATGGGAAAGAATGAATTTCATGCTTGGTCGTACCCATAACCGCATCAGGTCTCCAAGGTGAAAAGCCTCTAGTTG
ATGGAAGAATGTAGATAAGGGAAGTCGGCAAATTGGATCCGTAACTTCGGGAGAAGGATTGGCTCTAAGGGTTGGGT
GCTTTAAGAACCAGGCCTTAGCGGCCTGAGCAATCGGGCTGCTTCCAGGCTTGGAGCTCTTGGGCACGCTTAACAACC
AGCTTAGAACTGGTACGGACCAAGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATTGCCATAAAGTGGTATT
GACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAG
TAACTATGAGAGCTTTGTGATATAGTCCAGTTTCAGAACTGCTAATTAGTGACGCGCATGAATGGATTAACGAGATTC
CCACTGTCCCTATCTACTATCCAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAAAATCAGCGGGGAAAGAAGACC
CTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGGGGGTGTAGAATATGTGGGAGCTTCGGCGCCAGTG
AAATACCACAACCCTTATAGTTTTTTTACTTAAATAATCAAGTGGGAGAAGGCTTCACGGCCTATCTTCTAGCGTTAAG
CAGTCTTCGGGCTGCGACCCATGTTATTGACATTGTCAAGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGAT
AACGCAGGTGTCCTAAGGGGAGCTCAACGAGAACAGAAATCTCGTGTAGAGCAAAAGGGCAAAAGCTCCCTTGATTT
TGATTTTCAGCGTGAATACGAACCATGAAAGTGTGGCCTATCGATCCTTTATGCCATTTCCTTAGGATTTAAGGCTAGA
GGTGCCGGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTC
GATGTCGGCTCTTCCTATCATACAGAAGCAGAATTCTGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGC
TGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAATCAGTAGGCGTCCCGACAGTAATTGAAGTTA
GTACGAGAGGAACCCTTCATTCAGATAATTGGTTTTTGCGGTTGGTTGAAAGGCCAATGCCGCGAAGCTACCATCTGC
TGGATAATGGCTGAAAGCCTCTAAGTCAGAATCCATGCTGGTTAAGGGACGCTAAAACCAGACCTTTAAAGCGCGAG
AAAGTGCTCAAATAGATCTCTTATGGGATCGAATGCCTAATATGAGGTTATCCTCTTGGGTTGAAAGGCTCAAGTCGG
ATACCTCTCATGATAATGTCTAGCTTAAAGGTTGTAAATCTCGAGCAGACGACTTGAAATCGACGGGCTATTGTAAGC

Figure 15

Rhodotorula glutinis rRNA gene (SEQ ID NO: 62)

CGATTGAATGGCTTAGTGAGGCCTCCGGATTGGCTATTGGGAGCTCGCGAGAGCACCTGACTGCTGAGAAGTTGTACG
AACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAGTGAATCT
AGGGTGTCCAATTTAACTTGGAGCCCGAACTCTCACTTTCTAACCCTGTGCATCTGTTATTGGTTAGTAGCTCTTCGGA
GTGAACTCCATTCACTTACAAACACAAAGTCTATGAATGTATACAAAATTATAACAAAACAAAACTTTCAACAACGGA
TCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCG
AATCTTTGAACGCACCTTGCGCTCCTTGGTATTCCGAGGAGCATGCCTGTTTGAGTGTCATGAAATCTTCAACCCACCT
CTTTCTTAGTGAATCTGGTGGTGCTTGGTTTCTGAGCGCTGCTCTGCTTCGGCTTAGCTCGTTCGTAATGCATTAGCATC
CGCAACCGAACTTCGGATTGACTTGGCGTAATAGACTATTCGCTGAGGATTCTAGTCTCGTACTAGAGCCGGGTTGGG
TTAAAGGAAGCTTCTAATCCTAAAGTCTATTTTTTGATTAGATCTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCA
TATCAATAAGCGGAGGAAAAGAAACTAACAAGGATTCCCCTAGTAGCGGCGAGCGAAGCGGGAAGAGCTCAAATTTA
TAATCTGGCACCTTCGGTGTCCGAGTTGTAATCTCTAGAAGTGTTTTCCGCGTTGGACCGCACACAAGTCTGTTGGAAT
ACAGCGGCACAGTGGTGATACCCCCGTACACGGTGCGGACGCCCAGCGCTTTGTGATACACTTTCAATGAGTCGAGTT
GTTTGGGAATGCAGCTCAAATTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGT
ACCGTGAGGGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAACAGTACGTGAAATTGTTGGAAGGGAAACGCTTGAA
GTCAGACTTGCTTGCCGGAGCTTGCTTCGGTTTGCAGGCCAGCATCAGTTTTCCGGGGTGGATAATGGTGGTTTGAAG
GTAGCAGCCTCGGCTGTGTTATAGCTTTCCACTGGATACATCCTGGGGGACTGAGGAACGCAGCGTGCTTTTTGCGAA
GGTTTCGACCTTTTCACGCTTAGGATGCTGGTGTAATGACTTTAAACGACCCGTCTTGAAACACGGACCAAGGAGTCT
AACATGCTCGCGAGTATTTGGGTGTCAAACCCGGATGCGCAATGAAAGTGAATGTAGGTGGGAACCGCAAGGTGCAC
CATCGACCGATCTGGATCTTTTGAGATGGATTTGAGTAAGAGCGCGTATGTTGGGACCCGAAAGATGGTGAACTATGC
CTGAATAGGGCGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGG
GTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAACTCAC
ATCAGTTCTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATA
TGTAGGAAGTCCTTGCTACTTAATTGAGCGAGGACATGCGAATGAGAGTTTCTAGTGGGCCATTTTTGGTAAGCAGAA
CTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAG
TTCATCTAGACAGCCGCACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCAACGGCCGAATGA
ACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGTTACCCATACCTCGCCGTCAGCGCTATTGATACGTTGACGAGTAG
GCAGGCGTGGAGGTCCGTATAGAAGCTTTCGGAGTGATCCGGAGTAGAACGGCCTCTAGTGCAGATCTTGGTGGTAGT
AGCAAATATTCAAGTGAGAACCTTGAAGACTGAAGTGGGGAAGGGTTCCATGGTAACAGCAGTTGGACATGGGTGAG
TCGGTCCTAAGAGATAGGGAAACTCCGTTTTAAAGTGTGCGCTTGTTCGCACGGCCTATCGAAAGGGAATACGGTTAA
AATTCCGTAACCGCGATGCAGATTCTGAACGGCAACGTAAATGAACTTGGAGACGTCGGTGAAGGCCCTGGGAAGAG
TTATCTTTTCTCCTTTACAGCTTATAACCCTGGAATCGGATTATCCGGAGATAGGGTCTAATGGCTGGTAGAGCAGCGC
TATTTTGTGCTGTCCGGTGCGTCTTCAACGGCCCGTGAAAATCCGAGGGAATGAAAAAGTCTTGCACGCGATCGTACC
CATATCCGCATCAGGTCCCCAAGGTGATCAGCCTCTAGTCCATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGA
TCCGTAACTTCGGGAAAAGGATTGGCTCATAGGGTAGGGTACGTCGGGGCCTTGGGCAAAGACAAGGGACCGCGGTG
GGACTACTGCGGCGCAAGCTGCGGCGGACCTGCTGTGGACCCGAGTCGGCGCCCCTGGCCAGTCTTCGGACGTCTGGC
GTACGATTAACTACCAACTATGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGG
CCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGG
GTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGA
TTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAAAATAAGCGGG
GAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAGAGACATAGAGGGTGTAGAATAAGTGGGAGCTTC
GGCGCCGGTGAAATACCACTACCTTTATCGTTTCTTTACTTATTCAATGAAGCGGAGCTGGGATTAACGTCCCACGTTT
TGGCATTAAGGTCCTTCGCGGGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTG
TTAAACAATAACGCAGGTGTCCTAAGGGGGACTCAATGAGAACAGAAATCTCATGTAGAACAAAAGGGTAAAAGTCC
CCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGC
TAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATC
CTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGT
GAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTTTTGAAGGGTTATCGTAATAGTAATTCAACTTAG
TACGAGAGGAACCGTTGATTCGCGTAATTGGTATTTGCGGCTGTCCGATCGGGCAATGCCGCGAAGCTACCACGCGTT
GGATTATGGCTGAACGCCTCTAAGCCAGAATCCGTGCTAGAAACGATGATGTTAGTCCCGCAAATCTTAGTCGAGTAA
AGATAGAGCTTCGGCTCGTAAACCATAGTTGGCTGGTCATGTTCAGTAGGGCGGAAAGGCCTTGCTGTTCTACCGGCG
AATAGCATTCGAAATATTTGCGGGGGTAAATCCTTGCAGACGACTTGAATAGAACGGAGTGCTGTACGCC

Figure 16

Scedosporium apiospermum rRNA gene (SEQ ID NO: 63)

CTACTACCCGATTGAATGGCTTAGTGAGACCCTCGGATTGGCGTTAAGAAGCCGGCAACGGCATCTTTTGGCCGAGAA
GTTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTA
GTGAATTGCTCTTTGAGCGTTAAACTATATCCATCTACACCTGTGAACTGTTGATTGACTTCGGTCAATTACTTTTACA
AACATTGTGTAATGAACGTCATGTTATTATAACAAAAATAACTTTCAACAACGGATCTCTTGGCTCTCGCATCGATGA
AGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCC
CGGCAGTAATCTGCCGGGCATGCCTGTCCGAGCGTCATTTCAACCCTCGAACCTCTGTTTCCCAGCGAAGCTCAGGGT
CGGCGTTGGGGCGCTACGGCGAGTCTTCGCGACCCCGTAGGCCCTGAAATACAGTGGCGGTCCCGCCGCGGTTGCCTT
CTGCGTAGTAAAAGTCTTCTTTTGCAAGCTTCGCATTGGGTCCCGGCGGAGGCCTGCCGTCAAACCACATTATAACTTA
AGATGGTTTGACCTCGGATCAGGTAGGGTTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAAC
AGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCAGCCTCCGGGCGGTCCGAGTT
GTAATTTGAAGAGGATGCTTTTGGCGAGGCGCCTTCCGAGTGCCCTGGAACGGGACGCCACAGAGGGTGAGAGCCCC
GTATGGTTGGACGCCGAGCCTCTGTAAAGCTCCTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCAAAATGGGAGGT
AAACCCCTTCTAAAGCTAAATACTGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTT
GAAAAGAGAGTTAAATAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCGACCAGACTTGTGCCCGTCGAATCAGCC
GCCGCTCGTCGGCGGCGCACTTCGGCGGGCTCAGGCCAGCATCAGTTCGCTGCAGGGGGAGAAAGGCGGTGGGAATG
TGGCTCTTCGGAGTGTTATAGCCCGCCGCGCAATACCCCTCGGCGGACTGAGGACCGCGCATCTGCAAGGATGCTGGC
GTAATGGTCGTCAGCGACCCGTCTTGAAACACGGACCAAGGAGTCGTCCTAATATGCGAGTGTTCGGGTGTAAAACCC
CTGCGCGTAATGAAAGTGAACGGAGGTGAGAGCTTCGGCGCATCATCGACCGATCCTGATGTTCTCGGATGGATTTGA
GTAAGAGCATATTGGGCCGGACCCGAAAGAAGGTGAACTATGCCTGTATAGGGTAAAGCCAGAGGAAACTCTGGTGG
AGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATATGGGCATGGGGGCGAAAGACTAATCGAACCTTCTAGT
AGCTGGTTTCCGCCGAAGTTTCCCTCAGGATAGCAGTGTTGAATTTCTCAGTTTTATGAGGTAAAGCGAATGATTAGG
GACTCGGGGGCGCTATTAAGCCTTCATCCATTCTCAAACTTTAAATATGTAAGAAGCCCTTGTTACTTAACTGAACGTG
GGCATTCGAATGTATCAACACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGATCGCGGGGA
TAAGGTGCCGGAGTGGACGCTCATCAGACACCACAAAAGGTGTTATCACATCTTGACAGCAGGACGGTGGCCATGGA
AGTCGGAATCCGCTAAGGACTGTGTAACAACTCACCTGCCGAATGTGATAGCCCTGAAAATGGATGGCGCTCAAGCGT
CCCACCCATACCCCGCCCTCAGGGTAGACACTATGCCCTGAGGAGTAGGCGGACGTGGAGGTCAGTGACGAAGCCTA
GGGCGTGAGCCCGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTTCAATGAGATCTTGAAGGA
CCGAAGTGGGGAAAGGTTCCATATGAACAGCGGTTGGATATGGGTAAGCCGATCCTAAGCCATAGGGAAGTTCCGTTT
CAAAGGGGCACTAATCGCCCCGTATGGCGAAAGGGAAGCCGGTCAATATTCCGGCGCCTGGATGTGGGTTTTACGCGG
CAACGCAAACGAAAGCGGAGACGAGGGCGGGGGCCCTGGGTAGAGTTCTCTTTTCTTCTTAACGGCCTAGTGACCCTG
GAATCGGTTTGTCCGGAGATAGGGTTCAACGGCCGGAAGAGCCCAGCACTTCTGCTGGGTCCGGTGCGCTCCCGACCT
CCCTTGAAAATCCGCTGGAGGGAATAATTCTCACGCCAGTTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAACAG
CCTCTGGTTGATAGAACAACGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTA
AGGGTTGGGCACGTTGGGCTTCTGGCGGACGCCCCGGGAGCAGACGGCCACTAGCCGGGCAACCGGCCGGGGGCTGT
CAGCATCTGGGCGCGGAAGCCTTTAGCAGGCCTTCGGGCCGTCCGGCGTGCAGTTAACAACCAACTTAGAACTGGTGC
GGACAGGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTC
TGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCAACG
TGCAGCTCCGGAACGGAAACGCACAGCGTTGCCTGTAGTGGAAGAAACAACAGCAACTTAAGAGGGTCAAGCAGCGT
AAAAGGCGACTGCTAGTGGACCCGGGCCTGCTGGGGAGGCCCGCGGATTCCGCGACACTGTCAAATTGCGGGGAGTT
CCTAAAGCCTCTTGCTACCGCGGCCCGCCGAAAGGTAGGGTGCAGCACCAGGGTAATGACCTCGGGGATGGTAAAAA
CGCAGAGGATGCTAACAATGGATGATCCGCAGCCAAGTCCTACGTCCCAGGGGGCCCCCGACACTTCGTTTTGCTCGG
AGGGGGCCAGGCACCGGGATAGGGATGCAGTTCAACGACTAGACGGCAGTGGGTCCGAGGGGGGCGAGCAAGCGTCC
CACCCGTGCTGGGTGGGAGCCCCCCGCTGAACGGGCTTAAGGTATAGTCTGCTGGTCTCCCGAAAGGGATGCACCCAC
TGAAGAAATGCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATCAACGAGATTCCCA
CTGTCCCTATCTACCATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTG
TTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGAGGTGTAGAATAGGTGGGAGCTTCGGCGCCGGTGAAAT
ACCACTACTCCTATTGTTTTTTTACTTATTCAGTGAAGCGGGGCTGGACTTACGTCCAACTTCTGGTGTTAAGGTCCTT
CGCGGGCCGACCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGCTAAACCATAACGCA
GATGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTT
CAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGGGTTTGAGGCTAGAGGTGCCAGAAA
AGTTACCACAGGGATTAACGAAAAAAACGTTACGGCTATCGTAATGAAAATAGTCCCAGGCGGCGCCATGACAAGCG
CCGCCTAGTCCGGCAGGCCCCGTACAGCGCTGGGGCCTGCGACTGTTCTGTAACTCAGTCGGCTTCGGGGGAGGTTCA
GGCCTCCCCCGCGGCTTGGGCAAAACACCTGGATGCGGGGAAGTCTCGTTAGGTCAGCGGTAGCAAGCCCGTGGTGGT
AACGCCCCCGGGTTAAGCCAGTGTCAAGGCGGCTAATAACCCACTGAATAGAGATAATCCGCAGCTCGACCCGGCCA
CACTCACCGGCAAACGGTGCAAGGGCTGGGCAGTTCAACGCTCGCTAAGGTGTTGGTGAGAGGGTCCCAGTGGACCT

CTTGCTTAAGGTACGGGCTACTCCCACCCGAGAGGGTGTCGTGTCTACCGGCTGCGCACGCCGAGAAGCACGAAGCAG
GGCGGTAAAACGAAGCCCTGTGGGTAGAAAGGAACTGGCTTGTGGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTGA
TCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAAC
GTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAACTCGCCGCAATGGTAATTCAGCTCA
GTACGAGAGGAACCGCTGATTCAGATAATTGGTTTTTGCGGCTGTCCGACCGGGCAGTGCCGCGACGCTACCATCTGC
TGGATAATGGCTGAACGCCTCTAAGTCAGAATCCATGCCAGAAAGCGGCGATATACCCGCACGTCTAGACGGACAAG
AATAGGCTCCGGCTTAGTGTCTTAGCGGGCGGATGGTCCGCCAGGCTCGAAGTGCCTGGCGGTGATTCGCGAATTGTA
ATTTCGATGCGCGCGGGGATGAATCCTTGCAGACGACTTAGTTGTGCGAAAGGGTCCTGTAAGCAGTAGAGTAGCCTG
TTTGGTTACG

Figure 17

Antrodia vaillantii rRNA gene (SEQ ID NO: 64)

CTTGGTCATTTAGAGGAAGTAAAAGTCGTAACATCCGTAGGTGAACCTGCGGAAGGATCATTAATGAATTTCAATGGA
GTTGTAGCTGGCTCTAACAAGGGCATGTGCACACTCTATTCGTTATATTATACACCTGTGCACCTTTTGTAGTTCGGTTG
TTACGGGGAGAGTCGAAAGGCTTTCTCAGACCCCCGTTCTATGTTTTTATTATAAACCTTTGAATGTCTTTGAATGTCTG
CATTAATAATGCATTTTATACAACTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGA
TAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTTGGTATTCCGAGGAGCA
TGCCTGTTTGAGTGTCATGGAATTATCAAACCTTTCTTTAAATTTATTTTAAAGGTTGGCTTGGACTTGGAGGTTGCTGG
CCGCGCCATTTTGTAGTCAGTCAGCTCCTCTTGAATGCATTAGCTTGAGTCTTTAATGAGTCGGCTTATCGGTGTGATAA
ACTTATGCCGTTAGTCAACTTGTAAACAAATCGAGCTTCTAATCGTCTTTGGACAAACATTATAATATGACCTCTGACTT
CAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACTAACAAGGATTCCCCTAGT
AACTGCGAGTGAAGCGGGAAAAGCTCAAATTTAAAATCTGGCAGTTTAATAGCTGTCCGAGTTGTAGTCTGGAGAAGT
GCTTTCCGTGCTAGACCGTGTACAAGTCCCTTGGAACAGGGCGTCATAGAGGGTGAGAATCCCGTCTTTGACACGGACT
ACTAGTGCTTTGTGATGCGCTCTCAAAGAGTCGAGTTGTTTGGGAATGCAGCTCAAAATGGGTGGTAAATTCCATCTAA
AGCTAAATACAGGCGAGAGACCGATAGCGAACAAGTACCGTGAGGGAAAGATGAAAAGCACTTTGGAAAGAGAGTTA
AACAGTACGTGAAATTGCTGAAAGGGAAACGCTTGAAGTCAGTCGCGTTGTCCGGAAATCAGCCTTGCATTTATTTGCT
TGGTGTATTTTCTGGTTGACGGGCCAGCATCGATTTTAATCGTTGGATAAAGGCGAGGGAAATGTGGCACCTTCGGGTG
TGTTATAGTCCCTTGTCACATACAACGGTCGGGATCGAGGAACTCAGCACGCCTTTATTGGTCGGGGTTCGCCCACGTT
TCGTGCTTAGGATGTTGGCATAATGGCTTTAAACGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATACCTGCGAG
TGTTTGGGTGGTAAACCCGAGCGCGTAATTAAAGTAATAGTTGAGATCCCCGTTACAAGGGAGCATCGACGCCCGGAC
TTGACCTTCTGTGATAGCTCTGCGGTAGAGCATGTATGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGA
AGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGATTCTGACGTGCAAATCGATCGTCAAATTTGGGTATAGGGGCGAA
AGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAACTCGTATCAGATTTATGTG
GTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAACGAGCC
GTCACTTAATTGGACCGCTCGGCGATTGAGGTTTCTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAA
CCGAACGTGAGGTTAAGGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCAGGAC
GGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGATG
GCGCTCAAGCGTGTTACCCATACCTCACCGTCAGTGTTTAAGTGAAACATTGACGAGTAGGCAGGCGTGGAGGTCAGT
GAAGAAGCCTAGGCAGTAATGCTGGGTGAAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAGTGAG
AACCTTGAAGACTGAAGTGGAGAAAGGTTCCATGGTAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGAGATAGGG
AAGCTCCGTTTCAAAGTGTACGATTTTTCGTACCGCCTATCGAAAGGGAATCCGGTTAAGATTCCGGAACCAGGATGTG
GATTTTTAACGGCAACGTAAATGAACTTGGAGACGCTGGCGAGGGCCCCGGGAAGAGTTATCTTTTCTCCTTAACAGTC
TAACACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAATGACTGGTAGAGCTCGACACTTCTGTCGGGTCCGGTGCGT
TCTTGACAGCCCTTGAAAATCCAAGGGAATGAATAATTTTCACACCTGGTCGTACTCATAACCGCAGCAGGTCTCCTAG
GTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGGATT
GGCTCTAAGGGTTGGGTACATCGGGCCTTAGTTGGAAGCTACGGGACCAGGCTAGGACTGTTTCGGGGCAACCTGGGA
CGGACTTGGCCAGGGACCTGTCAGTGGATGGCTTTGGCTGCTCTCGGGCGTCCGGTGTACGCTTAACAACCAACTTAGA
ACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAAT
GTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGA
CTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTA
TCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGA
CTCTAGTTTGACATTGTGAAAAGACATAGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCT
TTATCGTCTTTTTACTTATTCAATGAGGCGGAGCTGGGATTAACAGTCCCACCTTTTGGCTTCAAGGTCCTTTAAGGGCT
GATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTA
AGGGGGACTCATCGAGAACAGAAATCTCGAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAA
TACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACA
GGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATAC
CGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACA
GGTTAGTTTTACCCTACTGATGGAGTGTTATCGTAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCATTCAGATAT
TTGGTATTTGCGCCTGTCCGATCGGGCAATGGCGCGAAGCTATCATCTGCTGGATTATGGCTGAACGCCTCTAAGCCAG
AATCCGTGCTAGAAACGATGATGTTGGTCCCGCACATATAAGTTGCGTTGAAATAGAGCTTTGCTCGTGAACCAAATCA
GGTGGGCTGGGTCGTTCAAGCGGAAATGCTTGTTCGATTTGTCTACGAATTGTAATCATCATATGCGCGGGGGTGAATC
CTTTGCAGACGACTTGAATGGGAACGGGGTACTGTAAGCAGTAGAGTAGCCTTGTTGCTACGATCTGCTGAGGTTAAGC
CCTTGTTCTATAGATTTGTT

Figure 18

Aspergillus fumigatus rRNA gene (SEQ ID NO: 65)

GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCC
CTCTGGGTCCAACCTCCCACCCGTGTCTATCGTACCTTGTTGCTTCGGCGGGCCCGCCGTTTCGACGGCCGCCGGGGAG
GCCTTGCGCCCCCCGGGCCCGCGCCCGCCGAAGACCCCAACATGAACGCTGTTCTGAAAGTATGCAGTCTGAGTTGATTA
TCGTAATCAGTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTA
ATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTG
TCCGAGCGTCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCGTCCCCCTCTCCCGGGGGACGGGCCCGAAAG
GCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCTGCTCTGTANGCCCGGCCGGCGCCAGCCG
ACACCCAACTTTATTTTTCTAANGTTGACCTCGGATCANGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGA
GGAAAAGAAACCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAATTTGAAAGCTGGCCCCTTC
GGGGTCCGCGTTGTAATTTGCAGAGGATGCTTCGGGTGCAGCCCCCGTCTAAGTGCCCTGGAACGGGCCGTCATANAG
GGTGAGAATCCCGTCTGGGACGGGGTGTCTGCGTCCGTGTGAAGCTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGC
TCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGA
TGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGAAAGGGAAGCGTTTGCGACCAGACTCGCCCGC
GGGGTTCAGCCGGCATTCGTGCCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGGTCAAAGGCCCT
CGGAATGTATCACCTCTCGGGGTGTCTTATAGCCGAGGGTGCAATGCGGCCTGCCTGGACCGAGGAACGCGCTTCGGCT
CGGACGCTGGCGTAATGGTCGTAAATGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATCTACGCGAGTGTTCGG
GTGTCAAACCCGTACGCGCAGTGAAAGCGAACGGAGGTGGGAGCCCCCTCGCGGGGCGCACCATCGACCGATCNTGAT
GTCTTCGGATGGATTTGAGTACGAGCGTAGCTGTGGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGCGAAGCC
AGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGGGTATAGGGGCGAAAGAC
TAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGCGGATCAGTTTTATGAGGTAA
AGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGCGCTTGTTGC
TTAGTTGAACGTGCGCATTAGAATGAAGCGTTACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAA
CCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCCGAC
GGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACGGGCCGAATGAACTAGCCCTGAAAATGGATG
GCGCTCAAGCGTGCTACCCATACCTCGCCGTCGGGGTAGAAACGACGCCCCGACGAGTAGGCAGGCGTGGGGGTCCGT
GACGAAGCCTTGGGAGTGATCCCGGGTCGAACGGCCCCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTCAAATGAG
AACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGGCATAGGG
AAGTTCCGTTTGAAAGGCGCCCTCGTGCGCCGTGTGCCGAAAGGGAAGCCGGTTAACATTCCGGCACCTGGATGTGGA
TTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCGGGGGTCCTGGGAAGAGTTCTCTTTTCTTCTTGACAGCCTT
CCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTCCATGGCTGGCAGAGCCCCGCACCTTTGCGGGGTCCGGTGCGCCC
CCGACGACCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGG
TGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATGGATCCGTAACTTCGGGATAAGGATTG
GCTCTAAGGGTCGGGCCCGCTGGGCCTTGGGGGAAACCCCTCGGAGCAGGGGGGCACTAGCCGGGCAACCGGCCGGC
GCCCCCCAGCACTGGGGCGGGGACGCCCTTGGCAGGCTTCGGCCGTCCGGCGGGCGCTTAACGACCAACTTAGAACTG
GTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGA
TTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCT
CTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTA
CTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCT
AGTTTGACATTGTGAAAAGACATATGGGGTGTAGAATAGGTGGGAGCTTCGGCGCCAGTGAAATACCACTACCTTTATC
GTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTCACCGCCCATCTTCTGGCGTTAAGGTCCTTCGCGGGCCGATCCG
GGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCACAACGCAGGTGTCCTAAGGGGG
ACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAA
CCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATA
ACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGC
AGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATANGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGT
TTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTTAGTACNAGAGGAACCGTTGATTCAGATAATTGGTTTT
TGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGCCGGATAATGGCTGAACGCCTCTAAGTCAGAATCCGTG
CCGGAACGCGGCGATGTAGCCCCGCACGTCGTAGTTGGATACGAATAGGCCTCCGGGCCATGTACCTCAGCAGGCTGG
CGACGGCCCCCGGGGAGAAACCCCCGAGGGCTGGCTGGCGGATTGCAATGTCACCTCGCGCGGGGATGAATCCTCTGC
AGACGACTGAAGTGACCAAGCGGGTCGTGTAAGCGGTCAAGTAGCCTTGTTGCTACGAGTCGCTGAGCGTCAGCCCGA
TCCTTGGCTAGATTTGTTGGCAAACACCTCCCATCAACGGGCCCGGCAGC

Figure 19

Aspergillus niger rRNA gene (SEQ ID NO: 66)

GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGCGGGTC
CTTTGGGCCCAACCTCCCATCCGTGTCTATTGTACCCTGTTGCTTCGGCGGGCCCGCCGCTTGTCGGCCGCCGGGGGGG
CGCCTCTGCCCCCCGGGCCCGTGCCCGCCGGAGACCCCAACACGAACACTGTCTGAAAGCGTGCAGTCTGAGTTGATTG
AATGCAATCAGTTAAAACTTTCAACAATGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATAACT
AATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCT
GTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCGCCGTCCCCCTCTCCGGGGGGGACGGGCCCGAAA
GGCAGCGGCGGCACCGCGTCCGATCCTCGAGCGTATGGGGCTTTGTCACATGCTCTGTAGGATTGGCCGGCGCCTGCCG
ACGTTTTCCAACCATTCTTTCCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGG
AGGAAAAGAAACCAACCGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAATTTGAAAGCTGGCTCCTT
CGGAGTCCGCATTGTAATTTGCAGAGGATGCTTTGGGTGCGGCCCCCGTCTAAGTGCCCTGGAACGGGCCGTCAGAGA
GGGTGAGAATCCCGTCTTGGGCGGGGTGTCCGTGCCCGTGTAAAGCTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAG
CTCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAAAG
ATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCGACCAGACTCGCCCG
CGGGGTTCAGCCGGCATTCGTGCCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGGTCAAAGGCC
CCTGGAATGTAGTGCCCTCCGGGGCACCTTATAGCCAGGGGTGCAATGCGGCCAGCCTGGACCGAGGAACGCGCTTCG
GCACGGACGCTGGCATAATGGTCGTAAACGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATCTACGCGAGTGTT
CGGGTGTCAAACCCGTGCGCGCAGTGAAAGCGAACGGAGGTGGGAGCCCCCTTGCGGGGCGCACCATCGACCGATCCT
GATGTCTTCGGATGGATTTGAGTAAGAGCGTAGCTGTGGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGCGAA
GCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGGGTATAGGGGCGAAA
GACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGCAAAATCAGTTTTATGAG
GTAAAGCGAATGATTAGAGGCATTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGCCCTTG
TTGCTTAGTTGAACGTGGGCATTAGAATGGAGCGTTACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGAT
GAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCC
GACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACGGGCCGAATGAACTAGCCCTGAAAATGG
ATGGCGCTCAAGCGTGCTACCCATACCTCGCCGTCGGGGTAGAAACGATGCCCCGACGAGTAGGCAGGCGTGGGGGTC
CGTGACGAAGCCTTGGGAGTGATCCCGGGTCGAACGGCCCCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTCAAAT
GAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGGCATA
GGGAAGTTCCGTTTGAAAGGCGCCCTCGTGCGCCGTGTGCCGAAAGGGAAGCCGGTTAACATTCCGGCACCTGGATGT
GGATTCTCCACGGCAACGTAACTGAACGCGGAGACATCGGCGGGGGTCCTGGGAAGAGTTCTCTTTTCTTCTTGACGGC
CTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTCCACGGCCGGCAGAGCCCTGCACCTTTGCAGGGTCCGGTGCG
CCCCCGACGATCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCA
AGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATGGATCCGTAACTTCGGGATAAGGA
TTGGCTCTAAGGGTCGGGCTCGCTGGGCCTTGGGGGAAACCCCTCGGAGCAGGGGGGCACTAGCCGGGCAACCGGCCG
GCGCCCCCCAGCACCGGGTGGGGGACGCCCTTGGCAGGCTTCGGCCGTCCGGCGGGCGCTTAACGACCAACTTAGAAC
TGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGT
GATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACT
CTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATC
TACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACT
CTAGTTTGACATTGTGAAAAGACATATGGGGTGTAGAATAGGTGGGAGCTTCGGCGCCAGTGAAATACCACTACCTTTA
TCGTTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTCACCGCCCATCTTCTGGCGTTAAGGTCCTTCGCGGGCCGATC
CGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCACAACGCAGGTGTCCTAAGGG
GGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACA
AACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGG
ATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGA
AGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGT
TAGTTTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTTAGTACGAGAGGAACCGTTGATTCAGATAATTGG
TTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGCCGGATAATGGCTGAACGCCTCTAAGTCAGAATC
CGTGCCGGAACGCGGCGATGTTGCCCCGCACGTCGTAGTTGGATACGAATAGGCCTCCGGGCCATGCACCTCAGCAGG
CTGGCGACGGCTCCTAGGGAGAAGCCCCTGGGAGCTGGCTGGCGAATTGCAATGTCACCTCGCGCGGGGATGAATCCT
CTGCAGACGACTGAAGTGACCAAGCGGGTCGTGTACGCGGTCAAGTAGCCTTGTTGCTACGAGTCGCTGAGCGTCAGC
CCGTCCTTGGCTAGATTTGTGTTATACACCTCCCCCACTGACAGGTCCGGCAGC

Figure 20

Aspergillus oryzae rRNA gene (SEQ ID NO: 67)

GTCAAACCCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCGA
GTGTAGGGTTCCTAGCGAGCCCAACCTCCCACCCGTGTTTACTGTACCTTAGTTGCTTCGGCGGGCCCGCCATTCATGGC
CGCCGGGGGCTCTCAGCCCCGGGCCCGCGCCCGCCGGAGACACCACGAACTCTGTCTGATCTAGTGAAGTCTGAGTTG
ATTGTATCGCAATCAGTTAAAACTTTCAACAATGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGAT
AACTAGTGTGAATTGCAGAATTCCGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCAT
GCCTGTCCGAGCGTCATTGCTGCCCATCAAGCACGGCTTGTGTGTTGGGTCGTCGTCCCCTCTCCGGGGGGGACGGGCC
CCAAAGGCAGCGGCGGCACCGCGTCCGATCCTCGAGCGTATGGGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGC
TTGCCGAACGCAAATCAATCTTTTTCCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA
AGCGGAGGAAAAGAAACCAACCGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAATTTGAAAGCTGG
CTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTTCGGGTGCGGCCCCTGTCTAAGTGCCCTGGAACGGGCCGTC
AGAGAGGGTGAGAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGACGAGTCGAGTTGTTTGGGA
ATGCAGCTCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGAT
CGAAAGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCGACCAGAC
TCGCCTCCAGGGTTCAGCCGGCATTCGTGCCGGTGTACTTCCCTGGGGGCGGGCCAGCGTCGGTTTGGGCGGCCGGTCA
AAGGCTCCCGGAATGTAGTGCCCTCCGGGGCACCTTATAGCCGGGAGTGCAATGCGGCCAGCCTGGACCGAGGAACGC
GCTTCGGCACGGACGCTGGCATAATGGTCGTAAACGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATCTACGCG
AGTGTTCGGGTGTCAAACCCGTACGCGCAGTGAAAGCGAACGGAGGTGGGAGCCCCCTCGTGGGGCGCACCATCGACC
GATCCTGATGTCTTCGGATGGATTTGAGTAAGAGCGTAAATGTGGGGACCCGAAAGATGGTGAACTATGCCTGAATAG
GGCGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGGGTATAGGG
GCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGCGAATTCAGTTT
TATGAGGTAAAGCGAATGATTAGAGGCATTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAA
GCCCTTGTTGCTTAGTTGAACGTGGGCATTAGAATGGAGCGTTATTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGAT
GCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAG
ACAGCCCGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACGGGCCGAATGAACTAGCCCTG
AAAATGGATGGCGCTCAAGCGTGTTACCCATACCTCGCCGCCGGGGTAGAAACGATGCCCCGGCGAGTAGGCAGGCGT
GGAGGTCCGTGACGAAGCCTTGGGAGTGATCCCGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATA
CTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTA
AGGCATAGGGAAGTTCCGTTTGAAAGGCGCCCTCGTGCGCCGTGTGCCGAAAGGGAAGCCGGTTAACATTCCGGCACC
TGGATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCGGGGGTCCTGGGAAGAGTTCTCTTTTCTTCT
TGACAGCCTACCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTCAATGGCTGGCAGAGCCCCGCACCTTTGCGGGGTC
CGGTGCGCCCCCGACGACCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAG
GTCTCCAAGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATGGATCCGTAACTTCGGG
ATAAGGATTGGCTCTAAGGGTCGGGCTCGCTGGGCCTTGGGGGGAACCCCTCGGAGCAGGGGGGCACTAGCCGGGCAA
CCGGCCGGCGCCCCCCAGCACCGGGTGGGGGACGCCCTTGGCAGGCTTCGGCCGTCCGGCGGGCGCTTAACGACCAAC
TTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGAC
GCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAAC
TATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGT
CCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAG
CTTGACTCTAGTTTGACATTGTGAAAAGACATATGGGGTGTAGAATAGGTGGGAGCTCCGGCGCCAGTGAAATACCAC
TACCTTTATCGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTCACCGCCCATCTTCTGGCGTTAAGGTCCTTCGCG
GGCCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCACAACGCAGGTGT
CCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTG
TGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTAC
CACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATC
ATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGA
GACAGGTTAGTTTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTTAGTACGAGAGGAACCGTTGATTCAGA
TAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGCCGGATAATGGCTGAACGCCTCTAAGT
CAGAATCCGTGCCGGAACGCGGCGATGTTGCCCCGCACGTCGTAGTTGGATACGAATAGGCCTCCGGGCCACGAACCT
CAGCAGGCTGGCGACGGCTCCCCGGGAGAAGCCCCGGGGAGCTGGCTGGCGGATTGCAATGTCACCTCGCGCGGGGAT
GAATCCTCTGCATACGACTGAAGTGACCAAGCGGGTCGTGTAAGCGGTCAAGTAGCCTTGTTGCTACGAGTCGCTGAGC
GTCAGCCCGACCTTGGCTAGATTTGTGTACCA

Figure 21

Aspergillus terreus rRNA gene (SEQ ID NO: 68)

CGGAAAGTTGGTCAAACCCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
TCATTACCGAGTGCGGGTCTTTATGGCCCAACCTCCCACCCGTGACTATTGTACCTTGTTGCTTCGGCGGGCCCGCCAGC
GTTGCTGGCCGCCGGGGGGCGACTCGCCCCCGGGCCCGTGCCCGCCGGAGACCCCAACATGAACCCTGTTCTGAAAGC
TTGCAGTCTGAGTGTGATTCTTTGCAATCAGTTAAAACTTTCAACAATGGATCTCTTGGTTCCGGCATCGATGAAGAAC
GCAGCGAAATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGG
TATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCTCGTCCCCCGGCTC
CCGGGGGACGGGCCCGAAAGGCAGCGGCGGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTCGTCTTCCGCTCCGT
AGGCCCGGCCGGCGCCCGCCGACGCATTTATTTGCAACTTGTTTTTTTCCAGGTTGACCTCGGATCAGGTAGGGATACC
CGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACCGGGATTGCCTCAGTAACGGCGAGTGAAGCGGC
AAGAGCTCAAATTTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTTCGGGTGCAGCCCCCGTC
TAAGTGCCCTGGAACGGGCCGTCATAGAGGGTGAGAATCCCGTATGGGGCGGGGTGTCTGCGTCCGTGTGAAGCTCCT
TCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATACTGGCCGGAGACC
GATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGAA
AGGGAAGCGCTTGCAACCAGACTCGCTCGCGGGGTTCAGCCGGGCTTCGGCCCGGTGTACTTCCCCGCGGGCGGGCCA
GCGTCGGTTTGGGCGGCCGGTCAAAGGCCTCCGGAATGTAGCGCCCTTCGGGGCGCCTTATAGCCGGGGGTGCAATGC
GGCCAGCCTGGACCGAGGAACGCGCTTCGGCACGGACGCTGGCATAATGGTTGTAAACGACCCGTCTTGAAACACGGA
CCAAGGAGTCTAACATCTACGCGAGTGTTCGGGTGTCAAACCCGTACGCGCAGTGAAAGCGAACGGAGGTGGGAGCCC
CCTCGCGGGGCGCACCATCGACCGATCCTGATGTCTTCGGATGGATTTGAGTACGAGCGTAGCTGTGGGGACCCGAAA
GATGGTGAACTATGCCTGAATAGGGCGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATC
GATCGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTGGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGA
TAGCAGTAACGCGGATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCATTGGGGTTGAAACAACCTTAACCTATTCT
CAAACTTTAAATATGTAAGAAGCGCTTGTTGCTTAGTTGAACGTGCGCATTAGAATGGAGCGTTACTAGTGGGCCATTT
TTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACACCAC
AAAAGGTGTTAGTTCATCTAGACAGCCCGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCAC
GGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCCATACCTCGCCGTCGGGGTAGAAACGATG
CCCCGACGAGTAGGCAGGCGTGGAGGTCCGTGACGAAGCCTTGGGCGTGAGCCCGGGTCGAACGGCCTCTAGTGCAGA
TCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTG
GACATGGGTTAGTCGATCCTAAGGCATAGGGAAGTTCCGTTTGAAAGGCGCCCTCGTGCGCCGTGTGCCGAAAGGGAA
GCCGGTTAACATTCCGGCACCTGGATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCGGGAGTCCT
GGGAAGAGTTCTCTTTTCTTCTTGACAGCCTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTCCATGGCTGGCAG
AGCCCCGCACCTTTGCGGGGTCCGGTGCGCTCCCGACGACCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCCAG
GTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGC
AAAATGGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTCGGGCTCGCTGGGCCTTGGGGGGAACCCCCCGGAG
CAGGGAGGCACTAGCCGGGCAACCGGCCGGCGCTTCCCAGCACCGGGGCGGGGACGCCCTTGGCAGGCTTCGGCCGTC
CGGCGGGCGCTTAACGACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCG
ATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGC
GCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAAT
GGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGC
GGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATATGGGGTGTAGAATAGGTGGGAGC
TCCGGCGCCAGTGAAATACCACTACCTTTATCGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTCACCGCCCATCT
TCTGGCGTTAAGGTCCTTCGCGGGCCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCT
GTTAAACCACAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTC
CCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGC
TAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCC
TTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGA
GCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTTAGTAC
GAGAGGAACCGTTGATTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGCCGGAT
AATGGCTGAACGCCTCTAAGTCAGAATCCGTGCCGGAACGCGGCGATGTAGCCCCGCACGTCGTAGTTGGATACGAAT
AGGCCTTCGGGCCCTGAACCTCAGCAGGCTGGCGACGGCGCCCGGGGAGAAGCCCTCGGGTGCTGGCTGGCGGATTGC
AATGTCACCTCGCGCGGGGATGAATCCTCTGCAGACGACTGAAGTGACCAAGCGGGTCGTGTAAGCGGTCAAGTAGCC
TTGTTGCTACGAGTCGCTGAGCGTCAGCCCGCCCTTGGCTAGATTTGTGTTTACACCCTCC

Figure 22

Batrachochytrium dendrobatidis rRNA gene (SEQ ID NO: 69)

TTTAAAAGAAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTACCAAGGTAACCGTAGGTGACCCTGCGGT
TGGATCATTAATATTTGTTTGGGGGGGGGGTTGTTTTATTGATGTGTAAATGTTGATGGAATGACCCATTGTTTTTTCAA
AAAACACCCTTGATATAATACAGTGTGCCATATGTCACGAGTCGAACAAAATTTATTTATTTTTTCGACAAATTAATTG
GAAATTGAATAATTTAATTGAAAAAAATTGAAAATAAATATTAAAAACAACTTTTGACAACGGATCTCTTGGCTCTCGC
AACGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAACCTTTGTGAATCATTAAATCTTTGAACGCAC
ATTGCACTCGTAAAAGAGTATACATGTTTGAGAATTATAAAAATACATTGTCCGAATTGACTGGACAGATATGAACCAT
GTCAAAAATATTTGACAGGTTTTAAAAGTAGTAGTAAAAAAGAGTGATACAAAAAGTAGTAATACAACGTCACACCAA
CAAAAATATAATCTCAAATCATGCAAGATTACCCGCTGAACTTAAGCATATCAATAAGCGGTGGAAAAGAAACTAACA
AGGATTCCCCTAGTAACGGCGAGTGAAGCGGGAATAGCTCAAATTTGAAATCTCACAATAGTGCGAATTGTAGTTTAG
AGAAACCCCATTTTTTTACTAGACAATCAAAAAGTTTTTTGGAATAAAACATCATAGAGGGTGACAATCCCGTTTTTGA
TTGCCAAGTAATAATGTATTGGGATATCCAAGAGTCGGTTTGTTTGGGAATGCAGACCAAAATGGGTGGTAAATACCAT
CTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACCGTGAGGGAAAGATGAAAAGAACTTTGAAAAGAGA
GTTAAACAGTACGTGAAATTGTCAAAAGGGAAACGCTTGAAACCAGTATTTAAACATGAATTTCAATTCACCATGTGGT
GAGTCTATATTTGATGATTAGAGTCAACAAGGGTTTGACAAGTGATAAAAACGGCTAGAGTAGACCTATTAGGACAAA
GTCTAGTCAAATGTCACGGGTTGGACTTTTTTTAGTGTAATGTATAACATGTCTTGTTTTGACTGTGGTGGTGTTGAAAT
GCATGCAGATCAATGACACTCCAACAAATCAATTCATACTTACCCACCACAAAAACGTTGAGGAAATGGTTTTAAACG
ACCCGTCTTGAAACACGGACCAAGGAGTCCAACATATATGCAAGTATTTGAGTGAATAAACCCAAATGCAAAATAAAA
GTGAAAAGGTGGGAATATATAGCACCATTGGCCAATTAATAATAATTGAGCAAGAGCATACATGTTGGGACCCGAAAG
ATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCG
ATCGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCCTCCGAAGTTTCCCTCAGGAT
AGCAGAAGCTCAGTATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTCGGGGAAGTAAATTCCTTGACCTATTCT
CAAACTTTAAATATGTAAGACGTTGTGGTTACTTGAATGAACCGCGACAGCGAATGAGAGTTTCTAGTGGGCCATTTTT
GGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGTCGAGTTAAGGTGCCAGAATGCACGCTCATTTAGACACCACA
AAAGGTGTTGGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTTGGAACCCGCCAAGGAGTGTGTAACAACTCACC
TGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCCATACTCGACCGTCGGACCAAATACAATGG
TTTGACGAGTAGGAGGGCGTGGAGGTTTGTGTGGAAGCTTTGGATGTGAATCCGAGTGAAACGGCCTCTAGTGCAGAT
CTTGGTGGTAGTAGCAAATATTCAAAAGAGAACTTTGAAGACTGAAGTGGAGAAAGGTTCCGTGTGAACAGCAGTTGG
ACACGGGTCAGTCGATCCTAAAGAGTAAGGGAAACCTGGTAATGCACAGTGTGCGGACTCTGAAAGGGCATCCGGTTA
ATATTCCGGAACTGGGAGGTGGAATAAGCGGCAACGCAAGACAACTTGGTGACGTTGGTAGGAACCCTAGAAAGAGA
TGTCTTTTCTTTTTAACCAAACAACAACCTTGGAAACGGATGAACCGGAGAAGAGGTTTGGGATGGGCAAAGCACTGCT
TCAGCAGTGTCTGGAGCGTTTCTAACGACCCGTGAAAAACCAAGGGACTAATTTTCACACCTAGTCGTACTCATAACCG
CAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAAC
TTTGGGAAAAGGATTGGCTCCAGGGGTTGCGATGTAATCGATATCAACTAATCTGGAACTGGTACGGACATGGGGAAT
CTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTG
AATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGC
CTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACA
GCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAA
AACATGGGGGGCGTAGAATAAGTGGGAGCTTTGGCACCGGTGAAATACCACTACCCCCAATGTTTTTTTACTTATTCAA
TGAAGCAGGATTGGCCGTCATGGCCATATTGTAGTGTTTGAACCTGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCT
GGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCCAAGGGAAACTCATCGAGAACAGAAATCTCGAGTAGAACA
AAAGGGTAAACGTTTCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAAATTC
TGGGTATTTCAGGTTAGAGGTGTCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGAC
GTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATTGAGAAGCAAAATTCTCAAAGCGTCGGATTGTTCACCCGCC
AACAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGGAGGGTTGTCACAATAGT
AATTCAACGTAGTACGAGAGGAACTGTTGATTCACATAATTGGTTTTTGCGGTTAGCTGATCAGCTAGTGCCGCGACGC
TACCATGTGTAGGATTACGGCTGAACGCCTCTAAGTCGGAATCCATGCTAAAAGTGATGATGTGTCTCTGGATTGTTGA
TGAAAATAGATGCAAATCGTGTATTGTTTTGGTGTTGAGATGAAAGGGATGAAATCCGTTTTATTTGCGCCTAATAACA
AGTTTGGAATTCAGAGTGGAAATAAAGAGAAGACGACTTTTAATCACCCGGGTATTGTAAGCAGTAGAGTAGCCTTGT
TGTTACGATCTGGTGAGATTAAGCCTTGGGTTTTTTGATTTTTTTTTGGGGTGGAGTTACCTGAGGGTGTTGTATT

Figure 23

Botrytis cinerea rRNA gene (SEQ ID NO: 70)

CTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGAGTTCAT
GCCCGAAAGGGTAGACCTCCCACCCTTGTGTATTATTACTTTGTTGCTTTGGCGAGCTGCCTTCGGGCCTTGTATGCTCG
CCAGAGAATACCAAAACTCTTTTTATTAATGTCGTCTGAGTACTATATAATAGTTAAAACTTTCAACAACGGATCTCTTG
GTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTT
GAACGCACATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCTTAGCTTGGTA
TTGAGTCTATGTCAGTAATGGCAGGCTCTAAAATCAGTGGCGGCGCCGCTGGGTCCTGAACGTAGTAATATCTCTCGTT
ACAGGTTCTCGGTGTGCTTCTGCCAAAACCCAAATTTTTCTATGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAAC
TTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAAAGCTC
AAATTTGAAATCTGGCTCTTTTAGAGTCCGAATTGTAATTTGTAGAAGATGCTTCGGGTGTGGTTCCGGTCTAAGTTCCT
TGGAACAGGACGTCATAGAGGGTGAGAATCCCGTATGTGACTGGATACCTATGCTCATGTGAAGCTCTTTCGACGAGTC
GAGTTGTTTGGGAATGCAGCTCAAAATGGGAGGTATATTTCTTCTAAAGCTAAATATTGGCCAGAGACCGATAGCGCAC
AAGTAGAGTGATCGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAACAGTACGTGAAATTGTTGAAAGGGAAGCGC
TTGCAATCAGACTTGCACTTGGTGTTCATCAGGGTCTCGTACCCTGTGTACTTCATCAAGTTCAGGCCAGCATCAGTTTG
AGTGGTTAGATAAAGGCTTAGAGAATGTGGCCCTCTTCGGGGGGTGTTATAGCTCTAGGTGCAATGTAGCCTACTTGGA
CTGAGGACCGCGCTTCGGCTAGGATGCTGGCGTAATGGTTGTAAGCGACCCGTCTTGAAACACGGACCAAGGAGTGTA
CCTAATATGCGAGTGTTTGGGTGTTAAACCCATACGCGTAATGAAAGTGAACGCTGGTGAGAACCCTTAAGGGTGCATC
ATCGACCGATCTTGATGTCTTCGGATGGATTTGAGTAAGAGCATATTGGGTGCGACCCGAAAGATGGTGATCTATACGT
GAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGCGT
ATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTGTTGTTTTCA
GTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAA
GAAGTCCTTGTTACTTAATTGAACGTGGACATTCGAATGTACCAACACTAGTGGGCCATTTTTGGTAAGCAGAACTGGC
GATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATATACGCTCATCAGACACCACAAAAGGTGTTAGTTCATC
TAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAATGTGTAACAACTCACCTGCCGAATGAACTAGCC
CTGAAAATGGATGGCGCTTAAGCGTATTACCCATACCTCGCCGCCAGGGTAGAAACTATGCCCTGGCGAGTAGGCAGG
CGTGGAGGTTGTGACGAAGCCTTGGGAGTGATCCCGGGTAGAACAGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAA
TACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCC
TAAGAGATAGGGAAACTCCGTTTTAAAGTGCGCACTTGTGCGCCGTCCCTCGAAAGGGAAACCGGTTAATATTCCGGTA
CCTGGATTTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGACGGCGGGGGCCCCGGGAAGAGTTCTCTTTTCTT
CTTAACAGCCTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAACGGTTGGTAGAGCTCGACACCTCTGTCGGG
TCCGGTGCGCTCTCGACGTCCCTTGAAAATCCGCGGGAAGGAATAGCTTTCAAGCCAGGTCGTACTCATAACCGCAGCA
GGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGG
GAAAAGGATTGGCTCTAAGGGTTGGGTACGTTGGGCCATTAGGGGATGCTCTTGGAGCAGAGGAGCACTAGCCTCACG
GCCGGCGCACCTCAGCATCGAGGGTTTGACGCTTTTGGCAGACTTCGGTCGTCCGGCGTACAATTAACAACCAACTTAG
AACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAA
TGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGTAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATG
ACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCT
ATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTG
ACTCTAGTTTGACATTGTGAAAAGACATAGGGGGTGTAGAATAGGTGGGAGCGCAAGCGCCGGTGAAATACCACTACC
CTTATCGTTTTTTTACTTATTCAATAAAGCGGAACTGGGTGTCAAAGCCCAACTTCTAGCATTAAGGTCCTTCGCGGGCT
GATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCATAACGCAGGTGTCCTA
AGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAA
TACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACA
GGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATAC
CGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACA
GGTTAGTTTTACCCTACTGATGACCGTCGCCGCAATGGTAATTCAGCTTAGTACGAGAGGAACCGCTGATTCAGATAAT
TGGTTTTTGCGGCTGTCTGACAAGGCAGTGCCGCGAAGCTACCATCTGCTGGATAATGGCTGAACGCCTCTAAGTCAGA
ATCCATGCCAGAAAGCGGTGATTTATACCCACACATCGTAGTCGGATACGAATAGGCCTTTGGCCCTGAATCTTAGCTG
GCTGGTAACGGTCCTATTGAAGAAACTCTTTAGGACTAACTGGCGTCTTGCAATTTTACAATGCGTGGGGTTGAATCCT
TTGCATACGACTTAATTGTGCTATACGGTCCTGTAAGTAGTAGAGTAGCCTTGTTGTTACGATCTACTGAGGGTAAGCC
GTCCATAGCCTAGATTTGATTTATAATCTCCCATTTTTAGCTTGTC

Figure 24

Candida albicans rRNA gene (SEQ ID NO: 71)

TTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGATTTGCTTA
ATTGCACCACATGTGTTTTTCTTTGAAACAAACTTGCTTTGGCGGTGGGCCCAGCCTGCCGCCAGAGGTCTAAACTTAC
AACCAATTTTTTATCAACTTGTCACACCAGATTATTACTAATAGTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCA
TCGATGAAGAACGCAGCGAAATGCGATACGTAATATGAATTGCAGATATTCGTGAATCATCGAATCTTTGAACGCACA
TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTTTGAGCGTCGTTTCTCCCTCAAACCGCTGGGTTTGGTGTTGAGCAA
TACGACTTGGGTTTGCTTGAAAGACGGTAGTGGTAAGGCGGGATCGCTTTGACAATGGCTTAGGTCTAACCAAAAACAT
TGCTTGCGGCGGTAACGTCCACCACGTATATCTTCAAACTTTGACCTCAAATCAGGTAGGACTACCCGCTGAACTTAAG
CATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAAATT
TGAAATCTGGCGTCTTTGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGCCCGGCTCTTGTCTATGTTCCTTGGA
ACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGACCCGGGTCTGTGTAAAGTTCCTTCGACGAGTCGAGT
TGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG
TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTG
AGATCAGACTTGGTATTTTGCATGCTGCTCTCTCGGGGGCGGCCGCTGCGGTTTACCGGGCCAGCATCGGTTTGGAGCG
GCAGGATAATGGCGGAGGAATGTGGCACGGCTTCTGCTGTGTGTTATAGCCTCTGACGATACTGCCAGCCTAGACCGA
GGACTGCGGTTTTTACCTAGGATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACG
TCTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGGTGGGGGCCCATTAGGGTGCACCAT
CGACCGATCCTGATGTGTTCGGATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTG
AATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTA
TAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTATCA
GTTTTATGAGGTAAAGCGAATGATTAGAAGTCTTGGGGTTGAAATGACCTTAACTTATTCTCAAACTTTAAATATGTAA
GAAGTCCTTGTTGCTTAATTGAACGTGGACAATTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGC
GATGCGGGATGAACCGAACGTGAAGTTAAAGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATC
TAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCC
CTGAAAATGGATGGCGCTCAAGCGTGCTACTTATACTTCACCGTGATTGCTGTTTTGACGCTTTCACGAGTAGGCAGGC
GTGGAGGTCAGTGACGAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAA
TATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGTTGGACATGGGTTAGTCGATCC
TAAGAGATGGGGAAGCTCCGTTTCAACGTGCTTGATTTTTCAGGCCAACCATCGAAAGGGAATCCGGTTAAAATTCCGG
AACTTGGATATGGATTCTTCACGGCAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTATCTTTTC
TTCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAGAGCGCGGTAATTTTGCCG
CGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAAGTCGTACTCATAACCGCAG
CAGGTCTCCAAGGTTAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTC
GGGATAAGGATTGGCTCTAAGGATCGGGTGTCTTGGGCCTTGTGTAGACGCGGCGGTGACTGTTGGCGGGCTGTTTTAC
GACGGACTGCTGGTGGATGCTGCTGTAGACACGCTTGGTAGGTCTTTATGGCCGTCCGGGGCACGTTTAACGATCAACT
TAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTTGACA
CAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACT
ATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTC
CCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGC
TTGACTCTAGTTTGACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATACCACT
ACCTCTATAGTTTTTTTACTTATTCAATGAAGCGGAGCTGGAGGTCAAACTCCACGTTCTAGCATTAAGCCCTCTGGGCG
ATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGTCCTAA
GGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAAT
ACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACA
GGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATAC
CGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACA
GGTTAGTTTTACCCTACTGATGAATGTTATCGCAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCATTCAGATAAT
TGGTTTTTTGCGGCTGTCTGATCAGGCAACGCCGCGAAGCTACCATCTGCTGGATTATGGCTGAACGCCTCTAAGTCAGA
ATCCATGCTAGAACGCGATGATTTTTGCCCTGCACATTTTAGATGGATACGAATAAGACTTTTTAGTCGCTGGACCATA
GCAGGCTGGCAACGGTGCGCTTAGCGGAAAGGCTTTGTGCGCTTGCCGGCGGATAGCAATGTCAACATGCGCGGGGAT
AAATCCTTTGCATACGACTTAGATGTACAACGGAGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGA
TTAAGCTCTTGTTGTCTGATTTGT

Figure 25

Candida dublineinsis rRNA gene (SEQ ID NO: 72)

CTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGATTTGCTT
AATTGCACCACATGTGTTTTGTTCTGGACAAACTTGCTTTGGCGGTGGGCCCCTGCCTGCCGCCAGAGGACATAAACTT
ACAACCAAATTTTTTATAAACTTGTCACGAGATTATTTTTAATAGTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGC
ATCGATGAAGAACGCAGCGAAATGCGATACGTAATATGAATTGCAGATATTCGTGAATCATCGAATCTTTGAACGCAC
ATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTTTGAGCGTCGTTTCTCCCTCAAACCCCTAGGGTTTGGTGTTGAGC
AATACGACTTGGGTTTGCTTGAAAGATGATAGTGGTATAAGGCGGAGATGCTTGACAATGGCTTAGGTGTAACCAAAA
ACATTGCTAAGGCGGTCTCTGGCGTCGCCCATTTTATTCTTCAAACTTTGACCTCAAATCAGGTAGGACTACCCGCTGAA
CTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAAAGCT
CAAATTTGAAATCTGGCGTCTTTGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGCCCGGCTCTTGTCTATGTTC
CTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGGCCCGGGTCTATGTAAAGTTCCTTCGACGAG
TCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCG
AACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAG
GGCTTGAGATCAGACTTGGTATTTTGCAAGTTACTCTTTCGGGGGTGGCCTCTGCGGTTTACCGGGCCAGCATCGGTTTG
GAGCGGTAGGATAATGGCGGGGGAATGTGGCACGACTTTGGTTGTGTGTTATAGCCTCTGACGATACTGCCAGCCTAG
ACCGAGGACTGCGGTTTTTACCTAGGATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTC
TAACGTCTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGATGGGGGCCTGTATGGGTGC
ACCATCGACCGATCCTGATGTGTTCGGATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTAT
GCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTT
GGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTC
GTATCAGTTTTATGAGGTAAAGCGAATGATTAGAAGTCTTGGGGTTGAAATGACCTTAACTTATTCTCAAACTTTAAAT
ATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGACAATTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGA
ACTGGCGATGCGGGATGAACCGAACGTGAAGTTAAAGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAG
TTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAA
CTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACTTATACTTCACCGTGATTGCTTTTTTGACGCTTTCACGAGTAGG
CAGGCGTGGAGGTCAGTGACGAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTA
GCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGTTGGACATGGGTTAGTC
GATCCTAAGAGATGGGGAAGCTCCGTTTCAACGCGCTTGATTTTTCAGGCCAACCATCGAAAGGGAATCCGGTTAAAAT
TCCGGAACTTGGATATGGATTCTTCACGGCAACGTAACTGAATGTGGAGACGTCGGCGTGAGCGCTGGGAGGAGTTAT
CTTTTCTTCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAGAGCGCGGTAATTT
TGCCGCGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAAGTCGTACTCATAAC
CGCAGCAGGTCTCCAAGGTTAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTA
ACTTCGGGATAAGGATTGGCTCTAAGGATCGGGTGTTTTGGGCCTTGTGTAGACGCGGTGGTGACTGGTGGCGGGCTGT
TTCACGACGGACTGCTGTTGGACGCTGCTGTAGACACGCTTGGTAGGCTCTTGTAGCCGTCCGGGGCACGCTTAACGAT
CAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGT
TGACACAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAG
TAACTATGACTCTCAACCTATAAGGGAGGCAAAAGTAGGGACGCTATGGTTTCCAGAAATGGGCCGAGGTGTTTTTGA
CCTGCTAGTCGATCTGGTTAATTAGGTATTTTGTATATTACTTATCAGAGTATTCTCCTGGTATTATACATTTTACTTTAT
GACGACAACTATTACCCGCGGGACAACCATTTCTTGATTTATTTACTGCAAGTGATTCTAGAATATGGTGATTCCAGTTA
TAACACCAACTGTTATGACACAAGTGTGATACAGTCATAAGCTGTGGGTAACCAGCGGCGACATAACCTGGTACGGGG
AAGGCCTCGAAGCAGTATATATTTTGGGATTGAAAATCGGGTTGCAAAACTTTTGTTTTTGGAAACACGGTTGGTGAGG
AAAAAAAAATATTTTTTCCCCGCACTTGAAGAAATATATGTTGTATGGGGTTAATCCCGTGGCGAGCCGTCAGAGCGCG
AGTTCTGGCAGTGGCCGTCGTAGAGCACGGAAAGGTATGGGCTGGCTCTCTGAGTCGGCTTAAGGTACGTGCCGTCCCA
CACGATGAAAAGTGTGCGGTGCAGAATAGTTCCCACAGAACGAAGCTGCGCCGGAGAAAGCGATTTCTTGGAGCAATG
CTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTA
CTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCT
AGTTTGACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCTCTAT
AGTTTTTTTACTTATTCAATGAAGCGGAGCTGGAGGTCAAACTCCACGTTCTAGCATTAAGTCCTTTTGGGCGATCCGGG
TTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGTCCTAAGGGGGAC
TCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACC
ATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAA
CTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCA
GAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTT
TTACCCTACTGATGAATGTTATCGCAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCATTCAGATAATTGGTTTTTG
CGGCTGTCTGATCAGGCAACGCCGCGAAGCTACCATCTGCTGGATTATGGCTGAACGCCTCTAAGTCAGAATCCATGCT
AGAACGCGATGATTTTTGCCCTGCACATTTTAGATGGATACGAATAAGACTTTTGTCGCTGGACCATAGCAGGCTGGCA
ACGGTGCGCTTAGCGGAAAGGCTTTGTGTGCTTGCCGGCGGATAGCAATGTCAACATGCGCGGGGATAAATCCTTTGCA
TACGACTTAGATGTACAACGGAGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGATTAAGCTTTTGT
TGTCTGATTTGTCTAATCCTGGTTGCCC

Figure 26

Candida glabrata rRNA gene (SEQ ID NO: 73)

GGTCATTTAGAGGAACTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAAGAAATTTAATT
GATTTGTCTGAGCTCGGAGAGAGACATCTCTGGGGAGGACCAGTGTAGACACTCAGGAGGCTCCTAAAATATTTTCTCT
GCTGTGAATGCTATTTCTCCTGCCTGCGCTTAAGTGCGCGGTTGGTGGGTGTTCTGCAGTGGGGGGAGGGAGCCGACAA
AGACCTGGGAGTGTGCGTGGATCTCTCTATTCCAAAGGAGGTGTTTTATCACACGACTCGACACTTTCTAATTACTACA
CACAGTGGAGTTTACTTTACTACTATTCTTTTGTTCGTTGGGGGAACGCTCTCTTTCGGGGGGGAGTTCTCCCAGTGGAT
GCAAACACAAACAAATATTTTTTTAAACTAATTCAGTCAACACAAGATTTCTTTTAGTAGAAAACAACTTCAAAACTTT
CAACAATGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCCGT
GAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCA
AACACATTGTGTTTGGTAGTGAGTGATACTCGTTTTTGAGTTAACTTGAAATTGTAGGCCATATCAGTATGTGGGACAC
GAGCGCAAGCTTCTCTATTAATCTGCTGCTCGTTTGCGCGAGCGGCGGGGGTTAATACTGTATTAGGTTTTACCAACTCG
GTGTTGATCTAGGGAGGGATAAGTGAGTGTTTTGTGCGTGCTGGGCAGACAGACGTCTTTAAGTTTGACCTCAAATCAG
GTAGGGTTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACTGGGATTGCCTTAGTAACGGCGA
GTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTTTGGTGCCCGAGTTGTAATTTGGAGAGTACCACTTTGGGAC
TGTACTTTGCCTATGTTCCTTGGAACAGGACGTCATGGAGGGTGAGAATCCCGTGTGGCGAGGGTGTCAGTTCTTTGTA
AAGGGTGCTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATACAGG
CGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAA
ATTGTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGCGCCCCTTGCCTCTCGTGGGCTTGGGACTCTCGCAGC
TCACTGGGCCAGCATCGGTTTTGGCGGCCGGAAAAAACCTAGGGAATGTGGCTCTGCGCCTCGGTGTAGAGTGTTATAG
CCCTGGGGAATACGGCCAGTCGGGACCGAGGACTGCGATACTTGTTATCTAGGATGCTGGCATAATGGTTATATGCCGC
CCGTCTTGAAACACGGACCAAGGAGTCTAACGTCTATGCGAGTGTTTGGGTGTTAAACCCGTACGCGTAATGAAAGTG
AACGTAGGTTGGGGCCCTCCACCTGGGGGGTGCACAATCGACCGATCCTGATGTCTTCGGATGGATTTGAGTAAGAGC
ATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTA
GCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCC
TGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGTACCGGGGTTG
AAATGACCTTGACCTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGACATTTGAATGAA
GAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGTGGAGTTAAGGTGCCGGAAT
ACACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTA
AGGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGTTACCTATACTCCG
CCGTCAGGGTTGAAATGAGGCCCTGACGAGTAGGCAGGCGTGGGGGTCAGTGACGAAGCCTAGGCCGTAAGGTCGGGT
CGAACGGCCCCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGG
TTCCACGTCAACAGCAGTTGGACGTGGGTTAGTCGATCCTAAGAGATGGGGAAGCTCCGTTTCAAAGGCCTGATTTATG
CAGGCCACCATCGAAAGGGAATCCGGTTAAGATTCCGGAACCTGGATGTGGATTCTTCACGGCAACGTAACTGAATGT
GGAGACGTCGGCGCGAGCCCTGGGAGGAGTTATCTTTTCTTCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAG
ATGGGGTCTTATGGCTGGAAGAGGCGAGCTCATATGCTCGCTCCGGTGCGCTTGCGACGGCCCTTGAAAATCCACAGG
AAGGAATAGTTTTCACGCCAGGTCGTACTGATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAATA
ATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTCGGGTAGTGAGGGC
CTTGGTCAGACGCGGCGGGGCTGCGTGCGGACTGCCTGGTGGGGCTTGCTCTGCCGGGCGGACTGCATGCGGCTCCTGT
CGTAGACGGTCTTGGTAGGTCTCTTGTAGGCCGTCGCTTGCTGCGATTAACGATCAACTTAGAACTGGTACGGACAAGG
GGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGTCAGAAAGTGATGTTGACGCAATGTGATTTCTGCCCAGTG
CTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCA
AATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAA
CCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGT
GAAGAGACATAGAGGGTGTAGCATAAGTGGGAGCTCCGGCGCCAGTGAAATACCACTACCTTTATAGTTTCTTTACTTA
TTCAATTAAGCGGAGCTGGAATTCATTTTCCACGTTCTAGCTTTCAAAGTGCCATTCGGTGCTGATCCGGGTTGAAGAC
ATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGCAGATGTCCTAAGGGGGACTCATGGAG
AACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGT
GTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGT
GGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGT
AAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTAC
TGATGAATGTTACCGCAATAGTAATTGAACTTAGTACGAGAGGAACAGTTCATTCGGATAATTGGTTTTTGCGGCTGTC
TGATCAGGCAATGCCGCGAAGCTACCATCCGCTGGATTATGGCTGAACGCCTCTAAGTCAGAATCCATGCTAGAACGC
GGTGATTCTTTGCCCTGCACAACGTAGATGGATACGAATAAGGCGTCCTTTTGGGCGTCGCTGAACCATAGCAGGCTGG
CGACGGTGCGCTTGGCGGAAAGGCCTTGCGTGCTTGCCGGCGGATAGCAATGTCATTTTGCGCGGGGATAAATCATTTG
TATACGACTTAGATGTACAACGGGGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATC

Figure 27

Candida gulliermundei rRNA gene (SEQ ID NO: 74)

TTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTT
GCCAGCGCTTAACTGCGCGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTCTGCTTTGGGTTTGGCCT
AGAGATAGGTTGGGCCAGAGGTTTAACATAAACACAATTTAATTATTTTTACAGTTAGTCAAATTTTGAATTAATCTTC
AAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA
GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGGTATTCCAGAGGGCATGCCTGTTTTGAGCGTCA
TTTCTCTCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGGACTAGGCGTTTGCTTGAAAAGTAATTGGCA
TGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAACTCGTTGAATGGTGTGGCGGGATATTTC
TGGTATTGTTGGCCCGGCCTTACAACAACCAAACAAGCTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCA
TATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAAATTTG
AAATCTGGCGCCTTCGGTGTCCGAGTTGTAATTTGAAGATTGTAACCTTGGGGGTTGGCTCTTGTCTATGTTTCTTGGAA
CAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAACGGTGCTTTCGAAGAGTCGAGTT
GGTTTGGGGAATGCAGCTCCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACA
AGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGTT
TGAGATCAGACTCGATATTTTGTGAGCCTTGCCTTCGTGGCGGGGTGACCCGCAGCTTATCGGGCCAGCATCGGTTTGG
GCGGTAGGATAATGGCGTAGGAATGGTGACTTTACTTCGGTGAAGTGTTAATAGCCTGCGTTGATGCTGCCTGCCTAGA
CCGAGGACTGCGATTTTATCAAGGATGCTGGCATAATGATCCCAAACCGCCCGTCTTGAAACACGGACCCAAGGAGTC
TAACGTCTATGCGAGTGTTTGGGTGTTAAACCCGTACGCGTAATGAAAGTGAACGTAGGTGAGGGCTCTTTTGAGTGCA
TCATCGACCGATCCTGATGTCTTCGGATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATAC
CTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGG
GTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGT
ATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGTATTGGGGTTGAAATGACCTTAACCTATTCTCAAACTTTAAATAT
GTAAGAAGTCCTTGTTGCTTAATTGAAACGTGGACATTTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAA
CTGGCGATGCGGGATGAACCGAACGTGAAGTTAAAGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGT
TCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAAC
TAGCCCTGAAAAGTGGATGGCGCTCAAGCGTGTTACTTATACTTCGCCGTCGAGGGTTGATATGATGCCCTGACGAGTA
GGCAGGCGTGGAGGTCAGTGACGAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAG
TAGCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGTTGGACATGGGTTAG
TCGATCCTAAGAGATGGGGAAGCTCCGTTTCAAAGTGCTTGATTTTTCAAGCCGCCATCGAAAGGGAATCCGGTTAATA
TTCCGGAACTTGGATATGGATTCTTCACGGTAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTCT
CTTTTCTTCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATAGGGTCTTATGGCTGGAAGAGCGCAATACTTT
TGTTGCGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAAGTCGTACTCATAAC
ACGCAGCAGGTCTCCAAGGTTAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGT
AACTTCGGGATAAGGATTGGCTCTAAGGATCGGGTGTCTTGGGCCTTTACCAGACGCAGCGGAACCGGCGGTGGACTG
TCTAGGAGCAATCTTGGACGGACCGCTGTTGGATCTTGTTGTAGACGGTTTTGGTAGGCTTTTAGCCGTCCGGGGCACG
CTTAACGATCAACTTAGAACTGGTACGGACAAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGTCAG
AAAGGTGAATGTTGACGCAATGTGATTTCTGCCCCAGTTGCTCTGAAATGTCAAAGTGGAAGAAATTCAACCAAGCGC
GGGTAAACGGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAAT
GGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGC
GGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGAGGGTGTAGAATAAGTGGGAGC
TTTCGGCGCCGGTGAAATACCACTACCTCTATAGTTTTTTTACTTATTCAATTAAGCGGAGCTGGACTTCATCGTCCACG
TTCTAGCATTAAGGTCTCATTAGAGGCTGATCCCGGGTTGAAGACATTGTCAGGTGGGGGAGTTTGGCTGGGGCGGCAC
ATCTGTTAAACGATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGGTAA
AAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGGATCCTTTAGTCCCTCGGAATT
TGAGGCTAGAGGTGCCAGGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTT
TTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGAATTGTTCACCCCACTAATAG
GGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAATGTTATCGCAATAGTAATTGA
ACTTAGTACGAGAGGAACCGTTCATTCGGATAATTGGTTTTTGCGGCTGTCTGATCAGGCAACGCCGCGAAGCTACCAT
CCGCTGGATTATGGCTGAACGCCTCTAAGTCAGAATCCATGCTAGAAAGCGATGATTCTTGCCTCGCACATTTTAGTTG
GATAAGAATAAGGCTCTTTGAGTCGCTGAACCATAGCAGGCCTAGGTAACGGTACACTTAACGGAAAGGTTTTGTGTG
CTTGCCGGCGGATAGCAATGTCATAATGAGCGGGGATAAATCCTTTGCATACGACTTACATGTACAACGGAGTATTGTA
AGCAGTAGAGTAGCCTTGTTGTTACAGATCTGCTGAGATTAAGCTTCAGTTGTCCGATTTGTTTAGTGTCTAC

Figure 28

Candida kefyr rRNA gene (SEQ ID NO: 75)

TCCGTAGGTGAACCTGCGGAAGGATCATTAAAGATTATGAATGAATAGATTACTGGGGGAATCGTCTGAACAAGGCCT
GCGCTTAATTGCGCGGCCAGTTCTTGATTCTCTGCTATCAGTTTTCTATTTCTCATCCTAAACACAATGGAGTTTTTTCTC
TATGAACTACTTCCCTGGAGAGCTCGTCTCTCCAGTGGACATAAACACAAACAATATTTTGTATTATGAAAAACTATTA
TACTATAAAATTAATATTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAATTGCGA
TATGTATTGTGAATTGCAGATTTTCGTGAATCATCAAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGGGGGCAT
GCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTTGGGTTTGGTAGTGAGTGATACTCGTCTCGGGTTAACTTGAAAGTGG
CTAGCCGTTGCCATCTGCGTGAGCAGGGCTGCGTGTCAAGTCTATGGACTCGACTCTTGCACATCTACGTCTTAGGTTTG
CGCCAATTCGTGGTAAGCTTGGGTCATAGAGACTCATAGGTGTTATAAAGACTCGCTGGTGTTTGTCTCCTTGAGGCAT
ACGGCTTTAACCAAAACTCTCAAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCAATAAGCG
GAGGAAAAGAAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCGTCT
TCGACGTCCGAGTTGTAATTTGAAGAAGGCGACTTTGTAGCTGGTCCTTGTCTATGTTCCTTGGAACAGGACGTCATAG
AGGGTGAGAATCCCGTGTGGCGAGGATCCCAGTTATTTGTAAAGTGCTTTCGACGAGTCGAGTTGTTTGGGAATGCAGC
TCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGA
TGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATGGCGTT
TGCTTCGGCTTTCGCTGGGCCAGCATCAGTTTTAGCGGTTGGATAAATCCTCGGGAATGTGGCTCTGCTTCGGTAGAGT
GTTATAGCCCGTGGGAATACAGCCAGCTGGGACTGAGGATTGCGACTTTTGTCAAGGATGCTGGCGTAATGGTTAAATG
CCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGTCTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAA
AGTGAACGTAGGTGAGGGCCCGCAAGGGTGCATCATCGACCGATCCTGATGTCTTCGGATGGATTTGAGTAAGAGCAT
AGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGC
GGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTG
CCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGTACCGGGGTTGA
AATGACCTTGACCTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGACATTTGAATGAAG
AGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGTGGAGTTAAGGTGCCGGAATA
CACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAA
GGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGTTACCTATACTCCAC
CGTCAGGGTTAATATGATGCCCTGACGAGTAGGCAGGCGTGGAGGTCAGTGACGAAGCCTAGGCTGTAAAGCTGGGTA
GAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGT
TCCACGTCAACAGCAGTTGGACGTGGGTTAGTCGATCCTAAGAAATGGGGAAGCTCCGTTTCAAAGGCCTAATTTTCTA
GGCCACCATCGAAAGGGAATCCGGTTAATATTCCGGAACCTGGATATGGATTCTTCACGGTAACGTAACTGAATGTGG
AGACGTCGGCGCGAGCCCTGGGAGGAGTTATCTTTTCTTCTTAACAGCTTATCACCCCGGAATTGGTTTATCCGGAGAG
GGGGTCTTATGGCTGGAAGAGCCCAGCCCTTGTGCTGGGTCCGGTGCGCCCGCGACGGCCCTTGAAAATCCACAGGAA
GGAATAGTTTTCATGCCAGGTCGTACTGATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAATAATG
TAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGAAGTCGGCAAAATAGATCCG
TAATTTCGGGATAAGGATTGGCTCTAAGGATCGGGTAGTGAGGGCCTTGGTCAGACGCGGCGGGCATGCTTGTGGACT
GTCTTACTGGGCTTGCTCGGTGGGACGGACTGCTTGCGGGCCTTGTCGTAGACGGCCTTGGTAGGTCTCTTGTAGACCG
TCGCTTGCTACAATTAACGATCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTG
CGATGGTCAGAAAGTGATGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAA
GCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATG
AACGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATC
AGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAGAGACATAGAGGGTGTAGCATAAGTGGG
AGCTTCGGCGCCAGTGAAATACCACTACCTTTATAGTTTCTTTACTTATTCAATTAAGCGGAGCTGGAATTCATTTTCCA
CGTTCTAGCATTCAAAGTCCTATACGGGCTGATCCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCA
CATCTGTTAAACGATAACGCAGATGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAA
AGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGGTCCTCGGAATTTG
AGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTG
ATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAAC
GTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAATGTTATCGCAATAGTAATTGAACCTA
GTACGAGAGGAACAGTTCATTCGGATAATTGGTTTTTGCGGCTGTCTGACCAGGCATTGCCGCGAAGCTACCATCCGCT
GGATTATGGCTGAACGCCTCTAAGTCAGAATCCATGCTAGAACGCGATGATTTCTTTGCCTTGCACAATATAGAAGGAT
ACGAATAAGGCGTCTTTATGGCGTCGCTGAACCATAGCAGGCTGGCAACGGTGCTCTTAGCGGAAAGGCTTTGGGTGCT
TGCCGGCGAATTGCAATGTCATTTTGCGCAAGGATAAATCATTTGTATACGACTTAAATGTACAACAGGGTATTGTAAG
CAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGATTAAGCCTTCGTTGTCTGATTTGT

Figure 29

Candida krusei rRNA gene (SEQ ID NO: 76)
(GenBank® Accession # EF550222 + GenBank® Accession # AB369918)

GGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGTGATTTAGTACTACACTGCGTG
AGCGGAACGAAAACAACAACACCTAAAATGTGGAATATAGCATATAGTCGACAAGAGAAATCTACGAAAAACAAACA
AAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAGCGCAGCGAAATGCGATACCTAGTGTGAATTGCAGC
CATCGTGAATCATCGAGTTCTTGAACGCACATTGCGCCCCTCGGCATTCCGGGGGGGCATGCCTGTTTGAGCGTCGTTTCC
ATCTTGCGCGTGCGCAGAGTTGGGGGAGCGGAGCGGACGACGTGTAAAGAGCGTCGGAGCTGCGACTCGCCTGAAAG
GGAGCGAAGCTGGCCGAGCGAACTAGACTTTTTTTCAGGGACGCTTGGCGGCCGAGAGCGAGTGTTGCGAGACAACAA
AAAGCTCGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAG
GGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAGAGCTCAGATTTGAAATCGTGCTTTGCGGCACGAGTTGTAGATTG
CAGGTTGGAGTCTGTGTGGAAGGCGGTGTCCAAGTCCCTTGGAACAGGGCGCCCAGGAGGGTGAGAGCCCCGTGGGAT
GCCGGCGGAAGCAGTGAGGCCCTTCTGACGAGTCGAGTTGTTTGGGAATGCAGCTCCAAGCGGGTGGTAAATTCCATC
TAAGGCTAAATACTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAAAAGCACTTTGAAAAGAGAG
TGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGTATTGCGCCCGACATGGGGATTGCGCACCGCTGCCTCTCGTGGG
CGGCGCTCTGGGCTTTCCCTGGGCCAGCATCGGTTCTTGCTGCAGGAGAAGGGGTTCTGGAACGTGGCTCTTCGGAGTG
TTATAGCCAGGGCCAGATGCTGCGTGCGGGGACCGAGGACTGCGGCCGTGTAGGTCACGGATGCTGGCAGAACGGCGC
AACACCGCCCGTCTTGAAACATGGACCAAGGAGTCTAACGTCTATGCGAGTGTTTGGGTGTGAAACCCGTACGCGTAAT
GAAAGTGAACGTAGGTCGGACCCCCTGCCCTCGGGGAGGGGAGCACGATCGACCGATCCCGATGTTTATCGGAAGGAT
TTGAGTAGGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGG
TGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCT
AGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTATCAGTTTTATGAGGTAAAGCGAATGATTAGA
CGTCTCGGGGTCGAAATGACCTTAGCGTATTCTCAAACTTTAAATATGTAAGAAGTCCCTGTTGCTTTATTGAACGCGG
ACGTTTGAATGCAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAAGTT
AAGGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCCAGACAGCCGGACGGTGGCCATGGAAG
TCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGT
TACCTATACTTCGCCGCCATGGCGCAAGGCCTTGGCGAGTAGGCAGGCGTGGGGGTTTGTGACGAAGCCTTGGGCGTG
AGCCTGGGTCGAACGGCCCCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGGGAACTTTGAAGACTGAAGT
GGGGAAAGGTTCCGCGTCAACAGCAGTTGGACGCGGGTCAGTCGATCCTAAGAGATGGGGAAGCTCCGTTTCAACGAG
CGCAATTCGCTTGCGCCACCATCGAAAGGGAATCCGGTTAAGATTCCGGAACTTGGATGTGGATTCTTCACGGCAACGT
AACAGAATGCGGAGACGCCGGCGGGAGCCCTGGGAGGAGTTTTCTTTTCTTCTTAACAGCCTAACACCCTGGAATTGGT
TTATCCGGAGAGGGGGTCTTATGGCTGGAAGAGCGTCGCCCTTGCTGCGACGTCCGGTGCGCTTGCGACGGTCCTTGAA
AATCCGCAGGAAGGAATAGTTTTCACGCCAAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTTAACAGCCTCTAGTT
GATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGC
GGAGTGCTGGGGCTGCCGGCGCGTGCCGGGTGCTGCGGAGACGCATCTGTGTTTCTGCGGCTGCCTGGCGGCGGGCTTG
CGGCCTGTTTTTCAGTCCCGCGGTTAACAACCGACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAA
CATAGCATTGCGATGGTCAGAAAGTGATGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAA
TTCAACCAAGCGCGGGTAAACGGCGGNAGTAACTATGACTCTCTTAAGGTAGCCNAATGCCTCGTCATCTAATTAGTGA
CGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTG
GCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGAGGGTGTAGCA
TAAGTGGGAGCTCCGGCGCCAGTGAAATACCACTACCTTTATCGTTTTTTTACTTATTCAATGAAGCGGAGCTGGTCTTG
ACGACCACGTTCTGGAGCGAAGGCGCCTTGTGCGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGG
GCGGCACATCTGTTAAACGATAACGCAGATGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAG
GGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGG
AATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGCTCATAGCGACATTG
CTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATA
GGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAATGTTGTCGCAATAGTAATTG
AACTTAGTACGAGAGGAACCGTTCATTCAGATAATTGGTTTTTGCGGCTGTCTGAGCAGACACTGCCGCGACGCTACCA
TCTGCTGGATAATGGCTGAACGCCTCTAAGTCAGAATCCATGCTAGAACGCGACGATTACCTGCCCTCGCACATTTGAG
AAGGATACGAATAAGGCCCTGTGGCCGCAGAACCGTAGCAGGCCGGCAGCGGTGCGCATGGCGGAAAGGCCGTGTGT
GCTTGCCGGCGGATGGCAATGTCAGGATGCGCGAGGATAAATCCTATGCATACGACTTAGATGTACAACGGGGTATTG
NAAG

Figure 30

Candida lipolytica rRNA gene (SEQ ID NO: 77)
(GenBank® Accession # AJ616903 + GenBank® Accession # DQ680839)

ACGAATCTTTGGAAGTAAAAAAGCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATTGATTTTATCTAT
TTCTGTGGATTTCTATTCTATTACAGCGTCATTTTATCTCAATTATAACTATCAACAACGGATCTCTTGGCTCTCACATCG
ATGAAGAACGCAGCGAACCGCGATATTTTTTGTGACTTGCAGATGTGAATCATCAATCTTTGAACGCACATTGCGCGGT
ATGGCATTCCGTACCGCACGGATGGAGGAGCGTGTTCCCTCTGGGATCGCATTGCTTTCTTGAAATGGATTTTTTTAAAC
TCTCAATTATTACGTCATTCACCTCCTCATCCGAGATAGCTTAGCCACGGATTTCACCTCCTTCATCCGAGATTACCCGC
TGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAA
AGCTCAAATTTGAAACCCTCGGGATTGTAATTTGAAGATTTGGCATTGGAGAAAGCTAACCCAAGTTGCTTGGAATAGT
ACGTCATAGAGGGTGACAACCCCGTCTGGCTAACCGTTCTCCATGTATTGCCTTATCAAAGAGTCGAGTTGTTTGGGAA
TGCAGCTCAAAGTGGGTGGTAAACTCCATCTAAAGCTAAATACTGGTGAGAGACCGATAGCGAACAAGTACTGTGAAG
GAAAGGTGAAAAGAACTTTGAAAAGAGAGTGAAATAGTATGTGAAATTGTTGATAGGGAAGGAAATGAGTGGAGAGT
GGCCGAGGTTTCAGCCGCCCCTCGTGGGCGGTGTACTGCCGACGCCGAGTCATCGATAGCGAGACGAGGGTTACAAAT
GGGAGCGCCTTTCGGGCGTTCTCCCCTAACCCTCCACACTGCCACCGACGACATAATCCACCCATTTCACCCGTCTTGA
AACACGGACCAAGGAGTCTAATGGATATGTGAGTGTTAGGGTGGCAAACCCCAGCGCGCAATGAAAGTGAATGGATTC
GTTCAGAATCGACCGAACTTGATTATTATGACAGTTTTGAGTAAACACATCCATTGGGACCCGAAAGATGGTGAACTAT
GCCTGGATAGGGTGAAGTCAGAGGAAACTCTGATGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTAGGATCT
GGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTC
ATATCAGTTTTATGAGGTAAAGCGAATGATTAGAAGTATTGGGGGCGAAATGCCCTCGGCTTATTCTCAAACTTTAAAT
ATGTAAGAAGCCTTGGTTACTTAATCGAACCGTGGCTACGAATGAAGAGCTTCTAGTGGGCCATTTTTGGTAAGCAGAA
CTGGCGATGCGGGATGAACCGAACGTGGAGTTAAGGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGT
TTATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTCACAACTCACCGGCCGAATGAAC
TAGCCCTGAAAATGGATGGCGCTTAAGCGTGTTACCTATACTCTACCGAGAGGAGGTTTCCTCTCGAGTAGGCAGGCGT
GGGGGTTGTTGAGAAGCGTTGGCCGAGAAGCTGCGTCGAACGGCCCCTAGTGCAGATCTTGGTGGTAGTAGCAAATAT
TCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCGTGTGAACAGCAGTTGGACACGGGTAAGTCGATCCTAA
GGGGTGGCATAACTGTCGCGTACGGCCCGATAAGGGCCTTCTCCAAAAGGGAAGCCGGTTGAAATTCCGGCACTTGGA
TGTGGATTCTCCACGGCAACGTAACTGAATGTGGGGACGGTGGCACAAGTCTTGGAAGGAGTTATCTTTTCTTTTTAAC
GGAGTCAACACCCTGGAATTAGTTTGTCTAGAGATAGGGTATCGTTCCGGAAGAGGGGGGCAGCTTTGTCCCCTCCGAT
GCACTTGTGACGCCCCTTGAAAACCCGCAGGAAGGAATAGTTTTCACGCCAAGTCGTACTGATAACCGCAGCAGGTCT
CCAAGGTGAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAA
GGATTGGCTCTGGGGGTTGGTGGATGGAAGCGTGGGAGACCCCAAGGGACTGGCAGCTGGGCAACTGGCAGCCGGAC
CCGCGGCAGACACTGCGTCGCTCCGTCCACATCATCAACCGCCCCAGAACTGGTACGGACAAGGGGAATCTGACTGTC
TAATTAAAACATAGCTTTGCGATGGTTGTAAAACAATGTTGACGCAAAGTGATTTCTGCCCAGTGCTCTGAATGTCAAA
GTGAAGAAATTCAACCAAGCGCGCGGGTAAACGGCGGGAGTAACTATGCTCTCTTAAGGTAGCCAAATGCCTCGTCAT
CTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATGTAGCGAAACCACAGCCAAGGG
AACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAGAGACATAGG
GGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCCTTATCGTTTCTTTACTTATTTAGTAAGTGGA
AGTGGTTTAACAACCATTTTCTAGCATTCCTTTCCAGGCTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCAC
ATCTGTTAAAAGATAACGCAGATGTCCTAAGGGGGACTCAATGAGAACAGAAATCTCATGTAGAACAAAAGGGTAAA
AGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTTGTTCGGAGTTTG
AACCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTG
ATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAAC
GTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGGACTTGTTGCAATAGTAATTGAACTTAG
TACGAGAGGAACAGTTCATTCGGATAATTGGTGTTTGCTGCTGTCTGACCAGGCAATGCAGCGAAGCACCACCCGCTGG
GTTATGGCCGAACGCCTCCAAGTCAGAACCCATGCCAGAAGGGAAGAATCAGGGGGAAGGAGGGATATGAAGAAGTA
CCGCAGTACCGGAGGGGGAGGGGGGGTGGATAAGGAAACCGCCCGCCCCCCCCCGACTGGAAAGACCCACCCTTGTG
AAATCCATTGTAGACGACTTTAGTATGCGACGAGGTATTGTAAGTAGTAGAGTAGCCTTGTTGTTACGATCTATTGAGA
TTAAGCCTTTGTTGTTTAGATTCGA

Figure 31

Candida lusitaniae rRNA gene (SEQ ID NO: 78)

TTTTGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAAAAATACATTACACATT
GTTTTTGCGAACAAAAAAAATAAATTTTTTTATTCGAATTTCTTAATATCAAAACTTTCAACAACGGATCTCTTGGTTCT
CGCATCGATGAAGAACGCAGCGAATTGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCACA
TTGCGCCTCGAGGCATTCCTCGAGGCATGCCTGTTTGAGCGTCGCATCCCCTCTAACCCCCGGTTAGGCGTTGCTCCGA
AATATCAAGCCGCGCTGTCAAACACGTTTACAGCACGACATTTCGCCCTCAAATCAGGTAGGACTACCCGCTGAGACTT
AAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAAAGCTCAA
ATTTGAAATCCTGCGGGAATTGTAATTTGAAGGTTTCGTGGTCTGAGTCGGCCGCGCCCAAGTCCATTGGAACATGGCG
CCTGGGAGGGTGAGAGCCCCGTATGGCGCACGCCGACTCTTTGTACACCGCGGCTCCGACGAGTCGAGTTGTTTGGGA
ATGCAGCTCTAAGTGGAGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGA
TGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGA
CACGGTTTTACCGGGCCAGCGTCGAAAAGGGGGGAGGAACAAGAACTCGAGAATGTGGCGCGCACCTTCGGGCGCGC
GTGTTATAGCTCGTGTTGACGCCTCCATCCCTTTTCGAGGCCTGCGATTCTAGGACGCTGGCGTAATGGTTGCAAGCCGC
CCGTCTTGAAACACGGACCAAGGAGTCTAACGTCTATGCGAGTGTTTGGGTGCAAAACCCCAGCGCGGAATGAAAGTA
AGAGGTTGGAGCCGCAAGGCGCACAATCGACCGACCCTGAAGTGCTCGGACGGGTTTGAGTAGGAGCATAGCTGTTGG
GACCCGAAAGATGGTGAACTATGCCTGGATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGAC
GTGCAAATCGATCGTCGAATCTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGCTCTTATGCTCTTCCT
GCCGAAGTTCCTGACGCCTCCATCCCTTTTCGAGGCCTGCGATTCTAGGACGCTGGCGTAATGGTTGCAAGCCGCCCGT
CTTGAAACACGGACCAAGGAGTCTAACGTCTATGCGAGTGTTTGGGTGCAAAACCCCAGCGCGGAATGAAAGTAAGAG
GTTGGAGCCGCAAGGCGCACAATCGACCGACCCTGAAGTGCTCGGACGGGTTTGAGTAGGAGCATAGCTGTTGGGACC
CGAAAGATGGTGAACTATGCCTGGATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGC
AAATCGATCGTCGAATCTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCT
CAGGATAGCAGAAGCTCGTTACAAACAGTTTTATGAGGTAAAGCGAATGATTAGAGGTCTCGGGGCGGAAATAGCCTT
AGCCTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGACATACGAATGTAGAGCTTTTAGT
GGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAAGTTAAAGTGCCGGAATGCACGCTCATC
AGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATTCCGCTAAGGAGTGTGT
AACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACTTATACTTCGCCGGCATTTTT
TTTGGAAATGCCGAGTAGGCAGGCGTGGAGGTGGTGACGAAGCCTTGGCTGTGAAGCTGGGTCGAACCGCCTCTAGTG
CAGATCTTGGTGGTAGTAGCAAATATTCAAATGGGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCA
GATGGACATGGGTGAGTCGATCCTAAGAGCTAAGGTAGTTCTGACTGAACAGCTTCTTTGCGAAGTGTGCTCGAAAGG
GAATCCGGTTAAGATTCCGGAACTTGGATGCGGAACTACACGGCAACGTAACTGAATGCGGAGACGCCGGCGTGGGCC
CTGGGAGGAGTTTTCTTTTTCTTCTAACAGCCTGTGACCCTGGAATTGGATTATCCGGAGAGGGGGTTTTGTGGCTGGA
AGAGCGCGGCATCTTCGCCGCGTCCGGTGCGCCTACGACGGTCCTTGAAAATCCGCAGGAAGCAATTGTTTTCGCGCCA
AGTCGTACTGATAACCGCAGCAGGTCTCCAAGGTTAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGG
CAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGAGTGTAAGGGACGGGGGTGACGTGGATGAG
TGTAGTGTGGACGGTGCTGGCTTCAAGGCCGGCGCTGTCTGCGCCGTGCTTGTCCTCCAACCCCCCGTTCCCCGCTTCAA
TAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGTCAGAAA
GTGATGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACG
GCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAG
ATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAG
ACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGA
GTGAAATACCACTACCTCCATCGTTTTTTTACTTACTGAATGAAGGGGAGCTGGTTGTCATGACCACGTTCTGGATTTAA
GCAGCAATGCAATCCCGGTTCAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGC
AGATGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGCCCCCTTGATTTTGATTT
TCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAA
AGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTT
CCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGT
CGTGAGACAGGTTAGTTTTACCCTACTGATGGACCGTTGTTGCAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCA
TTCAGATAATTGGTATTTGGCCCTGTCTGATCAGGCACCGGGCCGAAGCTACCATCTGCTGGATTATGGCTGAACGCCT
CTAAGTCAGAATCCATGCTAGAAGCGACGACTCTGCCTCGCGCGTTGCAGTTGGATACAAATACGATGTGGACCATAC
AAGGCGGCGTTTGGCGGCGGTGCGGAAAGGCGCTGTCGCTGGCTGCGGATAGCAATGTCTCGATGCGCGGGGATAAAT
CCTTTGCATACGACTTAGATGTACAACGGAGTATTGTAAGCGGTAGAGTAGCCTTGTTGTTACGATCCGCTGAGATTAA
GCTCTTGTTGGCTGGTTTGTCTACCTAGA

Figure 32

Candida parapsilosis rRNA gene (SEQ ID NO: 79)

TTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGAATGAAAA
GTGCTTAACTGCATTTTTTCTTACACATGTGTTTTTCTTTTTTTGAAAACTTTGCTTTGGTAGGCCTTCTATATGGGGCCT
GCCAGAGATTAAACTCAACCAAATTTTATTTAATGTCAACCGATTATTTAATAGTCAAAACTTTCAACAACGGATCTCTT
GGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATATTCGTGAATCATCGAATCTTT
GAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCCCTCAAACCCTCGGGTTTGGT
GTTGAGCGATACGCTGGGTTTGCTTGAAAGAAAGGCGGAGTATAAACTAATGGATAGGTTTTTTCCACTCATTGGTACA
AACTCCAAAACTTCTTCCAAATTCGACCTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGG
AAAAGAAACCAACAGGGATTGCCTTAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACTTTCAG
TGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGTCTGGCTCTTGTCTATGTTTCTTGGAACAGAACGTCACAGAGGGT
GAGAATCCCGTGCGATGAGATGTCCCAGACCTATGTAAAGTTCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA
AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAA
AAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGATCAGACTTGGTATTTTGT
ATGTTACTCTCTCGGGGGTGGCCTCTACAGTTTACCGGGCCAGCATCAGTTTGAGCGGTAGGATAAGTGCAAAGAAATG
TGGCACTGCTTCGGTAGTGTGTTATAGTCTTTGTCGATACTGCCAGCTTAGACTGAGGACTGCGGCTTCGGCCTAGGAT
GTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGTCTATGCGAGTGTTTGGGTGTAA
AACCCGTACGCGTAATGAAAGTGAACGTAGGTAGGACCTCCTTTAGGAGTGCACTATCGACCGATCCTGATGTCTTCGG
ATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAA
CTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAA
CCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTATCAGTTTTATGAGGTAAAGCGAATG
ATTAGAAGTCTTGGGGTTGAAATGACCTTAACTTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAA
CGTGGACATATGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGTG
AAGTTAAAGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCGGACGGTGGCCAT
GGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAG
CGTGTTACTTATACTTCGCCGTGAGAGGTTGATATGATGCCCTCACGAGTAGGCAGGCGTGGAGGTCAGTGAAGAAGC
CTTTGCTGTGAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGAACTTTGAA
GACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGAGATGGGGAAGCTCCGT
TTCAATGCGCTTGATTTTTCAAGCCAACCATCGAAAGGGAATCCGGTTAAAATTCCGGAACTTGGATATGGATTCTTCA
CGGCAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTATCTTTTCTTCTTAACAGCTTATCACCCT
GGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAGAGCGCGGTAATTTTGCCGCGTCCGGTGCGCTCACGACGG
TCCTTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTTAACAGC
CTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAG
GATCGGGTGGTTTGGGCCTTGCGTAGAAGTGGTGGTGACTGGCGGCGGGCTGCTTTCGGGCGGACTGCTGTTGGACGTC
GCTATAGACACACTTGGTAGGCATTTATGTCGTCCGGATCACGCTTAACGATCAACTTAGAACTGGTACGGACAAGGGG
AATCTGACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTTGACACAATGTGATTTCTGCCCAGTGCT
CTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAA
TGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACC
ACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGA
AAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCTCTATAGTTTTTTTACTTATT
CAATGAAGCGGAGCTGGAGGTAAAACTCCACGTTCTAGCATTAAGGCCTTTTGGCTGATCCGGGTTGAAGACATTGTCA
GGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAA
ATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTA
TCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCA
AGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTG
GATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAAT
GTTATCGCAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCATTCAGATAATTGGTTTTTGCGGCTGTCTGATCAGG
CAACGCCGCGAAGCTACCATCTGCTGGATTATGGCTGAACGCCTCTAAGTCAGAATCCATGCTAGAAAGCGATGATTTT
TGCCCTGCACATTTTAGATGGATAAGAATAAGACTTTTTAGTCGCTAGACCATAGCAGGCTGGCAACGGTGCGCTTAGC
GGAAAGGCTTTGTGTGCTTGCCGGCGAATAGCAATGTCGACATGCGCGGGGATAAATCCTTTGTATACGACTTAGATGT
ACAACGGAGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGATTAAGCTTCAGTTGTCTGATTTGTCTA
CGAGTTTGCGGGCGAGAG

Figure 33

Candida tropicalis rRNA gene (SEQ ID NO: 80)

CTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGATTTGCTT
AATTGCACCACATGTGTTTTTTATTGAACAAATTTCTTTGGTGGCGGGAGCAATCCTACCGCCAGAGGTTATAACTAAA
CCAAACTTTTTATTTACAGTCAAACTTGATTTATTATTACAATAGTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGC
ATCGATGAAGAACGCAGCGAAATGCGATACGTAATATGAATTGCAGATATTCGTGAATCATCGAATCTTTGAACGCAC
ATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCCCTCAAACCCCCGGGTTTGGTGTTGAGCA
ATACGCTAGGTTTGTTTGAAAGAATTTAACGTGGAAACTTATTTTAAGCGACTTAGGTTTATCCAAAACGCTTATTTTGC
TAGTGGCCACCACAATTTATTTCATAACTTTGACCTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAA
GCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGC
TCTTTCAGAGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGTCTGGCTCTTGTCTATGTTTCTTGGAACAGAACGTCA
CAGAGGGTGAGAATCCCGTGCGATGAGATGATCCAGGCCTATGTAAAGTTCCTTCGAAGAGTCGAGTTGTTTGGGAAT
GCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGG
AAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGATCAGACTT
GGTATTTTGTATGTTACTTCTTCGGGGGGTGGCCTCTACAGTTTATCGGGCCAGCATCAGTTTGGGCGGTAGGAGAATTGC
GTTGGAATGTGGCACGGCTTCGGTTGTGTGTTATAGCCTTCGTCGATACTGCCAGCCTAGACTGAGGACTGCGGTTTAT
ACCTAGGATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGTCTATGCGAGTGTT
TGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGTAGGTGGGGGCCCGTATGGGTGCACCATCGACCGATCCTGAT
GTCTTCGGATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCC
AGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGAC
TAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTATCAGTTTTATGAGGTAA
AGCGAATGATTAGAAGTATTGGGGTTGAAATGACCTTAACTTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGC
TTAATTGAACGTGGACAATTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAA
CCGAACGTGAAGTTAAAGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCGGAC
GGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATG
GCGCTCAAGCGTGCTACTTATACTTCACCGTGATTGCTAATTTATGATGCTTTCACGAGTAGGCAGGCGTGGAGGTCAG
TGAAGAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAG
AACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGAGATGGGG
AAGCTCCGTTTCAAAGCGCTTGATTTTTCAAGCCTACCATCGAAAGGGAATCCGGTTAAAATTCCGGAACTTGGATATG
GATTCTTCACGGTAACGTAACTGAATGTGGAGACGTCGGCATGAGCCCTAGGAGGAGTTATCTTTTCTTCTTAACAGCT
TATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAGAGCGCGGTAATTTTGCCGCGTCTGGTGCGC
TCATGACGGTCCTTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAAGTCGTACTCATAACCGCAGCAGGTCTCCTAG
GTTAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTTCGGGATAAGGAT
TGGCTCTAAGGATCGGGTGTCTTGGGCCTTGTGTAGACGCGGTGGTGACTGATGGCGGGCTGTCTTCGGACGGACTGCT
GCCGGACGCTGCTGTAGACACGCTTGGTAGGTTCTTGTAACCGTCCGGGGCACGCTTAACGATCAACTTAGAACTGGTA
CGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTTGACACAATGTGATTTC
TGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTA
AGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTAT
CTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTT
TGACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCCTCTAGTT
TTTTTACTTATTCAATGAAGCGGAGCTGGAGGTCAAACTCCACGTTCTAGCATTAAGCCTTTTTAGGTGATCCGGGTTGA
AGACATTGTCAGGTGGGGAGTTTGGCTGGGGGCGGGCACATATTGTTTAACGATAACGCAGGTGTCCTAAGGGGGACT
CATGGAGAACAGGAAATCTCCCAGTAGAACAAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAA
CCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATA
ACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGC
AGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGT
TTTACCCTACTGATGAATGTTGTCGCAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCATTCAGATAATTGGTTTTT
GCGGCTGTCTGATCAGGCAACGCCGCGAAGCTACCATCTGCTGGATTATGGCTGAACGCCTCTAAGTCAGAATCCATGC
TAGAACGCGACGATTTTTGCCCTACACATTTTAGATGGATACGAATAAGACTTTATGTCGCTGGACCATAGCAGGCTGG
CAACGGTACACTTAGCGGAAAGGCTTTGTGTGCTTGCCGGCGGATAGCAATGTCAACATGCGTGGGGATAAATCCTTTG
CATACGACTTAGATGTACAACGGAGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGATTAAGCTCTT
GTTGTCTGATTTGTCTAGGTGTAGTACTGT

Figure 34

Chaetomium globosum rRNA gene (SEQ ID NO: 81)

CCAAACTTCGGTCATTTAGAGGAAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATTACAG
AGTTGCAAAACTCCCTAAACCATTGTGAACGTTACCTATACCGTTGCTTCGGCGGGCGGCCCCGGGGTTTACCCCCCGG
GCGCCCCTGGGCCCCACCGCGGGCGCCCGCCGGAGGTCACCAAACTCTTGATAATTTATGGCCTCTCTGAGTCTTCTGT
ACTGAATAAGTCAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTA
ATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCGCCAGCATTCTGGCGGGCATGCCTG
TTCGAGCGTCATTTCAACCATCAAGCCCCCGGGCTTGTGTTGGGGACCTGCGGCTGCCGCAGGCCCTGAAAAGCAGTGG
CGGGCTCGCTGTCGCACCGAGCGTAGTAGCATACATCTCGCTCTGGTCGCGCCGCGGGTTCCGGCCGTTAAACCACCTT
TTAACCCAAGGTTGACCTCGGATCAGGTAGGAAGACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACC
AACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCTTCGGCCCGAGTTGTAAT
TTGCAGAGGAAGCTTTAGGCGCGGCACCTTCTGAGTCCCCTGGAACGGGGCGCCATAGAGGGTGAGAGCCCCGTATAG
TTGGATGCCTAGCCTGTGTAAAGCTCCTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCAAAATGGGAGGTAAATTTC
TTCTAAAGCTAAATACCGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGA
GGGTTAAATAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGTGACCAGACTTGCGCCGGGCGGATCATCCGGTGTTCT
CACCGGTGCACTCCGCCCGGCTCAGGCCAGCATCGGTTCTCGCGGGGGGATAAAGGTCCTGGGAACGTAGCTCCTCCG
GGAGTGTTATAGCCCCGGGGCGTAATGCCCTCGCGGGGACCGAGGTTCGCGCATCTGCAAGGATGCTGGCGTAATGGTC
ATCAGCGACCCGTCTTGAAACACGGACCAAGGAGTCAAGGTTTTGCGCGAGTGTTTGGGTGTAAAACCCGCACGCGTA
ATGAAAGTGAACGTAGGTGAGAGCTTCGGCGCATCATCGACCGATCCTGATGTTTTCGGATGGATTTGAGTAGGAGCGT
TAAGCCTTGGACCCGAAAGATGGTGAACTATGCTTGGATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGC
GGTTCTGACGTGCAAATCGATCGTCAAATCTGAGCATGGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTACC
GCCGAAGTTTCCCTCAGGATAGCAGTGTTGTCTTCAGTTTTATGAGGTAAAGCGAATGATTAGGGACTCGGGGGCGCTT
TTTAGCCTTCATCCATTCTCAAACTTTAAATATGTAAGAAGCCCTTGTTACTTAATTGAACGTGGGCATTCGAATGTACC
AACACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGGGGTTAAGGTGCCGGAGTGG
ACGCTCATCAGACACCACAAAAGGCGTTAGTACATCTTGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAG
GACTGTGTAACAACTCACCTGCCGAATGTACTAGCCCTGAAAATGGATGGCGCTCAAGCGTCCCACCCATACCCCGCCC
TCAGGGTAGAAACGATGCCCTGAGGAGTAGGCGGCCGTGGAGGTCAGTGACGAAGCCTAGGGCGTGAGCCCGGGTCG
AACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTTCAATGAGAACTTGAAGGACCGAAGTGGGGAAAGGTT
CCATGTGAACAGCGGTTGGACATGGGTTAGTCGATCCTAAGCCATAGGGAAGTTCCGTTTCAAAGGGGCACTCGTGCCC
CGTGTGGCGAAAGGGAAGCCGGTTAACATTCCGGCACCTGGATGTGGGTTTTGCGCGGTAACGCAACTGAACACGGAG
ACGACGGCGGGGGCCCCGGGCAGAGTTCTCTTTTCTTCTTAACGGTCCATCACCCTGAAAACAGTTTGTCTGGAGATAG
GGTTTAACGGCCGGAAGAGCCCGACACTTCTGTCGGGTCCGGTGCGCTCTCGACGTCCCTTGAAAATCCGTGGGAGGG
AATAATTCTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTGGTTGATAGAACAATGTA
GATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTTGGGCACGTTGGGCTTTGG
GCGGACGCCCTGGGAGCAGGTCGCCTCTAGCCGGGCAACCGGCGGGGGGCTTCCAGCATCCGGGTGCAGATGCCCTTA
GCAGGCTTCGGCCGTCCGGCGTGCGGTTAACAACCAACTTAGAACTGGTACGGACAGGGGGAATCTGACTGTCTAATT
AAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGA
AGAAATTCAACCAAGCGCGGGTAAACGGGCGGGGAGTAACTATTGACTCTTTCTTAAGGTTAGCCAAATGCCTCGTCAT
TCTAATTAAGTGACGCGCATGAAATGGATTTAACGAGATTCCCAACTGTCCCTTATCTACTATCTAGGCGAAACCACCA
GCCAAGGGAACGGGCTTGGCCAGAATCCAGCGGGGAAAGAAGACCCCTGTTGAGCTTGACTCTAGTTTTGACATTGTG
AAAAGACATAGGGAGGTGTAGAATAGGTGGGGAGCTTCGGCGCCCGGTGAAATACCACTACTCCTATTGTTTTTTTTAC
TTATTCAATGAAGCGGGGCTGGATTTTCGTCCCAACTTCTGGTTTTAAGGTCCTTCGCGGGCCGACCCGGGTTGAAGAC
ATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGGCTCATGGAG
AACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGT
GTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGT
GGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGT
AAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTAC
TGATGAACTCATCGCAATGGTAATTCAGCTTAGTACGAGAGGAACCGCTGATTCAGATAATTGGTTTTTGCGGTTGTCC
GACCGGGCAGTGCCGACGAAGCTACCATCTGCTGGATAATGGCTGAACGCCTCTAAGTCAGAATCCATGCCAGAACGC
GATGATACTACCCGCACGTTGTAGACGTATAAGAATAGGCTCCGGCCTCGTATCTTAGCAGGCGATTCCTCCGCCGGCC
TCGAAGTGGTCGGCGGTAATTCGCGTATTGTAATTTCGGCACGCGCGGGATCAAATCCTTTGCAGACGACTTAGCTGTG
CGAAAGGGGTCCTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGGGTAAGCCCTTCTTCGCCTAGATTTCC
CAGCGAGAGCCCGCCAGCGAA

Figure 35

Coccidioides immitis rRNA gene (SEQ ID NO: 82)

GTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAAGTGGCGTCCGGC
TGCGCACCTCCCCCGCGGGGGTCGCGCGGTCCGTACCTCCCACCCGTGTTTACTGAACTATTGTTGCCTTGGCAGGCCT
GCCGGGCCTCTGGCTGCCGGGGATCGCCCGCCTTGCGCGGCGTCCCGGGCGCGCGCCTGCCAGTGGATCAATTGAACTC
TTATGTGAAGATTGTCAGTCTGAGCATCATAGCAAAAAATCAAACAAAACTTTCAACAACGGATCTCTTGGTTCCGGCA
TCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACA
TTGCGCCCTCTGGTATTCCGGGGGGCATGCCTGTTCGAGCGTCATTGCAAACCCTTCAAGCACGGCTTGTGTGTTGGGC
CAACGTCCCCGCTTGTGTGGACGGGCCTGAAATGCAGTGGCGGCACCGAGTTCCTGGTGTCTGAGTGTATGGGAAATCA
CTTCATCGCTCAAAGACCCGATCGGGGCCGATCTTTTTTTTTTTTTAATATCCGGTTTGACCTCGGATCAGGTAGGAGTA
CCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCG
GCAAAAGCTCAAATTTGAAATCTGGCTCCATGCGGAGCCCGAGTTGTAATTTGGAGAGGACACTTCGGGTGCGGCCAC
GGCATAAGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTCTTTGGCTGCTGGACCGCGCCCATGCGAAGTT
CCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTTCATCTAAAGCTAAATATTGGCCGGAG
ACCGATAGCGCACAAGTAGAGTGATCGAAAGGTTAAAAGCACCTTGAAAAGGGAGTTAAATAGCACGTGAAATTGTTG
AAAGGGAAGCGCTTGCAACCAGACTCGGTCGTGGGGGCTCAGCGGGCATGAGTGCCCGTGTACTCCCCCATGCTCCGG
GCCAGCATCAGTTCTGGCGGTTGGTTAAAGGCCTCTGGAATGTATCGTCCTCCGGGACGTCTTATAGCCAGGGGCGCAA
TGCGGCCAGCCGGGACTGAGGAACGCGCTTCGGCACGGATGCTGGCATAATGGTTGTAAGCGGCCCGTCTTGAAACAC
GGACCAAGGAGTCTAACATCCACGCGAGTGTTCGGGTGTCAAACCCGTGCGCGCAGTGAAAGCGAACGGAGGTGGGA
GCTCCGCAAGGGTGCACCTATCGACCGATCCTGAAGTCTTCGGATGGATTTGAGTAAGAGCGTGGCTGTGTGGGACCCG
AAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAA
ATCGATCGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTGGTAGCTGGTTCCTGCCGAAGTTTCCCTCA
GGATAGCAGTAACGTTTTCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATT
CTCAAACTTTAAATATGTAAGAAGCCCTTGTTACTTAAGTGAATCGTGGGCATTAGAATGGATCGTTACTAGTGGGCCA
TTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACAC
CACAAAAGGTGTTAGTTCATCTAGACAGCCCGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACT
CACGGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCCATACCTCGCCGTCGGGGTAGAAACG
AAGCCCCGACGAGTAGGCAGGCGTGGAGGTTTGTGACGAAGCCTTGGGAGTGATCCCGGGTCGAACAGCCTCTAGTGC
AGATCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAG
TTGGACATGGGTTAGTCGATCCTAAGACATAGGGTAGTTCCGTTTGAAAGCGCGCCCTAGTGCGCCGTTTGTCGAAAGG
GAAGCCGGTTAATATTCCGGCACCTGGATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCAGGAGT
CCTGGGAAGAGTTCTCTTTTCTTCTTGACGGCCTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTCATGGCCGGC
AGAGCCCCGCACCTTTGCGGGGTCCGGTGCGCTCCTGACGACCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCC
AGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCG
GCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTCGGGCGCGTTGGGCCTTGGGGGAAAGCCTCCGG
AGCAGGAGGGCACTAGCCGGGCAACCGGCGGGCGCCTTCCAGCATCGGGGTGCGGACGCCCTTGGCAGGCTTCGGCCG
TCCGGCGCGCGATTAACGACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTG
CGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAA
GCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATG
AATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAAAATC
AGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATATCGGGTGTAGAATAGGTGGG
AGCTTCGGCGCCGGTGAAATACCACTACCTTTATTGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTTACCGCCCA
ACTTCTAGCGTTAAGGTCCTTCGCGGGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACA
TCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAG
TCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAG
GCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGAT
CCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGT
GAGCTGGGTTTAGACCGTCGTGAGACAGGGTTAGTTTTACCCTACTGATGAAGGGTCGCCGCAACGGTAATTCAATTTA
GTACGAGAGGGAACCGTTGATTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGAAGCTACCATCTGC
CGGATTATGGCTGAACGCCTCTAAGTCAGAATCCGTACCGGAACGCGGCGATGTTGCCCCGCACGTTGTAGTTGGATAC
GAATAGGCCTACGGGCCCTGAACCTCAGCAGGTCGGCGACGGCTCCCGGGAAGAGACTCTCGGGCGCCAGCTGACGGA
TTGCAATGTCACCACGCGCGGGGATAGATCCTCTGCAGACGACTGAAATGACCAAGCGGGTCGTGTAAGCGGTCAAGT
AGCCTAGTTGTTACGAGTCGCTGAGCGTCAGCCCGATCCTTGGCTCGATTTGTTGTAAACACCCTCCATCAACATGTTTG
TCTTCGGCAACGCCGG

Figure 36

Coccidioides posadasii rRNA gene (SEQ ID NO: 83)

ATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAAGTGGCGTCCGGCTGC
GCACCTCCCCCCGCGGGGGTTCGCGCCGTCCGTACCTCCCACCCGTGTTTACTGAACCATTGTTGCCTTGGCAGGCCTGC
CGGGCCTCCGGCTGCCGGGGATCGCCCGTCTTGCGCGGCGTCCCGGGCGCGCGCCTGCCAGCGGATCAATTGAACTCTT
ATGTGAAGATTGTCAGTCTGAGCATCATAGCAAAAATCAAACAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATCG
ATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTG
CGCCCTCTGGTATTCCGGGGGGCATGCCTGTTCGAGCGTCATTGCAAACCCTTCAAGCACGGCTTGTGTGTTGGGCCAA
CGTCCCCGCTTGTGTGGACGGGCCTGAAATGCAGTGGCGGCACCGAGTTCCTGGTGTCTGAGTGTATGGGAAATCACTT
CATCGCTCAAAGACCCGATCGGGGCCGATCTCTTTTTTTTATTATATCCGGTTTGACCTCGGATCAGGTAGGAGTACCCG
CTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAA
AAGCTCAAATTTGAAATCTGGCTCCATGCGGAGCCCGAGTTGTAATTTGGAGAGGACACTTCGGGTGCGGCCACGGCA
TAAGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTCTTTGGCTGCTGGACCGCGCCCATGCGAAGTTCCTT
CGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTTCATCTAAAGCTAAATATTGGCCGGAGACCG
ATAGCGCACAAGTAGAGTGATCGAAAGGTTAAAAGCACCTTGAAAAGGGAGTTAAATAGCACGTGAAATTGTTGAAA
GGGAAGCGCTTGCAACCAGACTCGGTCGTGGGGGCTCAGCGGGCATGCGTGCCCGTGTACTCCCCCATGCTCCGGGCC
AGCATCAGTTCTGGCGGTTGGTTAAAGGCCTCTGGAATGTATCGTCCTCCGGGACGTCTTATAGCCAGGGGCGCAATGC
GGCCAGCCGGGACTGAGGAACGCGCTTCGGCACGGATGCTGGCATAATGGTTGTAAGCGGCCCGTCTTGAAACACGGA
CCAAGGAGTCTAACATCCACGCGAGTGTTCGGGTGTCAAACCCGTGCGCGCAGTGAAAGCGAACGGAGGTGGGAGCCC
GCAAGGGTGCACCATCGACCGATCCTGAAGTCTTCGGATGGATTTGAGTAAGAGCGTGGCTGTTGGGACCCGAAAGAT
GGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGAT
CGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTGGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAG
CAGTAACGTTTTCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAA
CTTTAAATATGTAAGAAGCCCTTGTTACTTAAGTGAACGTGGGCATTAGAATGGATCGTTACTAGTGGGCCATTTTTGG
TAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACACCACAAA
AGGTGTTAGTTCATCTAGACAGCCCGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACGGG
CCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCCATACCTCGCCGTCGGGGTAGAAACGAAGCCC
CGACGAGTAGGCAGGCGTGGAGGTTTGTGACGAAGCCTTGGGAGTGATCCCGGGTCGAACAGCCTCTAGTGCAGATCT
TGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGAC
ATGGGTTAGTCGATCCTAAGACATAGGGTAGTTCCGTTTGAAAGCGCGCCCTAGTGCGCCGTTTGTCGAAAGGGAAGCC
GGTTAATATTCCGGCACCTGGATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCAGGAGTCCTGGG
AAGAGTTCTCTTTTCTTCTTGACGGCCTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTCATGGCCGGCAGAGCC
CCGCACCTTTGCGGGGTCCGGTGCGCTCCTGACGACCCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGT
ACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAAT
AGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTCGGGCGCGTTGGGCCTTGGGGGAAAGCCTCCGGAGCAGGA
GGGCACTAGCCGGGCAACCGGCGGGCGCCTTCCAGCATCGGGGTGCGGACGCCCTTGGCAGGCTTCGGCCGTCCGGCG
CGCGATTAACGACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGC
CAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGG
TAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATT
AACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAAAATCAGCGGGGA
AAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATATCGGGTGTAGAATAGGTGGGAGCTTCGG
CGCCGGTGAAATACCACTACCTTTATTGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTTACCGCCCAACTTCTAG
CGTTAAGGTCCTTCGCGGGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAA
ACCATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTG
ATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAG
GTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGA
TGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGG
GTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTTAGTACGAGAG
GAACCGTTGATTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGAAGCTACCATCTGCCGGATTATGG
CTGAACGCCTCTAAGTCAGAATCCGTACCGGAACGCGGCGATGTTGCCCCGCACGTTGTAGTTGGATACGAATAGGCCT
ACGGGCCCTGAACCTCAGCAGGTCGGCGACGGCTCCCGGGAAGAGACTCTCGGGCGCCAGCTGACGGATTGCAATGTC
ACCACGCGCGGGGATAGATCCTCTGCAGACGACTGAAATGACCAAGCGGGTCGTGTAAGCGGTCGAGTAGCCTAGTTG
TTACGAGTCGCTGAGCGTCAGCCCGATCCTTGGCTCGATTTGTTGTAAACACCCTCC

Figure 37

Cryptococcus neoformans rRNA gene (SEQ ID NO: 84)

AGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCAGTAGAGAATATTGGACTTTGGTCC
ATTTATCTACCCATCTACACCTGTGAACTGTTTATGTGCTTCGGCACGTTTTACACAAACTTCTAAATGTAATGAATGTA
ATCATATTATAACAATAATAAAACTTTCAACAACGGATCTCTTGGCTTCCACATCGATGAAGAACGCAGCGAAATGCGA
TAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCAACTTGCGCCCTTTGGTATTCCGAAGGGCA
TGCCTGTTTGAGAGTCATGAAAATCTCAATCCCTCGGGTTTTATTACCTGTTGGACTTGGATTTGGGTGTTTGCCGCGAC
CTGCAAAGGACGTCGGCTCGCCTTAAATGTGTTAGTGGGAAGGTGATTACCTGTCAGCCCGGCGTAATAAGTTTCGCTG
GGCCTATGGGGTAGTCTTCGGCTTGCTGATAACAACCATCTCTTTTTGTTTGACCTCAAATCAGGTAGGGCTACCCGCTG
AACTTAAGCATATCAATAAGCGGAGGAAAAGAAACTAACAAGGATTCCCTTAGTAACGGCGAGTGAACCGGGAAGAG
CTCAAATTTGAAATCTGGCGTCCTCCGGGCGTCCGAGTTGTAATCTACAGAAACGTTTTCCGTGCTGGACCGTGTCTAA
GTCCCTTGGAATAGGGTATCAAAGAGGGTGACAATCCCGTACTTGACACGATCACCAGTGCTCTGTGATACGTTTTCTA
CGAGTCGCGTTACTTGGGAGTGTAGCGCAAAATGGGTGGTAAACTCCATCTAAAGCTAAATATTGGTGGAAGACCGAT
AGCGAACAAGTACCGTGAGGGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAACAGTACGTGAAATTGTTGAAAGG
GAAACGATTGAAGTCAGTCGTGTCTATTGGGTTCAGCCAGTTCTGCTGGTGTATTCCCTTTAGACGGGTCAACATCAGTT
CTGATCGGTGGATAAGGGCTGGAGGAATGTGGCACTCTTCGGGGTGTGTTATAGCCTCCTGTCGCATACACTGGTTGGG
ACTGAGGAATGCAGCTCGCCTTTATGGCCGGGGTTCGCCCACGTTCGAGCTTAGGATGTTGACAAAATGGCTTTAAACG
ACCCGTCTTGAAACACGGACCAAGGAGTCTAACATATCTGCGAGTGTTTGAGTGTCAAACTCGAGCGCGAAATGAAAG
TGAATGTAGGAGGGATCCGCAAGGAGCACCTTCGACCGATCCGGATCTTCTGTGATGGATTTGAGTAAGAGCATATAT
GCTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGCGAAGCCAGGGGAAACTCTGGTGGAGGCTCGTAGCGATT
CTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGA
AGTTTCCCTCAGGATAGCAGAAACTCGCATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGACGAAACG
TCCTTAACCTATTCTCAAACTTTAAATGTGTAAGAAGCACTTGTCACTTAATTGGACGAGCGCATGCGAATGAGAGTTT
CTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGATCGTGAGGTTAAGGTGCCGGAATACACGC
TCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGT
GTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGTTACCCATACCTCACCGTCAG
CGTTGTAGTGACGCGCTGACGAGTAGGCAGGCGTGGAGGTCAGTGTAGAAGCCTAGGCAGTGATGTCGGGTGGAACGG
CCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAGTGAGAACCTTGAAGACTGAAGTGGAGAAAGGTTCCATG
GTAACAGCAGTTGGACATGGGTCAGTCGATCCTAAGAGATAGGGAAACTCCGTTTTAAAGCGCACGATTTTCCGTGCCG
CCTATCGAAAGGGAATCCGGTTAAGATTCCGGAACCAGGATGTGGATCATTGACGGTAACGTAAATGAAGTTGGAGAC
GTCGGCAAGGGCCCTGGGAAGAGTTCTCTTTTCTCCTTAACCGCCTACGACCTCGAAATCGGATTATCCGGAGCTGAGG
TTATATGGTGGGTAAAGCACAACACCTCTGTTGTGTCCGGTGCGTCCTTGACGATCCTTGAAAATCCGACGGAACGTAT
AAGTCTCACGCCTGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTGATGGAACAATGTAGAT
AAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGTGCGTCGGGCCGTTGACG
GAAGGAAGCTGGACCTGGCGGGACTGCATGGGGCAACCTGTGTGGACCTGCTGGGATCGGCGACTGGAAGTCTTTGGC
AGCCCTCGGGCGTCCGGCGTACGCTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAA
AACATAGCATTGCGATGGCCAGAAAATGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAG
AAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTA
GTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGG
CTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATGGAGGGTGT
AGAATAAGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCTCCATCGTTTTTTTACTTATTCAATGAAGCGGAGCTGG
GATGAAAGTCCCACCTTCTAGCGTTAAGGTCGTTTACCGGCCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGG
CTGGGGCGGCACATCTGTTAAAAAATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTGGAAC
AAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTC
CCTCGGAGTTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCG
ACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCA
CTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGGAGTGTCGTCGTAATA
GTAATTGAGGGTAGTACGAGAGGAACTGCTCATTCGTATAATTGGTATTTGCGTCTGTCCGATCGGGCAATGACGCGAA
GCTATCATACGCCAGATTATGGCTGAACGCCTCTAAGTCAGAATCTGTACTAGAAACGACGATTTTGGTCCCGCACATG
TTAGTTGTGTTTAAATAGGCTTCGGCTGTGAACCATATCTGAGGGTTGGGCTGCTTAGGCGGAAAGGCTTAGGTAGTCT
CCTTCGTATTGAAATGGAATATGGGCGGGGGTAAATCCTTTGCAGACGACTTGAATGGGAACGGGGTGCTGTAAGTGG
TAGAGTAGCCTTGTTGCTACGATCCACTGAGGCTAAGCCCTTGTTCTATAGATTTGTCTCTAACATGTTGGGTCTC

Figure 38

Fusarium graminearum rRNA gene (SEQ ID NO: 85)

CGGAAAGCTCTCCAAACTCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGA
TCATTACCGAGTTTACAACTCCCAAACCCCTGTGAACATACCTTATGTTGCCTCGGCGGATCAGCCCGCGCCCCGTAAA
AAGGGACGGCCCGCCGCAGGAACCCTAAACTCTGTTTTTAGTGGAACTTCTGAGTATAAAAAACAAATAAATCAAAAC
TTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTC
AGTGAATCATCGAATCTTTGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAAC
CCTCAAGCCCAGCTTGGTGTTGGGAGCTGCAGTCCTGCTGCACTCCCCAAATACATTGGCGGTCACGTCGAGCTTCCAT
AGCGTAGTAATTTACACATCGTTACTGGTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGG
ATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCTAGTAAC
GGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCTTTCGGGCCCGAGTTGTAATTTGTAGAGGATGATTTTGAT
GCGGTGCCTTCCGAGTTCCCTGGAACGGGACGCCATAGAGGGTGAGAGCCCCGTCTGGTTGGATGCCAAATCTCTGTAA
ATCTCCTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCTAAATGGGAGGTATATGTCTTCTAAAGCTAAATACCGGCC
AGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGTACGTGAAAT
TGTTGAAAGGGAAGCGTTTATGACCAGACTTGGGCTTGGTTAATCATCTGGGGTTCTCTCCAGTGCACTTTTCCAGTCCA
GGCCAGCATCAGTTTTCGCCGGGGGATAAAGGCTTCGGGAATGTGGCTCCCCTCGGGGAGTGTTATAGCCCGTTGTGTA
ATACCCTGGTGGGGACTGAGGTTCGCGCTTCTGCAAGGATGCTGGCGTAATGGTCATCAACGACCCGTCTTGAAACACG
GACCAAGGAGTCGTCTTCGTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGTAATGAAAGTGAACGCAGGTGAGAGC
TTCGGCGCATCATCGACCGATCCTGATGTTCTCGGATGGATTTGAGTAAGAGCATACGGGGCCGGACCCGAAAGAAGG
TGAACTATGCCTGTGTAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCG
TCAAACATGGGCATGGGGGCGAAAGACTAATCGAACCTTCTAGTAGCTGGTTTCCGCCGAAGTTTCCCTCAGGATAGCA
GTGTTGAACTCAGTTTTATGAGGTAAAGCGAATGATTAGGGACTCGGGGGCGCTATTTAGCCTTCATCCATTCTCAAAC
TTTAAATATGTAAGAAGCTCTTGTTGCTTAATTGAACGTGAGCATTCGAATGTATCAACACTAGTGGGCCATTTTTGGTA
AGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCAGAGTAGACGCTCATCAGACACCACAAAAG
GTGTTAGTACATCTTGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGACTGTGTAACAACTCACCTGCC
GAATGTACTAGCCCTGAAAATGGATGGCGCTCAAGCGTCTCACCCATACCTCGCCCTCAGGGTAGAAACGAAGCCCTG
AGGAGTAGGCGGACGTGGAGGTCAGTGACGAAGCCTAGGGCGTGAGCCCGGGTTGAACGGCCTCTAGTGCAGATCTTG
GTGGTAGTAGCAAATACTTCAATGAGAACTTGAAGGACCGAAGTGGGGAAAGGTTCCATGTGAACAGCGGTTGGACAT
GGGTTAGTCGATCCTAAGCTATAGGGAAGTTCCGTTTCAAAGGCGCACTTTGCGCCGTCTAGCGAAAGGGGAGCCGGT
CAATATTCCGGCACCTGGATGTGGGTTTTGCGCGGCAACGCAACTGAACGTGGAGACGACGGCGGGGGCCCCAAGCAG
AGTTCTCTTTTCTTCTTAACAGTCTCTCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAATGGCTGGAAGAGCCCGG
CACCTCTGCCGGGTTTGGTGCGCTCTCGACGTCCCTTGAAAATCCACGGGAAGAAATAATTCTCACGCCAGGTCGTACT
CATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTGGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGA
TCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTTGGGCACGTTGGGCCTTGGGCGGACGTCCTGGGAGCAGGCAGC
CACTAGTCGGGCAACCGACCGGAGGCGGCCAGCATCCGGGTGCTGATGCCCTTGGCAGGCTTCGGCCGTCCGGCGTGC
GGTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAG
AAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGTAATTCAACCAAGCGCGGGTAA
ACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAAC
GAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAG
AAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGAGGTGTAGAATAGGTGGGAGCTTCGGCGC
CGGTGAAATACCACTACTCCTATTGTTTTTTTACTTATTCAATGAAGCGGGGCTGGATTTACGTCCAACTTCTGGTTTTA
AGGTCCTTCGCGGGCCGACCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCA
TAACGCAGGTGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTT
TGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGACATTTGAGGCTAGAGGTGC
CAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTGATCCTTCGATGTC
GGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTT
AGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCTCACCGCAATGGTAATTCAGCTTAGTACGAGAGGAACC
GCTGATTCAGATAATTGGTTTTTGCGGCTGTCCGACCGGGCAGTGCCGCGAAGCTACCATCTGCTGGATAATGGCTGAA
CGCCTCTAAGTCAGAATCCATGCCAGAACGCGGTGATACCACCCGCACGTATAGATGGACAAGAATAGGCCTCGGCTT
AGCGTCTTAGCAGGCGATTCCTCCACGGCGCTCGAAGCGCGTCGTGGTATTTCGCGTATTGTAATTTCAACACGAGCGG
GGTCAAATCCTTTGCAGACGACTTAGCTGTGCGAAACGGTCCTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCT
GAGGGTAAGCCGTCCTTCGCCTCGATTTCCCCAACGATGACTCTCGCAGGGCGAGGGCGTGG

Figure 39

Fusarium oxysporum rRNA gene (SEQ ID NO: 86)

GCCGGAAAGCTCTCCAAACTCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGG
GATCATTACCGAGTTTACAACTCCCAAACCCCTGTGAACATACCACTTGTTGCCTCGGCGGATCAGCCCGCTCCCGGTA
AAACGGGACGGCCCGCCAGAGGACCCCTAAACTCTGTTTCTATATGTAACTTCTGAGTAAAACCATAAATAAATCAAA
ACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAA
TTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCTGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCA
ACCCTCAAGCACAGCTTGGTGTTGGGACTCGCGTTAATTCGCGTTCCCCAAATTGATTGGCGGTCACGTCGAGCTTCCA
TAGCGTAGTAGTAAAACCCTCGTTACTGGTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGACCTCG
GATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCTAGTA
ACGGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCTCTCGGGCCCGAGTTGTAATTTGTAGAGGATACTTTTG
ATGCGGTGCCTTCCGAGTTCCCTGGAACGGGACGCCATAGAGGGTGAGAGCCCCGTCTGGTTGGATGCCAAATCTCTGT
AAAGTTCCTTCAACGAGTCGAGTAGTTTGGGAATGCTGCTCTAAATGGGAGGTATATGTCTTCTAAAGCTAAATACCGG
CCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGTACGTGAA
ATTGTTGAAAGGGAAGCGTTTATGACCAGACTTGGGCTTGGTTAATCATCTGGGGTTCTCCCCAGTGCACTTTTCCAGTC
CAGGCCAGCATCAGTTTTCCCCGGGGGATAAAGGCGGCGGGAATGTGGCTCTCTTCGGGGAGTGTTATAGCCCACCGT
GTAATACCCTGGGGGGGACTGAGGTTCGCGCATCTGCAAGGATGCTGGCGTAATGGTCATCAACGACCCGTCTTGAAA
CACGGACCAAGGAGTCGTCTTCGTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGTAATGAAAGTGAACGCAGGTGA
GAGCTTCGGCGCATCATCGACCGATCCTGATGTTCTCGGATGGATTTGAGTAAGAGCATACGGGGCCGGACCCGAAAG
AAGGTGAACTATGCCTGTATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCG
ATCGTCAAATATGGGCATGGGGGCGAAAGACTAATCGAACCTTCTAGTAGCTGGTTTCCGCCGAAGTTTCCCTCAGGAT
AGCAGTGTTGAACTCAGTTTTATGAGGTAAAGCGAATGATTAGGGACTCGGGGGCGCTATTTAGCCTTCATCCATTCTC
AAACTTTAAATATGTAAGAAGCTCTTGTTGCTTAATTGAACGTGAGCATTCGAATGTATCAACACTAGTGGGCCATTTTT
GGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCAGAGTAGACGCTCATCAGACACCACA
AAAGGTGTTAGTACATCTTGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGACTGTGTAACAACTCACC
TGCCGAATGTACTAGCCCTGAAAATGGATGGCGCTCAAGCGTCTCACCCATACCTCGCCCTCAGGGTAGAAACGATGC
CCTGAGGAGTAGGCGGACGTGGAGGTCAGTGACGAAGCCTAGGGCGTGAGCCCGGGTTGAACGGCCTCTAGTGCAGAT
CTTGGTGGTAGTAGCAAATACTTCAATGAGAACTTGAAGGACCGAAGTGGGGAAAGGTTCCATGTGAACAGCGGTTGG
ACATGGGTTAGTCGATCCTAAGCCATAGGGAAGTTCCGTTTCAAAGGTGCACTTTGCACCGTCTGGCGAAAGGGAAGC
CGGTCAATATTCCGGCACCTGGATGTGGGTTTTGCGCGGCAACGCAACTGAACGTGGAGACGACGGCGGGGGCCCCGG
GCAGAGTTCTCTTTTCTTCTTAACAGTCTCTCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAATGGCTGGAAGAGC
CCAGCACCTCTGCTGGGTCCGGTGCGCTCTCGACGTCCCTTGAAAATCCACGGGAGGAAATAATTCTCACGCCAGGTCG
TACTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTGGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAA
TAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGCACGTTGGGCCTTGGGCGGACGCCTTGGGAGCAGG
CTGCCACTAGTCGGGCAACCGACCGGCGGCGGCCAGCATCCGAGTGTTGATGCCCTTGGCAGGCTTCGGCCGTCCGGC
GTGCGGTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGG
CCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGTAATTCAACCAAGCGCGG
GTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGAT
TAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGG
AAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGAGGTGTAGAATAGGTGGGAGCTTCG
GCGCCGGTGAAATACCACTACTCCTATTGTTTTTTTACTTATTCAATGAAGCGGCGCTGGATTTACGTCCAACTTCTGGT
TTTAAGGTCCTTCGCGGGCCGAGCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAA
CCATAACGCAGGTGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGA
TTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGACATTTGAGGCTAGAGGT
GCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTGATCCTTCGATG
TCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGT
TTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCTCACCGCAATGGTAATTGAGCTTAGTACGAGAGGAA
CCGCTCATTCAGATAATTGGTTTTTGCGGCTGTCCGACCGGGCAGTGCCGCGAAGCTACCATCTGCTGGATAATGGCTG
AACGCCTCTAAGTCAGAATCCATGCCAGAACGCCGGTGATACCACCCGCACGTATAGATGGACAAGAATAGGCTTCGGC
TTAGCGTCTTAGCAGGCGATTCTTCCACGGCGCTCGAAGCGCGTCGTGGTATTTCGCGTATTGTAATTTCAACACGAGC
GGGGTCAAATCCTTTGCAGACGACTTAGCTGTGCGAAACGGTCCTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTG
CTGAGGGTAAGCCGTCCTTCGCCTCGATTTCCCCAATGGGTTCTCCGGATTTCTGGAGACTTG

Figure 40

Histoplasma capsulatum rRNA gene (SEQ ID NO: 87)

GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCACGCCGTGGGG
GGCTGGGAGCCTCTGACCGGGACCCCTCCGCCCTCCTACCCGGCCACCCTTGTCTACCGGACCTGTTGCCTCGGCGGTC
CTGCAGCGATGCTGCCGGGGGAGCTTCTCCTCCCCGGGCCCGTGTCCGCCGGGGACACCGCAAGAACCGTCGGTGAAT
GATTGGCGTCTGAGCATGAGAGCGATAATAATCCAGTCAAAACTTTCAACAACGGATCTCTTGGTTCCGACATCGATGA
AGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCC
CCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCAACCCTCAAGCGCGGCTTGTGTGTTGGGCCATCGTCCC
CCTGACCGGTGGGACGTGCCCGAAATGCAGTGGCGGTGTCGAGTTCCGGTGCCCGAGTGTATGGGGCTTTGCCACCCG
CTCTGGAGGCCCGGCCGGCTCCGGCCCACCATCTCAACCTCCTTTTTCACACCAGGTTGACCTCGGATCAGGTAGGGAT
ACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGC
GGCAAGAGCTCAAATTTGAAATCCGGCCCCTCTGGGGGCCTGAGTTGTAATTTGCAGAGGATGCTTCGGGCGCGACCG
CGGTCCAAGTCCCCTGGAACGGGGCGTCGTAGAGGGTGAGAATCCCGTCTCCGGCCGGCCGGTCTCGCCCGTGTGAAG
CTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATACTGGTCGG
AGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCATGTGAAATTG
TTGAAAGGGAAGCGCTTGCGATCAGAGTCGGCCGCGGGGGTTCAGCGGGCATTCGTTGCCCGTGCAATCCCCCGCGGC
CGGGCCAGCGTCGGTTTCGACGGCCGGTCAAAGGCCCCCGGAATGTGTCGCCTCTCGGGGCGTCTTATAGCCGGGGGT
GCAATGCGGCCAGTCGGGACCGAGGAACGCGCTCCGGCACGGACGCTGGCTTAATGGTCGTCAGCGACCCGTCTTGAA
ACACGGACCAAGGAGTCTAACATCCACGCGAGTGTTCGGGTGTCAAACCCGTCCGCGCAGTGAAAGCGAATGGAGGTG
GGAACCCCTGAGGGTGCACCATCGACCGATCCTGAAGTTTTCGGATGGATTTGAGTAGGAGCGTGGCTGTTGGGACCC
GAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCA
AATCGATCGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTGGTAGCTGGTTCCTGCCGAAGTTTCCCTC
AGGATAGCAGTAACGTTTTCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTAT
TCTCAAACTTTAAATATGTAAGAAGCCCTTGTTACTTCGTTGAACGTGGGCACTGGAATGGATCGTTACTAGTGGGCCA
TTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACAC
CACAAAAGGTGTTAGTTCATCTAGACAGCCCGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACT
CACGGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCCATACCTCGCCGTCGGGGTAGGATCG
ATGCCCCGACGAGTAGGCAGGCGTGGAGGTCCGTGACGAAGCCCGGGGAGTGATCCCGGGTCGAACGGCCTCTAGTGC
AGATCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAG
TTGGACATGGGTTAGTCGATCCTAAGACATAGGGAAATTCCGTTTGAAAGCGCGCCCTCGTGCGCCGTCCGTCGAAAGG
GAAGCCGGTTAACATTCCGGCACCTGGATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCGGGGGT
CCTGGGAAGAGTTCTCTTTTCTTCTTGACGGCCTGTCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTCAATGGCCGGC
AGAGCCCCGCACCTTTGCGGGGTCCGGTGCGCCCCCGACGACCCTTGAAAATCCGCGGGAGGGAATAGTTTTCACGCC
AGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCG
GCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTTGGGCACGTTGGGCCTTGGGCGGAGACCTCTGG
AGCAGGGGGGCACTAGCCGGGCAACCGGTGGGGGCCCTCCAGCATCGGGGCGTGGACGCCCTCGGCAGGCTTCGGCC
GTCCGGCGTGCGATTAACAACCGACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATT
GCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCA
AGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCAT
GAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCGGAAT
CAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATATCGGGTGTAGAATAGGTGG
GAGCTTCGGCGCCGGTGAAATACCACTACCTTTATCGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTCACCGCCC
AACTTCTGGCGTTAAGGTCCCTCGCGGACCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCA
CATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAA
AGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTG
AGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTT
GATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAA
CGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTT
AGTACGAGAGGAACCGTTGATTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGC
CGGATTATGGCTGAACGCCTCTAAGTCAGAATCCGTGCCGGAACGCGGCGATGTCGCCCCGCACGTCGTAGTTGGATA
CGAATAGGCCTCCGGGTCCAGAACCTCAGCAGGCCGGCGATGGTGTTCCGGGGAGAGACCCCCGGGGACCCGCCGGCG
GATTGCAATGTCACCACGCGCGGGGATAGATCCTCTGCAGACGACTGAAATGACCAAGCGGGTCGTGTAAGCGGTCAA
GTAGCCTTGTTGCTACGAGTCGCTGAGCGTCAGCCCGATCCTTGGCTCGATTTGTTGTAACAACCCCC

Figure 41

Hypocrea jecorina rRNA gene (SEQ ID NO: 88)

TCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATTACCGAGTTTACA
ACTCCCAAACCCCAATGTGAACGTTACCAATCTGTTGCCTCGGCGGGATTCTCTGCCCCGGGCGCGTCGCAGCCCCGGA
TCCCATGGCGCCCGCCGGAGGACCAACTCAAACTCTTTTTTCTCTCCGTCGCGGCTTCCGTCGCGGCTCTGTTTTACCTT
TGCTCTGAGCCTTTCTCGGCGACCCTAGCGGGCGTCTCGAAAATGAATCAAAACTTTCAACAACGGATCTCTTGGTTCT
GGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACG
CACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTCCGAGCGTCATTTCAACCCTCGAACCCCTCCGGGGGGTCGG
CGTTGGGGATCGGCCCCTCACCGGGCCGCCCCCGAAATACAGTGGCGGTCTCGCCGCAGCCTCTCCTGCGCAGTAGTTT
GCACACTCGCACCGGGAGCGCGGCGCGGCCACAGCCGTAAAACACCCCAAACTCTGAAATGTTGACCTCGGATCAGGT
AGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCCAGTAACGGCGAG
TGAAGCGGCAACAGCTCAAATTTGAAATCTGGCCCTTTCGGGTCCGAGTTGTAATTTGTAGAGGATGCTTTTGGCAAGG
CGCCGCCCGAGTTCCCTGGAACGGGACGCCACAGAGGGTGAGAGCCCCGTCTGGCTGGCCGCCGAGCCTCTGTAAAGC
TCCTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCAAAATGGGAGGTATATGTCTTCTAAAGCTAAATATTGGCCAGA
GACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACCTTGAAAAGAGGGTTAAATAGTACGTGAAATTGTT
GAAAGGGAAGCGCTTGTGACCAGACTTGGGCGCGGCGGATCATCCGGGGTTCTCCCCGGTGCACTTCGCCGTGTCCAG
GCCAGCATCAGTTCGTCGCGGGGGAAAAAGGCTTCGGGAACGTGGCTCCCCTGGGAGTGTTATAGCCCGTTGCATAAT
ACCCTGCGGTGGACTGAGGACCGCGCATCTGCAAGGATGCTGGCGTAATGGTCACCAGCGACCCGTCTTGAAACACGG
ACCAAGGAGTCGTCTTCGTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGTAATGAAAGTGAACGCAGGTGAGAGCT
TCGGCGCATCATCGACCGATCCTGATGTTCTCGGATGGATTTGAGTAAGAGCATACGGGGCCGGACCCGAAAGAAGGT
GAACTATGCCTGTATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGT
CAAATATGGGCATGGGGGCGAAAGACTAATCGAACCTTCTAGTAGCTGGTTTCCGCCGAAGTTTCCCTCAGGATAGCA
GTGTTGAACTCAGTTTTATGAGGTAAAGCGAATGATTAGGGACCCGGGGGCGCTATATTGCCTTCATCCATTCTCAAAC
TTTAAATATGTAAGAAGCCCTTGTTGCTTAATTGAACGTGGGCATTCGAATGTATCAACACTAGTGGGCCATTTTTGGTA
AGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCAGAGTAGACGCTCATCAGACACCACAAAAG
GCGTTAGTACATCTTGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGACTGTGTAACAACTCACCTGCC
GAATGTACTAGCCCTGAAAATGGATGGCGCTCAAGCGTCTCACCCATACCTCGCCCTCGGGGTAGAAACGATGCCCCG
AGGAGTAGGCGGACGTGGAGGTCGTGACGAAGCCTAGGGCGTGAGCCCGGGTCGAACGGCCTCTAGTGCAGATCTTGG
TGGTAGTAGCAAATACTTCAATGAGAACTTGAAGGACCGAAGTGGGGAAAGGTTCCATGTGAACAGCGGTTGGACGTG
GGTTAGTCGATCCTAAGCCATAGGGAAGTTCCGTTTCAAAGGCGCACTTCGCGCCGTTTGGCGAAAGGGGAGCCGGTC
AATATTCCGGCACCTGGATGTGGGTTTTGCGCGGCAACGCAACTGAACGCGGAGACGACGGCGGGGGCCCCGGGCAGA
GTTCTCTTTTCTTCTTAACAGTCTATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAATGGCTGGAAGAGCCCAGC
ACCTCTGCTGGGTCCGGTGCGCCCTCGACGTCCCTTGAAAATCCGCGGGAAGGAATAATTCTCACGCCAGGTCGTACTC
ATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTGGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGAT
CCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGCACGTTGGGCTTTGGACGGACGCCTCGGGAGCAGGCGGCC
ACTAGCCGGGCAACCGGCCGGCGGCTGCCAGCATCTGGGTGCTGATGTCCCTTGCAGGCTTCGGCCGTCCGGCGTGCG
GTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGA
AAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGTAATTCAACCAAGCGCGGGTAAAC
GGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGA
GATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAA
GACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGAGGTGTAGAATAGGTGGGAGCTTCGGCGCCG
GTGAAATACCACTACTCCTATTGTTTTTTTACTTATTCAATGAAGCGGGGCTGGATTTACGTCCAACTTCTGGTATTAAG
GTCCTTCGCGGGCCGACCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCATA
ACGCAGGTGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTG
ATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGACATTTGAGGCTAGAGGTGCCA
GAAAAGTTACCACAGGGATAACTGGCTTGTGGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTGATCCTTCGATGTCGG
CTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAG
ACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCTCACCGCAATGGTAATTGAGCTTAGTACGAGAGGAACCGC
TCATTCAGATAATTGGTTTTTGCGGCTGTCCGACCGGGCAGTGCCGCGAAGCTACCATCTGCTGGATAATGGCTGAACG
CCTCTAAGTCAGAATCCATGCCAGAACGCGGTGATAGCACCCGCACGTATAGACGGACAAGAATAGGCTTCGGCTTAG
TGTCTCAGCAGGCGATTCCTCCGCGGTCCTCGAAGCGGGCCGCGGTATTTCGCGTATTGTAATTTCAACACGAGCGGGG
TTAAATCCTTTGCAGACGACTTAGCTGTGCGAAACGGTCC

Figure 42

Lodderomyces elongisporus rRNA gene (SEQ ID NO: 89)

TTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGAATTTTGAGAATTGT
GCTTAACTGCACTTTTCTTATCTACACACGTGTTTTTGTTTTATTCTTAAAACTTGCTTTGGCAGTGGCTGCTTAATTGCT
CTGCTGCCAGAGGATAAACTCAACCTAAATTTTTTATTTTAAACTAGTCAACTGATTATATTTATTAATAGTCAAAACTT
TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATATTCG
TGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTTTGAGCGTCATTTCTCCCTC
AAACCCCCGGGTTTGGTGATGAGCAATACGCCAGGTTTGCTTGAAAGTTAGGAGGAGTATTTATAACAATGTATTAGGT
CTAACCACTCCATTGTGCTTAATAAAAAGCTCCAATCTATATTTCAAACTTCGACCTCAAATCAGGTAGGATTACCCGCT
GAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAGCGGCGAGTGAAGCGGCAATA
GCTCAAATTTGAAATCTGGCACTTTCAGTGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGTCTAGCTCTTGTCTATG
TTTCTTGGAACAGAACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGTCTAGATCTATGTAAAGTTCCTTCGAAGA
GTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATAATGGCGAGAGACCGATAGC
GAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAA
GGGCTTGAGATCAGACTTGGTATTTTGTATGTTACTCTCTCGGGGGTGGCCTCTACAGTTTACCGGGCCAGCATCAGTTT
GAGCGGTAGGAGAATTGCGTAGGAATGTGGCTCGGCCTCGGTCGAGTGTTATAGCCTTCGTCGATACTGCCAGCTTAGA
CTGAGGACTGCGGCTTCGGCCTAGGATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCT
AACGTCTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGTAGGTAGGACCTTCTTTTGAAGCGC
ACTATCGACCGATCCTGATGTCTTCGGATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATG
CCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTG
GGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCG
TATCAGTTTTATGAGGTAAAGCGAATGATTAGAAGTCTTGGGGTTGAAATGACCTTAACTTATTCTCAAACTTTAAATA
TGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGACATATGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAA
CTGGCGATGCGGGATGAACCGAACGCGAAGTTAAAGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGT
TCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAAC
TAGCCCTGAAAATGGATGGCGCTCAAGCGTGTTACTTATACTTCGCCGTGAGAGGTTGATATGATGCCCTCACGAGTAG
GCAGGCGTGGAGGTCAGTGAAGAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGT
AGCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGTTGGACATGGGTTAGT
CGATCCTAAGAGATAGGGAAGCTCCGTTTCAATGCGCCTGATTATTCAGGCCACTATCGAAAGGGAATCCGGTTAAAAT
TCCGGAACTTGGATATGGATTCTTCACGGTAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTATC
TTTTCTTCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAGAGCGTGGTAATTTT
GCCACGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAAGTCGTACTCATAACC
GCAGCAGGTCTCCAAGGTTAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAA
CTTCGGGATAAGGATTGGCTCTAAGGATCGGGTGTTTTGGGCCTCGCGAAGACGTGGTGGCGACTGACGGCGGACTGC
TTTCGGGCGGACTGCTGTTGGATGCTGCCATAGACACGCTTGGTAGGGATTTATCCCGTCCGGAGCACGCTTAACGATC
AACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTT
GACACAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGT
AACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCAC
TGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTT
GAGCTTGACTCTAGTTTGACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATAC
CACTACCTCTATAGTTTTTTTACTTATTCAATGAAGCGGAGCTGGAGGTAAAACTCCACGTTCTAGCATTAAGGCCTTTT
GGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGT
CCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGCCCCCTTGATTTTGATTTTCAGTG
TGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAAAGTTAT
CACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATC
ATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGA
GACAGGTTAGTTTTACCCTACTGATGAATGTTATCGCAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCATTCAGA
TAATTGGTTTTTGCGGCTGTCTGATCAGGCAACGCCGCGAAGCTACCATCTGCTGGATTATGGCTGAACGCCTCTAAGT
CAGAATCCATGCTAGAAAGCGATGATTTTTGCCCTGCACATTTTAGATGGATACGAATAAGACTTTTAATAGTCGCTGG
ACCATAGCAGGCTGGCAGCGGTGCACTTAGCGGAAAGGCTTTGTGTGCTTGCCGGCGAATAGCAATGTCAACATGCGC
GGGGATAAATCCTTTGCATACGACTTAGATGTACAACGGAGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTG
CTGAGATTAAGCTTCAGTTGTCTGATTTGTCTAGGAGT

Figure 43

Magnaporthe grisea rRNA gene (SEQ ID NO: 90)

CATGTGCCGGAAAGTTGTACGAACTCGGTCGTTTAGAGGAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGC
GGAGGGATCATTACTGAGTTGAAAAACTCCAACCCCTGTGAACATAACCTCTGTCGTTGCTTCGGCGGGCACGCCCGCC
GGAGGTTCAAAACTCTTATTTTTTCCAGTATCTCTGAGCCTGAAAGACAAATAATCAAAACTTTCAACAACGGATCTCT
TGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCT
TTGAACGCACATTGCGCCCGCCGGTATTCCGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCTCGGCTTG
GTGTTGGGGCGCCCGGGCCCTCCGCGGCCCGGGGCCCCCAAGTTCATCGGCGGGCTCGGCGGTACACTGAGCGCAGTA
AAACGCGGTAAAACGCGAACCTCGTTCGGATCGTCCCGGCGTGCTCCAGCCGCTAAACCCCCAATTTTTTAAAGGTTGA
CCTCGGATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCC
AGTAACGGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCCCCCCGGCCCGAGTTGTAATTTGCAGAGGATGC
TTTTGGTGAGGCACCTACCGAGTCCCCTGGAATGGGGCGCCATAGAGGGTGAGAGCCCCGTATGGTAGGACGCCGAAC
CTCTGTAAAGCTCCTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCTAAATGGGAGGTAAATTTCTTCTAAAGCTAAA
TACCGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGGGTTAAAAAGTA
CGTGAAATTGTTGAAAGGGAAGCGCTTGTGACCAGACTTGCGCCGGGCGGATCATCCAGCGTTCTCGCTGGTGCACTCC
GCCCGGTTCAGGCCAGCATCGGTTTTCGCCGGGGGACAAAGGCTTCGGGAACGTGGCTCCTTTCGGGGAGTGTTATAGC
CCGTTGCGTAATACCCCGGCGGGGACCGACGACCGCGCTTCGGCAAGGATGCTGGCGTAATGGTCATCAGCGACCCGT
CTTGAAACACGGACCGAGGAGTCAAGCATTAGTGCGAGTGTTTGGGTGTAAAACCCGCACGCGTAATGAAAGTGAACG
TAGGTGAGAGCTTCGGCGCATCATCGACCGATCCTGATGTTTTCGGAAGGATTTGAGTAGGAGCATTAACGCTTGGACC
CGAAAGATGGTGAACTATACTTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGC
AAATCGATCGTCAAATTTGAGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTTCAGCCGAAGTTTCCCT
CAGGATAGCAGTGTCGTCTTCAGTTTTATGAGGTAAAGCGAATGATTAGGGACTCGGGGGCGATTTTTAGCCTTCATCC
ATTCTCAAACTTTAAATATGTAAGAAGCCCTTGTTACTTAGTTGAACGTGGGCCTTCGAATGTACCGACACTAGTGGGC
CATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGGGGTTAAGGTGCCGGAGTGGACGCTCATCAGAC
ACCACAAAAGGCGTTAGTACATCTTGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGACTGTGTAACAA
CTCACCTGCCGAATGTACTAGCCCTGAAAATGGATGGCGCTCAAGCGTCCCACCCATACCCCGCCCCCAGGGTAGAAA
CGATGCCCTGGGGAGTAGGCTGACGCGGGGGTAGCGACGAAGGCTAGGGCGTGAGCCCGGCTAGAGCTGCCCCTGGT
GCAGATCTCGGTGAGAGTAGCAAATACTTCAATGAGAACTTGAAGGACCGAAGTGGGGAAAGGTTCCATGTGAACAGC
AGTTGGACGTGGGTTAGCCGATCCTGAGCCATAGGGAAGTTCCGTTTCAAAGGGGCGCTAGCGCCCCGTATGGCGAAA
GGGAAGCAGGTTAATATTCCTGCGCCTGGATGTGGGTTTTTCGCGGCAACGCAACTGAACGCGGAGACGGCGGCGGGG
GCCCCGGGCAGAGTTCTCTTTTCTTCTTAACGATCCACCACCCTGGAAACGGTTTGTCCGGAGATAGGGTTCAGCGGTC
GGAAGAGCCCAGCACTTCTGTTCGCCCTCGACGTCCCTTGAAAATCCGCGGGAGGGAATAATTCTCACGCCAGGTCGTA
CTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTGGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAACA
GATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTTGGGTACGTTGGGCCTTTGGCGGACGCGCCGGGGGCAGGTC
GCCACTAGCCGGGCAACCGGCCGGGGGCTTCCAGCACCTGGTTGCCGACGCCTTTGGCAGGCTTCGGCCGTCCGGCGT
ACGGTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCC
GGAAAGCGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCACAGCAAAGTAATTTGACCAAGCGCGGGT
AAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTA
ACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAA
AGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGAGGTGTAGAATAGGTGGGAGCTTCGGC
GCCGGTGAAATACCACTACTCCTATTGTTTTTTTACTTATTCGATTAAGCGGGGCTGGATTTACGTCCAACTTCTGGTTTT
AACGTCCTTCGCGGGCGGACCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACC
ATAACGCAGGTGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATT
TTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTG
CCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTGATCCTTCGATGT
CGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTT
TAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCTCGTCGCAATGGTAATTGAGCTTAGTACGAGAGGAAC
CGCTCATTCAGATAATTGGTTTTTGCGGTTGTCCGACAGGGCAGTGCCGCGAAGCTACCATCTGCAGGATAACGGCTGA
ACGCCTCTAAGTCGGAATCCTTGCCAGAACGCGACGATACCTCCCGCACGTTTAGACGGATAAGAATAGGCTTCGGCCT
CGTATCTCAGCAGGCGATAACCCCGCCGGGCTCGAAGCGCCCGGTGGTGATTCGCGTATTGTAATTTTGACACGCGCGG
GGTCAAATCCTTTGCAGACGACTTAGCTGTGCGAAAGGGTCCTGTAAGCAGTAGAGTAGCTTTATCGTTACGATCTGCT
GAGGGTAAGCCCTCCTTCGCCTAGATTTCCCAGACTTTCTACCCCATTC

Figure 44

Metarhizium anisopliae rRNA gene (SEQ ID NO: 91)

CCGGAAAGCTCTCCAAACTCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGG
ATCATTACCGAGTTATCCAACTCCCAACCCCTGTGAATTATACCTTTAATTGTTGCTTCGGCGGGACTTCGCGCCCGCCG
GGGACCCAAACCTTCTGAATTTTTTAATAAGTATCTTCTGAGTGGTTAAAAAAATGAATCAAAACTTTCAACAACGGAT
CTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGA
ATCTTTGAACGCACATTGCGCCCGTCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACGCCCCTCAAGTCCCCTG
TGGACTTGGTGTTGGGGATCGGCGAGGCTGGTTTTCCAGCACACCGTCCCTTAAAATTAATTGGCGGTCTCGCGTGGCC
CTCCTCTGCGCAGTAGTAAAACTCGCAACAGGAGCCCGGCGCGGTCCACTGCCGTAAAACCCCCCAACTTTTTATAGTT
GACCTCGAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCC
CCAGTAACGGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGTCCCCAGGGCCCGAGTTGTAATTTGCAGAGGA
TGCTTTTGGTGAGGTGCCTTCCGAGTTCCCTGGAACGGGACGCCATAGAGGGTGAGAGCCCCGTCTGGTTGGATACCGA
GCCTCTGTAAAGCTCCTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCTAAATGGGAGGTATATGTCTTCTAAAGCTA
AATATTGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGGGTTAAATAG
TACGTGAAATTGTTGAAAGGGAAGCACTTATGACCAGACTTGGCCCCGGTGAATCATCCAGCGGTTCCCCGTGTGCACT
TTGCCGGGGTTCAGGCCAGCATCAGTTCGCTCCGGGGGATAAAGGCTTTGGGAATGTGGCTCCCTCGGGAGTGTTATAG
CCCATTGCGCAATACCCTGTGGCGGGCTGAGGTTCGCGCTTTATGCAAGGATGCTGGCATAATGGTCATCAGTGACCCG
TCTTGAAACACGGACCAAGGAGTCGTCTTCGTATGCGAGTGTTCGGGTGTTAAACCCCTACGCGTAATGAAAGTGAACG
CAGGTGAGAGCCCTCCAGGGCGCATCATCGACCGATCCTGATGTTCTCGGATGGATTTGAGTAAGAGCATACGGGGCC
GGACCCGAAAGAAGGTGAACTATGCCTGTATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGA
CGTGCAAATCGATCGTCAAATATGGGCATGGGGGCGAAAGACTAATCGAACCTTCTAGTAGCTGGTTTCCGCCGAAGTT
TCCCTCAGGATAGCAGTGTTGATTTCTCAGTTTTATGAGGTAAAGCGAATGATTAGGGACCCGGGGGCGGCTTATAGCC
TTCATCCATTCTCAAACTTTAAATATGTAAGAAGCCCTTGTTGCTTAGGTGAACGTGGGCATTCGAATGTATCAACACTA
GTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCAGAGTAGACGCTCA
TCAACACCACCAAAGGTGTTAGTACATCTTGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGACTGTGT
AACAACTCACCTGCCGAATGTACTAGCCCTGAAAATGGATGGCGCTCAAGCGTCTCACCCATACCTCGCCCTCGGGGTA
GGAACGATGCCCCGAGGAGTAGGCGGACGTGGGGGTCAGTGACGAAGCCCAGGGCGTGAGCCCGGGTCGAACGGCCC
CTAGTGCAGATCTTGGTGGTAGTAGCAAATACTTCAATGAGAACTTGAAGGACCGAAGTGGGGAAAGGTTCCATGTGA
ACAGCGGTTGGACGTGGGTTAGTCGATCCTAAGCCATAGGGAAGTTCCGTTTCAAAGGTGCACTTGTGCGCCGTCTGGG
CGAAAGGGAAGCCGGTCAATATTCCGGCACCTGGATGTGGGTTTTTCGCGGCAACGCAACTGAACGCGGAGACGACGG
CGGGGGCCCCGAGCAGAGTTCTCTTTTCTTCTTAACAGTCTGTCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAAT
GGCTGGAAGAGCGGCACCTCTGCCGGGTTCGGTGCGCTCCCGACGTCCCTTGAAAATCCGCGGGAGGGAATAATTCTC
ACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTGGTTGATAGAACAATGTAGATAAGGGA
AGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGTGCGTTGGGCCTCGGGGGGACGCC
TTGGGAGCAGGCAGCCACTAGCCGGGCAACCGTCGGCGGCCGCAGCATCCGAGCGCTGAATCCCTTGGCAGGCTTCGG
CCGTCCGGCGCACGATTAACAACCAACTTAGAACTGGTACGGACAAGGGAATCTGACTGTCTAATTAAAACATAGCA
TTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGTAATTCAACC
AAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCA
TGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAA
TCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGAGGTGTAGAATAGGTG
GGAGCTTCGGCGCCGGTGAAATACCACTACTCCTATTGTTTTTTTACTTATTCAATGAAGCGGGGCTGGATTTTCGTCCA
ACTTCTGGTCTTAAGGTCCTTCGCGGGCTGTACCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCAC
ATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAA
GTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGACATTTGA
GGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCGGCCAAGCGTTCATAGCGACGTCGCTTTTTG
ATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTGCCTAAGCGTTGGATTGTTCACCCACTAATAGGGAAC
GTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCTCACCGCAATGGTAATTCAGCTTAG
TACGAGAGGAACCGCTGATTCAGATAATTGGTTTTTGCGGCTGTCCGACCGGGCAGTGCCGCGACGCTACCATCTGCTG
GATAATGGCTGAACGCCTCTAAGTCAGAATCCATGCCAGAACGCGGTGATACCCGCCGCACGTACAGATGGACAAGAA
TAGGCTCCGGCTTAGCGTCTTAGCAGGCGATTGTTCCGCTGCGCAGGAAGCGCAGTATTTCGCGTATTGTAATTTCACC
ACGAGCGGGGTCAAATCCTTTGCAGACGACTTAGCTGTGCGAAACGGTCCTGTAAGCAGTAGAGTAGCCTTGTTGTTAC
GATCTGCTGAGGGTTAGCCGTTCTTCGCCTCGATTTCCCCAATATCAGCGCATCCCGTTTCGCGGGGCGGG

Figure 45

Microsporum gypseum rRNA gene (SEQ ID NO: 92)

TCGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAACGCGCAGGCC
GTAGACGGCCCGTCCCCGGATGCGTCCGGGGGCGGTGTCGCCGGCCACACGCCCATTCTTGTCTATTTACCCAGTTGCC
TCGGCGGGCCGCGCACTCGTGCCGCGCCTCGAGGAGCCGTCCGGGGACAATCAACTCCCTGGATCGCGCCCGCCGGAG
GAGTGATTAAAATCCATGAATACTGTTCCGTCTGAGCGTTAGCAAGTAAAATCAGTTAAAACTTTCAACAACGGATCTC
TTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATC
TTTGAACGCACATTGCGCCCTCTGGTATTCCGGGGGGCATGCCTGTTCGAGCGTCATTTCAACCCCTCAAGCCCGGCTT
GTGTGATGGACGACCGTCCCGCCCTCCCTACTCCAGGGGAGGGGGACGCGCCCGAAAAGCAGTGGCCAGGCCGCGATT
CCGGCTCCTGGGCGAATGGGCAACAAACCAACGCCTCTAGGACCGGCCGGTTTTCTGGCCTAGTTTTAGTTAGGGATGA
ACTTCCCTACAATCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAA
GAAACCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCCTCCTACGGGGG
TCCGAGTTGTAATTTGTAGAGGATGCTTCGGGTGTGGCCGCCGTCTAAGTTCCTTGGAACAGGACGTCAGAGAGGGTGA
GAATCCCGTCTTGGGCGGCCGGTCCGCGCCCGTGTGAAGCTCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAA
GCGGGTGGTAAATTTCATCTAAAGCTAAATACTGGTCGGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGGTTAAA
AGCACCTTGAAAAGGGAGTTAAACAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCGGCCAGACTCGGGGGCGGGG
TTCAGCGGGTGCTCGTCGCCCGTGCACTCCCCGTCTCCCGGGCCAGCATCAGTTTCGACGGCCGGTCAAAGGCCTCCGG
AATGTGTCGTCTCTCGGGACGTCTTATAGCCGGGGGTGCAATGCGGCCCGTCGGGACTGAGGAACGCGCTTCGGCTCGG
ATGCTGGCGTAATGGCCGTAAGCGGCCCGTCTTGAAACACGGACCAAGGAGTCTAACATCCACGCGAGTGTTCGGGTG
TCAAACCCGTGCCGCGCAGTGAAAGCGAACGGAGGTGGGAGCCTTAGGGCGCACCATCGACCGATCCTGAAGTCTTCGG
ATGGTTAGGGTTAGGTTAGGGTTAGGTTAGGTTTTAGGGTTTAGGGTTAGGGTTTAGGGTGTGAAGCCAGAGGAAACTC
TGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGGGCATAGGGGCGAAAGACTAATCGAACCA
TCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTGACGATATTCCAGTTTTATGAGGTAAAGCGAATGAT
TAGAGGCCTTGGGGATGAAACATCCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGCCCTTGTTTCTTAAGTGAAC
GTGGGCACTAGAATGGAACGTCACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGA
GGTTAAGGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCCGACGGTGGCCATG
GAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACGGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGC
GTGCTACCCATACCTCGCCGCCGGGGTTGAAATGACGCCCCGGCGAGTAGGCAGGCGTGGAGGTCCGTGACGAAGCCC
TGGGGGTGACCCCGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGG
ACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGGCATAGGGTAGTTCCGAT
TGCATGTGCGCCCTGGTGCGCCGTCAGCCGAAAGGGAAGCCGGTTAAAATTCCGGCACCTGGATGTGGATTCTCCACG
GCAACGTAACTGAACGCGGAGACGTCGGCGGGGGTCCTGGGAAGAGTTATCTTTTCTTCTTGACGGCCTATCACCCTGA
AATCGGTTTGTCCGGAGCTAGGGTTCAATGGCCGGCAGAGCGCCGCACCTTTGCGGCGTCCGGCGTGCCCCCGACGAC
CCTTGAAAATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGC
CTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAG
GATCGGGCGCGTTGGGCCTTGGGTGGAGACCCTCGAGGCAGGGCAGCACTAGCCGGGCAACCGGCCGGCGCCGCCCA
GCATCGGGGCGTGGACGCCCTTGGCAGGCCTCTGGCCGTCCGGCGCGCGCTTAACGATCAACTTAGAACTGGTACGGA
CAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCC
CAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGT
AGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAG
CGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGAC
ATTGTGAAAAGACATATCGGGTGTAGAATAGGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCTTTATTGTTTTTTT
ACTTATTCAATGAAGCGGAACTGGCCTTTACTGGCCAACTTCTAGCGTTAAGGTCCCTCGCGGGCTGATCCGGGTTGAA
GACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACAATAACGCAGGTGTCCTAAGGGGGACTCATG
GAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAA
AGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCT
TGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTC
GGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCC
TACTGATGAAGTTCGCCGCAACGGTAATTCAATTTAGTACGAGAGGAACCGTTGATTCAGATAATTGGTTTTTGCGGCT
GTCTGACAAGGCATTGCCGCGACGCTACCATCTGCCGGATTATGGCTGAACGCCTCTAAGTCAGAATCCGTGCCGGAA
AGCGGCGATACCTGCCCCGCACGTTGTAGTTGGATACAAATAGGCTTCGGCCCTGAACCTCAACAGGCCGGCACCGGC
GCCTCGGCGCTAGCTGGCGGATTGCAATGTCACCACGCGCGGGGATAAATCCTCTGCAGACGACTGAAGTGAGCAAGC
GGGTCGTGTAAGCGGTCAAGTAGCCTTGTTGTTACGAGTCGCTGAGCGTCAGCCCGATCCTTGCCTAGATTTGTTGTAA
CACCCTCCC

Figure 46

Mucor racemosus rRNA gene (SEQ ID NO: 93)

TAGGCTATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAATAATCAATA
ATTTTGGCTTGTCCATCATTATCTATTTACTGTGAAACGTATTATTACTTGACGCCTGAGGGATGTTCCACTGCTATAAG
GATAGGCAGCGGAAATGTTAACCGAGTCATAATCAAGCTTAGGCTTGGTATCCTATTATTATTTACCAAAAGAATTCAG
AATTAATATTGTAACATAGACGTAAAAAATCTATAAAACAACTTTTAACAACGGATCTCTTGGTTCTCGCATCGATGAA
GAACGTAGCAAAGTGCGATAACTAGTGTGAATTGCATATTCAGTGAATCATCGAGTCTTTGAACGCAACTTGCGCTCAT
TGGTATTCCAATGAGCACGCCTGTTTCAGTATCAAAACAAACCCTCTATCCAACTTTTGTTGAATAGGATGACTGAGAG
TCTCTTGATCGTCAGATCTCGAACCTCTTGAAATGTACAAAGGCCTGATCTTGTTTGATGCCTGAACTTTTTTTTAATAT
AAAGAGAAGCTCTTGCGGTAAACTGTGCTGGGGCCTCCCAAATAACACTTTTTTAAATTTGATCTGAAATCAGGTGGGA
TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAAATAACAATGATTTCCCTAGTAACGGCGAGTGAAG
AGGAAAGAGCTCAAAGTTGGAAACTGTTTGGCTTAGCTAAACCGTATTGTAAACTGTAGAAACATTTTCCTGGCACACC
AGATTAATAAGTCCTTTGGAACAAGGCATCATGGAGGGTGAGAATCCCGTCTTTGATCTGAGTAGTTGTCTTTTGTGAT
ATGTTTTCAAAGAGTCAGGTTGTTTGGGAATGCAGCCTAAATTGGGTGGTAAATCTCACCTAAAGCTAAATATTTGCGA
GAGACCGATAGCGAACAAGTACCGTGAGGGAAAGATGAAAAGAACTTTGAAAAGAGAGTTAAACAGTATGTGAAATT
GTTAAAAGGGAACCGTTTGGAGCCAGACTGGTTTGCTTGTAATCAACCTAGAATTCGTTTTGGGTGCACTTGCAGGCTA
TACCTGCCAACAACAGTTTGATTTGGAGGAAAAAATTAGTAGGAATGTAGCCTCTCGAGGTGTTATAGCCTACTATCAT
ACTCTGGATTGGACTGAGGAACGCAGCGAATGCCTTTAGGCAAGATTGCTGGGTGCTTTCGCTAATAAATGTTAGAATT
TCTGCTTCGGGTGGTGCTAATGTTTAAAGGAGGAACACATCTAGTATATTTTTTATTCGCTTAGGTTGTTGGCTTAATGA
CTCTAAATGACCCGTCTTGAAACACGGACCAAGGAGTCCACCATAAGTGCAAGTATTTGAGTGACAAACTCATATGCGT
AAGGAAACTGATTGATACGAAGTCTTTTGATGGCAGTATCACCCGGCGTCGACGTTTTAACTGAAATGACCGAGGTAA
AGCACTTATGATGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTC
GTAGCGATTCTGACGTGCAAATCGATCGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGG
TTCCTGCCGAAGTTTCCCTCAGGATAGCAAAAACTTAAACGCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGG
GGACGAAATGTCCTTAACCTATTCTCAAACTTTAAATATGTAAGACGACCTGTTTGCTTAATTGAAGCAGGTCATTGAA
TGTGAGTTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGAGAAGTTAAGGTGCCGG
AATACACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCG
CTAAGGAGTGTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTTAAGCGTGTTACCCATACTT
CTCCGTTATTGTAAAAGCGAAGCAATAACGAGTAGGCAGGCGTGGAGGTTTTTATAAACTGTTAAGAAGCTCTTGGAGT
GATCCGGAGTGAAACAGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGAACTTTGAAGACTGAAG
TGGAGAAAGGTTCCTGGAGAACATTATTTGGTCCAGGGTTAGTCGATCCTAAGAGATAGGGAAATTCCGTTTTTTCAAA
GCAATCAATCTTGATTCGCCTATCGAAAGGGAAACAGTTTAATATTACTGTACTAGGATGAGGATTTTCTGCGGTAACG
CAAATGAACTTGGAGACATCAGTGTGGATCCCAGGAAGAGTTATCTTTTCTTTTTAACAACTTTGTTGTAGACCTTGAA
ATCTGTTTAGCAGGAGAAAAGGTTTACCGGTTGGTAGAGCATAGTACTTTTTGCTATGTCTGGTGCATTCACAACGATC
CTTGAAAATCCAAGGGAAAGAATAATTTTCTCGCCTAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCT
CTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGG
TTGGGTAGATATGGACTCTTGGTATGGTTGGTTTCTAGGCGATTTTAAGTGATTTCGGTTGCTTGATTTTGCTTGGAGAT
CTTCGTAACCAGGAGAGCCCAGTTTACGCTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTA
ATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGT
GAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTA
ATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAAC
GGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGAGGG
TGTAGCATAAGTGGGAGCTTCGGCGCCAGTGAAATACCACTACCTTTATCGTTTTTTTACTTAAATAATTAAGTGGGATT
GAGTCGCAAGATTAACCTTCTAGTATTAAGCATCTTCGGATGTGACCCACGTTATTGACATTGTCAAGTGGGGAGTTTG
GCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGGGGGACTCAACGAGAACAGAAATCTCGTGTAGAA
TAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGA
ATCTCAAGATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGC
GACGTTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACTGAAGCAGAATTCAGTAAGCGTTGGATTGTTCACCC
ACTAATAGGGAACGTCAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGGTATTGGTATCGTAA
CAGTAATTGAAGTTAGTACGAGAGGAACCCTTCATTCAGATAATTGGTATTTGCGGCTGGTTGAAAGGCCAATGCCGCG
AAGCTACCATCTGCTGGATAATGCTGAACGCCTCTAAGTCAGAATCCATGCTGAAAACGATACTACTGTGTTTTGATTG
TACCAGATGAGTACTAATAAAGCTTCGGCTTGAAAACCTTACTTGTGAGCTAGGTTTGGTAGCGGAAATGCTGCTAGAT
CTACTTGCTAATGATAATGCTAATACATCAAAATGATAAATCGCATGCAGACGACATGAAATGGACGGGGTATTGTAA
GTACTAGAGTAGCCTTTGTTGCTACGATGTACTGAGATTAAGCCTTTGTCATTGAATTTGTTCCTCTAAGGAACATTTCT
CATCAAAAATTAATAAATTTTTATCTATTTTTTTTTATCTGT

Figure 47

Neurospora crassa rRNA gene (SEQ ID NO: 94)

CGGTTATTTAAAGGAAATAAAAATTGTAATAAAGTTTCTGTTAGTAAATTAGTAGAAAGATTATTATAGAATTACAAAA
CTCCTATAAATTATTGTAAATTTTACTTATATAGTTACTTCGGCGTTAGTAGTTTAAAAAAGCCTTCGAGCCCTCCCGGA
TCCTCGGGTCTCCTACTCGTAAGAAGTTACCCGCCGGAATACTAAAACTAAACTCTTAATATTTTATATCTCTTTAAGTA
AACTTTTAAATAAATTAAAACTTTTAATAATAAATCTCTTAGTTCTAACATTAATAAAAAACGTAATAAAATATAATAA
GTAATATAAATTATAGAATTTAGTAAATTATTAAATCTTTAAACGCACATTGCGCTTACTAATATTCTAGTAAGTATACT
TATTCGAATATTATTTCAACTATTAAGCTCTACTTACGTTAGGGATCCGTAGCTATCCGTAGTCCTTTAAAATTAATAGC
GGGTTTATTAATTATATTGAGTATAGTAATTCTATATTATTATAATTATATAGCGGGTTCTTACTATAAAACCCCCTATTT
TTAAAATTGACCTCGGATTAGGTAGGAATACCCGCTGAATTTAAGTATATTAATAAGTAGAAGAAAAAAAATTAATAG
GGATTACCTTAATAATAGCGAATAAAATAGTAATAGTTCAAATTTGAAATCTAGCTTCGGCCCGAATTATAATTTGTAA
AAGAAGCTTTTAGTAAGGCACTTTCTAAATCCCCTAGAACGGAGCGCTATAGAGGGTGAGAGCCCTATATAATTGGAT
GCCAATCTAATATAAAGCTCCTTTAATAAATCGAATAGTTTAGGAATATTATTTAAAATAGGAGGTAAATTTCTTTTAA
AGCTAAATACCGGCTAGAGATTAATAGTATATAAGTAGAGTAATTAAAAAATGAAAAGTACTTTAAAAAGAGGGTTAA
ATAGTATATGAAATTATTAAAAGGAAAGTGTTTATAATTAGATTTATACTGTTTTAATTATTTAGTATTCTTATTAGTAT
ATTTAGGACGGTTTAAACTAATATTAGTTTTAGTAGGGGGATAAAGGTTTAGGGAATATAACTCCTCTAGGAATATTAT
AGCCCTAGGCGTAATACCTTTACTAGAACTGAAGTTCGTATATTTATAAGAATACTAGTATAATAATTATTAATAACCC
GTTTTAAAATACAGACTAAGGAATTAAAGTTTTACGCAAGTATTTAGGTATAAAACCCGTACGTATAATAAAAGTAAAT
GTAGGTGAGAGCTTCGGTATATTATTAATTAATTCTAATATATTTAGATAAATTTAAATAAGAATATTAAACCTTAAAC
CCGAAAAATAATAAACTATACTTAGATAGGGTAAAGCTAGAAGAAACTCTAATAGAGGCTCGCAACGGTTCTAACGTA
CAAATCGATTGTTAAATCTAAGTATGGGGGCGAAAGACTAATTGAACTATCTAATAGCTAATTACCGCCGAAGTTTCCC
TTAAGATAATAATATTATTCTTCAATTTTATAAGGTAAAGCGAATAATTAGGGACTCGGGGGCGCTTTTTAGCCTTCATC
CATTCTTAAACTTTAAATATATAAGAAGCCCTTATTATTTAATTAAATATAGGTATTCGAATATATTAATACTAATAGGC
TATTTTTAATAAGTAGAACTAGTAATACGGAATAAACCGAACGTAGGGTTAAAGTACTAGAGTAAATACTTATTAAATA
CTATAAAAAGCGTTAGTATATTTTAATAATAGGACGGTGGCTATAGAAATCGGAATTTGCTAAGGACTATATAATAATT
TACTTACCGAATATACTAGCTTTGAAAATAAATAGTACTTAAACGTCCTACTTATACCCCGCCCTTAAAGTAGAAACGA
TATTCTAAAGAGTAGGCGGCTATAGAGGTTAGTAACGAAGCCTAGGGCGTAAGCCCGGGTCGAACGGCCTTTAATATA
AATTTTAATAGTAGTAATAAATATTTTAATAAGAATTTAAAGGACTAAAGTAGGGAAAGGTTCTATATAAATAGCGGTT
GGATATAGGTTAATTAATCTTAAACTATAGGGAAGTTCCGTTTTAAAGGGGTATTTATACTCTATATAGCGAAAGGGAA
GCCGGTTAATATTCCGGTACCTAAATATAGGTTTTACGCGGTAATGTAATTAAATATAGAAACGATAGCGGAGGCCCCA
GGTAAAATTCTCTTTTCTTTTTAATAGTCTATTACCCTAAAAATAATTTATTTAGAGATAGGGTTTAATAGCCGGAAGAG
CCCAATATTTCTATTGGGTCCAGTACGTTTTTAATATCCCTTAAAAATCCGTAGGAGGGAATAATTCTTATATTAAGTTA
TATTTATAATTATAGTAGGTCTTTAAAGTGAATAGCTTCTAATTAATAGAATAATATAGATAAGGGAAGTTAGTAAAAT
AGATTTATAATTTTAGGAAAAGGATTAATTCTAAGGGTTAAGTACGTCGGGCTTTAGGTAAACGCCCTAAGAGTAGATT
GCTATTAGTTAGGTAACCGGCCGGTAGCTTTCAATATCCGGGTATAGAAGCTTTTAATAGACTTCGGTCGTCCGGTGTA
CGTTTAATAATTAATTTAAAATTAGTATAGATAGGGGGAATTTAATTATCTAATTAAAATATAGTATTACGATAGTTAG
AAAGTAGTATTAACGTAATATAATTTCTATTTAGTATTTTAAATATTAAAATAAAAAAATTCAACTAAGCGCGGGTAAA
TAGCAGGAATAACTATAATTCTCTTAAAGTAGCCAAATACTTTATTATTTAATTAGTAACGCATATAAATAGATTAATG
AGATTCCTATTATCCCTATTTATTATCTAGCGAAACTATAATTAAAGGAACGGGCTTAGTAGAATTAATGGAGAAAGAA
GACCCTATTAAACTTAATTTTAGTTTAATATTATAAAAAAATATAGGAAGTATAGAATAGGTAGGAGCTTCGGCGCCGG
TAAAATACTACTACTCCTATTGTTTTTTTACTTATTTAATTAAGCGGGGCTAGATTTTTATTCAACTTCTAATTTTAAGGT
CCTTCGTAGGCTAACCCGGATTAAAAATATTATTAAGTAGGGAATTTAGCTAGGGCAGTACATCTATTAAACTATAATG
CAAATATCCTAAGGGGGGCTTATAGAGAATAAAAATCTCTAGTAGAACAAAAGGGTAAAAATCCCCTTAATTTTAATTT
TTAATATAAATATAAATTATAAAAGTATAGCCTATTAATCCTTTAGTCCCTCGAAATTTAAAGTTAGAAGTACTAGAAA
AATTACTATAAGGATAATTAACTTATAATAGCCAAACGTTTATAGCAATATCGCTTTTTAATCCTTCAATATCAGCTCTT
CCTATTATACCGAAGTAGAATTCGGTAAATATTAGATTATTTACCTATTAATAGGGAATGTAAGCTAAATTTAGACTAT
TATAAAATAAATTAGTTTTACCCTACTAATAACTTTATCGCAATAGTAATTAAATTTAGTATAAAAGGAACTACTTATTT
AAATAATTAGTTTTTATAATTATCTAACCGGATAGTACTATAACGCTACTATCTACTAGATAATAACTGAACGCCTCTAA
ATTAGAATTTATATTAGAATACGATAATACTTTTAGTATATTATAGATATATAAAAATAAGCTCCGGCTTTGTATCTTAG
TAAGCAATTCCTCTATTAGCCTTAAAGTAGCTAGCGGTAATTCGTATATTATAATTTTAATATATATTAGATTAAATCCT
TTATAAATAATTTAAATATACGAAAGGGTTTTATAAATAATAGAATAGCCTTATTATTATAATTTATTAAGAGTAAGCC
CTCCTTCGCTTAAATTTCCCAATAGAAGGATCCGCTTAATAAATAGGCATTT

Figure 48

Paracoccidioides brasiliens rRNA gene (SEQ ID NO: 95)

GTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAACGCGCCGTGGGGG
GACGGGGCCCGATCGGGTTCCCGGCCCTCTCACCTGGCCACCCTTGTCTATTCTACCTGTTGCTTCGGCGGGCCTGCAGC
GATGCTGCCGGGGGGGCTCGGCCTCCCGGGCTCGTGCCCGCCGGGGACACCGTTGAACTTCTGGTTCGGAGCTTTGACG
TCTGAGACCTATCATAATCAGTAAAAACTTTCAACAACGGATCTCTTGGTTCCGACATCGATGAAGAACGCAGCGAAAT
GCGATAAGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGGG
GGCATGCCTGTCCGAGCGTCATTTCAACCCTCAAGCGCGGCTTGCGTGTTGGGCCCGCGTCCCCCCGTGGACGTGCCCG
AAATGCAGCGGCGGCGTCGCGTTCCGGTGCCCGAGCGTATGGGGCTTCGTCACACGCTCTCAGAGGCCCGGCCGACTC
CGGCCCCACTCATCGACCCCGGCGGGGGGGAAAAAGGTGTCCTCTCTCGATCGACACCCTTCCCCCTTGCCGACCAAGG
TTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTG
CCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAATTTGAAATCTGGCTCCTTCGGGGCCCGAGTTGTAATTTGTAGA
GGATGCTTCGGGCGTGGCCGCGGTCTAAGTCCCCTGGAACGGGGCGTCGCAGAGGGTGAGAATCCCGTCTTCGGCCGG
CCGGCCCCGCCCGTGTGAAGCTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATC
TAAAGCTAAATACTGGTCGGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGAG
TTAAACAGCATGTGAAATTGTTGAAAGGGAAGCGCTTGCGACCAGAGTCGGCCGCCGGGGGCTCAGCGGGCACTCGTTG
CCCGTGCACTCCCCCGTGGTCGGGCCAGCGTCGGTTTCGACGGCCGGTCAAAGGCCCCCGGAATGTGTCGCCTCTCGGG
GCGTCTTATAGCCGGGGGTGCAATGCGGCCAGTCGGGACCGAGGAACGCGCTCCGGCACGGACGCTGGCTTAATGGTC
GTAAGCGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATCCACGCGAGTGTTCGGGTGTCAAACCCGTCCGCGCA
GTGAAAGCGAACGGAGGTGGGAACCCTCAAGGGTGCACCATCGACCGATCCTGAAGTCTTCGGATGGATTTGAGTAAG
AGCGTGGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTC
GCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGGGCATAGGGGCGAAAGACTAATCGAACCATCTGGTAGCTGG
TTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGTTTTCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGG
TTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGCCCTTGTTGCTTAGTTGAACGTGGGCACTGGAAT
GGATCGTTACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGG
AATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCCGACGGTGGCCATGGAAGTCGGAATCCG
CTAAGGAGTGTGTAACAACTCACGGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCCATACC
TCGCCGTCGGGGCAGAAACGACGCCCCGACGAGTAGGCAGGCGTGGAGGTCCGTGACGAAGCCCTGGGAGTGATCCC
GGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGA
AAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGACATAGGGAAGTTCCGTTTCAAAGCGCGCCCT
CGTGCGCCGTCCGTCGAAAGGGAAGCCGGTTAATATTCCGGCACCTGGATGTGGATTCTCCACGGCAACGTAACTGAA
CGCGGAGACGTCGGCGGGGGTCCTGGGAAGAGTTATCTTTTCTTCTTGACGGCCTATCACCCTGAAATCGGTTTGTCCG
GAGCTAGGGTTCAACGGCCGGCAGAGCCCCGCACCTTTGCGGGGTCCGGTGCGCCCCCGACGACCCTTGAAAATCCGC
GGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTAGTTGATAGA
ACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTTGGGCACGTTG
GGCCTTGGGCGGAGACCCCCGGAGCAGGAAGGCACTAGCCGGGCAACCGGTGGGGGCCCTCCAGCATCGGGGCGTGG
ACGCCCTTGGCAGGCTTCGGCCGTCCGGCGTGCGATTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGAC
TGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGT
CAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGT
CATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAA
GGGAACGGGCTTGGAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATA
TCGGGTGTAGAATAGGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCTTTATTGTTTTTTTACTTATTCAATGAAGCG
GAACTGGGCTTTGCTGCCCAACTTCTGGCGTTAAGGTCCCTCGCGGGCCGATCCGGGTTGAAGACATTGTCAGGTGGGG
AGTTTGGCTGGGGCGGCACATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCA
GTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCC
TTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTC
ATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTT
CACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGTGGTCGCCGC
AACGGTAATTCAATTTAGTACGAGAGGAACCGTTGATTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCG
CGACGCTACCATCTGCCGGATTATGGCTGAACGCCTCTAAGTCAGAATCCGTGCCGGAACGCGGCGATGTTGCCCCGCA
CGTTGTAGTTGGATACGAATAGGCCTCCGGGCCCAGAACCTCAGCAGGCCGGCGACGGTGCCCGGGGAGAGACCCCCG
GGCGCCAGCTGGCGGATTGCAATGTCACCACGCGCGGGGATAGATCCTCTGCAGACGACTGAAATGACCAAGCGGGTC
GTGTAAGCGGTCAAGTAGCCTTGTTGTTACGAGTCGCTGAGCGTCAGCCCGATCCTTGGCTCGATTTGTTGTAGACAAC
CCCCATCGGTACGAACTAGCCCTGGTATATCCGGGGGATCG

Figure 49

Pneumocystis carinii rRNA gene (SEQ ID NO: 96)

CGAAAGAGAGGAGGTAGCACCGTTCCGTAGGTGAACCTGCGGAAGGATCATTAATGAAATGTTGTCAAGAACTAGTTT
ATCTGGTTCTTGACATTTTCATCATAACACTTGTGAACATTAAAGATTTGCTTTGACAGGATGGGAGTTAGCTTTCGTCC
TGTCAGAGGTTTTCAATTAAAACTTTTTTGGTGTTTCGGTTAAAAATATAATTTTTAAAAACTTTCAGCAATGGATCTCT
TGGTTCCCGCGTCGATGAAGAACGTGGCAAAATGCGATAAGTAGTGTGAATTGCAGAATTCAGTGACTCATCGAATTTT
TGAACGCATATTGCGCTCCTCAGTATTCTGTGGAGCATGCCTGTTTGAGCGTCATTTTTATACTTGAACCTTTTTAAGGT
TTGTGTTGGGCTATGCATTTTAGTATTTTTACAAGATGCTAGTCTAAAATGGAATCCAGAATATTATTTCGTGCAGCGTA
ATAGGGTTAAATTCCAATTCGCTGTTTTTAGAAATGATAGACTGGTTTGTCTATTGTTCCTAGAGAGCAATTTTTGAACC
TTTGACCTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACTAACAAGGATT
CCCTCAGTAACGGCGAGTGAAGTGGGAAAAGCTCAAAATTAAAATCTGGCGAGGATCCTCGTCCGAGTTGTAATTTAG
AGAAGTGCTTTTGGCTTGATGCTCTATTTAAAGTCCTTTGGAACAAGGCATCATAGAGGGTGATAATCCCGTACGAGTA
GGGTTATTAAGCTATGTAAAAGCACATTCGAAGAGTCGAGTTGTTTGGGATTGCAGCTCAAAATGGGTGGTAAATTTCA
TCTAAAGCTAAATATTAGCGGGAGACCGATAGCGAACAAGTAGAGTGATCGAAAGATGAAAAGAACTTTGAAAAGAG
AGTTAAATAGTACGTGAAATTGCTGAAAGGGAAGCGCTTGCGATCAGACATGCCTTATCAGGATGTTGTTGTCTTGACA
ATAACTATTACTTGGTTTGGCAGGCCAACATCGGTTTCAGCTGCTAGGTAAGTGTCAAGAGAGGGTAGCCTCTTTCGTG
GGGTGGTTAGCTCTTGGCTTCTGTAGTAGCAGGGACCGGAAGGTCTAGCGTCAGCTTGGTTGTTGGCTTAATGGTCTTA
AGCGACCCGTCTTGAAACACGGACCAAGGAGTCTAATATCTATGCGAGTGTTTGAGTGGAAAACTCATACGCGAAATG
AAAGTGAAGCAAAAGGTAGGAACCCTTTAAGGGTGCACTATCGACCGGTTCAAATTTATTTGGATTGAGTAAGAGCAT
AGCTATTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGC
GGTTCTGACGTGCAAATCGATCGTCAAATTTGGGCATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTG
CCGAAGTTTCCCTCAGGATAGCAGAAACTCAATATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCATTGGGGTTG
AAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACATGGACATTAGAATGAG
AGTTTCTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAAGC
ACGCTCATCAGATACCACAAAAGGTGTTAGTTCATCTAGACAGTAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAG
GAGTGTGTAACAACTCACCTACCGAATGAACTGGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCTATACCTCGCC
GTCTGGGATAATGATTCCTAGACGAGTAGGCAGGCGTGGGGGTCGTGGCGAAGCCTAGGGCGTGAGCCCGGGTTGAAC
GGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGGACTTTGAAGACTGAAGTGGGGAAAGGTTCCA
TGCGAACAGTTATTGGGCATGGGTTAGTCGATCCTAAGAGATAGGGAAACTCCGTTTTAAAGTGCGCGATTTTTCGCGC
CTCTATCGAAAGGGAATCCGGTTAATATTCCGGAACCAGGATATGGATTCTTCACGGCAACGTAAATGAAGTCGGAGA
CGTCAGCGGGGGGCCTGGGAAGAGTTATCTTTTCTTCTTAACAGCCTATCACCCTGGAATCGGTTTATCCGGAGATAGG
GTTCAATGGCTGGTAGAGTTCAGCACTTCTGTTGAATCCAGTGCGCTTTCGATGACCCTTGAAAATCCGACGGAAGGAA
TAGTTTTCATGCCTGGTCGTACTCATAACCGCAACAGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAATAATGTAGA
TAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGATTGGGTGCATTGGGCTTTAATC
GGAAGCTATTGGACCAGACGGGAACTACCTTGGGAAACCGAGGCGGATCCTGTTAGGATCGATCAGTGAATGATTTTA
GCAGCCCTTTGGGCGTCCGATGCACGCTTAACAATCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATT
AAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCGATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGA
AGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCACCTTTTGAGGGTCATGAAAGCGGCGCGAAAG
TGTTAGCTAGTGATCCGAAAAATAAATTCGGGTTGCGACACTGTCAAATTGCGGGGAGTCCCTAAAGATTCAACTACTA
AGCAGCTTGTGGAAACACAGTTGTGGCCGAGTTAATAGCCCTGGGTATAGTAACAATGTTGAATATGACTCTTAATTGA
GGAAATGGGTGATCCGCAGCCAAATCCTAAGGACATTTTATTGTCTATGGATGCAGTTCAGCGACTAGACGGCAGTGG
GTATTGTAGAGATATGGGGTTATTTATGGCCTTATCTACAATGCTTAAGGTATAGTCTAATCTCTTTCGAAAGAAAGAG
TAGTGTGCTCTTAAGGTAGCCAAATGCCTCGTCATCTGATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGT
CCCTATCTACGATCTAGCGAAACCACAGCCAAGGGAATGGGCTTGGCAAAATCAGCGGGGAAAGAAGACCCTGTTGAG
CTTGACTCTAGTTTGACATTGTGAAAAGACATAGAGGATGTAGAATAGGTGGGAGCTTCGGCGCCTGTGAAATACCAC
CGCCTTTATTGTTTTTTTACTTAATCAGTGGAGCGGGACTGAGCTTTTGCTCATCTTTTAGCGTTAAGGTCCTTTTACGGG
CCGACCCGAGTTGATGACATTGTCAGATGGGGAGTTTGGCTGGGGCGGCACATCTGTCAAAAGATAACGCAGGTGTCC
TAAGGGGAGCTCATTGAGAACAGAAATCTCAAGTAGAATAAAAGGGTAAAAGTTCCCTTGATTTTGATTTTCAGTACG
AATACAAACCATGAAAGTGTGGCCTATCGATCCTCTAAATCCTCGAAATTTGAGGCTAGGGGTGCCAGAAAAGTTACC
ACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCA
TACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAG
ACAGGTTAGTTTTACCCTGCTGATGAAGTTATCGCAATGGTAATTCAGCTTAGTACGAGAGGAACCGTTGATTCAGATA
TTTGGTTTTTGCGGTTGTCTGACCAGGCAGTGCCGCGAAGCTATCATCTGTTGGATTATGGCTGAAAGCCTCTAAGTCAG
AATCCATGCCAGAAAGCGATGATATTTCCTCACGTTTTTTGATACAAATAGGCATCTTGCCAATATCAGTATTTGGACG
GGTGGAGGCGGACGGAAGTGTTCGTCTCTGTCCATTAATATTAATTAATATTCGTGAGGGCGAATCCTTTGTAGACGAC
TTAGTTGAGGAACGGGGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGATTAAGCCTTTGTTCCCAA
GATTTGT

Figure 50

Penicillium verrucosum rRNA gene (SEQ ID NO: 97)

CTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGCGG
GCCCTCGCGGCTCAACCTCCCACCCTTGTCTCTATACACCTGTTGCTTTGGCGGGCCCACCGGGGCCACCTGGTCGCCG
GGGGACGTCGTCTCCGGGCCCGCGCCCGCCGAAGCGCTCTGTGAACCCTGATGAAGATGGGCTGTCTGAGTACTATGA
AAATTGTCAAAACTTTCAACAATGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGT
GAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGCATTCCGGGGGGCATGCCTGTCCG
AGCGTCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGTGCGGTCCCCCCGGGGACCTGCCCGAAAGGCAGCGGCGAC
GTCCGTCTGGTCCTCGAGCGTATGGGGCTCTGTCACTCGCTCGGGACGGACCTGCGGGGGTTGGTCACCACCATATTTT
ACCACGGTTGACCTCGGATCAGGTAGGAGTTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAAC
CGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAATTTGAAATCTGGCCCCTTTGGGGTCCGAGTTGTA
ATTTGCAGAGGATGCTTCGGGTGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTGAGAATCCCGTCT
GGGATGGGCGGCCGCGCCCGTGTGAAGCTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGCGGGTGGTAA
ATTTCATCTAAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAA
AAGAGAGTTAAACAGCACGTGAAATTGTTGAAAGGGAAGCGTTGTCCACCAGACTCGCCCGGGGGGGGTTCAGCCGGCA
CGTGTGCCGGTGTACTCCTCTCCGGGCGGGCCAGCATCGGTTTGGGCGGCTGGTGAAAGGCCCCGGGAATGTAACACC
CTTCGGGGTGCCTTATAGCCCGGGGTGCCATACAGCCAGCCTGGACCGAGGCCCGCGCTTCGGCGAGGATGCTGGCGT
AATGGTGGTCAACGGCCCGTCTTGAAACACGGACCAAGGAGTCTAACATCTATGCGAGTGTTCGGGTGTCAAACCCGT
CCGCGCAGTGAAAGCGAACGGAGGTGGGAGCCCCTCGGGGCGCACCATCGACCGATCCTGATGTCTTCGGATGGATTT
GAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGCGAAGCCAGAGGAAACTCTGGT
GGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTG
GTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGACATCAGTTTTATGAGGTAAAGCGAATGATTAGAGG
CCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGCCCTTGTTGCTTAGTTGAACGTGGGC
GTTAGAATGAAACGTTACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAA
GGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCCGACGGTGGCCATGGAAGTC
GGAATCCGCTAAGGAGTGTGTAACAACTCACGGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTA
CCCATACCTCGCCGTCGGGGTAGAAACGATGCCCCGACGAGTAGGCAGGCGTGGGGGTCCGTGACGAAGCCTTGGGAG
TGATCCCGGGTCGAACGGCCCCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAA
GTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTGAGTCGATCCTAAGACATAGGGTAGTTCCGTTTGAAAG
TGCGCCCTCGTGCGCCGTCCGTCGAAAGGGAAGCCGGTTAATATTCCGGCACCTGGATGTGGATTCTCCACGGCAACGT
AACTGAACGCGGAGACATCGGCGGGGGTCCTGGGAAGAGTTCTCTTTTCTTCTTGACAGCCTATCACCCTGAAATCGGT
TTGTCCGGAGCTAGGGTTCCACGGCTGGCAGAGCTCGGCACCTTTGCCGGGTCCGGTGCGCCCCCGACGATCCTTGAAA
ATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTG
ATAGAACAATGTAGATAAGGGAAGTCGGCAAAATGGATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTCGGGCA
CGTTGGGCCTTGGGGGGAAGCCCCTGGAGCAGGTGGGCACTAGCCGGGCAACCGGCCGGCGCCCGCCAGCATCGGGTG
GTGGACGCCCTTGGCAGGCTTCGGCCGTCCGGCGTGCGCTTAACGACCAACTTAGAACTGGTACGGACAAGGGGAATC
TGACTGTCTAATTAAAACATAGCATTGTGATAGCCAGAAAGTGGTATTGACACAATGTGATTTCTGCCCAGTGCTCTGA
ATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCC
TCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAG
CCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAG
ACATATGGGGTGTAGCATAGGTGGGAGCTTCGGCGCCAGTGAAATACCACTACCTTTATCGTTTTTTTACTTATTCAATG
AAGCGGAACTGGGCTTCACCGCCCAATTTCTAGCGTTAAGGTCCTTCGCGGGCCGATCCGGGTTGAAGACATTGTCAGG
TGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGRCTCATGGAGAACAGAAAT
CTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATC
GATCCTTTAGTCCCTCGAMATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCGGCCAA
GCGTTCATAGCGACGTCGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGG
ATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCT
CACCGCAATGGTAATTGAGCTTAGTACGAGAGGAACCGCTCATTCAGATAATTGGTTTTTGCGGCTGTCCGACCGGGCA
GTGCCGCGAAGCTACCATCTGCTGGATAATGGCTGAACGCCTCTAAGTCAGAATCCATGCCAGAACGCGGTGATAGCA
CCCGCACGTATAGACGGACAAGAATAGGCTTCGGCTTAGTGTCTCAGCAGGCGATTCCTCCGTGGTCCTCGAAGCGGG
CCGCGGTATTTCGCGTATTGTAATTTCAACACGAGCGGGGTTAAATCCTTTGCAGACGACTTAGCTGTGCGAAACGGTC
C

Figure 51

Pichia stipitis rRNA gene (SEQ ID NO: 98)

CTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTT
TTGCCAGCGCTTAACTGCGCGGCGAAAAAACCTTACACACAGTGTTTTCTTTATTAGAAACTATTGCTTTGGTCTGGCTC
AGAAATGAGTTGGGCCAGAGGTTTACCAAACTTCAATTTTATTGAATTGTTATTTTATTAATTTGTCAATTTGTTGATTA
AATTCAAAAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAG
TAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCT
GTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAA
AGTATTGGCACGAGTGGTACTAAATAGTACTGACAGAATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT
GGCGGTGAATTTTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCG
CTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAA
AAGCTCAAATTTGAAATCTGGCACCTTCGGTGTCCGAGTTGTAATTTGAAGAAGGTAACTTTGGAGTCAGCTCTTGTCT
ATGTTCCTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGTCTGATTCTATGTAAAGTGCTTTCGA
AGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGAT
AGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGG
GAAGGGTTTGAGATCAGACTTGGTATTTTGTATGTCTTGCTTTCGGGTGGGGCCTCTACAGTTTACTGGGCCAGCATCGG
TTTGGACGGTAGGATAATGACATTGGAATGTGGCACCACTTCGGTGGTGTGTTATAGACTTTGTTGATACTGCCTGTCTA
GACCGAGGACTGCGTCTTTGACTAGGATGCTGGCATAATGATCTTAAACCGCCCGTCTTGAAACACGGACCAAGGAGT
CTAACGTCTATGCAAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGTAGGTGAGAGCTCTTTTGAGTGC
ATCATCGACCGATCCTGATGTCTTCGGATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATG
CCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTG
GGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCG
TATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGTCTTGGGGTTGAAATGACCTTAACCTATTCTCAAACTTTAAATA
TGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGACATATGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAA
CTGGCGATGCGGGATGAACCGAACGTGAAGTTAAAGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGT
TCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAAC
TAGCCCTGAAAATGGATGGCGCTCAAGCGTGTTACTTATACTTCACCGTCAGGGTTGATATGATGCCCTGACGAGTAGG
CAGGCGTGGAGGTCAGTGACGAAGCCTTTGCTGTAAAGCTGGGTAGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTA
GCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGTTGGACATGGGTTAGTC
GATCCTAAGAGATGGGGAAGCTCCGTTTCAAAGATTTGATTTTTCAAGTCACCATCGAAAGGGAATCCGGTTAAAATTC
CGGAACTTGGATATGGATTCTTCACGGTAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTCTCTT
TTCTTCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATAGGGTCTTATGGCTGGAAGAGTGCAATACTTTTGT
TGCATCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAAGTCGTACTCATAACCGC
AGCAGGTCTCCAAGGTTAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACT
TCGGGATAAGGATTGGCTCTAAGGATCGGGTGTCTTGGGCCTTTACCAGACGCAGCGGAACTGGTGGTGGACTGTTCTT
CCTTGTGTTGAACGGACCGCTACCGGATCTTGCTGTAGACGGTTTAGGTAGGCTTCGGCCGTCCGGGGCACGCTTAACG
ATCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGTCAGAAAGTGAT
GTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGG
AGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCC
CACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCT
GTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGCACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAA
TACCACTACCTCTATAGTTTTTTTACTTATTCAATTAAGCGGAGCTGGACTTCATCGTCCACGTTCTAGCATTAAGGTCT
CTTTAGAGGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACG
CAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATT
TTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAA
AAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCT
TCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCG
TCGTGAGACAGGTTAGTTTTACCCTACTGATGAATGTTATCGCAATAGTAATTGAACTTAGTACGAGAGGAACCGTTCA
TTCGGATAATTGGTTTTTGCGGCTGTCTGATCAGGCAACGCCGCGAAGCTACCATCCGCTGGATTATGGCTGAACGCCT
CTAAGTCAGAATCCATGCTAGAAAGCGATGATTCTTGCCTCGCACATTTTAGTTGGATAAGAATAAGGCTCTTTGAGTC
GCTGAACCATAGCAGGCTGGCAATGGTACACTTAACGGAAAGGTTTTGTGTGCTTGCCGGCGAATAGCAATGTCATAAT
GCGCGGGGATAAATCCTTTGCAAACGACTTAAATGTACAACGGAGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGA
TCTGCTGAGATTAAGCTTCAGTTGTCCGATTTGTTTGTGTTACACAACACAATCTCCTCTAAGTGATAGTTGGCAGGTGC
TAACTA

Figure 52

Rhizomucor miehei rRNA gene (SEQ ID NO: 99)

GACTGGCAACGGTCCGAAGCTTTAGCCGAACTATGGCAAACTACTCCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT
TCCGTAAGTGAACCTGCGGAAGGATCATTAAAAAAAAGTTGATATCATGGTGACCCCTTTACGGGGGTGAGCCATGAT
TTCTTCTCCCTTTTTGTGCAATGTTTGAGGGATTGCTCCAAATCTCTCCTTCCCTTTTTTTACGTATTGATTTGACTGAAC
ATTTTTGTTTTAAAATGAAAAAAAGTTTTGAAGCCAATCAATTGGTTCAAGACAAATCAAATTTTGAAACAACTTTAAG
CAATGGATCACTTGGTTCTCGCATCGATGAAGAACGTAGCAAATTGCGAAAAGTAATGCGATCTGCAACCTTTGCGAAT
CATCGAATTCTCGAACGCATCTTGCACCCTTTGGTCATCCAATGGGTACGTCTAGTTCAGTATCTTTTTGAAACCCTAAA
GGTTCAATTTTGTTGTTGACCTTTGGATTTGCGGTAATGATGGGGGGGAAGACAAAGCAAATTTTTTTTTTTTCCCCCGT
TAAAAGAAACGGAACAGTTTTTGGGTTTTTGGCCTTTTTGGATTGGGGAACATTTTGGAAGGGCTTACTTTGAAAATAA
AAAATTTGGAATTTTGGGTTACCATTGCTTTGGGAAAACCCAATTTAAAAGCAAAAACTTTTTTTAAACTTTTTTTTTTT
CATTCATGGATCTGAACTTAGACGGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAAATAACAA
TGATACCCTTAGTAGCGGCGAGCGAAGTGGGTAAAGCTCAAGTTTAAAACCTGTTTGTCATAGACAAACCGGATTGTA
AACTATGGACATGTTATCCAGGCTCTTTGGACCTTCAAGTCCTTTGGAATAAGGCTTCACAGAGGGTGACAATCCCGTT
AGAGGGTCTTGAACAGAGTCTATTGCGATGCATGCTCCAAGAGTCAAGTTGTTTGGGAATGCAACCTAAATTGCAGGGT
AAATCCCTCCTAAAGCTAAATATTGGCGAGAAACCGATAGCAAACAAGTACCGTGAGGGAAAGTTGAAAAGAACTTTG
AAAAGAGAGTCAAAAGTACGTGAAATTGCTTAAAGGGAAGCGTTTGGAGCTAGTTTGGCTAGTCTGTTATCAGCCTGA
GCTTCGGCTTTGGTGTACTATCAGGCTATTTTTGCCGGCCAACTCTCAGGATTGAAAGGAAAGCTTGGTGCTTTGGAGTC
TAAAGAGACCCTCTCCTGAAGCCTCTGGTGGAGCGTGGTCTGCCCTTGGCCCTTTTGAGCCTATAGTTTGGCTTAATGGC
TCTAAACGGCCCGTCTTGAAACACGGGCCAAGGAGTCCACCACTGTTGCGAGTATTTTGGTGGCAAACCCATACGCGA
AATGAAATTGAAAGCTATGAAATCCGCAAGGATGGCAATAGCGTCCAGGCCTTTAGGACCGAGACAAAGCAATAGTGA
TGGGACCCGAAAGATGGTGAACTATGCTTGAGTAGAGTGAAGCCAGAAGAAATTCTGGTGGAAGCTCGTAACGGTTCT
GACGTGCAAATCGATCGTCGAACTTGAGCATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCATGGTTCCTGCCGA
AGTTTCCCTCAGGATAGCAGAAGCTTATAGGCAGTTTTATGTGGTAAAGCGAATGATTAGAGGTCTTGGGACGCAATCC
TTAACCTATTCTCAAACTTTAAATATGTAAGACGTTCTTGCTGCTTGAATTATGAGCTTGAACCGTCGAATGCTGAGCTT
CTAGTGGGCCGTTCTTGGTAAGCAGGACTGGCGATGCGGGATGAACCGAACGCAAAGATAAGGCGTCAAAGAACACG
CTCATCAGACACCACAAAAGGTGTTGGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGCTAAGGAGTGTGTA
ACAACTCACCTGCCGAATGAACCACGCCCTGGAAATAAATGGCGCTGAAGCGTGTCGCCCATACTTTCCCGTCAAAGTT
AAAAGCGAAGCTTTGACGAGTAGGCAGGCGTGGAGTTTTATTGAGCGTTGGAACCCTTTGGCGGTGAGCCGGAGTGGA
CAGCCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCCAATTGAAATCTTTGAGGACTGAAGTGGAGAAGGTTTC
CTCGAGAACATTAGTTGGTCGAGGGTTAGTCGATCCTAAGAGATAGGGTAGTTCCGTTTTACCAAATGGTCCTTTGGAC
CATCCTATCGAAAGGGAAGCTGGTTAATATTCCAGCACCAAGACATGGATTCTATGCGGCAACGCAGATGAACATAGG
GACATTGGCATGGATCCTGGGAAGAGTTCTCTTTTCTTTTTGACAGCGTTTTCTTAAGCCATGAAATCGGTCTAAACCGG
GGCAATGTTTGCTTAAGAGCTGTTAGAGTAACGCAATTTTTGTGGTAGCCACAGCATTCATGACGATCCTTGAAGACCT
ACGGGAAAGAATGAATTTCATGCTTGGGCGTACCATAACCGCAGCAGGTCCCCAAGGTCTAGAAGCCTCTACTTGATG
GAAGAATGTAGATAAGGGAAGTCGGCAAATTGGATCCGTAACTTCGGGAGAAGGATTGGCTCTAAGGGTTGGGTGCTT
TAAGAACCATGGCCTTAGCGGCCTGAGCAATCGGGCTGCTTCCAGGCTTGGAGCTCTTGGGCACGCTTAACAACCAGCT
TAGAACTGGTACGGACCAAGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATTGCCATAAAGTGGTATTGACG
CAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAGTTGAATAAATTCAACCAAGCGCGGGTAAACCGCGGGTATTACTA
TGAGAGCTTTGTGATATAGTCCAAGTTTCTAGAACTGCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACT
GTCCCTATCTACTATCCAGCGAAACCACAACCAAGGGAACGGGCTTGGCAAAATCAGCGGGAAAGAAGCGCCAGTTGA
GCTTGACTCTAGTTTGACATTGTGAAAGGACATAGGGGTGTAGAATATGTGGGAGCTTCGGCGCCAGTGAATACCACA
ACCCTTATAGTTTTTTTTACTTAAATAATCAAGTGGGAGAAGGCTTCACGGCCTATCTTCTAGCGTTAAGCAGTCTTCGG
GCTGCGACCCATGTTATTGACATTGTCAAGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGT
CCTAAGGGGAGCTCAACGAGAACAGAAATCTCGTGTAGAGCAAAAGGGCAAAAGCTCCCTTGATTTTGATTTTCAGCG
TGAATACGAACCATGAAAGTGTGGCCTATCGATCCTTTATGCCATTTCCTTAGGATTTAAGGCGCCAGAAAAGTTACCA
CAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCAT
ACAGAAGCAGAATTCTGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGA
CAGGTTAGTTTTACCCTACTGATGAATCAGTAGGCGTCCCGACAGTAATTGAAGTTAGTACGAGAGGAACCCTTCATTC
AGATAATTGGTTTTTGCGGTTGGTTGAAAGGCCAATGCCGCGAAGCTACCATCTGCTGGATAATGGCTGAAAGCCTCTA
AGTCAGAATCCATGCTGGTTAAGGGACGCTAAATACCAGACCTTTAAAGCGCGAGAAAGTGCTCAAATAGATCTCTTAT
GGGATCGAATGCCTAATATGAGGTTATCCTCTTGGGTTGAAAGGCTCAAGTCGGATACCTCTCATGATAATGTCTAGCT
TAAAGGTTGTAAATCTCGAGCAGACGACTTGAAATCGACGGGCTATTGTAAGCACTAGAGTAGCCTTTGTTGCTACGAT
GTGCTGAGATTAAGGCCTTGTCTTTAGATTTGT

Figure 53

Rhizopus oryzae rRNA gene (SEQ ID NO: 100)

CTAGGCTATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAATTATGTTAA
AGCGCCTTACCTCTTAGGGTTTCCTCTGGGGTAAGTGATTGCTTCTACACTGTGAAAATTTGGCTGAGAGACTCAGACT
GGTCATGGGTAGACCTATCTGGGGTTTGATCGATGCCACTCCTGGTTTCAGGAGCACCCTTCATAATAAACCTAGAAAT
TCAGTATTATAAAGTTTAATAAAAAACAACTTTTAACAATGGATCTCTTGGTTCTCGCATCGATGAAGAACGTAGCAAA
GTGCGATAACTAGTGTGAATTGCATATTCAGTGAATCATCGAGTCTTTGAACGCAGCTTGCACTCTATGGTTTTTCTATA
GAGTACGCCTGCTTCAGTATCATCACAAACCCACACATAACATTTGTTTATGTGGTAATGGGTCGCATCGCTGTTTTATT
ACAGTGAGCACCTAAAATGTGTGTGATTTTCTGTCTGGCTTGCTAGGCAGGAATATTACGCTGGTCTCAGGATCTTTTTC
TTTGGTTCGCCCAGGAAGTAAAGTACAAGAGTATAATCCAGCAACTTTCAAACTATGATCTGAAGTCAGGTGGGATTAC
CCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAAATAACAATGATTTCCCTAGTAACGGCGAGTGAAGAGG
AAAGAGCTCAAAGTTGGAACCTGTTTGGCCTAGCTAAACCGGATTGTAGACTGTAGAAGTGTTTTCCAGGCAAGCCGA
GTAAATAAGTCCTTTGGAACAGGGCATCATAGAGGGTGAGAATCCCGTCTTTGGCTTGAGCATTTGCCTTTTGTGATAC
GCTTTCAAAGAGTCAGGTTGTTTGGGAATGCAGCCTAAATTGGGTGGTAAATCTCACCTAAAGCTAAATATTGGCGAGA
AACCGATAGCGAACAAGTACCGTGAGGGAAAGATGAAAAGAACTTTGAAAAGAGAGTTAAACAGTATGTGAAATTGT
TAAAAGGGAACCGTTTGGAGCCAGACTGGCTTGTCTGTAATCAATCTAGGCTTCGGCCTGGATGCACTTGCAGGCTATG
CCTGCCAACGACAATTTGACTTGAGGGAAAAAACTAAGGGAAATGTGGCCCACTTGTGGGTGTTATAGTCCCTTAGAA
AATACCTTGGGTTGGATTGAGGAACGCAGCGAATGCTTTTTGGCGAGTTTTCCAGGAAGGTTTTCTGAGGTACTACGGT
ATCAAGGTTGATCTTTTTGGTTATACTTCTATTCGCTTAGGTTGTTGGCTTAATGACTCTAAATGACCCGTCTTGAAACA
CGGACCAAGGAGTCCACCATTAGTGCGAGTATTTGGGTGCCAAACCCATATGCGTAAGGAAACTGATTGATACGAATC
CATTAAGGAGGCAGTATCGTCCGGCGCTGACGTTTTATACTGAATTGACCGAGACAAAGCACTAATGATGGGACCCGA
AAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGATTCTGACGTGCAAA
TCGATCGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAG
GATAGCAGAAACTTATACGCAGTTTTATGTGGTAAAGCGAATGATTGGGGTCACGGGGGGCTAAACGCCCTTCAACCA
CTCTCAAACTTTAAATATGTAAGACGACCTGTTTGCTTAATTGAAGCAGGTCATTGAATGCAGAGTTTCTAGTGGGCCA
TTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCAGAGTTAAGGTGCCGGAATACACGCTCATCAGACAC
CACAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACT
CACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTTAAGCGTGTTACCCATACTCTGCCGTTATTGTAAAAGCGA
AGCAATAACGAGTAGGCAGGCGTGGAGGTTTTTATAAACTGTTAAGAAGCTCTTGGTGTGAACCGGAGTGAAACAGCC
TCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGAGAAAGGTTCCTGGAG
AACATCAGTTGGTCCAGGGTTAGTCGATCCTAAGAGATAGGGAAGTTCCGTTTTTTCAAAGCGCCCAATTTTTGGGCCG
CCTATCGAAAGGGAAACCGGTTAATATTCCGGTACTAGGACGAGGATTTTTTGCGGCAACGCGATTGAACTTGGAGAC
ATCAGTATGGGTCCCGGGAAGAGTTATCTTTTCTTTTTGACAGTTAGTATAAACCTTGAAATCTGTTTAGCAGGAGAAA
AGGTTTATCTGCTGGTAGAGCACAGTACTTTTTGCTGTGTCCGGTGCATTCATAACGATCCTTGAAAATCCAAGGGAAA
GAATAATTTTCTCGCCTAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTAGTTGATAGAACAATGT
AGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGAATAAGGATTGGCTCTAAGGGTTGGGTAGAAATGGACCCT
TGGTATTGACCTTGAGGAAGAGAGAATGGGGGCAACTCTGTTCTTTCATCTTCTTGGTCTACAACCAAGGGAACCCAGT
CTACGCTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGG
CCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGG
GTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGAT
TAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGG
AAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGAGGGTGTAGCATAAGTGGGAGCTTCG
GCGCCAGTGAAATACCACTACCTCTATTGTTTTTTTACTTAAATAATTAAGTGGGATTGAGTCGCAAGACTCACCTTCTA
GCTTTAAGCATCCATTAGGGTGCGACCCATGTTATTGACATTGTCAAGTGGGGAGTTTGGCTGGGGCGGCACATCTGTT
AAAAGATAACGCAGGTGTCCTAAGGGGGACTCAAGGAGAACAGAAATCTCCTGTAGAATAAAAGGGTAAAAGTCCCC
TTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGAATCTCAAGATTTGAGGCTAG
AGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTC
GATGTCGGCTCTTCCTATCATAATGAAGCAGAATTCATTAAGTGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCT
GGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGGTATTGGTATCGCAACAGTAATTGAAGTTAGTACG
AGAGGAACCCTTCATTCAGATAATTGGTATTTGCGGCTGGTTGAAAGGCCAATGCCGCGAAGCTACCATCTGCTGGATA
ATGGCTGAACGCCTCTAAGTCAGAATCCATGCTGGAAGCGATACTACTGTGCTTTGATTGTACTAGTTGTGTACAAATA
AAGCTTCGGCTTGAAAACCTTACTTGCGGGATAGGCTTTGCAGCGGAAATGCTGTGATTCACTACCCTGTGATGATAAT
GCAAATGATCAAAGTGATAAATCGCATGCAGACGACATGAAATGGACGGGGTATTGTAAGTACTAGAGTAGCCTTTGT
TGCTACGATGTACTGAGATTAAGCCCTTGTCATTGAATTTGTTCCTTACG

Figure 54

Saccharomyces cerevisiae rRNA gene (SEQ ID NO: 101)

GGTCATTTAGAGGAACTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAAGAAATTTAATA
ATTTTGAAAATGGATTTTTTTGTTTTGGCAAGAGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCA
GCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTG
TGCTTTTGTTATAGGACAATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTCATATCTTTGCAACTTTTTCTTTGG
GCATTCGAGCAATCGGGGCCCAGAGGTAACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAA
TTTTCGTAACTGGAAATTTTAAAATATTAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAG
CGAAATGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATT
CCAGGGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACT
TGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACG
GTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGT
CTAGGCGAACAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCAATAAGCGG
AGGAAAAGAAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCTT
CGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCTTGTCTATGTTCCTTGGAACAGGACGTCATAGA
GGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCT
CTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGAT
GAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTT
TGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA
TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAGGACTGCGACGTAAGTC
AAGGATGCTGGCATAATGGTTATATGCCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGTCTATGCGAGTGTTTGG
GTGTAAAACCCATACGCGTAATGAAAGTGAACGTAGGTTGGGGCCTCGCAAGAGGTGCACAATCGACCGATCCTGATG
TCTTCGGATGGATTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCA
GAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGACT
AATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAGCTCGTATCAGTTTTATGAGGTAAA
GCGAATGATTAGAGGTTCCGGGGTCGAAATGACCTTGACCTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTACT
TAATTGAACGTGGACATTTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACC
GAACGTAGAGTTAAGGTGCCGGAATACACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCGGACGG
TGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGC
GCTCAAGCGTGTTACCTATACTCTACCGTCAGGGTTGATATGATGCCCTGACGAGTAGGCAGGCGTGGAGGTCAGTGAC
GAAGCCTAGACCGTAAGGTCGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATATTCAAATGAGAAC
TTTGAAGACTGAAGTGGGGAAAGGTTCCACGTCAACAGCAGTTGGACGTGGGTTAGTCGATCCTAAGAGATGGGGAAG
CTCCGTTTCAAAGGCCTGATTTTATGCAGGCCACCATCGAAAGGGAATCCGGTTAAGATTCCGGAACCTGGATATGGAT
TCTTCACGGTAACGTAACTGAATGTGGAGACGTCGGCGCGAGCCCTGGGAGGAGTTATCTTTTCTTCTTAACAGCTTAT
CACCCCGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAGAGGCCAGCACCTTTGCTGGCTCCGGTGCGCTTG
TGACGGCCCGTGAAAATCCACAGGAAGGAATAGTTTTCATGCCAGGTCGTACTGATAACCGCAGCAGGTCTCCAAGGT
GAACAGCCTCTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGATAAGGATTGG
CTCTAAGGGTCGGGTAGTGAGGGCCTTGGTCAGACGCAGCGGGCGTGCTTGTGGACTGCTTGGTGGGGCTTGCTCTGCT
AGGCGGACTACTTGCGTGCCTTGTTGTAGACGGCCTTGGTAGGTCTCTTGTAGACCGTCGCTTGCTACAATTAACGATC
AACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGTCAGAAAGTGATGTT
GACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGT
AACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCAC
TGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTT
GAGCTTGACTCTAGTTTGACATTGTGAAGAGACATAGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCAGTGAAATAC
CACTACCTTTATAGTTTCTTTACTTATTCAATGAAGCGGAGCTGGAATTCATTTTCCACGTTCTAGCATTCAAGGTCCCA
TTCGGGGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACGATAACGCA
GATGTCCTAAGGGGGGCTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGCCCCCTTGATTTTGATTTT
CAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGTGCCAGAAA
AGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATTGCTTTTTGATTCTTCGATGTCGGCTCTT
CCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGT
CGTGAGACAGGTTAGTTTTACCCTACTGATGAATGTTACCGCAATAGTAATTGAACTTAGTACGAGAGGAACAGTTCAT
TCGGATAATTGGTTTTTGCGGCTGTCTGATCAGGCATTGCCGCGAAGCTACCATCCGCTGGATTATGGCTGAACGCCTCT
AAGTCAGAATCCATGCTAGAACGCGGTGATTTCTTTGCTCCACACAATATAGATGGATACGAATAAGGCGTCCTTGTGG
CGTCGCTGAACCATAGCAGGCTAGCAACGGTGCACTTGGCGGAAAGGCCTTGGGTGCTTGCTGGCGAATTGCAATGTC
ATTTTGCGTGGGGATAAATCATTTGTATACGACTTAGATGTACAACGGGGTATTGTAAGCAGTAGAGTAGCCTTGTTGT
TACGATCTGCTGAGATTAAGCCTTTGTTGTCTGATTTGTTTTTTATTTCTTTCTAAG

Figure 55

Schizosaccharomyces japonicus rRNA gene (SEQ ID NO: 102)

ATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAGAAAGTAATTATTTGAG
TTTTCAACATTCACCTGCTGAACTCTCAAAAAATCTCTCTATATCTTTCTGTGAACATGTTTTCATATGAGAATGTTTGGT
CAGTCGGTCGAAAGGTTGGTTGGCCAAGCATTTGAACTATAAACTTCATTTTATATTTGATGTCTGATTTATATTTAACT
AAATGTTAAAACTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTG
AATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCTTTGGGTTATTCCCAAAGGCATGCCTGTTTGA
GTGTCATTACATTCTTCTTAAATCTAACTTTTTGTTATGGGTTAAGGTGTTGAACTATAATCGCGAAAGCAGATTTGGTT
TTAAATTTAAAGGTAGATTATGGAGATGCTTCAGCAATTCGTTAAGCACGCATATTCATATTTGAACGTAATAGGTTTT
ACCAACTCGTTCAAGTTCATTGATTGTGTTGTGTGAGTTGCTATAGTAAGCATTATCGAACTAATCCTTAATGTCTTTCG
AGACTACATTCATTTGAATGTACTCCTTTGTTTGACCTCAGATCAGGTAGGACTACGCGCTGAACTTAAGCATATCAAT
AAGCGCAGGACAAGAAAATAACCATGATTCCCCTAGTAACGGCGAGTGAAGCGGGAAAAGCTCAAATTTGAAATCTG
GCAAAGTTTTATTCTTTGCCCGAGTTGTAATTTCAAGAAGCTGCTTTGAGTATTGCTACGTCGGTCTAAGTTCCTTGGAA
CAGGACGTCAGAGAGGGTGAGAACCCCGTCTTTGGCCGATGTGCTTTGCCATATAAAGCGCTTTCTAAGAGTCGAGTTG
TTTGGGAATGCAGCTCTAAATGGGTGGTGAATTTCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTA
GAGTGATCGAAAGATGAAAAGAACTTTGAAAAGAGAGTTAAATAGTACGTGAAATTGCTGAAGGGGAAGCATTGGAA
ACCAGTCTTACCTTGGTGAGATCAGCTGTTTACTTGTAGACAGTGCACTCTGAACCTAGGTAGGTCAGCATCAGTTTTCG
GGGACGGAAAAAGAATAAGGGAAAGTGGCTTTTGGGCTTGCTCAGAAGTGTTATAGCCCTTATTGTAATACGCCCACT
GGGGACTGAGGTCTGCGACTTTGTCAAGGATGCTGACATAATGGTTTTCAATGGCCCGTCTTGAAACACGGACCAAGG
AGTCTAGCATCTATGCGAGTGTTTGGGTGGCTAAACCCATACGCGAAATGAAAGTGAATGCAGGTGGGAACTTTTTGTG
CACCACCGGCCGATCCGGAAGTTTGTCAATGGAAGGATTTGAGCAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGA
ACTATGCCTGAATAGGGCGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGGTTCTGACGCGCAAATCGATCGTCA
AATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGA
AACTCAGATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGAAGTAATTTCCTCAACCTATTCTCAAACTT
TAAATATGTAAGACGCCCTTGTCGCTTAATTGGACGTGGGCTTTCGAATGAGAGTTTCTAGTGGGCCATTTTTGGTAAG
CAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAATGCACGCTCATCAGACACCAGAAAAGGT
GTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCTGCCGA
ATGAACTAGCCCTGAAAATGGATGGCGCTTAAGCGTGCTACCCATACCTCGCCGTCTGGGTTAATTATGAAGCTTAGAC
GAGTAGGCAGGCGTGGAGGTCAGTGACGAAGCCTTGGGCGTAAGCCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGT
GGAAGTAGCAAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGG
GTTAGTCGATCCTAAGAGATAGGGAAGCTCCGTTTGAAAGTACACGATTCTTCGTGTCACCTATCGAAAGGGAATCCGG
TTAATATTCCGGAACCAGGATGTGGATTCTCCACGGCAACGTAAATGAAGTTGGAGACGTCGGTGGGAGCCCTGGGAA
GAGTTCTCTTTTCTTTTTAACAAACCAATCACCCTGAAATCGGTTTATCCGGAGCTAGGGTATAGTGTTTGGTAGAGCTC
AGCGCCTCTGCTGGGTCCGGTGCGCTCTCAACGGCCCTTGAAAATCCAACGGAAGGAATAGTTTTCACGCCTGGTCGTA
CTCATAACCGCAGCAGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATA
GATCCGTAACTTCGGGATAAGGATTGGCTCTAAGGGTTGGGTACGTTGGGCCTTGGTTTTGAACAATTGCTGGACTGGT
TAGGAACTGTCTGACTTCCCCGGAAGACGGATAGATCTTGACTAGACCTTGGCAGTTGGGATGGCCTTGGTAAGGCCTC
TACTTTGTAGAGTGTCCCTCACTGGCGTACGCTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTC
TAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAA
GTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATC
TAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGA
ACGGGCTTGGCAAAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAGAGACATAGAG
GGTGTAGCATAAGTGGGAGCTTCGGCGCCAGTGAAATACCACTACCTTTATAGTTTCTTTACTTAATCAATGAAGCGGA
ATTGGAATTCATTTTCCACATTCTAGCGTTAAAGTTCTTTACGAACCGATCCGTGTTGATGACATTGTCAGGTGGGGAGT
TTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGGGGGACTCATCGAGAACAGAAATCTCGAGTA
GAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTT
AGTCCCTCGAAATTCGAGGATAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCAT
AGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCA
CCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAATGTCGTCGCA
ATGGTAATTCAACTTAGTACGAGAGGAACCGTTGATTCAGATAATTGGTATTTGCGGCTGCCTGACAAGGCAATGCCGC
GAAGCTATCATCTGCCGGATAACGGCTGAACGCCTCTAAGTCAGAATCCGTGCCAGAAAGCGACGATACCTTATTCCG
CGCATCTTTGGTGCATACAAATAGAGCTTTGCTCCTGTATCGTATAAGGTGGGCGATGGCTAGTAGAACGGAAATGTTT
TATTAGTTTGTCCACGAAATTCCATTGAAAATTTGTGCGGAGTCGAATCCTTTGCATACGACTTAAATGTGGAACGGGG
TATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGATTAAGCCTTTGTTCCCAAGATTTGTTCTATAAGAAC

Figure 56

Schizosaccharomyces pombe rRNA gene (SEQ ID NO: 103)

CATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAGAAAAGTTATATGAAA
AGGTTTTAAAAAATTTCCATCTTTTAACTTTTTGGGAATTTTTTTTACCTTTTTCTTCTCTTATCCATTTACCTTTCTGTGA
AAATGTAAAATATTTTCAATTTTGATTTTTTTTTCTTTTTCTTTATATTTTTTTATTAAAAAAAAGTGTTTAGAAAAGAGA
AAAGATGAAAAAAAAAATGAAATTGTAAATATTACGAGTGGATGATTTTTGTTTGGTGTGTTTTTGTTGCATGCCAAGC
ATATCATTACTTTTTTTACTATTTTATTTTATTTTATCATTTTTCTATTCTTTCTCTTTTTTTTTAATATAAGGAAATTGGAA
AAGAAGCAAAATTAAATTATAAACCTTGAAATTTGTTTTTGAAGTCTGAATTAATTATATCTAATATATAAAATTATTTA
AAACTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAG
AATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCTTTGGGTTCTACCAAAGGCATGCCTGTTTGAGTGTCATTA
CAATCTTCTCACAAAAAATGTTTTTTTTTTAAATATTTTTGATGAGGTGTTGAACGAAAATTTGTTTTTTTTTTAAAATATA
AATTTAGTTTGAAATCGATTGGTGAAAACAAAAGGAAGATTGAAATTATTTTTCTATGCCTTTTTTCATTTTTTTTCTATT
GAACGTAATAGGTTTTACCACTTTGTTTGATAGAAAAAAAGAAATTAGGAAAGAAAAATAACTAAAAAGTTTTAATCT
CTTTTATATTTGAACCTTAACGAAAAAAAAAGTTATTTTTTTTTCACAGTACCTTTTTTATTTGACCTCAAATCAGGTAG
GACTACGCGCTGAACTTAAGCATATCAATAAGCGCAGGAAAAGAAAATAACCATGATTCCCTCAGTAACGGCGAGTGA
AGCGGGAAAAGCTCAAATTTGAAATCTGGCAACATTTCTTTTGTTGTCCGAGTTGTAATTTCAAGAAGCTGCTTTGAGT
GTAGACGATCGGTCTAAGTTCCTTGGAACAGGACGTCAGAGAGGGTGAGAACCCCGTCTTTGGTCGATTGGATATGCC
ATATAAAGCGCTTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCTAAAGCTAAATA
TTGGCGAGAGACCGATAGCGAACAAGTAGAGTGATCGAAAGATGAAAAGAACTTTGAAAAGAGAGTTAAATAGTACG
TGAAATTGCTGAAAGGGAAGCATTGGAAATCAGTCTTACCTGGGTGAGATCAGTAGTCTCTTCGCGAGACTATGCACTC
TGAACCTGTGGTAGGTCAGCATCAGTTTTCGGGGGCGGAAAAAGAATAAGGGAAGGTGGCTTTCCGGGTTCTGCCTGG
GGAGTGTTTATAGCCCTTGTTGTAATACGTCCACTGGGGACTGAGGACTGCGGCTTCGTGCCAAGGATGCTGACATAAT
GGTTTTCAATGGCCCGTCTTGAAACACGGACCAAGGAGTCTAGCATCTATGCGAGTGTTTGGGTGATGAAAACCCATCC
GCGAAATGAAAGTGAATGCAGGTGGGAACGCCCTTGTGGCGTGCACCATCGACCGACCCGGAAGTTTGTCAATGGAAG
GGTTTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTC
TGGTGGAGGCTCGTAGAGATTCTGACGTGCAAATCGATCTTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCA
TCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGAAACTCAGATCAGTTTTATGAGGTAAAGCGAATGATT
AGAGGTCTTGGGGAAGGAATTTCCTCAACCTATTCTCAAACTTTAAATATGTAAGACGCCCTTGTCGCTTAATTGGACG
TGGGCCATCGAATGAGAGTTTCTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGTGAGG
TTAAGGTGCCGGAATGTACGCTCATCAGACACCAGAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGA
AGTCGGAATCCGCTAAGGAGTGTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTTAAGCGT
ACTACCCATACCTCACCGTCTGGGTTAGCTTTGAGAAGCTCAGACGAGTAGGCAGGCGTGGAGGTTTGTGACGAAGCCT
TGGGCGTGAGCCTGGGTCGAACAGCCTCTAGTGCAGATCTTGGTGGAAGTAGCAAATATTCAAATGAGAACTTTGAAG
ACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGAGATAGGGAAGCTCCGTA
TGAAAGTTGCACGATTTTTCGTGCCTCCTATCGAAAGGGAATCCGGTTAATATTCCGGAACCAGAAGGTGGAATCAACA
CGGCAACGTAAATGAAGTTGGAGACGTCGGCGGGAGCCCTGGGAAGAGTTCTCTTTTCTTTTTAACAAACCATTGAACT
ACCCTGAAATCGGTTTATCCGGAGCTAGGGTATGGTGTTTGGAAGAGTTCAGCGCCTCATGCTGAATCCGGTGCGCTCT
CGACGGCCCTTGAAAATCCAACGGAAGAATGGACCTTCGGGTCCTTGTTTTCACATCTGGTCGTACTCATAACCGCAGC
AGGTCTCCAAGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATGGATCCGTAACTTCG
GGATAAGGATTGGCTCTAAGGGTTGGGTACGTTGGGCCTTGGAACCTGAACGGTTGCTGGACTGAGCGTGGACCGATG
TCTTTTCTCGCCTTTCGGGGTGAGAAGGGATGTTGGACCTGCTTGGACCTTGGCGGCCGGGAAGTCCTTGGTCGGGCTTT
TCTCCTTCTCGGGGATTATGCTCTTACTGGCGTACGTTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGA
CTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATG
TCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCG
TCATCTAACTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCT
GGGGAACGGGCCAGGCAAAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAGAGACA
TAGAGGGTGTAGGATAAGTGGGAGTATGTTTCGGCATACGCCGGTGAAATACCACTACCTTTATCGTTTCTTTACTTAA
TCAATGAAGCGGAATTGGGATTTATTTCCCATATTCTAGCGTTAAAGTTTCTTCGCGAACTGATCCGCGTTGATGACATT
GTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGGGGGACTCATCGAGAAC
AGAAATCTCGAGTAGAATAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTG
GCCTATCGATCCTTTGTTCCCTCGAAATTTGAGGACAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGC
AGCCAAGCGTTCATAGCGACGTTGCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAG
CGTTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGA
TGAAGTGTCGTCGCAATGGTAATTCAACTTAGTACGAGAGGAACCGTTGATTCAGATCATTGGTATTTGCGGCTGCCTG
ACAAGGCAATGCCGCGGAGCTATCATCTGCCGGATAACGGCTGAACGCCTCTAAGCCAGAATCCGTGCCAGAAAGCGA
CGATTTTTTGGTCCGCATGATTTATATGTATAAAAATAGAGGTAGGACTTGTTCCTACTCTCCTGTATCGTAGAAGATGG
GCGATGGTTGATGAAACGGAAGTGTTTTATTGACTTGTCCATGAAATTCCATTGAAATCTTGTGCGGAATCGAATCCAT
TGCATACGACTTTAATGTGGAACGGGGTATTGTAAGCAGTAGAGTAGCCTTGTTGTTACGATCTGCTGAGATTAAGCCT
TTGTTCCCAAGATTTGTTCCATTAAG

Figure 57

Sclerotinia sclerotiorum rRNA gene (SEQ ID NO: 104)

TTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGAGTTCATGCCCGAAAG
GGTAGACCTCCCACCCTTGTGTATTATTACTTTGTTGCTTTGGCGAGCTGCTCTTCGGGGCCTTGTATGCTCGCCAGAGA
ATATCAAAACTCTTTTTATTAATGTCGTCTGAGTACTATATAATAGTTAAAACTTTCAACAACGGATCTCTTGGTTCTGG
CATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA
CATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCTCAGCTTGGTATTGAGTCC
ATGTCAGTAATGGCAGGCTCTAAAATCAGTGGCGGCGCCGCTGGGTCCTGAACGTAGTAATATCTCTCGTTACAGGTTC
TCGGTGTGCTTCTGCCAAAACCCAAATTTTCTATGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATA
TCAATAAGCGGAGGAAAAGAAACCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAA
ATCTGGCTCTTTCAGAGTCCGAGTTGTAATTTGTAGAAGATGCTTCGGGTGTGGTTCCGGTCTAAGTTCCTTGGAACAGG
ACGTCATAGAGGGTGAGAATCCCGTATGTGACTGGATACCTATGCTCATGTGAAGCTCTTTCGACGAGTCGAGTTGTTT
GGGAATGCAGCTCAAAATGGGTGGTATATTTCATCTAAAGCTAAATATTGGCCAGAGACCGATAGCGCACAAGTAGAG
TGATCGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAACAGTACGTGAAATTGTTGAAAGGGAAGCGCTTGCAATCA
GACTTGCACTTGGTGTTCATCAGGGTTTCGTGCCCTGTGTACTTCATCAAGTTCAGGCCAGCATCAGTTTGAGTGGTTAG
ATAAAGGCTTGGAGAATGTGGCCCTCTTCGGGGGGTGTTATAGCTCCAGGTGCAATGTAGCCTACTTGGACTGAGGACC
GCGCTTCGGCTAGGATGCTGGCGTAATGGTTGTAAGCGACCCGTCTTGAAACACGGACCAAGGAGTGTACCTAATATG
CGAGTGTTTGGGTGTTAAACCCATACGCGTAATGAAAGTGAACGCTGGTGAGAACCCTTAAGGGTGCATCATCGACCG
ATCTTGATGTCTTCGGATGGATTTGAGTAAGAGCATATTGGGTGCGACCCGAAAGATGATGATCTATACGTGAATAGGG
TGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGCGTATAGGGGC
GAAAGACTAATCGAATCATTAAGGAATAGACCAAGCTCTAGGTGATTGAGAAACCTCCTTTGGGGTATTAGTCCTGGA
GACAGGGCGACATTGTCAAATTGTTCGGGGACCACCTGTTAAATTATATGCTACTGCAGCAGTGCTGAAAGGCCTGTGA
GCACTGAGGGTAACGCCCTCAGGGATGGTAATAACGCATATATAGGGTATATCCGCAGCGAAGTTCTAAGGCTTTCGA
GCTATGAATCGCGTTCACAGACTAGACGGCAATGGGCTCCTCGCGGGGCTTAAGATATAGTCGAACCCCTCAGAGATG
AGGATGGAATCAATGCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTGTTGTTTTCAGTTTTATGAGGT
AAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTT
ACTTAATTGAACGTGGACATTCGAATGTACCAACACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATG
AACCGAACGCGAGGTTAAGGTGCCGGAATATACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCAGG
ACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAATGTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGA
TGGCGCTTAAGCGTATTACCCATACCTCGCCGCCAGGGTAGAAACTATGCCCTGGCGAGTAGGCAGGCGTGGAGGTTG
TGACGAAGCCTTGGGAGTGATCCCGGGTAGAACAGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTCAAATGA
GAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGAGATAGG
GAAACTCCGTTTTAAAGTGCGCACTTGTGCGCCGTCCCTCGAAAGGGAAACCGGTTAATATTCCGGTACCTGGATTTGG
ATTCTCCACGGCAACGTAACTGAACGCGGAGACGACGGCGGGGGCCCCGGGAAGAGTTCTCTTTTCTTCTTAACAGCCT
ATCACCCTGAAATCGGTTTGTCCGGAGCTAGGGTTTAACGGTTGGTAGAGCTCGACACCTCTGTCGGGTCCGGTGCGCT
CTCGACGTCCCTTGAAAATCCGCGGGAAGGAATAGCTTTCAAGCCAGGTCGTACTCATAACCGCATGCAGGTGCTCCA
AGGTGAACAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGG
ATTGGCTCTAAGGGTTGGGTACGTTGGGCCATTAGGGGATGCTCTTGGAGCAGAGGAGCACTAGCTTCACGGCCGGCG
CTCTTCAGCATCGAGGGTTTGACGCTTTTGGCAGGCTTCGGTCGTCCGGCGTACAATTAACAACCAACTTAGAACTGGT
ACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATT
TCTGCCCAGTGCTCTGAATGTCAAAGTGAAGTAATTCAACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCAAC
CCTAAGAGGGTCGTAAGAGGGGATGCGAATAGCATTCCTTTAGTGATGAGATCGCAACACTGTCAAATTGCGGGGAGT
TCCTAAAGCTCAGGCTACCGCCTCAGGTGCTGAAAAGCCCTGAAGGCACCAAGGTTAGCAACCTTGGGTATGGTAATA
ACGCCTGTAGATACTACAATGGATGATCCGCAGCCAAGCTCTAACAATCTTTTCACGATTCACGAGCGGGGTTCAACGA
CTAGACGGCAGTGGGCCTGCAAAACAGGTTTAAGATATAGTCTGCGCCTAGGGAAAAATCCCAAGGAAATAAGTGCTC
TTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTAC
TATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTA
GTTTGACATTGTGAAAAGACATAGGGGGTGTAGAATAGGTGGGAGCGCAAGCGCCGGTGAAATACCACTACCCTTATC
GTTTTTTTACTTATTCAATAAAGCGGAACTGGGTGTCAAAGCCCAACTTCTAGCATTAAGGTCCTTCGCGGGCTGATCCG
GGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGG
ACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAA
CCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATA
ACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGC
AGAATTCGGTAAGCGTTGGATTGTTCACCCACTAGACCTTATTGGTGGGAAAAAGATCTTATTGATCACTTAGTCGAGT
CACCCACAACTATTGCGGGCGGTGACCGGCGAGACAACCTGGTTCGGGGGAGGCTGTAAAATGCTAATCTCGAGTGCA
GTCTGCTGGGAGTGATCCCTACAAGACGCACGTAACGCGCGGAAAGGTGTCGGTTGCCTCTTTTACAGAGGGAGCTTAT
GGGACGTGCTAAACCTATCCGAAAGGATAACACTGATCTAAGGGCCCGCAGCCTGGAGTTTAGTGTGACCGTCAAGAG
CCTGGGAGGAAATGCCCAAGGTCAGGTTGGTATATTAATGAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGAC
AGGTTAGTTTTACCCTACTGATGACCGTCGCCGCAATGGTAATTCAGCTTAGTACGAGAGGAACCGCTGATTCAGATAA
TTGGTTTTTGCGGCTGTCTGACAAGGCAGTGCCGCGAAGCTACCATCTGCTGGATAATGGCTGAACGCCTCTAAGTCAG
AATCCATGCCAGAAAGCGGTGATTTATACCCACACATCGTAGTCGGATACGAATAGGCCTTTGGCCCTGAATCTTAGCT
GGCTGGTAACGATCCTATTGAAGAAACTCTTTAGGATTAACTGGCGTCTTGCAATTTTACAATGCGTGGGGTTGAATCC
TTTGCATACGACTTAATTGTGCTACACGGTCCTGTAAGTAGTAGAGTAGCCTTGTTGTTACGATCTACTGAGGGTAAGC
CGTCTCGTAGCCTAGATTTGATTTTCAAT

Figure 58

Stagonospora nodorum rRNA gene (SEQ ID NO: 105)

TTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACACTCAGTAGTTTACTACT
GTAAAAGGGGCTGTTAGTCTGTATAGCGCAAGCTGATGAGCAGCTGGCCTCTTTTATCCACCCTTGTCTTTTGCGTACCC
ACGTTTCCTCGGCAGGCTTGCCTGCCGGTTGGACAAATTTATAACCTTTTTAATTTTCAATCAGCGTCTGAAAAACTTAA
TAATTACAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAGTGTGAAT
TGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCATGGGGCATGCCTGTTCGAGCG
TCATTTGTACCCTCAAGCTCTGCTTGGTGTTGGGTGTTTGTCCTCTCCCTAGTGTTTGGACTCGCCTTAAAATAATTGGCA
GCCAGTGTTTTGGTATTGAAGCGCAGCACAAGTCGCGATTCGTAACAAACACTTGCGTCCACAAGCCTTTTTAACTTTT
GACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGC
CCTAGTAACGGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCTCTTTCAGAGTCCGAGTTGTAATTTGCAGAG
GGCGCTTTGGCGTTGGCAGCGGTCCAAGTTCTTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTACGTGGTCGCT
AGCCTTCGCCGTGTAAAGCCCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGAGGTAAATTTCTTCTA
AAGCTAAATACTGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGGAAAGAGAGTC
AAATAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCAGCCAGACTTGCCTGTAGTTGCTTATCTGGACTTTTGTCCAG
TGCACTCTTCTGCGGGCAGGCCAGCATCAGTTTGGGCGGTTGGATAAAGGTCTCTGTCATGTACCTCCTTTCGGGGAGG
CCTTATAGGGGAGACGACATGCAACCAGCCTGGACTGAGGTCCGCGCATCTGCTAGGATGCTGGCGTAATGGCTGTAA
GCGGCCCGTCTTGAAACACGGACCAAGGAGTCTAACATCTATGCGAGTGTTTGGGTGTCAAGCCCAGACGCGTAATGA
AAGTGAACGGAGGTGGGAACCTTTTAGGTGCACCATCGACCGATCCTGATGTCTTCGGAAGGATTTGAGTAAGAGCAT
AGCTGTTGGGACCCGAAAGATGGTGAACTATGCTTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGC
GGTTCTGACGTGCAAATCGATCGTCAAATTTGGGCATAGGGGCGAAAGACTAATCGAACTATCTAGTAGCTGGTTCCTG
CCGAAGTTTCCCTCAGGATAGCAGTAACGTATTCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTGGGGGTTGAA
ACAACCTTCACCTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTACTTGATTGAACGTGGACACTTGAATGTACCG
TTACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGGGGTTAAGGTGCCAGAATATA
CGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGG
AGTGTGTAACAACTCACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTATTACCCATACCCCGCCG
CCGGGGCAGAATTTATGCCCCGGCGAGTAGGCAGGCGTGGAGGCTCGTGACGAAGCCTTGGGGGTGACCCCGGGTCGA
ACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTC
CGTGTGAACAGCAGTTGGACACGGGTTAGTCGATCCTAAGAGATAGGGTAGTTCCGTTTTAATGTTGGCGCTTGCGCCA
CGCCCTCGAAAGGGAAGCCGGTTAACATTCCGGCACCTGGATGTAGATTCTCCGCGGCAACGCAACTGAGAGCGGAGA
CCTTGGCGGGAGCCCCAAGAAGAGTTCTCTTTTCTTCTTAACGGTCTGTCACCCTGAAATCGGTTTGTCCGGAGCTAGG
GTTCAATGGCCGGAAGAGCGCTGCACTTTTGTGGCGTTTGGTGCGCTCCCGACGAGCCTTGAAAATCCGCTTGAAGAAA
TAGTTTTTACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTAGTTGATAGAACAATGTAGA
TAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTTGGGTACGTTGGGCCTTGGAG
AGAAGCCTCTGGCGCAGAAGGGCACTAGCCGCAAGGTGGGCGCCTTTCAGCGCTGGGGTGCGGGCATCCTTGGCAGGC
TTCGGCCGTCCGGCGTACGTTTAACAACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACAT
AGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGCGAAGAGATTC
GACCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACG
CGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGC
CAAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATAGGGGGTGTAGAATA
GGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCCTTATCGTTTTTTTACTTATTCGATGAAGCGGAGCTGGGCCTCA
CCGCCCAACTTCTAGCGTTAAGGTCCTTCGTGGGCCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGG
CGGCACATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAGCAAAAGG
GCAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAA
ATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGC
TTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAG
GGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGACCTTGCCCCAATGGTAATACCG
CTTAGTACGAGAGGAACCGCGGTTTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCATTGCCGCGAAGCTACCATC
TGCTGGATTATGGCTGAACGCCTCTAAGTCAGAATCCATGCCAGAACGGGGTGATTTCCGCCTGCACCAGTCGGATACG
AATAGGCCTTTGGCCCAGAACCTTACCAGATCAGCGTTGGCAGTCTCATTGAAATTGGGGCTGCTAGCTGGTGTATTGC
AATTGTACAGTGCGCAGGATTGAATCCTTTGCAGACGACTTAGTTGTCTAGCCGGGTCGTGTAAGTAGTCGAGTAGCCT
TGTTGTTACGAGCTACTGAGCGTAAGCCCGATGCTAGCTTGGTTGAATATGGGAAT

Figure 59

Umbilicaria esculenta rRNA gene (SEQ ID NO: 106)

CTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAAGAGATAGG
GCCCTCTCTGGGCCCGACCCTCCAACCCTTTGTCTACCTTACCTTCGTTGCTTTGGCGGGCCCGCTGGGGATGACCCACC
GCCGGCGCCAGCCGGTGAGCGCCCGCCGGAGGCCATCAAAACTCCGTCTGTCGGTGCTGTCTGAGTACCCCACAATCG
TTAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGC
AGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTTCGAGCGTCA
TTACAACCCTCAAGCTCTGCTTGGTATTGGGCTTTCACCCCTCCCCCGGGGGGGCGTGCCTGAAAGTGAGTGGCGGTGC
AGCCTGACTTCAAGCGTAGTAACTTCAAAACCCGCTTCGGAAGCCTTTCAGGTTGGGCCGGCCAGACAGCCCAACATTA
TTTCTATGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAA
CAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAACAGCTCAAATTTGAAATCTGGCCCCCCCGGGGTCCGAGTTGT
AATTTGTAGAGGATGCTTCGGGTGCGGCGCCGGTCTAAGTTCCTTGGAACGGGACGTCATAGAGGGTGAGAATCCCGT
ATGTGACCGGTGACCCAGCCCGTGTGAAGCTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTA
AATTTCATCTAAAGCTAAATACCGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGG
AAAGAGAGTTAAAAAGTACGTGAAATTGTTGAAAGGGAAGCGCTTGCGACCAGACTTGCTCGGGGGTGATCAGCCGTC
CTTCTGGGCGGCGCACTCGCCCACGATCGGGCCAGCATCGGTTCAGGCGGCCGGATAAAGGCCCCGGGAACGTGGCTC
CCTCCGGGGGAGTGTTACAGCCCGGGGTGCAATGCGGCCAGCCCGGACCGAGGACCGCGCTTCGGCTAGGATGCTGGC
GTAATGGTCGCAAGCGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATCTATGCGAGTGTTTGGGTGTCAAACCC
ATGCGCGCAATGAAAGTGAACGGAGGTGGGAACCCTCCAGGGTGCACCATCGACCGATCCTGATGTCTTCGGATGGAT
TTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGG
TGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCT
AGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAACGTTTTCAGTTTTATGAGGTAAAGCGAATGATTAGAG
GCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAAATATGTAAGAAGTCCTCGTTGCTCATTTGAACGTGGA
CATTTGAATGCACCGTTACTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGAACGCGAGGTTA
AGGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGT
CGGAACCCGCTAAGGAGTGTGTAACAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCT
ACCCATACCTCGCCGCCAGGGTAGAAACGATGCCCTGGCGAGTAGGCAGGCGTGGGGGTCGGTGACGAAGCCTCGGG
GGTGATCCCGGGTCGAACGGCCCCTAATGCAGATCTTGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTG
AAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGACATGGGTTAGTCGATCCTAAGAGATAGGGAAACTCCGTTTTAA
AGCGCGCACTCGTGCGCCGTCCCTCGAAAGGGAAGCCGGTCAACATTCCGGCACCTGGATGTGGATTCTCCACGGCAA
AGTAACCGAACGCGGAGACGTCGGCGGGGGCCCCGGGAAGAGTTCTCTTTTCTTCTTAACGGCCCATCACCCTGAAATC
GGTTTGTCCGGAGCTAGGGTTTAACGGCCGGTAGAGCCCCACACCTTTGTGGGGTCCGGTGCGCTCCCGACGACCCTTG
AAAATCCGCGGGAAGGAATAGTTTTCACGCCAGGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTGAAAAGCCTCTA
GTTGATAGAACAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTTG
GGTGCGTTGGGCCTTGGGGGGATGCCCCCGGAGCAGGTGGGCACTAGCCGGGCAACCGGCCGGCGCCCTCCAGCATCG
GGCGGCGGACGCCCGTGGCAGGTTTCGGCCGTCCGGCGCACGCTTAACGACCGACTTAGAACTGGTACGGACAAGGGG
AATCTGACTGTCTAATTAAAACATAGCATTGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCT
CTGAATGTCAAAGTGAAGAAATTCAAATAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAA
TGCCTCGTCATCTAATTAGTGACGCGCATGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACC
ACAGCCAAGGGAACGGGCTTGGCGGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGA
AAAGACATAGGGGGTGTAGAATAGGTGGGAGCTTCGGCGCCGGTGAAATACCACTACCCTTATCGTTTTTTTACTTATT
CAATGAAGCGGAACTGGGTTTTACCGCCCAACTTCTGGCGTCAAGGTCCCTCGCGGGCCGATCCGGGTTGAAGACATTG
TCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACA
GAAATCTCCAGTGGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGC
CTATCGATCCTTTAGTCCCTCGAAATTTGAGGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAG
CCAAGCGTTCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCG
TTGGATTGTTCACCCACTAATAGGGAACGTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATG
ACCGTCACCGCAACGGTAATTCAACTTAGTACGAGAGGAACCGTTGATTCAGATAATTGGTCTTTGCGGCTGTCTGACC
AGGCAGTGCCGCGAAGCTACCCTTCTTT

Figure 60

Uncinocarpus reesii rRNA gene (SEQ ID NO: 107)

TTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGTGGTTTCGG
GCCGTGCCGTTTCCCCGCTCGGGGGGCGCGCGGCCTGCACCTCCCACCCATGTTTACTTGAAACCCTTTGTTGCCTTGGC
AGGACTGCCGCTTGTCGGCTGCCGGGGACCTGCAGCCATGCAGCCCGGGCGAGTGCCTGCCAGAGGACTATTTGAACC
CTAAGTGAAGATTGACAGTCTGAGTATTCTAGCAAGAATAAGTTAAAACTTTCAACAACGGATCTCTTGGTTCCAGCAT
CGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACAT
TGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCAAATCCTTCAAGCACGGCTTGTGTGTTGGACT
GCGTCCCCGATGGTGTGGACGAGTCTGAAATGCAGTGGCGGCGCCGAGTTCCTGGTGTCTGAGTGTATGGGAAATCTCT
CTTTGCTCAAAGACCCGATCGGTACCGACCGTAGATCTTTCTTTCCGGTTTGACCTCGGATCAGGTAGGAGTACCCGCT
GAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAAA
GCTCAAATTTGAAATCTGGCCCCGTCAGGGGTCCGAGTTGTAATTTGGAGAGGATACTTCGGGTGTGGCCGTGGCTTAA
GTCCCTTGGAACAGGGCGTCATAGAGGGTGAGAATCCCGTCTTGAGTCACCGGTCCACGCCCATGCGAAGTTCCTTCGA
CGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTTCATCTAAAGCTAAATATTGGCTGGAGACCGATA
GCGCACAAGTAGAGTGATCGAAAGGTTAAAAGCACCTTGAAAAGGGAGTTAAATAGCACGTGAAATTGTTGAAAGGG
AAGCGCTTGCAACCAGACTCGAGCGCAGGGTTCAGCGGGCATGCGTGCCCGTGTACTCCCTGTGCTCGGGCCAGCATC
AGTTTCGGCGGTTGGTTAAAGGCCTCTGGAATGTATCGTCCTCCGGGACGTCTTATAGCCAGAGGCGCAATGCGGCCAG
CCGGGACTGAGGAACGCGCTTCGGCACGGATGCTGGCATAATGGTTGTAAGCGGCCCGTCTTGAAACACGGACCAAGG
AGTCTAACATCCACGCGAGTGTTCGGGTGTCAAACCCGTGCGCGCAGTGAAAGCGAACGGAGGTGGGAGCCCATCAGG
GTGCACCATCGACCGATCCTGAAGTCTTCGGATGGATTTGAGTAAGAGCGTGGCTGTTGGGACCCGAAAGATGGTGAA
CTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAA
ATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTGGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAGTAA
CGTTTTCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGTTGAAACAACCTTAACCTATTCTCAAACTTTAA
ATATGTAAGAAGCCCTTGTTACTTAAGTGAACGTGGGCATTAGAATGGATCGTTACTAGTGGGCCATTTTTGGTAAGCA
GAACCTGGCGATGCGGGATGAACCGAACGCGAGGTTAAGGTGCCGGAAATGCACGCTCATCAGACACCACAAAAGGT
GTTAGTTCATCTAGACAGCCCGACGGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAACAACTCCCGGGCCG
AAATGAACTAGCCCCTGAAAATGGATGGCGCTCAAGCGTGCTACCCCATACCTCGCCGTCCGGGTAGAAACGATGCCC
CGACGAGTAGGCAGGCGTGGAGGTTTGTGACGAAGCCTTGGGAGTGATCCCGGGTCGAACAGCCTCTAGTGCAGATCT
TGGTGGTAGTAGCAAATACTCAAATGAGAACTTTGAGGACTGAAGTGGGGAAAGGTTCCATGTGAACAGCAGTTGGAC
ATGGGTTAGTCGATCCTAAGACATAGGGTAGTTCCGTTTGAAAGCGCGCCCTCGTGCGCCGTTCGTCGAAAGGGAAGCC
GGTCAATATTCCGGCACCTGGATGTGGATTCTCCACGGCAACGTAACTGAACGCGGAGACGTCGGCAGGAGTCCTGGG
AAGAGTTCTCTTTTCTTCTTGACGGCCTATCACCCTGAAATCGGTTTGGTCCGGGGCTTGGGGTTTCATGGCAGGCAGAC
CCCCCGCACCTGTGTGGGGTCCCGGGACACTCCTGACGACCCCTAGAAAAACCGCGGGAAGGGAATAGTTTTCACGCC
AGGTCGTACTCATAAACCGCAGCAGGTCTCCAAGGTGAAAAAGCCTCTAGTTGATAGAACAATGTAGATAAGGGAAGT
CGGCAAAATAGATCCGTAACTTCGGGAAAAGGATTGGCTCTAAGGGTCGGGCGCGTTGGGCCTTGGGGGAAAGCCTCT
GGAGCAGAAGGGCACTAGCCGGGCAACCGGCGGGCGCCTTTCAGCATCGGGGTGCGGACGCCCTTGGCAGGCTTCGGC
CGTCCGGCGCGCGATTAACGACCAACTTAGAACTGGTACGGACAAGGGGAATCTGACTGTCTAATTAAAACATAGCAT
TGCGATGGCCAGAAAGTGGTGTTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCA
AGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCAT
GAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAGGGAACGGGCTTGGCAGAAT
CAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTGACATTGTGAAAAGACATATCGGGTGTAGAATAGGTGG
GAGCTTCGGCACAAGTGAAATACCACTACCTTTATTGTTTTTTTACTTATTCAATGAAGCGGAACTGGGCTTTACCGCCC
AACTTCTAGCGTTAAGGTCCTTCGCGGGCTGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCAC
ATCTGTTAAACCATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAACAGAAATCTCCAGTAGAACAAAAGGGTAAAA
GTCCCCTTGATTTTGATTTTCAGTGTGAATACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGAAATTTGA
GGCTAGAGGTGCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGCCAAGCGTTCATAGCGACGTTGCTTTTTG
ATCCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGTTGGATTGTTCACCCACTAATAGGGAAC
GTGAGCTGGGTTTAGACCGTCGTGAGACAGGTTAGTTTTACCCTACTGATGAAGGTCGCCGCAACGGTAATTCAATTTA
GTACGAGAGGAACCGTTGATTCAGATAATTGGTTTTTGCGGCTGTCTGACCAGGCAGTGCCGCGACGCTACCATCTGCC
GGATTATGGCTGAACGCCTCTAAGTCAGAATCCGTGCCGGAACGCGGCGATGTTGCCTCGCACGTCGTAGTTGGATACG
AATAGGCCTTCGGGCCCCGAACCTCAGCAGGTTGGCGGCGGTGTCCGGGGAGAGACCCTCGGGCGCCAGCTAACGGAT
TGCAATGTCACAACGCGCGGGGATAGATCCTCTGCAGACGACTGAAATGACCAAGCGGGTCGTGTAAGCGGTCAAGTA
GCCTAGTTGTTACGAGTCGCTGAGCGTCAGCCCGATCCTTGGCTCGATTTGTTGTAAACACCCTCCATCAAT

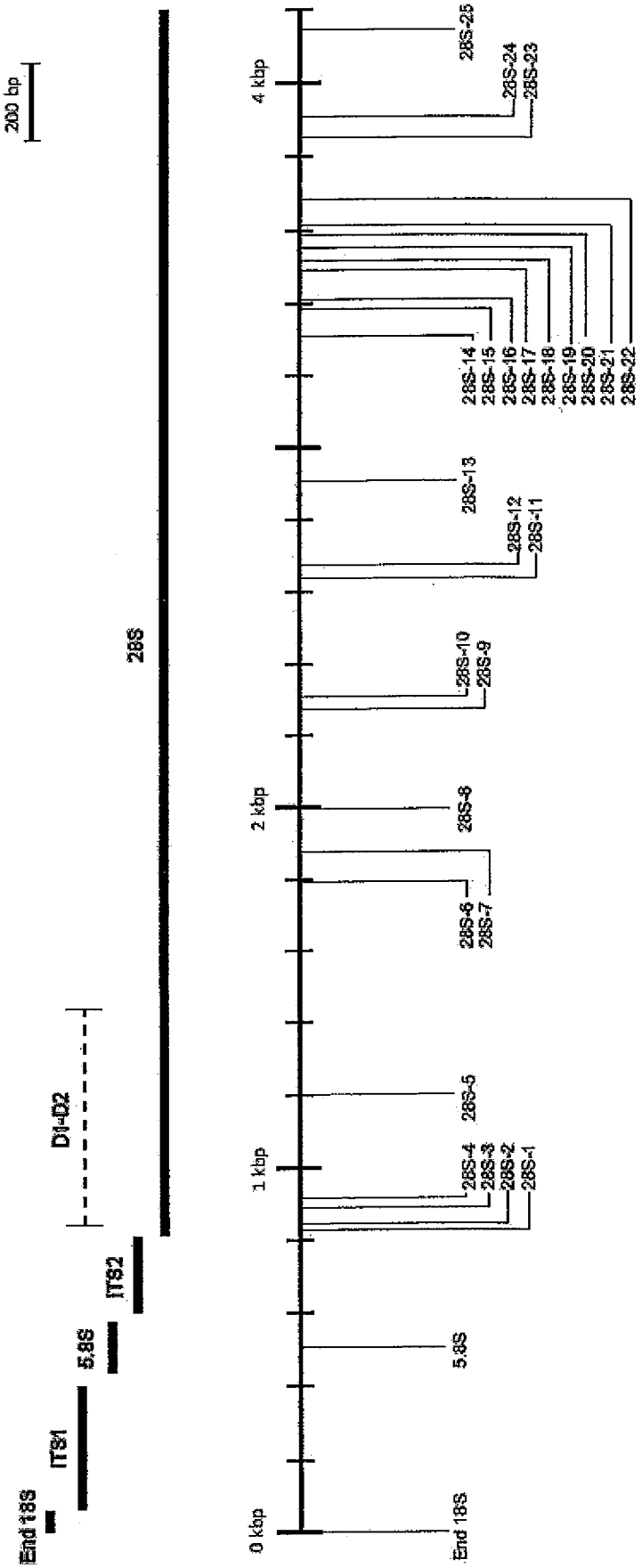
200 bp
End 18S
ITS1
5.8S
ITS2
D1-D2
28S
0 kbp
1 kbp
2 kbp
4 kbp
End 18S
5.8S
28S-1
28S-2
28S-3
28S-4
28S-5
28S-6
28S-7
28S-8
28S-9
28S-10
28S-11
28S-12
28S-13
28S-14
28S-15
28S-16
28S-17
28S-18
28S-19
28S-20
28S-21
28S-22
28S-23
28S-24
28S-25

FIG. 61

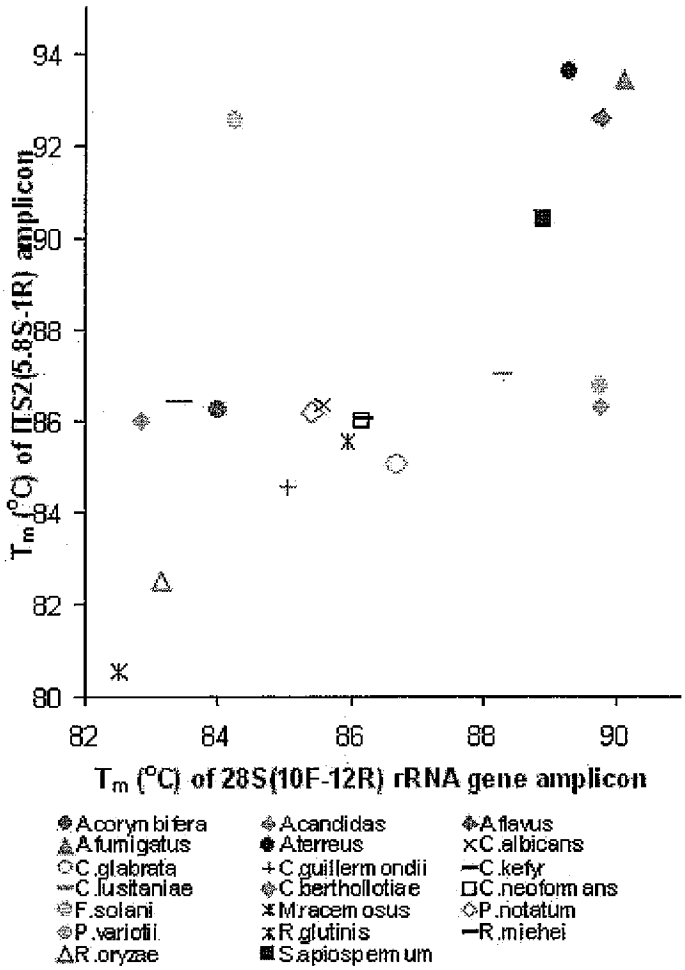
94
92
90
88
86
84
82
80
82
84
86
88
90
T_m (°C) of ITS2(5.8S-1R) amplicon
T_m (°C) of 28S(10F-12R) rRNA gene amplicon
A.corymbifera
A.fumigatus
C.glabrata
C.lusitaniae
F.solani
P.variotii
R.oryzae
A.candidas
A.terreus
C.guillermondii
C.berthollotiae
M.racemosus
R.glutinis
S.apiospermum
A.flavus
C.albicans
C.kefyr
C.neoformans
P.notatum
R.miehei

FIG. 62

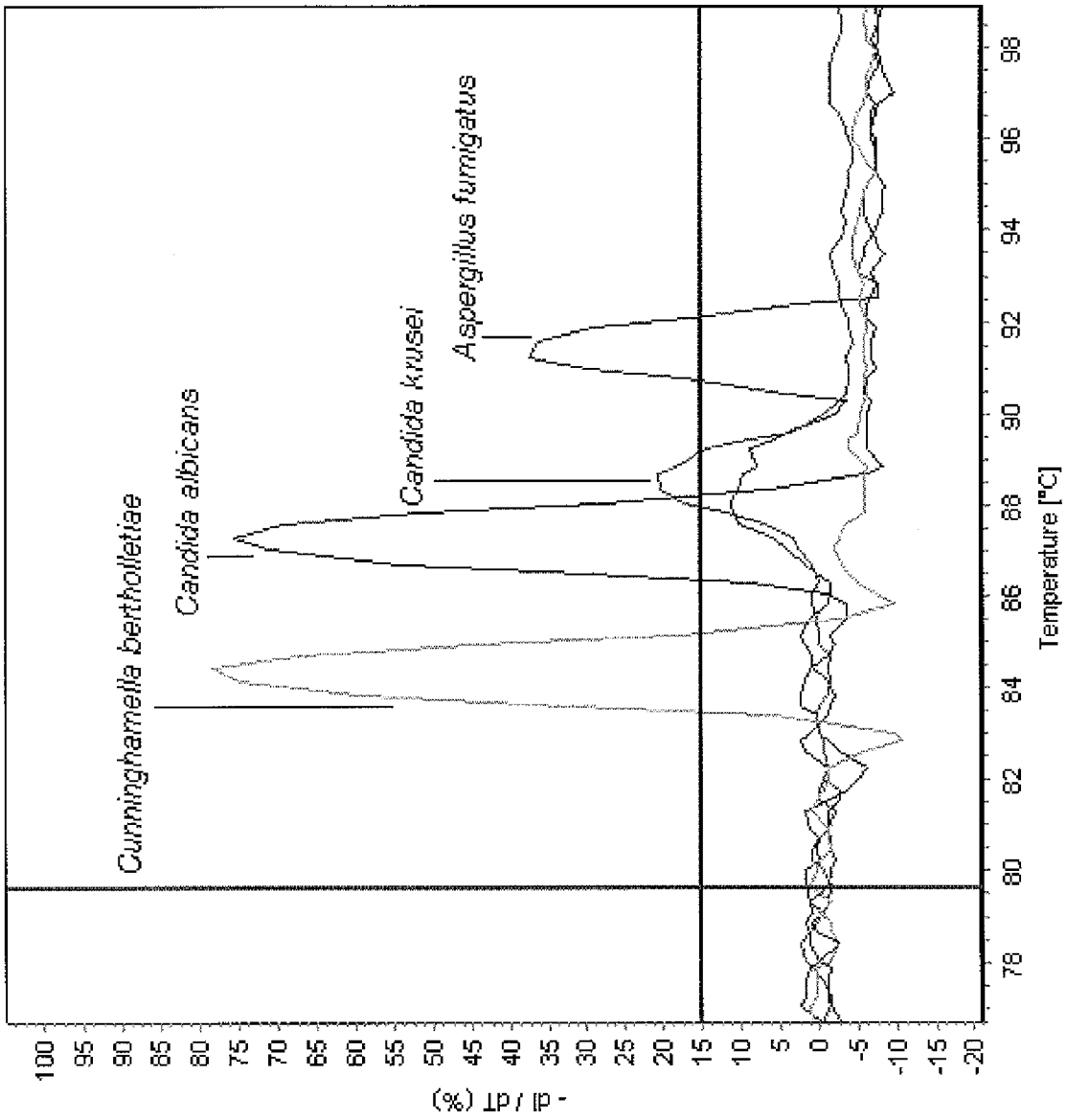
Cunninghamella bertholletiae
Candida albicans
Candida krusei
Aspergillus fumigatus
- dI / dT (%)
Temperature [°C]

FIG. 63

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 09/65770

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - G01N 33/48; C12Q 1/68 (2010.01)
USPC - 436/63, 94; 435/6
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
USPC - 436/63, 94; 435/6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
USPC - 436/63, 94; 435/6, 91.2

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
PubWEST(DB=PGPB,USPT,USOC,EPAB,JPAB; PLUR=YES; OP=ADJ), Google Scholar (David N. FREDRICKS fungus, Prasanna D. KHOT fungus, Daisy L. KO fungus, Fungus 18S rRNA 28S rRNA PCR patient)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	KHOT et al., "Development and optimization of quantitative PCR for the diagnosis of invasive aspergillosis with bronchoalveolar lavage fluid". BMC Infectious Diseases, 29 May 2008 (29.05.2008), vol 8, no 73, pp 1-13; abstract, pg 3-4, fig 1, DNA extraction from BAL fractions, ; pg 5, (iii) Aspergillus targeted 18S qPCR; pg 6, right col, para 1	1-2, 6-9, 21-29, 31 --- 3-5, 10-11, 15-16, 30
X --- Y	HENRY et al., "Identification of Aspergillus Species Using Internal Transcribed Spacer Regions 1 and 2". JOURNAL OF CLINICAL MICROBIOLOGY, April 2000, vol 38, no 4, pp 1510?1515; abstract; pg 1511, Primers.; pg 1512, fig 1, Table 1	32, 34, 45 --- 10, 11, 33, 35, 39, 46
Y	HINRIKSON et al., "Assessment of Ribosomal Large-Subunit D1-D2, Internal Transcribed Spacer 1, and Internal Transcribed Spacer 2 Regions as Targets for Molecular Identification of Medically Important Aspergillus Species". JOURNAL OF CLINICAL MICROBIOLOGY, May 2005, vol 43, no 5, pp 2092?2103; abstract, pg 2093, PCR amplification of the D1-D2 region of the large-subunit (28S) rRNA gene.	3-5, 33
Y	JP 2008/054563 A (NOZOMI et al.) 13 March 2008 (13.03.2008); para [0017], [1]-[3]; SEQ ID NO: 28	11, 15, 35, 39, 46
Y	US 2007/0042354 A1 (ENGELHARD et al.), 22 February 2007 (22.02.2007); para [0006], [0016], [0025]; table 1; SEQ ID NO: 1061	16, 46
Y	US 7,427,472 B2 (LINDSEY et al.), 23 September 2008 (23.09.2008); abstract; col 5, ln 37-40	30

☐ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 April 2010 (15.04.2010)	29 APR 2010
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-3201	Authorized officer: Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 09/65770

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I: claims 1-11, 15, 16, 21-35, 39, 45 and 46, directed to a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product; limited to wherein the forward primer comprises SEQ ID NO: 1, and is complementary to a fungal 18S rRNA gene, and the reverse primer is limited to SEQ ID NO: 30, and is complementary to a fungal 28S rRNA gene.
Group II: claims 1, 12, 13, 15, 16, 20, 32, 36, 37, 39, 40 and 44, directed to a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product; limited to wherein the forward primer comprises SEQ ID NO: 2 and is complementary to a fungal 5.8S rRNA gene, and the reverse primer is limited to SEQ ID NO: 30, and is complementary to a fungal 28S rRNA gene.

- Please see extra sheet for continuation -

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11, 15, 16, 21-35, 39, 45 and 46; limited to SEQ ID NO: 1 and SEQ ID NO: 30.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 09/65770

Continuation of Box III: Lack of Unity of Invention

Group III: claims 1, 14-16, 32 and 38-40, directed to a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product; limited to wherein the forward primer comprises SEQ ID NO: 3 and is complementary to a fungal 28S rRNA gene, and the reverse primer comprises SEQ ID NO: 30, and is complementary to a fungal 28S rRNA gene.
Group IV: claims 1, 17 and 41, directed to a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product; limited to wherein the primer set comprises forward and reverse primers consisting of SEQ ID NO: 2 and SEQ ID NO: 31, respectively.
Group V: claims 1, 18 and 43, directed to a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product; limited to wherein the primer set comprises forward and reverse primers consisting of SEQ ID NO: 11 and SEQ ID NO: 41, respectively.
Group VI: claims 1, 17, 19, and 42, directed to a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product; limited to wherein the primer set comprises forward and reverse primers consisting of SEQ ID NO: 1 and SEQ ID NO: 29, respectively.
Group VII: claims 1, 32, 47, 48 and 68, directed to a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product; limited to wherein the primer set comprises forward and reverse primers consisting of SEQ ID NO: 12 and SEQ ID NO: 41, respectively; further wherein the set may comprise a second reverse primer, consisting of SEQ ID NO: 108.
Group VIII: claims 49-52, directed to a method for determining the identity of a fungal species in a patient, comprising: isolating a patient sample; carrying out a first PCR reaction to generate a product, wherein the region amplified comprises a fungal ribosomal RNA gene comprising an internal transcribed spacer 2 (ITS-2) sequence; carrying out a second PCR reaction to generate a second product, wherein said second reaction comprises a second primer set capable of amplifying a fungal 28S rRNA gene and; determining the melting temperature of the first and second PCR products, wherein the identity of the fungal species is determined by comparing the melting point of the first and second PCR products to known standards.
Group IX: claims 53-67, directed to a method of identifying a primer set capable of detecting a fungal pathogen in a sample, comprising: obtaining the nucleic acid sequence of at least the 28S rRNA region of a fungal genome; designing a forward primer capable of hybridizing with a specific site in the 28S region; designing a reverse primer capable of hybridizing with the 28S rRNA at a point which is 3' to the region to the forward primer, and; determining whether the forward and reverse primer are capable of generating a PCR amplicon that is useful for identifying said fungal DNA.

The inventions listed as Groups I - IX do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The special technical feature of the claims of Groups I - VII is a method for detecting a fungal pathogen in a patient sample comprising: isolating a patient sample and carrying out PCR on the sample, wherein the region amplified comprises a region of a fungal ribosomal RNA gene, and detecting the PCR product, wherein each Group is directed to a particular set of primers used for the PCR detection reaction. The special technical feature of the Group VIII claims is a method for determining the identity of a fungal species in a patient. The special technical feature of the Group IX claims is a method of identifying a primer set capable of detecting a fungal pathogen in a sample.

The only common technical element shared by the above groups is that they are related to PCR-based amplification of fungal rRNA for detection and identification. This common technical element does not represent an improvement over the prior art of US 2008/0248970A1 to Morrison et al. (see para [0010], [0013], [0017], and [0050]). While some of the Groups share further common technical elements of primers having the same sequences, particularly SEQ ID NO: 1, SEQ ID NO: 2 and SEQ ID NO: 30, these common technical elements do not represent an improvement over the prior art of US 5,693,501 A to Lee et al. (see abstract, SEQ ID NO: 1 in comparison to Applicants' SEQ ID NO: 1), US 2008/0014582 A1 to Hooper et al. (see abstract, and SEQ ID NO: 85 in comparison to Applicants' SEQ ID NO: 2), and US 2007/0042354 A1 to Englehard (see abstract, para [0003], [0025], [0026] and SEQ ID NO: 1061 in comparison to Applicants' SEQ ID NO: 30). Therefore, the inventions of Groups I - IX lack unity of invention under PCT Rule 13 because they do not share a same or corresponding special technical feature.

Note: applicants may elect for additional sequences to be searched by specifying the SEQ ID NO: and by paying an additional invention fee for each identified sequence.