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The nucleic acid sequence encoding the internal transcribed spacer (2) region of Candida, the organism causing candidiasis, for various Candida species. Nucleic acid molecules useful as probes for detecting Candida species are described. The nucleic acid molecules are useful in methods for the detection and diagnosis of Candida infection in a sample or subject.

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(54) Title: NUCLEIC ACID PROBES FOR DETECTING *CANDIDA* SPECIES

(57) Abstract

The nucleic acid sequence encoding the internal transcribed spacer (2) region of Candida, the organism causing candidiasis, for various Candida species. Nucleic acid molecules useful as probes for detecting Candida species are described. The nucleic acid molecules are useful in methods for the detection and diagnosis of Candida infection in a sample or subject.

NUCLEIC ACID PROBES FOR DETECTING *CANDIDA* SPECIES

This invention was made by the Centers for Disease Control and Prevention, an agency of the United States Government.

TECHNICAL FIELD

The present invention relates in general to the field of microbiology. In particular, the invention relates to the species-specific detection of *Candida*, using DNA probes generated from the internal transcribed spacer 2 region of thirteen *Candida* species.

BACKGROUND OF THE INVENTION

Candidiasis is a fungal infection of mucosal membranes and other tissues. The infection is caused by the yeast-like organism *Candida*. Numerous species of *Candida* exist, including *C. albicans*. Rapid diagnosis of *Candida* infection has become important in recent years due to a substantial rise in the incidence of candidiasis. This increase in candidiasis is most likely caused by the rising incidence of AIDS, more intensive regimens of cancer therapy, complications of abdominal or cardio-thoracic surgery, organ transplantations, burns and trauma. While most candidiasis patients are infected with *C. albicans*, the number of non-*C. albicans* infections has been growing steadily and may reflect the increased use of azole drug prophylaxis and therapy since some non-*C. albicans* species are innately resistant to these drugs. Additional risk factors commonly associated with the onset of candidiasis

include protracted, broad-spectrum antibiotic therapies, invasive devices, and prolonged hospital stays. Under these conditions, an antibiotic resistant replacement flora, including one or more *Candida* species, can proliferate in the gastrointestinal tract and invade from mucosal foci to deep tissues, especially when mucosal integrity has been disrupted as a result of chemotherapy or surgery. As the number of risk factors increases, the odds of developing candidiasis multiplies. (Jarvis, W.R. 1995. Epidemiology of nosocomial fungal infections, with emphasis on *Candida* species. *Clin. Inf. Dis.* 20:1526-30; Wenzel, R.P. 1995. Nosocomial candidemia: risk factors and attributable mortality. *Clin. Inf. Dis.*. 20:1531-4; Wingard, J.R. 1995. Importance of *Candida* species other than *C. albicans* as pathogens in oncology patients. *Clin. Inf. Dis.*. 20:115-25; and Fridkin, S.K. *et al.*, 1996. Epidemiology of nosocomial fungal infections. *Clin. Micro. Rev.* 9:499-511).

Candida species such as *C. glabrata* and *C. krusei* are emerging as the causative agents of candidiasis possibly because these species are innately less susceptible to azole drugs. In addition, the ability of species such as *C. parapsilosis* to survive in the hospital environment increases the possibility of nosocomial transmission. Consequently, rapid identification to the species level is necessary for more timely, targeted, and effective antifungal therapy, and to facilitate hospital infection control measures.

Current methods available in the clinical laboratory to identify *Candida* species rely on morphology and assimilation tests. These tests require approximately three to five days to complete, sometimes requiring additional tests. (Warren, N.G. and K.C. Hazen, 1995. *Candida, Cryptococcus*, and other yeasts of medical importance, p. 723-737. *In* P.R. Murray, E.J. Barton, M.A. Pfaller, F.C. Tenover, and R.H. Yolken (ed.) Manual of Clinical Microbiology, 6th ed., American Society for Microbiology, Washington, D.C.)

U.S. Patent No. 5,426,027 describes a method for detecting five species of *Candida* using the polymerase chain reaction (PCR) technique. The five species detected by the method are *C. albicans, C. glabrata, C. tropicalis, C. parapsilosis, and C. krusei.* U.S. Patent No. 5,426,027 provides a rapid method for the

isolation, release, purification, amplification and detection of DNA from the above-identified species of *Candida* from blood and other body fluids. The method uses universal fungal primers that amplify the multi-copy internal transcribed spacer 2 region (ITS2) of rDNA, located between the 5.8S and the 28S rDNA coding regions, to enhance the amount of *Candida* target DNA in samples. Once amplified, target DNA is hybridized to probes which are then used in a microtitration plate format for the identification of specific species of *Candida*. However, the method described in U.S. Patent No. 5,426,027 is incapable of differentiating between *Candida* species other than those listed above.

Due to the increase in infections caused by other species of *Candida*, and the differences in therapeutic strategies for treating candidiasis caused by various *Candida* species, it is desirable to have a method for detecting and differentiating additional *Candida* species.

Therefore, there is a need for sensitive, rapid, species-specific methods for the detection of *Candida*. In addition, there is a need for universal fungal primers to amplify all fungal DNA followed by species-specific probes for *Candida* to be used in detection methods and as scientific research tools to investigate the *Candida* organism and to implement appropriate therapies and treatments for candidiasis.

SUMMARY OF THE INVENTION

Isolated nucleic acid molecules that selectively hybridize with nucleic acid molecules encoding the internal transcribed spacer 2 (ITS2) region of various species of *Candida*, or complementary sequences thereof, are described herein. The nucleic acid molecules are useful as probes to detect the presence and identity of a *Candida* species in a sample or specimen with high sensitivity and specificity. The nucleic acid molecules are also useful as laboratory research tools to study the organism and related diseases and to guide therapies and treatments for those diseases. In addition, methods are described for the detection of and differentiation between *Candida* species.

The *Candida* species detected by the probes and methods described herein include *C. guilliermondii, C. haemulonii, C. kefyr, C. lambica, C. lusitaniae, C. norvegensis, C. norvegica, C. rugosa, C. utilis,*

C. viswanathii, *C. zeylanoides*, *C. dubliniensis*, and *C. pelliculosa*. The method provides a simple, rapid, and feasible means for identifying and distinguishing these *Candida* species in clinical laboratories.

Therefore, it is an object of the present invention to provide probes and sensitive methods for detecting and differentiating *Candida* organisms in clinical and laboratory settings.

It is a further object of the present invention to provide nucleic acid probes specific for various *Candida* species.

It is a further object of the present invention to provide species-specific nucleic acid probes that hybridize to the internal transcribed spacer 2 region of particular *Candida* species.

It is a further object of the present invention to provide simple, rapid and reliable methods for detecting, diagnosing, or monitoring the progress of therapy for diseases caused by *Candida* organisms.

It is a further object of the invention to provide methods for detecting *Candida* in a tissue specimen or biological fluid sample of an infected patient, including a blood sample, or in cultures of *Candida* from any source.

These and other objects, features, and advantages of the present invention will become apparent after a review of the following detailed description of the disclosed embodiments and the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a chart showing absorbance values for the hybridization of eighteen species-specific probes to DNA from the same *Candida* species, other *Candida* species, and other fungal organisms. The vertical axis identifies the *Candida* species name of the probe. The horizontal axis identifies the DNA using a two or three letter abbreviation. CA is an abbreviation for *C. albicans*. CT is an abbreviation for *C. tropicalis*. CG is an abbreviation for *C. glabrata*. CP is an abbreviation for *C. parapsilosis*. CK is an abbreviation for *C. krusei*. GU is an abbreviation for *C. guilliermondii*. CR is an abbreviation for *C. rugosa*. CU is an abbreviation for *C. utilis*. CZ is

an abbreviation for *C. zeylanoides*. CH is an abbreviation for *C. haemulonii*. LA is an abbreviation for *C. lambica*. KF is an abbreviation for *C. kefyr*. VS is an abbreviation for *C. viswanathii*. LU is an abbreviation for *C. lusitaniae*. NC is an abbreviation for *C. norvegica*. FA is an abbreviation for *C. famata*. NS is an abbreviation for *C. norvegensis*. DUB is an abbreviation for *C. dubliniensis*. PEL is an abbreviation for *C. pelliculosa*. Upper values in each grid are provided as a mean absorbance at A_{650nm}. The lower value in each grid represents the standard deviation from the mean absorbance for all samples tested. The absorbance value "0" represents Mean $A_{650nm} \leq$ 0.010.

Figure 2 is a chart showing absorbance values for the hybridization of eleven species-specific probes to DNA from other *Candida* species and other fungal organisms. The vertical axis identifies the *Candida* species name of the probe. The horizontal axis identifies the DNA using a three to five letter abbreviation. FUM is an abbreviation for *Aspergillus fumigatus*. FLAV is an abbreviation for *Aspergillus flavus*. NID is an abbreviation for *Aspergillus nidulans*. TER is an abbreviation for *Aspergillus terreus*. NIG is an abbreviation for *Aspergillus niger*. BLAS is an abbreviation for *Blastomyces dermatitidis*. HIST is an abbreviation for *Histoplasma capsulatum*. Scere is an abbreviation for *Saccharomyces cerevisiae*. Cr.hum is an abbreviation for *Cryptococcus humicolus*. Cr.nA is an abbreviation for *Cryptococcus neoformans, Serotype A*. Cr.nB is an abbreviation for *Cryptococcus neoformans, Serotype B* Cr.nC is an abbreviation for *Cryptococcus neoformans, Serotype C*. Cr.nD is an abbreviation for *Cryptococcus neoformans, Serotype D*. C.cat is an abbreviation for *Candida catenulata*. S.cif is an abbreviation for *Stephanoascus ciferrii*. T.cut is an abbreviation for *Trichosporon cutaneum*. Pmar is an abbreviation for *Penicillium marneffei*. Upper values in each grid are provided as a mean absorbance at A_{650nm}. The lower value in each grid represents the standard deviation from the mean absorbance for all samples tested. The absorbance value "0" represents Mean $A_{650nm} \leq$ 0.010. The term "Neg" denotes negative detection as previously reported by Fujita, *et al.*, 1995. *J. Clin. Microbiol.* 33:962-967.

DETAILED DESCRIPTION OF THE INVENTION

Nucleic acid molecules that selectively hybridize to all or a portion of the internal transcribed spacer 2 (ITS2) region of various *Candida* species are provided. The sequences of nucleic acid molecules encoding the ITS2 region of *C. guilliermondii, C. haemulonii, C. kefyr, C. lambica, C. lusitaniae, C. norvegensis, C. norvegica, C. rugosa, C. utilis, C. viswanathii, C. zeylanoides, C. dubliniensis,* and *C. pelliculosa* are set forth as SEQ ID NOs:1-13.

The nucleic acid molecules described herein are useful as probes to detect, identify, and distinguish or differentiate between *Candida* species in a sample or specimen with high sensitivity and specificity. The probes can be used to detect the presence of *Candida* in the sample, diagnose infection with the disease, quantify the amount of *Candida* in the sample, or monitor the progress of therapies used to treat the infection. The nucleic acid molecules are also useful as laboratory research tools to study the organism and the disease and to guide therapies and treatments for the disease.

Exemplary nucleic acid probes that selectively hybridize with nucleic acid molecules encoding the ITS2 region of the thirteen species of *Candida* identified above are set forth as SEQ ID NOs:22-35. Additional probes that selectively hybridize to the ITS2 region of the *Candida* species described herein can be identified by those skilled in the art using routine screening procedures as set forth in more detail below.

Detection of DNA or RNA by the probes is facilitated by means such as nucleic acid amplification including the polymerase chain reaction (PCR) or ligase chain reaction (LCR), for example. Alternatively, the probe is labeled with a detectable label and detected in accordance with methods well known to those skilled in the art.

The term "isolated" in the context of a compound, such as a nucleic acid, is defined herein as free from at least some of the components with which the compound naturally occurs. A nucleic acid which "selectively hybridizes" is defined herein as a nucleic acid that

hybridizes to a species-specific portion of a *Candida* ITS2 region nucleic acid, and does not hybridize with other nucleic acids so as to prevent determination of an adequate positive hybridization to the species-specific portion of the *Candida* ITS2 region. Therefore, in the design of hybridizing nucleic acid probes, selectivity will depend upon the other components present in a sample. The hybridizing nucleic acid probe should have at least 70% complementarity with the segment of the nucleic acid to which it hybridizes. As used herein to describe nucleic acid probes, the term "selectively hybridizes" excludes the occasional randomly hybridizing nucleic acids, and thus, has the same meaning as "specifically hybridizes." The selectively hybridizing nucleic acids of the invention can have at least 70%, 80%, 85%, 90%, 95%, 97%, 98%, and 99% complementarity with the segment of the sequence to which it hybridizes. Hybridization studies are preferably conducted under stringent hybridization conditions.

Candida Probes

Nucleic acid molecules having the sequences set forth as SEQ ID NOs: 1-13, or complementary sequences thereof, will selectively hybridize to ITS2 DNA or RNA from each respective *Candida* species. For example, a nucleic acid molecule having the sequence of SEQ ID NO: 1 will selectively hybridize to ITS2 DNA from *C. guilliermondii* under stringent hybridization conditions and will not hybridize under the same or similar conditions to ITS2 DNA from any of the other twelve *Candida* species set forth above. Similarly, nucleic acid molecules having the sequences set forth as SEQ ID NOs: 22-35, and complementary sequences thereof, will selectively hybridize under stringent hybridization conditions to ITS2 DNA from each respective *Candida* species. Nucleic acid molecules having the sequences set forth as SEQ ID NOs: 22-35 represent portions or fragments of the corresponding nucleic acid molecules having the sequences set forth as SEQ ID NOs: 1-13. Two exceptions include the cross-reactivity of the *C. guillermondii* probe (SEQ ID NO: 22) with *C. zeylanoides* DNA and the *C. glabrata* probe (SEQ ID NO: 19) with *S. cerevisiae* DNA. The *C. zeylanoides* probe (SEQ ID NO: 25) does not

cross-react with *C. guillermondii* DNA, however, so that, by a process of elimination, these two species can be differentiated using these probes. No probe for *S. cerevisiae* has been developed to date, but given the rare occurrence of this organism in infected patients and that drug therapy would be the same for both *C. glabrata* and *S. cerevisiae* infections (both azole resistant), the cross-reactivity of the *C. glabrata* probe with *S. cerevisiae* does not pose a clinical problem.

It will be understood that the probes provided herein are merely exemplary and that those skilled in the art could identify additional portions or fragments of each ITS2 sequence to be used as species-selective probes without undue experimentation from the sequences provided in SEQ ID NOs:1-13, or complementary sequences thereof, which hybridize with specificity to each *Candida* species respectively. Therefore, the probes shown in SEQ ID NOs: 22-35 are only provided as examples of probes specific for *Candida* that can be derived from the ITS2 regions of each species in SEQ ID NOs:1-13, respectively. The ITS2 region for each *Candida* species offers a number of very unusual sequences for use as PCR primers. Therefore, comparisons can be made between the *Candida* ITS2 sequence of two or more species to identify unique or non-homologous regions that would be useful to construct probes that would be specific for distinguishing between those *Candida* and have minimal cross-hybridization with ITS2 regions from other species. One useful computer program for generating selective probes is the Gene Jockey program available from Biosoft (Cambridge, UK).

The invention contemplates sequences, probes, and primers that selectively hybridize to the DNA or the complementary, or opposite, strand of DNA as those specifically provided herein. Specific hybridization with nucleic acid can occur with minor modifications or substitutions in the nucleic acid, so long as functional species-specific hybridization capability is maintained.

The term "probe" is defined herein to include nucleic acid sequences that can be used as primers for selective hybridization with complementary nucleic acid sequences for their detection or amplification. Therefore, the terms "probe" or "probes" as used herein

are defined to include primers. Such probes can vary in length from about 5 to 263 nucleotides, or preferably from about 10 to 50 nucleotides, or most preferably about 18-26 nucleotides. Isolated nucleic acids are provided herein that selectively hybridize with the species-specific nucleic acids under stringent conditions and should have at least 5 nucleotides complementary to the sequence of interest. *See generally,* Sambrook, J., et al., 1989. Molecular cloning: a laboratory manual, latest edition. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.

If used as primers, the invention also preferably provides compositions including at least two nucleic acids which hybridize with different regions so as to amplify a desired region. Depending on the length of the probe or primer, the target region can range between 70% complementary bases and full complementarity and still hybridize under stringent conditions. For example, when diagnosing the presence of a *Candida* species, the degree of complementarity between the hybridizing nucleic acid (probe or primer) and the sequence to which it hybridizes (e.g., *Candida* DNA from a sample) is at least enough to distinguish hybridization with a nucleic acid from other yeasts and filamentous fungi.

It may be desirable in some cases to construct probes from the ITS2 regions disclosed herein which can selectively hybridize with more than one *Candida* species, but that still do not hybridize with other species of *Candida*. Such probes are, therefore, useful for detecting a selective sub-group of one or more species within the *Candida* genus. Examples of nucleic acids unique to each species of *Candida* are provided in the listed sequences so that the degree of complementarity required to distinguish selectively hybridizing from nonselectively hybridizing nucleic acids under stringent conditions can be clearly determined for each nucleic acid.

Methods for the Detection and Identification of *Candida*

Methods of using the nucleic acids described herein to detect and identify the presence of *Candida* are also provided. The method involves the steps of obtaining a sample suspected of containing

Candida. The sample may be a biological fluid or tissue specimen taken from an individual, such as blood, saliva, vaginal mucosa, tissues, etc. Alternatively the sample may be taken from the environment, such as a swab of a potentially contaminated surface. The *Candida* cells in the sample are then lysed, and the DNA extracted and precipitated. The DNA is preferably amplified using universal primers derived from the genomic regions adjacent to or including portions of the ITS2 region of the *Candida* DNA sequence. Examples of such primers are described below. Detection of *Candida* DNA is achieved by hybridizing the amplified DNA with a *Candida* species-specific probe that selectively hybridizes with the DNA. Detection of hybridization is indicative of the presence of *Candida*.

Preferably, detection of nucleic acid hybridization with probes can be facilitated by the use of detectable moieties well known to those skilled in the art. For example, the probes can be labeled with digoxigenin and biotin and used in a streptavidin-coated microtiter plate assay where an enzymatically labeled antibody to digoxigenin and a colorimetric substrate allows for detection. Other detectable moieties include radioactive labeling, enzyme labeling, and fluorescent labeling, for example.

<u>*Candida* Detection Kit</u>

The invention further contemplates a kit containing one or more *Candida* ITS2 specific nucleic acid probes that can be used for the detection of *Candida* organisms in a sample. Such a kit can also contain the appropriate reagents for lysing cells, amplifying DNA, hybridizing the probe to the sample, and detecting bound probe.

EXAMPLE 1

Cloning and Sequencing of the ITS2 Region from *Candida*

This example describes the cloning and sequencing of the ITS2 region from various species of *Candida*. The organisms used in this example and their sources are listed below in Table 1. Isolates of *Candida* spp., *Cryptococcus humicolus*, *Stephanoascus ciferrii*, and *Trichosporon cutaneum* were grown in 10 ml of YPD broth (1% yeast

extract, 2% Bacto™ Peptone, 1% glucose; Difco Laboratories, Detroit, MI) at 35°C for 18 hours. *Cryptococcus neoformans*, serotypes A, B, C, and D were grown in YPD broth + 2.9% NaCl at 35°C for 18 hours to reduce capsule formation. All broth cultures were grown on a gyrarotary shaker at 150 rpm.

Table 1 — Microorganisms tested against all probes.

Organism	Number	Source
Candida albicans	B311	Human
Candida tropicalis	CDC 38	Reference strain
Candida glabrata	Y-65	Type culture, feces
Candida parapsilosis	ATCC 22019	Type culture, sprue
Candida krusei	CDC 259-75	Reference strain
Candida guilliermondii	ATCC 6260	Type culture, bronchitis
Candida rugosa	ATCC 10571	Type culture, human feces
Candida utilis	ATCC 22023	Type culture, factory
Candida zeylanoides	ATCC 7351	Type culture, blastomycotic macroglossia
Candida haemulonii	ATCC 22991	Type culture, gut contents of fish
Candida lambica	ATCC 24750	Type culture, beer
Candida kefyr	ATCC 46764	Clinical isolate
Candida viswanathii	ATCC 22981	Type culture, cerebrospinal fluid
Candida lusitaniae	ATCC 34449	Type culture, pig
Candida norvegica	ATCC 36586	Type culture, sputum
Candida norvegensis	ATCC 22977	Type culture, sputum
Candida pelliculosa	ATCC 8168	Type culture
Candida dubliniensis	CBS 7987	Type culture, human tongue
Candida famata	ATCC 36239	Type culture
Aspergillus fumigatus	ATCC 36607	Clinical isolate
Aspergillus flavus	ATCC 11497	Environmental isolate
Aspergillus nidulans	ATCC 10074	unspecified
Aspergillus terreus	ATCC 7860	unspecified
Aspergillus niger	ATCC 16404	Environmental isolate
Blastomyces dermatitidis	CDC B4478	Dog
Histoplasma capsulatum	G217B	Human
Saccharomyces cerevisae	AB 972	unspecified
Cryptococcus humicolus	ATCC 14438	Type culture, soil
Cryptococcus humicolus	ATCC 38294	Human leg
Cryptococcus neoformans, Serotypes A, B, C, D	A=9759-MU-1, B=BIH409, C=K24066TAN, D=9375	Reference Strains from Dr. Cherniak, GA. State Univ.
Candida catenulata	ATCC 18812	Perleche
Candida catenulata	ATCC 10565	Type culture, human feces
Stephanoascus ciferrii	ATCC 22873	Type culture of *Candida ciferrii*, neck of cow
Trichosporon cutaneum	ATCC 34148	Clinical isolate
Penicillin marneffei	CDC B3420	Human lymph node

DNA isolation. DNA was extracted from all species using the Puregene™ Gram Positive Bacteria and Yeast DNA Isolation Kit (Gentra, Inc., Research Triangle Park, NC). DNA from filamentous and dimorphic fungi was obtained as described by Fujita, S.-I., *et al.*, 1995, Microtitration plate enzyme immunoassay to detect PCR-amplified DNA from *Candida* species in blood. *J. Clin. Microbiol.* 33:962-967, or was a gift from Dr. Liliana de Aguirre, CDC Mycotic Diseases Laboratories, Atlanta, GA. Quantification of the DNA was performed on a fluorometer (Dyna Quant 200) using Hoechst™ 33258 Dye (Pharmacia Biotech, Piscataway, NJ). DNA was diluted in TE buffer (10 mM Tris-Cl, 1 mM EDTA) so that 1 ng of template DNA was added to each PCR reaction vial.

Oligonucleotide synthesis of primers and probes. Oligodeoxyribonucleotide primers and probes (Table 2) were synthesized as described by Fujita, 1995, *J. Clin. Microbiol.* 33:962-967. The universal fungal primers ITS3 and ITS4, as described by White *et al.*, were used to amplify the ITS2 region. (White, T.J., *et al.*, 1990, Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics, p.315-322. *In* M.A. Innis, et al., (ed.), PCR protocols. Academic Press, San Diego, CA.)

The 5.8S rDNA universal 5' primer (ITS3) has the following sequence:

5' GCA TCG ATG AAG AAC GCA GC 3' (SEQ ID NO: 14)

The 28S rDNA universal 3' primer (ITS4) has the following sequence:

5' TCC TCC GCT TAT TGA TAT GC 3' (SEQ ID NO: 15)

The 5.8S rDNA 5'-end-labeled, biotinylated probe (universal capture probe) has the following sequence:

5' Bio-CA TGC CTG TTT GAG CGT CRT T 3' (SEQ ID NO: 16)

The sequenced ITS2 regions were determined to be as follows:

Candida guilliermondii (SEQ ID NO:1)

CTCTCTCAAA CCCCCGGGTT TGGTATTGAG TGATACTCTT AGTCGGACTA GGCGTTTGCT 60

TGAAAAGTAT TGGCATGGGT AGTATGGATA GTGCTGTCGA CCTCTCAATG TATTAGGTTT 120

ATCCAACTCG TTGAATGGTG TGGCGGGATA TTTCTGGTAT TGTTGGCCCG GCCTTACAAC 180

AACCAAACAA GC 192

Candida haemulonii (SEQ ID NO:2)

GAGCGTGATA TCTTCTCACC GTTGGTGGAT TTGTTTCTAA ATATCATGCC ACAGTGAAGT 60

CTACGC 66

Candida kefyr (SEQ ID NO:3)

CTCTCTCAAA CCTTTGGGTT TGGTAGTGAG TGATACTCGT CTCGGGCTTA ACTTGAAAGT 60

GGCTAACCGT TGCCATCTGC GTGAGCAGGC TGCGTGTCAA GTCTATGGAC TCGACTCTTG 120

CACATCTACG TCTTAAGTAT GCGCCAATTC GTGGTAAGCT TGGGTCATAG AGACTCATAG 180

GTGTTATAAA GACTCGCTGG TGTTTGTCTC CTTGAGGCAT ACGGCTTTAC AACTCTCAAG 240

Candida lambica (SEQ ID NO:4)

CCTTCTTGGA GCGGTGCTTC AGACCTGGCG GGCTGTCTTT TTGGACGGCG CGCCCAAAGC 60

GAGGGGCCTT CTGCGCGAAC TAGACTGTGC GCGCGGGGCG GTCGGCGAAC TTATTACCAA 120

G 121

Candida lusitaniae (SEQ ID NO:5)

GAGCGTCGCA TCCCCTCTAA CCCCCGGTTA GGCGTTGCTC CGAAATATCA ACCGCGCTGT 60

CAAATACG 68

Candida norvegensis (SEQ ID NO:6)

CCTTCTTGCG CAAGCAGAAG TTGGGGTTGC CACGGCCCGT GCGGCCTGTG TGTGGCTCCC 60

CGAAACGGAA CGGCAGCGGG ACTGAGCGAA GTACACAACA CTCGCGCTTG GCCCGCCGAA 120

CTTTTTTTTA ATCTAAG 137

Candida norvegica (SEQ ID NO:7)

CCTTCTCAAG CGTGAGCTTG GTGTTGGCGG AGGTCTTTCG AGGCCCCGCT GAAATACGCA 60

GGGGGTGCGT GGAAACGAGC TTTCTCTCTA CTAATGTCTA GTTCTGCCAA CTCATTGGAC 120

GAGCGTCTGC TGGCTCCACA ATCCCACCCC CATTACCCCA AC 162

Candida rugosa (SEQ ID NO:8)

CTCTCTCGCA AGTGTTGGCA CCACGCCGGC AGGCGTCTGC CCGAAACGCG ACCGTCTAAA 60

ACAGTTAAGC TTGTTACAGA CTCACGATC 89

Candida utilis (SEQ ID NO:9)

CTCTCTCAAG ATCCTCTAGG GGACTTGGTA TTGAGTGATA CTCTGTGTTA ACTTGAAATA 60

CTCTAGGCAG AGCTCCCCCC TGGAAATCCT CTGGGCCGAA ATAATGTATT AGGTTCTACC 120

AACTCGTTAT TTTCCAGACA GACTTCCAGG CAGAGCTCGT GCCCCTAACA TAGCAGTCTA 180

AGC 183

Candida viswanathii (SEQ ID NO:10)

CTCCCTCAAC CCCGCGGGTT TGGTGTTGAG CAATACGCCA GGTTTGTTTG AAAGACGTAC 60

GTGGAGACAA TATTAGCGAC TTAGGTTCTA CCAAAACGCT TGTGCAGTCG GTCCCACACA 120

CAGTGTAAGC TAACA 135

Candida zeylanoides (SEQ ID NO:11)

CTCTCTCAAA TCTTCGGATT TGGTTTTGAG TGATACTCTT AGTCAGACTA AGCGTTTGCT 60

TGAAATGTAA TGGCATGAGT GGTACTAGAT AGTGCTGAAC TGTCGTCATG TATTAGGTTT 120

ATCCAACTCG TTGACCAGTA TAGTATTTGT TTATTACACA GGCTCGGCCT TACAACAACA 180

AACAAAG 187

Candida dubliniensis (SEQ ID NO:12)

CTCCCTCAAA CCCCTAGGGT TTGGTGTTGA GCAATACGAC TTGGGTTTGC TTGAAAGATG 60

ATAGTGGTAT AAGGCGGAGA TGCTTGACAA TGGCTTAGGT GTAACCAAAA ACATTGCTAA 120

GGCGGTCTCT GGCGTCGCCC ATTTTATTCT TCAAAC 156

Candida pelliculosa (SEQ ID NO:13)

CTCTCTCAAA CCTTCGGGTT TGGTATTGAG TGATACTCTG TCAAGGGTTA ACTTGAAATA 60

TTGACTTAGC AAGAGTGTAC TAATAAGCAG TCTTTCTGAA ATAATGTATT AGGTTCTTCC 120

AACTCGTTAT ATCAGCTAGG CAGGTTTAGA AGTATTTTAG GCTCGGCTTA ACAACAATAA 180

ACTAAAAG 188

EXAMPLE 2

Species-Specific detection of *Candida*

Synthesis of oligonucleotide probes. Oligonucleotide probes were designed from sequence data for the ITS2 region of *Candida* spp rDNA. (Lott, T.J., *et al.*, 1997. Sequence analysis of the internal transcribed

spacer 2 (ITS2) from yeast species within the genus *Candida*.

Table 2

Synthetic Oligonucleotides used in PCR and hybridization analyses

Nucleotide sequence (5' to 3') and Chemistry	Primer or Probe	Source
*Dig-AT TGC TTG CGG CGG TAA CGT CC	SEQ ID NO: 17	ITS2 region of *C. albicans*
Dig-AA CGC TTA TTT TGC TAG TGG CC	SEQ ID NO: 18	ITS2 region of *C. tropicalis*
Dig-TT TAC CAA CTC GGT GTT GAT CT	SEQ ID NO: 19	ITS2 region of *C. glabrata*
Dig-AC AAA CTC CAA AAC TTC TTC CA	SEQ ID NO: 20	ITS2 region of *C. parapsilosis*
Dig-GG CCC GAG CGA ACT AGA CTT TT	SEQ ID NO: 21	ITS2 region of *C. krusei*
Dig-CC CGG CCT TAC AAC AAC CAA AC	SEQ ID NO: 22	ITS2 region of *C. guilliermondii*
Dig-AG TTA AGC TTG TTA CAG ACT CA	SEQ ID NO: 23	ITS2 region of *C. rugosa*
Dig-AC TCG TTA TTT TCC AGA CAG AC	SEQ ID NO: 24	ITS2 region of *C. utilis*
Dig-TC GTT GAC CAG TAT AGT ATT TG	SEQ ID NO: 25	ITS2 region of *C. zeylanoides*
Dig-CC GTT GGT GGA TTT GTT TCT AA	SEQ ID NO: 26	ITS2 region of *C. haemulonii*
Dig-AA AGC GAG GGG CCT TCT GCG CG	SEQ ID NO: 27	ITS2 region of *C. lambica*
Dig-GC GAG GGG CCT TCT GCG CGA AC	SEQ ID NO: 28	ITS2 region of *C. lambica*
Dig-GA GAC TCA TAG GTG TCA TAA AG	SEQ ID NO: 29	ITS2 region of *C. kefyr*
Dig-CT ACC AAA ACG CTT GTG CAG TC	SEQ ID NO: 30	ITS2 region of *C. viswanathii*
Dig-CT CCG AAA TAT CAA CCG CGC TG	SEQ ID NO: 31	ITS2 region of *C. lusitaneae*
Dig-AC GAG CGT CTG CTG GCT CCA CA	SEQ ID NO: 32	ITS2 region of *C. norvegica*
Dig-AC TGA GCG AAG TAC ACA ACA CT	SEQ ID NO: 33	ITS2 region of *C. norvegensis*
Dig-AT CAG CTA GGC AGG TTT AGA AG	SEQ ID NO: 34	ITS2 region of *C. pelliculosa*
Dig-AA GGC GGT CTC TGG CGT CGC CC	SEQ ID NO: 35	ITS2 region of *C. dubliniensis*

*Dig= digoxigenin label

PCR amplification. The reaction mixture (100 µl) contained 10 µl of 10X PCR buffer [100 mM Tris-HCl, pH 8.3, 500 mM KCl (Boehringer Mannheim, Indianapolis, IN)], 6 µl of 25 mM $MgCl_2$, 8 µl of deoxynucleotide triphosphate mix (1.25 mM each of dATP, dCTP, dGTP, and dTTP), 1 µl of each primer (20 µM), 2.5 U of Taq DNA polymerase (TaKaRa Shuzo Co., Ltd., Shiga, Japan), 2 µl of template DNA (0.5 ng/µl), and sterile water to make the total volume 100 µl. Vials were placed in the heating block of a Model 9600 thermal cycler (Perkin-Elmer, Emeryville, CA) after it reached 95°C. PCR amplification conditions were: 5 minutes denaturation at 95°C, followed by 30 cycles of 95°C for 30 seconds, 58°C for 30 seconds, and 72°C for 1

minute. A final extension step was conducted at 72°C for 5 minutes. After amplification, samples were stored at 4°C for not more than 20 hours before use in the EIA. Appropriate positive and negative controls were included and PCR contamination precautions were followed in accordance with the method of Kwok, S., *et al.*, 1989. Avoiding false positives with PCR. *Nature* (London) 339:237-238; and Fujita, et *al.*, 1995, *J. Clin. Microbiol.* 33:962-967.

Agarose gel electrophoresis. Electrophoresis was conducted in TBE (0.1 M Tris, 0.09 M boric acid, 0.001 M EDTA, pH 8.4) buffer at 76 volts for approximately 1 hour using gels composed of 1% (wt/vol) agarose (Boehringer Mannheim) and 1% (wt/vol) NuSieve (FMC Bioproducts, Rockland, ME). Gels were stained with 0.5 µg of Et Br per ml of deionized water for 30 minutes followed by a 30 minute wash in deionized water. Gels were viewed with a UV illuminator and photographed.

PCR-EIA. PCR-amplified DNA was hybridized to species-specific digoxigenin-labeled probes and to an all-*Candida* species biotinylated probe, and the complex was added to streptavidin-coated microtitration plates and trapped. Then, an indirect EIA was conducted as described by Fujita, et *al.*, 1995, *J. Clin. Microbiol.* 33:962-967, and Shin, *et al.* 1997, *J. Clin. Micro.* 35:1454-1459. All probes were tested in a checkerboard manner against DNA from other *Candida* species as well as against DNA from other fungal organisms.

To facilitate hybridization, single-stranded DNA was prepared from double-stranded PCR products by heat denaturation. A thin-walled polypropylene (0.5 ml) vial with flat cap (Perkin-Elmer), containing 10 µl of the PCR product plus 10 µl of sterile distilled water was heated at 95°C for 5 minutes and then immediately cooled on ice. Two hundred microliters of hybridization solution containing 4X SSC (saline-sodium citrate buffer; 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0), 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween™20 supplemented with 50 ng/ml each of biotin- and digoxigenin-labeled probes were then added to the single-stranded DNA.

After hybridization at 37°C for 1 hour, 100 µl of each sample was added to duplicate wells of a streptavidin-coated microtitration plate (Boehringer Mannheim), and the plate was incubated at ambient temperature for 1 hour with shaking (Minishaker, manufactured for Dynatech by CLTI, Middletown, NY). After washing six times with 0.01 M potassium phosphate buffered saline, pH 7.2, containing 0.05% Tween 20 (PBST), 100 µl of horseradish peroxidase-conjugated, anti-digoxigenin Fab fragment (Boehringer Mannheim), diluted 1:1000 in hybridization buffer, was added to each well. After a 30 minute incubation at ambient temperature on the shaker, the plate was again washed six times with PBST. Each well then received 100 µl of a mixture of one volume of 3, 3', 5, 5'-tetramethylbenzidine peroxidase substrate (Kirkegaard & Perry Laboratories, Inc., Gaithersburg, MD) and one volume of peroxidase solution (Kirkegaard & Perry). The plate was kept at ambient temperature for 15 minutes, and the A_{650nm} of each well was determined with a microtitration plate reader (UV Max; Molecular Devices, Inc., Menlo Park, CA). The absorbance of a reagent blank in which target DNA was replaced with distilled water was subtracted from each test sample.

Statistical analyses. The student's t-test was used to determine significant differences between absorbance values of homologous and non-homologous probe reactions. Absorbance values for all probes versus their homologous DNA were significantly different from those with non-homologous DNA ($P<0.05$) except for the cross-reactivity of the *C. guillermondii* probe with *C. zeylanoides* DNA and the *C. glabrata* probe with *S. cerevisiae* DNA ($P>0.05$, Figures 1 and 2).

EXAMPLE 3

Specificity of digoxigenin-labeled probes

Eighteen species-specific DNA probes were designed and tested for hybridization specificity. The results are shown in Figures 1 and 2. Absorbance values for all probes versus their homologous DNA were significantly different from those with non-homologous DNA,

(P<0.05) except in two cases of cross-reactivity of the *C. guillermondii* probe with *C. zeylanoides* DNA and the *C. glabrata* probe with *S. cerevisiae* DNA (P>0.05, Figures 1 and 2). However, the probe for *C. zeylanoides* (CZ) did not hybridize with DNA from *C. guilliermondii*, so that by a process of elimination these probes could be used to specifically identify the *Candida* species. In the other case, the previously published (Fujita, et *al.*, 1995, *J. Clin. Microbiol.* 33:962-967; Shin, *et al.* 1997, *J. Clin. Micro.* 35:1454-1459) probe for *C. glabrata*, CG, cross-hybridized with *Saccharomyces cerevisiae* DNA. This probe for *C. glabrata* also cross-hybridized with *Candida* species not previously tested, i.e. *C. pelliculosa,* and *C. utilis* (P>0.05). Therefore, the CG probe was redesigned (CGE) resulting in the elimination of cross-hybridizations with all above mentioned species except for *S. cerevisiae.*

Multiple strains of several species were tested. Absorbance values were consistent among the strains of each species except in two cases as shown in Table 3. Absorbance values for the *C. parapsilosis* probe (CP) versus *C. parapsilosis* Lehmann Group III (Lin, D., L.-C. *et al.*, 1995. Three distinct genotypes within *Candida parapsilosis* from clinical sources. *J. Clin. Micro.* 33:1815-1821) and the CH probe for *C. haemulonii* versus one strain (*C. haemulonii* 90.00.3593) gave statistically lower values than for positive control samples using homologous DNA. These discrepant cases may indicate a finer taxonomic discrimination of isolates by genotypic compared to phenotypic methods (Lehmann, P.F., *et al.*, 1993. Unrelatedness of groups of yeasts within the *Candida haemulonii* complex. *J. Clin. Micro.* 31:1683-1687; Zeng, S., *et al.*, 1996. Random amplified polymorphic DNA analysis of culture collection strains of *Candida* species. *J. Med. Vet. Mycol.* 34:293-297; and Lin, *et al.*, 1995, *J. Clin. Micro.* 33:1815-1821).

In Table 3, strains designated in bold print were those which were sequenced and from which the species-specific probe was designed.

Table 3
Consistency of A_{650nm} Values for Multiple Isolates Within a Given Species

SPECIES (PROBE)	ISOLATE	MEAN $A_{650nm} \pm$ S.D.[a]	
		For Each Isolate	For Each Species
C. tropicalis (CT)	**CDC 38**	0.870 ± 0.354	1.038 ± 0.238
	ATCC 750	1.206 ± 0.066	
C. guilliermondii (GU)	**ATCC 6260**	0.821 ± 0.303	1.162 ± 0.256
	ATCC 34134	1.464 ± 0.188	
	KOR G1	1.025 ± 0.355	
	B4346	1.152 ± 0.396	
	B4347	1.349 ± 0.402	
C. rugosa (CR)	**ATCC 10571**	0.222 ± 0.098	0.239 ± 0.028
	ATCC 38772	0.271 ± 0.077	
	ATCC 58964	0.223 ± 0.069	
C. utilis (CU2)	**ATCC 22023**	1.161 ± 0.193	1.198 ± 0.053
	ATCC 64882	1.236 ± 0.416	
C. zeylanoides (CZ)	**ATCC 7351**	0.361 ± 0.170	0.433 ± 0.104
	B996	0.466 ± 0.110	
	B997	0.339 ± 0.170	
	B4232	0.565 ± 0.060	
C. lambica (LA)	**ATCC 24750**	0.640 ± 0.175	0.677 ± 0.052
	ATCC 22695	0.714 ± 0.170	
C. kefyr (KF)	**ATCC 46764**	1.184 ± 0.384	1.282 ± 0.166
	ATCC 66028	1.474 ± 0.208	
	ATCC 42265	1.187 ± 0.224	
C. lusitaniae (LU)	**ATCC 34449**	0.483 ± 0.162	0.539 ± 0.079
	ATCC 42720	0.595 ± 0.148	
C. norvegensis (NS)	**ATCC 22977**	0.716 ± 0.242	0.630 ± 0.122
	ATCC 32816	0.544 ± 0.164	
C. pelliculosa (PL)	**ATCC 8168**	0.624 ± 0.320	0.642 ± 0.086
	KOR P1	0.809 ± 0.242	
	KOR P2	0.574 ± 0.170	
	KOR P4	0.612 ± 0.106	
	KOR P5	0.587 ± 0.152	
	KOR P6	0.649 ± 0.156	

C. parapsilosis (CP)	**ATCC 22019**	0.493 ± 0.231	
Group I	MCO478	0.554 ± 0.228	0.484 ± 0.061
	MCO441	0.453 ± 0.199	
	MCO433	0.445 ± 0.173	
Group II	MCO456	0.455 ± 0.243	0.489 ± 0.041
	MCO462	0.478 ± 0.203	
	MCO471	0.534 ± 0.133	
Group III	MCO429	0.162 ± 0.058	0.158 ± 0.006
	MCO448	0.154 ± 0.072	
C. haemulonii (CH)	**ATCC 22991**	0.841 ± 0.332	
	CBS 5199	0.850 ± 0.082	
Variant	90.00.3593	0.088 ± 0.026	

[a] Mean A_{650nm} ± standard deviation for n = 2 to 5 experiments conducted in duplicate

Species-specific probes were designed to identify two species that share a common phenotype, namely *C. albicans* and *C. dubliniensis*. The new species, *C. dubliniensis*, has been described by Sullivan, D.J., *et al.*, 1995, *Candida dubliniensis* sp. nov.: phenotypic and molecular characterization of a novel species associated with oral candidiasis in HIV-infected individuals. *Microbiology* 141:1507-1521. By routine conventional phenotypic methods, *C. dubliniensis* is identified as *C. albicans*. The probes designed in this example discriminated *C. albicans* from *C. dubliniensis* as shown in Table 4, below. The CA probe which detects *C. albicans* did not react with DNA from *C. dubliniensis* strains and the DB probe for *C. dubliniensis* did not hybridize with DNA from *C. albicans*.

The data shown in Table 4 demonstrate that the sequences of the ITS2 regions for *C. albicans* and *C. dubliniensis* differ. Specific probes for each species provide a rapid method to differentiate microorganisms having virtually the same phenotype but which differ genotypically.

Table 4
Differentiation of *C. albicans* from *C. dubliniensis* By Species- specific Probes.

TARGET DNA	*C. albicans* Probe	*C. dubliniensis* Probe
C. albicans		
ATCC 11006 (stellatoidea)	0.485 ± 0.252[a]	0
ATCC 20408 (stellatoidea)	0.370 ± 0.168	0
ATCC 36232 (stellatoidea)	0.409 ± 0.178	0
B36	0.568 ± 0.236	0
Q10	0.640 ± 0.192	0
Lecoq	0.464 ± 0.124	0
2730	0.631 ± 0.192	0
3153A	0.528 ± 0.068	0
Mean A_{650nm} for CA Probe	**0.512 ± 0.095**	**0**
C. dubliniensis		
M1	0	0.351 ± 0.090
M4	0	0.407 ± 0.186
P30	0	0.346 ± 0.088
1419-2	0	0.402 ± 0.132
901013	0	0.393 ± 0.101
Mean A_{650nm} for DB Probe	**0**	**0.380 ± 0.029**

[a] Mean A_{650nm} ± standard deviation for n=2 to 5 experiments conducted in duplicate

The probes described herein extend the range of *Candida* probes to include a test matrix of 18 *Candida* species. This test matrix is capable of complementing species identification by the API20C carbohydrate assimilation system. The probes described herein are species-specific and can be used to identify cultures *Candida* species including *C. dubliniensis* which cannot currently be differentiated from *C. albicans* by routine phenotypic methods.

Standardization of DNA extraction for all *Candida* species is facilitated by using broth culture and a commercially available extraction kit. The PCR-EIA for identification requires less time (one day) than conventional methods which require an average of 3 to 5 days for species identification of most *Candida* spp. and can require up to 4 or 5 weeks for unusual species such as *C. norvegensis* or *C. utilis*.

Since choice of drug varies from species to species, an accurate and timely identification is important so that appropriately targeted therapy can be administered to a patient. Some species are innately resistant to certain drugs, i.e. *C. krusei* to fluconazole, so that when an identification of "*Candida* spp other than *albicans*" is made, it may be an inadequate guide to the selection of appropriate therapy.

C. dubliniensis has been recently described as a new species after it was found that some "*albicans*" strains did not behave as typical *C. albicans* by molecular methods. DNA from these strains, when probed with *C. albicans*-specific and mid-repetitive elements such as Ca3 or 27A, did not react positively. Molecular differences became apparent by sequencing the ITS2 region of both species, and probes were designed that hybridized only with their homologous DNA.

It should be understood that the foregoing relates only to preferred embodiments of the present invention, and that numerous modifications or alterations may be made therein without departing from the spirit and the scope of the invention as set forth in the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: The Government of the United States of America, As Represented by the Secretary of the Department of Health and Human Services

(ii) TITLE OF INVENTION: Nucleic Acid Probes for Detecting Candida Species

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:
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(F) ZIP: M5H 3Y2

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: CA 2,300,192
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(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Rudolph, John
(B) REGISTRATION NUMBER: 4213
(C) REFERENCE/DOCKET NUMBER: 6857-9

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(B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida guilliermondi

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTCTCAAA CCCCCGGGTT TGGTATTGAG TGATACTCTT AGTCGGACTA GGCGTTTGCT 60

TGAAAAGTAT TGGCATGGGT AGTATGGATA GTGCTGTCGA CCTCTCAATG TATTAGGTTT 120

ATCCAACTCG TTGAATGGTG TGGCGGGATA TTTCTGGTAT TGTTGGCCCG GCCTTACAAC 180

AACCAAACAA GC 192

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida haemulonii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGCGTGATA TCTTCTCACC GTTGGTGGAT TTGTTTCTAA ATATCATGCC ACAGTGAAGT 60

CTACGC 66

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida keyfr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCTCAAA CCTTTGGGTT TGGTAGTGAG TGATACTCGT CTCGGGCTTA ACTTGAAAGT 60

GGCTAACCGT TGCCATCTGC GTGAGCAGGC TGCGTGTCAA GTCTATGGAC TCGACTCTTG 120

CACATCTACG TCTTAAGTAT GCGCCAATTC GTGGTAAGCT TGGGTCATAG AGACTCATAG 180

GTGTTATAAA GACTCGCTGG TGTTTGTCTC CTTGAGGCAT ACGGCTTTAC AACTCTCAAG 240

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida lambica

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTTCTTGGA GCGGTGCTTC AGACCTGGCG GGCTGTCTTT TTGGACGGCG CGCCCAAAGC 60

GAGGGGCCTT CTGCGCGAAC TAGACTGTGC GCGCGGGGCG GTCGGCGAAC TTATTACCAA 120

G 121

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida lusitaniae

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCGTCGCA TCCCCTCTAA CCCCCGGTTA GGCGTTGCTC CGAAATATCA ACCGCGCTGT 60

CAAATACG 68

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida norvegensis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCTTCTTGCG CAAGCAGAAG TTGGGGTTGC CACGGCCCGT GCGGCCTGTG TGTGGCTCCC 60

CGAAACGGAA CGGCAGCGGG ACTGAGCGAA GTACACAACA CTCGCGCTTG GCCCGCCGAA 120

CTTTTTTTTA ATCTAAG 137

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida norvegica

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTTCTCAAG CGTGAGCTTG GTGTTGGCGG AGGTCTTTCG AGGCCCCGCT GAAATACGCA 60

GGGGGTGCGT GGAAACGAGC TTTCTCTCTA CTAATGTCTA GTTCTGCCAA CTCATTGGAC 120

GAGCGTCTGC TGGCTCCACA ATCCCACCCC CATTACCCCA AC 162

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida rugosa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCTCTCGCA AGTGTTGGCA CCACGCCGGC AGGCGTCTGC CCGAAACGCG ACCGTCTAAA 60

ACAGTTAAGC TTGTTACAGA CTCACGATC 89

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida utilis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCTCTCAAG ATCCTCTAGG GGACTTGGTA TTGAGTGATA CTCTGTGTTA ACTTGAAATA 60

CTCTAGGCAG AGCTCCCCCC TGGAAATCCT CTGGGCCGAA ATAATGTATT AGGTTCTACC 120

AACTCGTTAT TTTCCAGACA GACTTCCAGG CAGAGCTCGT GCCCCTAACA TAGCAGTCTA 180

AGC 183

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida viswanathii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCCCTCAAC CCCGCGGGTT TGGTGTTGAG CAATACGCCA GGTTTGTTTG AAAGACGTAC 60

GTGGAGACAA TATTAGCGAC TTAGGTTCTA CCAAAACGCT TGTGCAGTCG GTCCCACACA 120

CAGTGTAAGC TAACA 135

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida zeylanoides

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTCTCTCAAA TCTTCGGATT TGGTTTTGAG TGATACTCTT AGTCAGACTA AGCGTTTGCT 60

TGAAATGTAA TGGCATGAGT GGTACTAGAT AGTGCTGAAC TGTCGTCATG TATTAGGTTT 120

ATCCAACTCG TTGACCAGTA TAGTATTTGT TTATTACACA GGCTCGGCCT TACAACAACA 180

AACAAAG 187

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida dubliniensis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCCCTCAAA CCCCTAGGGT TTGGTGTTGA GCAATACGAC TTGGGTTTGC TTGAAAGATG 60

ATAGTGGTAT AAGGCGGAGA TGCTTGACAA TGGCTTAGGT GTAACCAAAA ACATTGCTAA 120

GGCGGTCTCT GGCGTCGCCC ATTTTATTCT TCAAAC 156

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida pelliculosa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCTCTCAAA CCTTCGGGTT TGGTATTGAG TGATACTCTG TCAAGGGTTA ACTTGAAATA 60

TTGACTTAGC AAGAGTGTAC TAATAAGCAG TCTTTCTGAA ATAATGTATT AGGTTCTTCC 120

AACTCGTTAT ATCAGCTAGG CAGGTTTAGA AGTATTTTAG GCTCGGCTTA ACAACAATAA 180

ACTAAAAG 188

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "ITS3 5.8S rDNA universal 5' primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCATCGATGA AGAACGCAGC 20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "ITS4 28S rDNA universal 3' primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCCTCCGCTT ATTGATATGC 20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /note= "5'-end labeled, biotinylated probe; 5.8S rDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGCCTGTT TGAGCGTCRT T 21

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida albicans

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CA probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATTGCTTGCG GCGGTAACGT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida tropicalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CT probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AACGCTTATT TTGCTAGTGG CC 22

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida glabrata

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CGE probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTACCAACT CGGTGTTGAT CT 22

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida parapsilosis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CP probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACAAACTCCA AAACTTCTTC CA 22

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida krusei

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CK probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCCCGAGCG AACTAGACTT TT 22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida guilliermondii

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "GU probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCGGCCTTA CAACAACCAA AC 22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida rugosa

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CR probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGTTAAGCTT GTTACAGACT CA 22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida utilis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CU2 probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACTCGTTATT TTCCAGACAG AC 22

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida zeylanoides

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CZ probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCGTTGACCA GTATAGTATT TG 22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida haemulonii

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "CH probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCGTTGGTGG ATTTGTTTCT AA 22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida lambica

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "Probe LA2 of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAAGCGAGGG GCCTTCTGCG CG 22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida lambica

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "Probe LA4 of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCGAGGGGCC TTCTGCGCGA AC 22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida kefyr

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "KF probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAGACTCATA GGTGTCATAA AG 22

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida viswanathii

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "VS probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTACCAAAAC GCTTGTGCAG TC 22

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida lusitaneae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "LU probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTCCGAAATA TCAACCGCGC TG 22

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida norvegica

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "NC probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACGAGCGTCT GCTGGCTCCA CA 22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida norvegensis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "NS probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACTGAGCGAA GTACACAACA CT 22

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida pelliculosa

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "PL probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATCAGCTAGG CAGGTTTAGA AG 22

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Candida dubliniensis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "DB probe of ITS region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGGCGGTCT CTGGCGTCGC CC 22

We Claim:

1. A species-specific nucleic acid probe for a *Candida* species, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NOs: 26, 27, 31, 33, 32, 23, 24, 30, 25, or 34 and selectively hybridizes with a nucleic acid molecule encoding a species-specific portion of an internal transcribed spacer 2 (ITS2) region, or a complementary sequence thereof, of a respective *Candida* species selected from the group consisting of *C. haemulonii* (SEQ ID NO:2), *C. lambica* (SEQ NO ID:4), *C. lusitaniae* (SEQ ID NO:5), *C. norvegensis* (SEQ ID NO:6), *C. norvegica* (SEQ ID NO:7), *C. rugosa* (SEQ ID NO:8), *C. utilis* (SEQ ID NO:9), *C. viswanathii* (SEQ ID NO:10), *C. zeylanoides* (SEQ ID NO:11), and *C. pelliculosa* (SEQ ID NO:13); or

wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:28 and selectively hybridizes with a nucleic acid molecule encoding a species-specific portion of an internal transcribed spacer 2 (ITS2) region, or a complementary sequence thereof, of *C. lambica* (SEQ ID NO:4); or,

wherein the probe comprises a nucleic acid sequence of SEQ ID NO:29 or SEQ ID NO:35 and selectively hybridizes with a nucleic acid molecule encoding a species-specific portion of an internal transcribed spacer 2 (ITS2) region, or a complementary sequence thereof, of a respective *Candida* species selected from the group consisting of *C. kefyr* (SEQ ID NO:3) and *C. dubliniensis* (SEQ ID NO:12);

wherein the probe selectively hybridizes in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

2. A *C. haemulonii*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20,with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:2, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:26 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

3. The nucleic acid probe of Claim 2, comprising a nucleic acid sequence of SEQ ID NO:26, or a complementary sequence thereof.

4. A *C. kefyr*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20, with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:3, or a complementary sequence thereof, wherein the nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:29 or a complementary sequence thereof, and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

5. A *C. lambica*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20, with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:4, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:27 or SEQ ID NO:28 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

6. The nucleic acid probe of Claim 5, comprising a nucleic acid sequence of SEQ ID NO:27 or SEQ ID NO:28, or a complementary sequence thereof.

7. A *C. lusitaniae*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20,with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:5, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:31 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

8. The nucleic acid probe of Claim 7, comprising a nucleic acid sequence of SEQ ID NO:31, or a complementary sequence thereof.

9. A *C. norvegensis*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20,with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:6, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:33 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

10. The nucleic acid probe of Claim 9, comprising a nucleic acid sequence of SEQ ID NO:33, or a complementary sequence thereof.

11. A *C. norvegica*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20,with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:7, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:32 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

12. The nucleic acid probe of Claim 11, comprising a nucleic acid sequence of SEQ ID NO:32, or a complementary sequence thereof.

13. A *C.rugosa*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20, with a nucleic acid molecule encoding a species-specific portion

of an ITS2 region set forth in SEQ ID NO:8, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:23 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

14. The nucleic acid probe of claim 13, comprising a nucleic acid sequence of SEQ ID NO:23, or a complementary sequence thereof.

15. A *C.utilis*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20, with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:9, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:24 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

16. The nucleic acid probe of Claim 15, comprising a nucleic acid sequence of SEQ ID NO:24, or a complementary sequence thereof.

17. A *C. viswanathii*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20, with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:10, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:30 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

18. The nucleic acid probe of Claim 17, comprising a nucleic acid sequence of SEQ ID NO:30, or a complementary sequence thereof.

19. A *C. zeylanoides*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20, with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:11, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:25 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

20. The nucleic acid probe of Claim 19, comprising a nucleic acid sequence of SEQ ID NO:25, or a complementary sequence thereof.

21. A *C. dubliniensis*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20,with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:12, or a complementary sequence thereof, wherein the nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:35 or a complementary sequence thereof, and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

22. A *C. pelliculosa*-specific nucleic acid probe that selectively hybridizes, in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20, with a nucleic acid molecule encoding a species-specific portion of an ITS2 region set forth in SEQ ID NO:13, or a complementary sequence thereof, wherein the probe comprises at least ten consecutive nucleotides of SEQ ID NO:34 and does not hybridize with an ITS2 nucleic acid sequence from a different *Candida* species.

23. The nucleic acid probe of Claim 22, comprising a nucleic acid sequence of SEQ ID NO:34, or a complementary sequence thereof.

24. A method for species-specific detection of *Candida* in a sample comprising

a) combining the sample with the species-specific nucleic acid probe of claim 1, wherein the sample comprises an isolated *Candida* nucleic acid molecule;

b) selectively hybridizing the species-specific nucleic acid probe to the isolated *Candida* nucleic acid molecule, wherein the isolated *Candida* nucleic acid molecule comprises a nucleic acid sequence encoding a portion of an internal transcribed spacer 2 (ITS2) region, or a complementary sequence thereof, and,

c) detecting the presence of hybridization,

thereby detecting a *Candida* species in the sample.

25. The method of claim 24 wherein the sample comprises cells which are lysed prior to step a).

26. The method of Claim 24, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:2, or a complementary sequence thereof, of a *C. haemulonii*.

27. The method of Claim 26, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:26, or a complementary sequence thereof.

28. The method of Claim 24, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:29, or a complementary sequence thereof.

29. The method of Claim 24, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:4, or a complementary sequence thereof, of a *C. lambica*.

30. The method of Claim 29, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:27 or SEQ ID NO:28, or a complementary sequence thereof.

31. The method of Claim 29, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:5, or a complementary sequence thereof, of a *C. lusitaniae*.

32. The method of Claim 31, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:31, or a complementary sequence thereof.

33. The method of Claim 24, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:6, or a complementary sequence thereof, of a *C. norvegensis*.

34. The method of Claim 33, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:33, or a complementary sequence thereof.

35. The method of Claim 24, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:7, or a complementary sequence thereof, of a *C. norvegica.*

36. The method of Claim 35, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:32, or a complementary sequence thereof.

37. The method of Claim 24, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:8, or a complementary sequence thereof, of a *C. rugosa.*

38. The method of Claim 37, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:23, or a complementary sequence thereof.

39. The method of Claim 24, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:9, or a complementary sequence thereof, of a *C. utilis.*

40. The method of Claim 39, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:24, or a complementary sequence thereof.

41. The method of Claim 24, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:10, or a complementary sequence thereof, of a *C. viswanathii.*

42. The method of Claim 41, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:30, or a complementary sequence thereof.

43. The method of Claim 29, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:11, or a complementary sequence thereof, of a *C. zeylanoides*.

44. The method of Claim 43, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:25, or a complementary sequence thereof.

45. The method of Claim 24, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:35, or a complementary sequence thereof.

46. The method of Claim 29, wherein the internal transcribed spacer 2 region comprises the sequence set forth in SEQ ID NO:13, or a complementary sequence thereof, of a *C. pelliculosa*.

47. The method of Claim 46, wherein the species-specific nucleic acid probe comprises a nucleic acid sequence of SEQ ID NO:34, or a complementary sequence thereof.

48. The nucleic acid probe of Claim 3, consisting of the nucleic acid sequence of SEQ ID NO:26, or a complementary sequence thereof.

49. The nucleic acid probe of Claim 4, consisting of the nucleic acid sequence of SEQ ID NO:29, or a complementary sequence thereof.

50. The nucleic acid probe of Claim 6, consisting of the nucleic acid sequence of SEQ ID NO:27 or SEQ ID NO:28, or a complementary sequence thereof.

51. The nucleic acid probe of Claim 8, consisting of the nucleic acid sequence of SEQ ID NO:31, or a complementary sequence thereof.

52. The nucleic acid probe of Claim 10, consisting of the nucleic acid sequence of SEQ ID NO:33, or a complementary sequence thereof.

53. The nucleic acid probe of Claim 12, consisting of the nucleic acid sequence of SEQ ID NO:32, or a complementary sequence thereof.

54. The nucleic acid probe of Claim 14, consisting of the nucleic acid sequence of SEQ ID NO:23, or a complementary sequence thereof.

55. The nucleic acid probe of Claim 16, consisting of the nucleic acid sequence of SEQ ID NO:24, or a complementary sequence thereof.

56. The nucleic acid probe of Claim 18, consisting of the nucleic acid sequence of SEQ ID NO:30, or a complementary sequence thereof.

57. The nucleic acid probe of Claim 20, consisting of the nucleic acid sequence of SEQ ID NO:25, or a complementary sequence thereof.

58. The nucleic acid probe of Claim 21, consisting of the nucleic acid sequence of SEQ ID NO:35, or a complementary sequence thereof.

59. The nucleic acid probe of Claim 23, consisting of the nucleic acid sequence of SEQ ID NO:34, or a complementary sequence thereof.

60. The method of claim 24, wherein selectively hybridizing under stringent conditions comprises hybridizing in a buffer comprising 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0, 20 mM HEPES, 2 mM EDTA, and 0.15% (vol/vol) Tween® 20.

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	CA	CT	CG	CP	CK	GU	CR	CU	CZ	CH	LA	KF	VS	LU	NC	FA	NS	DUB	PEL
albicans	0.426 0.275	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tropi-calis	0	0.870 0.354	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gla-brata	0	0	1.034 0.343	0	0	0.026 0.014	0	0	0.036 0.021	0	0	0	0	0	0	0.052 0.019	0	0	0
parap-silosis	0	0	0	0.493 0.231	0.025 0.018	0	0	0	0	0	0	0	0	0	0	0	0	0	0
krusei	0	0	0	0	0.389 0.136	0	0	0	0	0	0.114 0.042	0	0	0	0	0	0.085 0.045	0	0
guillier-mondii	0	0	0	0	0	0.821 0.303	0	0	0.639 0.172	0	0	0	0	0	0	0.094 0.014	0	0	0.097 0.085
rugosa	0	0	0	0	0	0	0.222 0.098	0	0	0	0	0	0	0	0	0	0	0	0
utilis	0	0	0	0	0	0	0	1.161 0.193	0	0	0	0	0	0	0	0	0	0	0
zeylan-noides	0	0	0	0	0	0	0	0	0.361 0.17	0	0	0	0	0	0	0	0	0	0
haemu-lonii	0	0	0	0	0	0	0	0	0	0.841 0.332	0	0	0	0	0	0	0	0	0
lambica	0	0	0	0	0	0	0	0	0	0	0.640 0.175	0	0	0	0	0	0	0	0
kefyr	0	0	0	0	0.037 0.008	0	0	0	0	0.014 0.009	0	1.184 0.384	0	0	0	0	0	0	0
viswa-nathii	0	0.175 0.093	0	0	0	0	0	0	0	0	0	0	0.988 0.419	0	0	0	0	0	0
lusit-taniae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.483 0.162	0	0	0	0	0
nor-vegica	0	0.015 0.028	0	0	0.019 0.032	0	0	0	0	0	0	0.012 0.013	0	0	0.258 0.102	0	0	0	0
norve-gensis	0	0	0	0	0.014 0.021	0	0	0	0	0.013 0.024	0.017 0.019	0	0	0	0.014 0.018	0	0.716 0.242	0	0
dublin-iensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.322 0.119	0
pellicu-losa	0	0.024 0.011	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.624 0.320

FIGURE 1

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	FUM	FLAV	NID	TER	NIG	BLAS	HIST	Scere	Cr.hum	Cr.hum	Cr.nA	Cr.nB	Cr.nC	Cr.nD	C.cat	C.cat	S.cif	T.cut	Pmar
albicans	neg	neg	0	0	0	neg	neg	neg	0	0	0	0	0	0	0	0	0	0	neg
tropi-calis	neg	neg	0	0.114 0.052	0	neg	neg	0	0	0	0	0	0	0	0	0	0	0	neg
gla-brata	0	0	0	0	0	0	0	0.755 0.229	0	0	0	0	0	0	0	0	0	0	0
parap-silosis	neg	0	0	0	0	neg	neg	neg	0	0	0	0	0	0	0	0	0	0	neg
krusei	0	0	0	0	0	0.071 0.025	0	0	0	0	0	0	0	0	0	0	0	0	0
guillier-mondii	0	0	0	0.017 0.034	0	0	0	0	0	0	0.024 0.012	0.054 0.028	0.034 0.015	0.071 0.016	0	0	0	0.039 0.029	0
rugosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
utilis	0	0	0	0.147 0.035	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
nor-vegica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.014 0.022	0	0	0	0
norve-gensis	0	0	0	0	0	0	0.014 0.012	0	0	0	0	0	0	0	0	0	0	0	0
dublin-iensis	0	0	0	0	0	0	0	0	0.041 0.019	0	0	0	0	0	0	0	0	0	0

FIGURE 2