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(72) Inventeurs/Inventors:
MORRISON, CHRISTINE J., US;
REISS, ERROL, US;
AIDOREVICH, LILIANA, VE;
CHOI, JONG SOO, KR

(73) Propriétaire/Owner:
THE GOVERNMENT OF THE UNITED STATES OF
AMERICA AS REPRESENTED BY THE
SECRETARY OF THE DEPARTMENT OF HEALTH
AND HUMAN SERVICES, US

(74) Agent: FINLAYSON & SINGLEHURST

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(54) Title: NUCLEIC ACIDS FOR DETECTING ASPERGILLUS SPECIES AND OTHER FILAMENTOUS FUNGI

(57) **Abrégé/Abstract:**

Nucleic acids for detecting *Aspergillus* species and other filamentous fungi are provided. Unique internal transcribed spacer 2 coding regions permit the development of nucleic acid probes specific for five different species of *Aspergillus*, three species of *Fusarium*, four species of *Mucor*, two species of *Penicillium*, five species of *Rhizopus*, one species of *Rhizomucor*, as well as probes for *Absidia corymbifera*, *Cunninghamella elagans*, *Pseudallescheria boydii*, and *Sporothrix schenkii*. The invention thereby provides methods for the species-specific detection and diagnosis of infection by *Aspergillus*, *Fusarium*, *Mucor*, *Penicillium*, *Rhizopus*, *Rhizomucor*, *Absidia*, *Cunninghamella*, *Pseudallescheria* or *Sporothrix* in a subject. Furthermore, genus-specific probes are also provided for *Aspergillus*, *Fusarium* and *Mucor*, in addition to an all-fungus nucleic acid probe.



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(21) International Application Number: PCT/US98/08926 (22) International Filing Date: 1 May 1998 (01.05.98) (30) Priority Data: 60/045,400 2 May 1997 (02.05.97) US (71) Applicant (for all designated States except US): THE GOVERNMENT OF THE UNITED STATES OF AMERICA as represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, c/o Centers for Disease Control and Prevention, Technology Transfer Office [US/US]; Atlanta, GA 30329 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): MORRISON, Christine, J. [US/US]; 3110 Tolbert Drive, Decatur, GA 30033 (US). REISS, Errol [US/US]; 3642 Castaway Court, Chamblee, GA 30341 (US). AIDOREVICH, Liliana [VE/VE]; Calle Circunvalación, Manzana B7 #16 Urlo, El Castan Maracay Edo Aragua (VE). CHOI, Jong, Soo [KR/KR]; 202-1506, Sinchungi-Town Apartment, Whangum-dong, Susung-gu, Taegu City 706-040 (KR). (74) Agents: WARREN, William, L. et al.; Jones & Askew, 37th floor, 191 Peachtree Street, N.E., Atlanta, GA 30303 (US).		(81) Designated States: AU, CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: NUCLEIC ACIDS FOR DETECTING <i>ASPERGILLUS</i> SPECIES AND OTHER FILAMENTOUS FUNGI (57) Abstract Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi are provided. Unique internal transcribed spacer 2 coding regions permit the development of nucleic acid probes specific for five different species of <i>Aspergillus</i>, three species of <i>Fusarium</i>, four species of <i>Mucor</i>, two species of <i>Penicillium</i>, five species of <i>Rhizopus</i>, one species of <i>Rhizomucor</i>, as well as probes for <i>Absidia corymbifera</i>, <i>Cunninghamella elagans</i>, <i>Pseudallescheria boydii</i>, and <i>Sporothrix schenkii</i>. The invention thereby provides methods for the species-specific detection and diagnosis of infection by <i>Aspergillus</i>, <i>Fusarium</i>, <i>Mucor</i>, <i>Penicillium</i>, <i>Rhizopus</i>, <i>Rhizomucor</i>, <i>Absidia</i>, <i>Cunninghamella</i>, <i>Pseudallescheria</i> or <i>Sporothrix</i> in a subject. Furthermore, genus-specific probes are also provided for <i>Aspergillus</i>, <i>Fusarium</i> and <i>Mucor</i>, in addition to an all-fungus nucleic acid probe.		

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**NUCLEIC ACIDS FOR DETECTING
ASPERGILLUS SPECIES AND OTHER FILAMENTOUS FUNGI**

15 This invention was made in the Centers for Disease Control
Mycotic Diseases Laboratories, an agency of the United States Government.

Technical Field

20 This application relates in general to the field of diagnostic
microbiology. In particular, the invention relates to the species-specific
detection of *Aspergillus*, *Fusarium*, *Mucor*, *Penicillium*, *Rhizopus*,
Rhizomucor, *Absidia*, *Cunninghamella*, *Pseudallescheria boydii*
(*Scedosporium apiospermum*), and *Sporothrix* species.

Background of the Invention

25 In recent years, chemotherapy for hematological
malignancies, and high-dose corticosteroid treatment for organ transplant
recipients, along with the spread of AIDS, have greatly increased the number
of immunocompromised patients (1, 12, 14, 43). Saprophytic filamentous
fungi, such as *Aspergillus*, *Rhizopus*, and *Mucor* species, found in the
30 environment and considered to be of low virulence, are now responsible for
an increasing number of infections in the immunocompromised host (17, 20,
43). In addition, these infections are often fulminant and rapidly fatal in
immunocompromised patients (7, 11, 12, 20, 44). Morbidity and mortality
is extremely high; for example, aspergillosis has a mortality rate of
35 approximately 90% (8, 11).

 To complicate matters, diagnosis is difficult and symptoms
are often non-specific (18, 27, 29, 42, 44). Antibody-based tests can be

unreliable due to the depressed or variable immune responses of immunocompromised patients (2, 9, 18, 46). Antigen detection tests developed to date have fallen short of the desired sensitivity (2, 9, 38). Radiographic evidence can be non-specific and inconclusive (5, 29, 36), although some progress in diagnosis has been made with the advent of computerized tomography (40). However, definitive diagnosis still requires either a positive blood or tissue culture or histopathological confirmation (3, 21). An added complication is that the invasive procedures necessary to obtain biopsy materials are often not recommended in thrombocytopenic patient populations (37, 41).

Even when cultures of blood, lung or rhinocerebral tissues are positive, morphological and biochemical identification of filamentous fungi can require several days for adequate growth and sporulation to occur, delaying targeted drug therapy. Some atypical isolates may never sporulate, making identification even more difficult (23). When histopathology is performed on tissue biopsy sections, the morphological similarities of the various filamentous fungi in tissue make differentiation difficult (16). Fluorescent antibody staining of histopathological tissue sections is not specific unless cross-reactive epitopes are absorbed out which can make the resultant antibody reactions weak (14, 19). Therapeutic choices vary (7, 41, 44) making a test to rapidly and specifically identify filamentous fungi urgently needed for the implementation of appropriately targeted therapy. Early and accurate diagnosis and treatment can decrease morbidity and increase the chances for patient survival (6, 27, 39). Furthermore, identification of filamentous fungi to at least the species level would be epidemiologically useful (24, 31, 43, 47).

PCR-based methods of detection, which show promise as rapid, sensitive means to diagnose infections, have been used in the identification of DNA from *Candida* species (13, 15, 30) and some other fungi, particularly *Aspergillus* species (31, 33, 45). However, most of these tests are only genus-specific (28, 38) or are directed to detect only single-copy genes (4, 35). Others have designed probes to detect multi-copy genes so as to increase test sensitivity (31, 33) but in doing so have lost test specificity because they have used highly conserved genes, which detect one or a few species but which are also plagued with cross-reactivities to human, fungal or even viral DNA (25, 31, 33).

Therefore, it is an object of the invention to provide improved materials and methods for detecting and differentiating *Aspergillus* and other filamentous fungal species in the clinical and laboratory settings.

Summary of the Invention

The present invention relates to nucleic acids for detecting *Aspergillus*, *Fusarium*, *Mucor*, *Penicillium*, *Rhizopus*, *Rhizomucor*, *Absidia*, *Cunninghamella*, *Pseudallescheria* (*Scedosporium*), and *Sporothrix* species. Unique internal transcribed spacer 2 coding regions permit the development of probes specific for five different *Aspergillus* species, *A. flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, and *A. nidulans*. The invention thereby provides methods for the species-specific detection and diagnosis of *Aspergillus* infection in a subject. In addition, species probes have been developed for three *Fusarium*, four *Mucor*, two *Penicillium*, five *Rhizopus* and one *Rhizomucor* species, as well as probes for *Absidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (*Scedosporium apiospermum*), and *Sporothrix schenckii*. Generic probes for *Aspergillus*, *Fusarium*, and *Mucor* species have also been developed.

In one aspect the invention pertains to an isolated nucleic acid probe for identifying a species of *Aspergillus* wherein the probe selectively hybridizing under stringent conditions to the nucleic acid of *Aspergillus flavus* (SEQ ID NO:1), *Aspergillus fumigatus* (SEQ ID NO:2), *Aspergillus niger* (SEQ ID NO:3), *Aspergillus terreus* (SEQ ID NO:4), *Aspergillus nidulans* (SEQ ID NO:5), or a complementary sequence thereof.

Another aspect of the invention pertains to a method of detecting a species of *Aspergillus* in a sample comprising combining the sample with a nucleic acid probe capable of selectively hybridizing under stringent conditions with a nucleic acid of *Aspergillus flavus* (SEQ ID NO:1), *Aspergillus fumigatus*

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(SEQ ID NO:2), *Aspergillus niger* (SEQ ID NO:3), *Aspergillus terreus* (SEQ ID NO:4), *Aspergillus nidulans* (SEQ ID NO:5), or a complementary sequence thereof, the presence of hybridization indicating the detection of the species in the sample.

The method of detecting and the isolated nucleic probe is also related to hybridizing to the nucleic and of SEQ ID NO:58 or a complementary sequence thereof.

These and other aspects, 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.

Detailed Description of the Invention

This invention provides a simple, rapid, and useful method for differentiating filamentous fungal species from each other and from other medically important fungi. This invention enables a rapid, simple and useful method to isolate fungal DNA from host samples, and to apply the species- and genus-specific probes for the diagnosis of a disease. Ultimately, these probes can be used for *in situ* hybridization or *in situ* PCR diagnostics so that the morphology of host tissue, and microorganisms, remain intact.

The invention provides nucleic acids containing regions of specificity for five *Aspergillus*, three *Fusarium*, four *Mucor*, two *Penicillium*, five *Rhizopus* and one *Rhizomucor* species as well as probes for *Absidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (*Scedosporium apiospreum*), and *Sporothrix schenckii*. These nucleic acids are from the internal transcribed spacer 2 ("ITS2") region of ribosomal deoxyribonucleic

acid (rDNA) of the genome of the aforementioned filamentous fungi. The ITS2 region is located between the 5.8S rDNA region and the 28S rDNA region.

In particular, the invention provides nucleic acids from
 5 *Aspergillus flavus* (SEQ ID NO:1), *Aspergillus fumigatus* (SEQ ID NO:2),
Aspergillus niger (SEQ ID NO:3), *Aspergillus terreus* (SEQ ID NO:4),
Aspergillus nidulans (SEQ ID NO:5), *Fusarium solani* (SEQ ID NO:6),
Fusarium moniliforme (SEQ ID NO:7), *Mucor rouxii* (SEQ ID NO:8), *Mucor*
racemosus (SEQ ID NO:9), *Mucor plumbeus* (SEQ ID NO:10), *Mucor indicus*
 10 (SEQ ID NO:11), *Mucor circinilloides f. circinelloides* (SEQ ID NO:12),
Rhizopus oryzae (SEQ ID NO:13 and NO:14), *Rhizopus microsporus* (SEQ ID
 NO:15 and 16), *Rhizopus circinans* (SEQ ID NO:17 and 18), *Rhizopus*
stolonifer (SEQ ID NO: 19), *Rhizomucor pusillus* (SEQ ID NO:20), *Absidia*
corymbifera (SEQ ID NO:21 and 22), *Cunninghamella elegans* (SEQ ID
 15 NO:23), *Pseudallescheria boydii* (teleomorph of *Scedosporium apiospermum*)
 (SEQ ID NO:24, 25, 26, and 27), *Penicillium notatum* (SEQ ID NO:28), and
Sporothrix schenkii (SEQ ID NO:29). These sequences can be used to identify
 and distinguish the respective species of *Aspergillus*, *Fusarium*, *Mucor*,
Rhizopus, and *Penicillium*, and identify and distinguish these species from
 20 each other and from *Absidia corymbifera*, *Cunninghamella elegans*,
Pseudallescheria boydii(*Scedosporium apiospermum*), and *Sporothrix*
schenkii.

Furthermore, the invention provides isolated nucleic acid
 probes derived from GenBank nucleic acid sequences (for *Penicillium*
 25 *marneffei* and *Fusarium oxysporum* only) or from the above nucleic acid
 sequences which may be used as species-specific identifiers of *Aspergillus*
flavus (SEQ ID NO:30 and 31), *Aspergillus fumigatus* (SEQ ID NO:32),
Aspergillus niger (SEQ ID NO:33), *Aspergillus terreus* (SEQ ID NO:34),
Aspergillus nidulans (SEQ ID NO: 35), *Mucor rouxii* (SEQ ID NO:36),
 30 *Mucor plumbeus* (SEQ ID NO:37), *Mucor indicus* (SEQ ID NO:38), *Mucor*
circinilloides f. circinelloides (SEQ ID NO:39), *Mucor racemosus* (SEQ ID
 NO:40), *Rhizopus oryzae* (SEQ ID NO:41), *Rhizopus circinans* (SEQ ID
 NO:42), *Rhizomucor pusillus* (SEQ ID NO:43), *Rhizopus stolonifer* (SEQ ID
 NO:44), *Pseudallescheria boydii* (*Scedosporium apiospermum*)(SEQ ID
 35 NO:45), *Penicillium notatum* (SEQ ID NO:46), *Penicillium marneffei* (SEQ
 ID NO:47 and 48), *Fusarium moniliforme* (SEQ ID NO:49), *Fusarium*
oxysporum (SEQ ID NO:50), *Fusarium solani* (SEQ ID NO:51),

Cunninghamella elegans (SEQ ID NO: 52, 53, and 54), *Absidia corymbifera* (SEQ ID NO:55), *Sporothrix schenkii* (SEQ ID NO:56), and *Rhizopus microsporus* (SEQ ID NO:57). Such probes can be used to selectively hybridize with samples containing nucleic acids from species of *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus* (or *Rhizomucor*), *Penicillium*, or from *Absidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (*Scedosporium apiospermum*), and *Sporothrix schenkii*. These fungi can be detected after polymerase chain reaction or ligase chain reaction amplification of fungal DNA and specific probing of amplified DNA with DNA probes labeled with digoxigenin, reacted with anti-digoxigenin antibodies labeled with horseradish peroxidase and a colorimetric substrate, for example. Additional probes can routinely be derived from the sequences given in SEQ ID NOs:1-29, which are specific for the respective species. Therefore, the probes shown in SEQ ID NOs:30-57 are only provided as examples of the species-specific probes that can be derived from SEQ ID NOs:1-29.

Generic probes for *Aspergillus* (SEQ ID NO:58), *Fusarium*, (SEQ ID NO:59) and *Mucor* (SEQ ID NO:60) species have also been developed to identify all members of their respective species which are listed above as well as an all-fungus biotinylated probe (SEQ ID NO:61) to capture all species-specific and generic probes listed above for their detection.

By "isolated" is meant nucleic acid free from at least some of the components with which it naturally occurs. By "selective" or "selectively" is meant a sequence which does not hybridize with other nucleic acids to prevent adequate determination of an *Aspergillus*, *Fusarium*, *Mucor*, *Penicillium*, *Rhizopus* or *Rhizomucor* genus or species or of *Absidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (*Scedosporium apiospermum*), or *Sporothrix schenckii* species.

The hybridizing nucleic acid should have at least 70% complementarity with the segment of the nucleic acid to which it hybridizes. As used herein to describe nucleic acids, the term "selectively hybridizes" excludes the occasional randomly hybridizing nucleic acids and thus has the same meaning as "specifically hybridizing". 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.

The invention contemplates sequences, probes and primers which selectively hybridize to 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 or genus-specific hybridization capability is maintained. By "probe" is meant nucleic acid sequences that can be used as probes or primers for selective hybridization with complementary nucleic acid sequences for their detection or amplification, which probes can vary in length from about 5 to 100 nucleotides, or preferably from about 10 to 50 nucleotides, or most preferably about 18 nucleotides. The invention provides isolated nucleic acids 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, Maniatis (26).*

If used as primers, the invention 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, target region can range between 70% complementary bases and full complementarity and still hybridize under stringent conditions. For example, for the purpose of diagnosing the presence of the *Aspergillus*, the degree of complementarity between the hybridizing nucleic acid (probe or primer) and the sequence to which it hybridizes (e.g., *Aspergillus* DNA from a sample) is at least enough to distinguish hybridization with a nucleic acid from other yeasts and filamentous fungi. The invention provides examples of nucleic acids unique to each filamentous fungus 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.

Alternatively, the nucleic acid probes can be designed to have homology with nucleotide sequences present in more than one species of the fungi listed above. Such a nucleic acid probe can be used to selectively identify a group of species such as the generic probes listed for *Aspergillus* (SEQ ID NO:58), *Fusarium* (SEQ ID NO:59), and *Mucor* (SEQ ID NO:60) as well as all fungi listed (SEQ ID NO:61). Additionally, the invention provides that the nucleic acids can be used to differentiate the filamentous fungi listed in general from other filamentous fungi and yeasts, such as *Candida* species. Such a determination is clinically significant, since therapies for these infections differ.

The invention further provides methods of using the nucleic acids to detect and identify the presence of the filamentous fungi listed, or

particular species thereof. The method involves the steps of obtaining a sample suspected of containing filamentous fungi. The sample may be taken from an individual, such as blood, saliva, lung lavage fluids, vaginal mucosa, tissues, etc., or taken from the environment. The filamentous fungal cells can then be lysed, and the DNA extracted and precipitated. The DNA is preferably amplified using universal primers derived from the internal transcribed spacer regions, 18S, 5.8S and 28S regions of the filamentous fungal rDNA. Examples of such universal primers are shown below as ITS1 (SEQ ID NO: 62), ITS3 (SEQ ID NO: 63), ITS4 (SEQ ID NO: 64). Detection of filamentous fungal DNA is achieved by hybridizing the amplified DNA with a species-specific probe that selectively hybridizes with the DNA. Detection of hybridization is indicative of the presence of the particular genus (for generic probes) or species (for species probes) of filamentous fungus.

Preferably, detection of nucleic acid (e.g. probes or primers) hybridization can be facilitated by the use of detectable moieties. For example, the species-specific or generic probes can be labeled with digoxigenin, and an all-fungus probe, such as described in SEQ ID NO:61, can be labeled with biotin and used in a streptavidin-coated microtiter plate assay. Other detectable moieties include radioactive labeling, enzyme labeling, and fluorescent labeling, for example.

The invention further contemplates a kit containing one or more species-specific probes, which can be used for the detection of particular filamentous fungal species and genera in a sample. Such a kit can also contain the appropriate reagents for hybridizing the probe to the sample and detecting bound probe. The invention may be further demonstrated by the following non-limiting examples.

Examples

In this example, PCR assay employing universal, fungus-specific primers and a simple, rapid EIA-based format for amplicon detection were used.

Extraction of Filamentous Fungal DNA

A mechanical disruption method was used to obtain DNA from filamentous fungal species and an enzymatic disruption method described previously (13) was used to obtain DNA from yeasts. Filamentous fungi were grown for 4 to 5 days on Sabouraud dextrose agar slants (BBL,

division of Becton Dickinson, Cockeysville, MD) at 35°C. Two slants were then washed by vigorously pipeting 5 mls of 0.01 M potassium phosphate buffered saline (PBS) onto the surface of each slant and the washes were transferred to 500 ml Erlenmeyer flasks containing 250 ml of Sabouraud dextrose broth (BBL). Flasks were then incubated for 4 to 5 days on a rotary shaker (140 rpm) at ambient temperature. Growth was then harvested by vacuum filtration through a sterile Whatman #1 filter paper which had been placed into a sterile Buchner funnel attached to a 2 L side-arm flask. The resultant cellular mat was washed on the filtration apparatus three times with sterile distilled water, removed from the filter paper by gentle scraping with a rubber policeman, and placed into a sterile Petri plate which was then sealed with parafilm and frozen at -20°C until used.

Just prior to use, a portion of the frozen cellular mat, equal in size to a quarter, was removed and placed into a cold mortar (6" diameter). Liquid nitrogen was added to cover the mat which was then ground into a powder with a pestle. Additional liquid nitrogen was added as needed to keep the mat frozen during grinding.

DNA was then purified using proteinase K and RNase treatment, multiple phenol extractions, and ethanol precipitation by conventional means (26).

PCR amplification

The fungus-specific, universal primer pair ITS3 (5'-GCA TCG ATG AAG AAC GCA GC-3') (SEQ ID NO: 63) and ITS4 (5'-TCC TCC GCT TAT TGA TAT GC-3') (SEQ ID NO: 64) was used to amplify a portion of the 5.8S rDNA region, the entire ITS2 region, and a portion of the 28S rDNA region for each species as previously described (13, 34). DNA sequencing used this primer pair and also the fungus-specific, universal primer pair ITS1 (5'-TCC GTA GGT GAA CCT GCG G-3') (SEQ ID NO: 62) and ITS4 to amplify a portion of the 18S rDNA region, the entire 5.8S region, the entire ITS1 and ITS2 regions, and a portion of the 28S rDNA region.

A DNA reagent kit (TaKaRa Biomedicals, Shiga, Japan) was used for PCR amplification of genomic DNA. PCR was performed using 2 µl of test sample in a total PCR reaction volume of 100 µl consisting of 10 µl of 10X Ex Taq buffer, 2.5 mM each of dATP, dGTP, dCTP, and dTTP, in 8 µl, 0.2 µM of each primer, and 0.5 U of TaKaRa Ex Taq DNA polymerase.

Thirty cycles of amplification were performed in a Perkin-Elmer 9600 thermal cycler (Emeryville, CA) after initial denaturation of DNA at 95°C for 5 minutes. Each cycle consisted of a denaturation step at 95°C for 30 seconds, an annealing step at 58°C for 30 seconds, and an extension step at 72°C for 1 minute. A final extension at 72°C for 5 minutes followed the last cycle. After amplification, samples were stored at -20°C until used.

Table 1
Synthetic Universal Oligonucleotides Used in PCR and Hybridization Analyses

Primers or Probes	Nucleotide Sequence (5' to 3')	Chemistry and Location
ITS3	GCA TCG ATG AAG AAC GCA GC (SEQ ID NO:63)	5.8S rDNA universal 5' primer
ITS4	TCC TCC GCT TAT TGA TAT GC (SEQ ID NO:64)	28S rDNA universal 3' primer
ITS1	TCC GTA GGT GAA CCT GCG G (SEQ ID NO:62)	18S rDNA universal 5' primer

DNA sequencing

Primary DNA amplifications were conducted as described above. The aqueous phase of the primary PCR reaction was purified using QIAquick Spin Columns (Quiagen, Chatsworth, CA). DNA was eluted from each column with 50 µl of heat-sterilized Tris-EDTA buffer (10 mM Tris, 1 mM EDTA, pH 8.0).

Purified DNA was labeled using a dye terminator cycle sequencing kit (ABI PRISM, Perkin Elmer, Foster City, CA). One mix was made for each of the primers so that sequencing could be performed in both the forward and reverse directions. The reaction volume (20 µl) contained 9.5 µl Terminator Premix, 2 µl (1 ng) DNA template, 1 µl primer (3.2 pmol) and 7.5 µl heat-sterilized distilled H₂O. The mixture was then placed into a pre-heated (96°C) Perkin Elmer 9600 thermal cycler for 25 cycles of 96°C

for 10 seconds, 50°C for 5 seconds, 60°C for 4 minutes. The PCR product was then purified before sequencing using CentriSep spin columns (Princeton Separations, Adelphia, NJ). DNA was then vacuum dried, resuspended in 6 µl of formamide-EDTA (5 µl deionized formamide plus 1 µl 50 mM EDTA, pH 8.0), and denatured for 2 min at 90°C prior to sequencing using an automated capillary DNA sequencer (ABI Systems, Model 373, Bethesda, MD).

The sequencing results were as follows:

Aspergillus flavus 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.

GCTGCCCATC AAGCACGGC TTGTGTGTTG GGTCGTCGTC
CCCTCTCCGG GGGGGACGGG CCCCAAAGGC AGCGGCGGCA
CCGCGTCCGA TCCTCGAGCG TATGGGGCTT TGTCACCCGC
TCTGTAGGCC CGGCCGGCGC TTGCCGAACG CAAATCAATC
TTTTTCCAGG TTGACCTCGG ATCAGGTAGG GATACCCGCT
GAACTTCAA (SEQ ID NO:1)

Aspergillus fumigatus 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.

AAACTTTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA
AGAACGCAGC GAAATGCGAT AACTAATGTG AATTGCAGAA
TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC
CTGGTATTCC GGGGGGCGATG CCTGTCCGAG CGTCATTGCT
GCCCATCAAG CACGGCTTGT GTGTTGGGCC CCCGTCCCCC
TCTCCCGGGG GACGGGCCCCG AAAGGCAGCG GCGGCACCGC
GTCCGGTCCT CGAGCGTATG GGGCTTGTCA CCTGCTCTGT
AGGCCCGGCC GGCGCCAGCC GACACCCAAC TTTATTTTTC
TAAGGTTGAC CTCGGATCAG GTAGGGATAC CCGCTGAACT TAAA
(SEQ ID NO:2)

Aspergillus niger 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.

AAACTTTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA
AGAACGCAGC GAAATGCGAT AACTAATGTG AATTGCAGAA

TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC
 CTGGTATTCC GGGGGGGCATG CCTGTCCGAG CGTCATTGCT
 GCCCTCAAGC ACGGCTTGTG TGTTGGGTCG CCGTCCCCCT
 CTCCCGGGGGG ACGGGCCCGA AAGGCAGCGG CGGCACCGCG
 5 TCCGATCCTC GAGCGTATGG GGCTTTGTCA CCTGCTCTGT
 AGGCCCGGCC GGCGCCTGCC GACGTTATCC AACCATTTT
 TTCCAGGTTG ACCTCGGATC AGGTAGGGAT ACCCGCTGAA CTAA
 (SEQ ID NO:3)

10 *Aspergillus terreus* 5.8S ribosomal RNA gene, partial sequence, internal
 transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial
 sequence.

AAAC TTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA
 AGAACGCAGC GAAATGCGAT AACTAATGTG AATTGCAGAA
 15 TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC
 CTGGTATTCC GGGGGGGCAT GCCTGTCCGA GCGTCATTGC
 TGCCCTCAAG CCCGGCTTGT GTGTTGGGCC CTCGTCCCCC
 GGCTCCCGGG GGACGGGGCC GAAAGGCAGC GGCGGCACCG
 CGTCCGGTCC TCGAGCGTAT GGGGCTTCGT CTTCCGCTCC
 20 GTAGGCCCGG CCGGCGCCCG CCGAACGCAT TTATTGCAA
 CTTGTTTTTT TTTCCAGGTT GACCTCGGAT CAGGT (SEQ
 ID NO:4)

25 *Aspergillus nidulans* 5.8S ribosomal RNA gene, partial sequence, internal
 transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial
 sequence.

AAAC TTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA
 AGAACGCAGC GAACTGCGAT AAGTAATGTG AATTGCAGAA
 TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC
 30 CTGGCATTCC GGGGGGGCAT CCTGTCCGAG CGTCATTGCT
 GCCCTCAAGC CCGGCTTGTG TGTTGGGTCG TCGTCCCCC
 CCCCGGGGGA CGGGCCCGAA AGGCAGCGGC GGCACCGGTC
 CGGTCCTCGA GCGTATGGGG CTTGGTCACC CGCTCGATTA
 GGGCCGGCCG GGCGCCAGCC GGCGTCTCCA ACCTTATCTT
 35 TCTCAGGTTG ACCTCGGATC AGGTAGGGAT ACCCGCTGAA CTAA
 (SEQ ID NO:5)

Fusarium solani (strain ATCC62877) internal transcribed spacer 2 and adjacent regions.

5 GAAAATGCGA TAAGTAATGT GAATTGCAGA ATTCAGTGAA
TCATCGAATC TTTGAACGCA CATTGCGCCC GCCAGTATTC
TGGCGGGGCAT GCCTGTTCGA GCGTCATTAC AACCCTCAGG
CCCCCGGGCC TGGCGTTGGG GATCGGCGGA AGCCCCCTGC
GGGCACAACG CCGTCCCCCA AATACAGTGG CGGTCCCGCC
GCAGCTTCCA TTGCGTAGTA GCTAACACCT CGCAACTGGA
GAGCGGCGCG GCCACGCCGT AAAACACCCA ACTTCTGAAT
10 GTTGACCTCG AATCAGGTAG GAATACCCGC TGA ACTTAA (SEQ ID
NO:6)

Fusarium moniliforme (strain ATCC38519) internal transcribed spacer 2 and adjacent regions.

15 AAATGCGATA AGTAATGTGA ATTGCAAAAT TCAGTGAATC
ATCGAATCTT TGAACGCACA TTGCGCCCGC CAGTATTCTG
GCGGGGCATGC CTGTTCGAGC GTCATTTCAA CCCTCAAGCC
CCCGGGTTTG GTGTTGGGGA TCGGCAAGCC CTTGCGGCAA
GCCGGCCCCG AAATCTAGTG GCGGTCTCGC TGCAGCTTCC
20 ATTGCGTAGT AGTAAAACCC TCGCAACTGG TACGCGGCGC
GGCCAAGCCG TTAAACCCCC AACTTCTGAA TGTTGACCTC
GGATCAGGTA GGAATACCCG CTGAACTTAA (SEQ ID NO:7)

Mucor rouxii (strain ATCC24905) internal transcribed spacer 2 and adjacent regions.

25 AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC
ATCGAGTCTT TGAACGCAAC TTGCGCTCAT TGGTATTCCA
ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC
CAGCATTTTG TTGAATAGGA AACTGAGAG TCTCTTGATC
30 TATTCTGATC TCGAACCTCT TGAAATGTAC AAAGGCCTGA
TCTTGTTTAA ATGCCTGAAC TTTTTTTTAA TATAAAGAGA
AGCTCTTGCG GTAAACTGTG CTGGGGCCTC CCAAATAATA
CTCTTTTAA ATTTGATCTG AAATCAGGCG GGATTACCCG
CTGAACTTAA (SEQ ID NO:8)

35 *Mucor racemosus* (strain ATCC22365) internal transcribed spacer 2 and adjacent regions.

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC
 ATCGAGTCTT TGAACGCAAC TTGCGCTCAT TGGTATTCCA
 ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC
 CAACTTTTGT TGTATAGGAT TATTGGGGGC CTCTCGATCT
 5 GTATAGATCT TGAAATCCCT GAAATTTACT AAGGCCTGAA
 CTTGTTTAAA TGCCTGAACT TTTTTTTAAT ATAAAGGAAA
 GCTCTTGTA TTTGACTTTGA TGGGGCCTCC CAAATAAATC
 TCTTTTAAAT TTGATCTGAA ATCAGGCGGG ATTACCCGCT
 GAACTTAA (SEQ ID NO:9)

10

Mucor plumbeus (strain ATCC4740) internal transcribed spacer 2 and adjacent regions.

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC
 ATCGAGTCTT TGAACGCAAC TTGCGCTCAT TGGTATTCCA
 15 ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC
 CAACTTTTGT TGTATAGGAT TATTGGGGGC CTCTCGATCT
 GTATAGATCT TGAAACCCTT GAAATTTACT AAGGCCTGAA
 CTTGTTTAAAT GCCTGAACTT TTTTTTAATA TAAAGGAAAG
 CTCTTGTAAT TGACTTTGAT GGGGCCTCCC AAATAAATCT
 20 TTTTTAAATT TGATCTGAAA TCAGGTGGGA TTACCCGCTG
 AACTTAA (SEQ ID NO:10)

Mucor indicus (strain ATCC4857) internal transcribed spacer 2 and adjacent regions.

25 AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC
 ATCGAGTCTT TGAACGCATC TTGCACTCAA TGGTATTCCA
 TTGAGTACGC CTGTTTCAGT ATCAAAAAC AACCTTATT
 CAAAATTCTT TTTTTGAATA GATATGAGTG TAGCAACCTT
 ACAAGTTGAG ACATTTTAAA TAAAGTCAGG CCATATCGTG
 30 GATTGAGTGC CGATACTTTT TTAATTTTGA AAAGGTAAAG
 CATGTTGATG TCCGCTTTTT GGGCCTCCCA AATAACTTTT
 TAAACTTGAT CTGAAATCAG GTGGGATTAC CCGCTGAACT
 TAA (SEQ ID NO:11)

35

Mucor circinelloides f. circinelloides (strain ATCC1209B) internal transcribed spacer 2 and adjacent regions.

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC
 ATCGAGTCTT TGAACGCAAC TTGCGCTCAT TGGTATTCCA
 ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC
 CAACATTTTT GTTGAATAGG ATGACTGAGA GTCTCTTGAT
 5 CTATTCTGAT CTCGAAGCTC TTGAAATGTA CAAAGGCCTG
 ATCTTGTTTG AATGCCTGAA CTTTTTTTTTA ATATAAAGAG
 AAGCTCTTGC GGTAAACTGT GCTGGGGCCT CCCAAATAAC
 ACATCTTTAA ATTTGATCTG AAATCAGGT GGGACTACCC
 GCTGAACTT AA (SEQ ID NO:12)

10

Rhizopus oryzae (strain ATCC34965) internal transcribed spacer 2 and adjacent regions.

15

AGTGCGATAA CTAGTGTGAA TTGCATATTC AGTGAATCAT
 CGAGTCTTTG AACGCAGCTT GCACTCTATG GTTTTTCTAT
 AGAGTACGCC TGCTTCAGTA TCATCACAAA CCCACACATA
 ACATTTGTTT ATGTGGTGAT GGGTCGCATC GCTGTTTTAT
 TACAGTGAGC ACCTAAAATG TGTGTGATTT TCTGTCTGGC
 TTGCTAGGCA GGAATATTAC GCTGGTCTCA GGATCTTTTT
 TTTTGGTTTCG CCCAGGAAGT AAAGTACAAG AGTATAATCC
 20 AGTAACTTTC AAACATATGAT CTGAAGTCAG GTGGGATTAC
 CCGCTGAACT TAA (SEQ ID NO:13)

Rhizopus oryzae (strain ATCC11886) internal transcribed spacer 2 and adjacent regions.

25

30

AGTGCGATAA CTAGTGTGAA TTGCATATTC AGTGAATCAT
 CGAGTCTTTG AACGCAGCTT GCACTCTATG GTTTTTCTAT
 AGAGTACGCC TGCTTCAGTA TCATCACAAA CCCACACATA
 ACATTTGTTT ATGTGGTAAT GGGTCGCATC GCTGTTTTAT
 TACAGTGAGC ACCTAAAATG TGTGTGATTT TCTGTCTGGC
 TTGCTAGGCA GGAATATTAC GCTGGTCTCA GGATCTTTTT
 CTTTGGTTTCG CCCAGGAAGT AAAGTACAAG AGTATAATCC
 AGCAACTTTC AAACATATGAT CTGAAGTCAG GTGGGATTAC
 CCGCTGAACT TAA (SEQ ID NO:14)

35

Rhizopus microsporus (strain ATCC14056) internal transcribed spacer 2 and adjacent regions.

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCGTGAATCA
TCGAGTCTTT GAACGCAGCT TGC ACTCTAT GGATCTTCTA
TAGAGTACGC TTGCTTCAGT ATCATAACCA ACCCACACAT
AAAATTTATT TTATGTGGTG ATGGACAAGC TCGGTTAAAT
5 TTAATTATTA TACCGATTGT CTAAAATACA GCCTCTTTGT
AATTTTCATT AAATTACGAA CTACCTAGCC ATCGTGCTTT
TTTGGTCCAA CCAAAAAACA TATAATCTAG GGGTTCTGCT
AGCCAGCAGA TATTTTAATG ATCTTTAACT ATGATCTGAA
GTCAAGTGGG ACTACCCGCT GAACTTAA (SEQ ID NO:15)

10

Rhizopus microsporus (strain ATCC12276) internal transcribed spacer 2 and adjacent regions.

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCGTGAATCA
TCGAGTCTTT GAACGCAGCT TGC ACTCTAT GGATCTTCTA
15 TAGAGTACGC TTGCTTCAGT ATCATAACCA ACCCACACAT
AAAATTTATT TTATGTGGTG ATGGACAAGC TCGGTTAAAT
TTAATTATTA TACCGATTGT CTAAAATACA GCCTCTTTGT
AATTTTCATT AAATTACGAA CTACCTAGCC ATCGTGCTTT
TTTGGTCCAA CCAAAAAACA TATAATCTAG GGGTTCTGCT
20 AGCCAGCAAA TATTTTAATG ATCTTTAACC TATGATCTGA
AGTCAAGTGG GACTACCCGC TGA ACTTAA (SEQ ID NO:16)

Rhizopus circinans (strain ATCC34106) internal transcribed spacer 2 and adjacent regions.

AAATTGCGAT AACTAGTGTG AATTGCATTT TCAGTGAATC
ATCGAGTCTT TGAACGCAT CTTGCGCTCT TGGGATTCTT
CCCTAGAGCA CACTTGCTTC AGTATCATAA CAAAACCCTC
ACCTAATATT TTTTTTTTTT AAAAAAAAAA TATTAGAGTG
GTATTGGGGT CTCTTTGGTA ATTCTTTGTA ATTATAAAG
30 TACCCTTAAA TGTCATAAAC AGGTTAGCTT TAGCTTGCCT
TTAAAGATCT TCTTAGGGTA TCATTACTTT TCGTAAATCT
TTAATAGGCC TGTCACATAA TTCTACCCTT AAATTTCTTA
AACCTTGATC TGAAGTCAAG TGGGAGTACC CGCTGAACTT AA
(SEQ ID NO:17)

35

Rhizopus circinans (strain ATCC34101) internal transcribed spacer 2 and adjacent regions.

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5  AAATTGCGAT  AACTAGTGTG  AATTGCATTT  TCAGTGAATC
   ATCGAGTCTT  TGAACGCATC  TTGCGCTCTT  GGGATTCTTC
   CCTAGAGCAC  ACTTGCTTCA  GTATCATAAC  AAAACCCTCA
   CCTAATATTT  TTTTTTAAAA  AAAAAAAAAATA  TTAGAGTGGT
   ATTGGGGTCT  CTTTGGTAAT  TCTTTGTAAT  TATAAAAGTA
   CCCTTAAATG  TCATAAACAG  GTTAGCTTTA  GCTTGCCTTT
   AAAGATCTTC  TTAGGGTATC  ATTACTTTTC  GTAAATCTTT
10  AATAGGCCTG  TCACATAATT  CTACCCTTAA  ATTTCTTAAA
   CCTTGATCTG  AAGTCAAGTG  GGAGTACCCG  CTGAACTTAA (SEQ
   ID NO:18)

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15 *Rhizous stolonifer* (strains ATCC14037 and 6227A) internal transcribed spacer 2 and adjacent regions.

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   AAAGTGCGAT  AACTAGTGTG  AATTGCATAT  TCAGTGAATC
   ATCGAGTCTT  TGAACGCAAC  TTGCACTCTA  TGGTTTTCCG
   TAAAGTACGC  TTGCTTCAGT  ATCATAAAGA  CCCCATCCTG
   ATTATTATTT  TTTTATTAAA  ATAATTAATT  TTGGAGATAA
20  TAAAAATGAG  GCTCTTTCTT  TTCTTTTTTT  TTTTTTTAAA
   AAAAAGGGGG  GGAAAGGGTC  TTTTAAAATG  GGCAAATTCT
   GGGTTTTTTA  CTAAACCTGA  ACTCCCCCCA  AAAATTCAAA
   AAAAAAAAAA  TGGGTTTTAC  CAAATTTTTT  TTTTTTTTCT
   CCTTTTTGTG  TAGTTAATAC  TCTATTAAAT  TTATTTACTT
25  GGTATTATAA  CGATTATGCA  AGAAGGGAGA  GAACAAAGAA
   TAATGAAAGA  GAGTTTTTAA  ATAAATTCTT  TTTTCATTTT
   TTCAATCAAT  GATCTGAAGT  CAAGTGGGAT  TACCCGCTGA
   ACTTAA (SEQ ID NO:19)

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30 *Rhizomucor pusillus* (strain ATCC36606) internal transcribed spacer 2 and adjacent regions.

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   AAATTGCGAA  AAGTAATGCG  ATCTGCAGCC  TTTGCGAATC
   ATCGAATTCT  CGAACGCACC  TTGCACCCTT  TGGTTCATCC
   ATTGGGTACG  TCTAGTTCAG  TATCTTTATT  AACCCCTAAA
35  GGTTTATTTT  TTGATAAATC  TTTGGATTGT  CGGTGCTGAT
   GGATTTTCAT  CCGTTCAAGC  TACCCGAACA  ATTTGTATGT
   TGTTGACCCT  TCAATATTCC  TTGAGGGGCT  GCATTGGTAT

```

CTAATTTTTT ACCAGTGTGC TTCGAGATGA TCAAGTATAA
 AGGTCAATCA ACCACAAATA AATTTCAACT ATGGATCTGA
 ACTTAGATGG GATTACCCGC TGA ACTTAA (SEQ ID NO:20)

5 *Absidia corymbifera* (strain ATCC46774) internal transcribed spacer 2 and adjacent regions.

AAAGTGCGAT AATTATTGCG ACTTGCATTC ATAGCGAATC
 ATCGAGTTCT CGAACGCATC TTGCGCCTAG TAGTCAATCT
 ACTAGGCACA GTTGTTTCAG TATCTGCAAC TACCAATCAG
 10 TTCAACTTGG TTCTTTGAAC CTAAGCGAGC TGGAAATGGG
 CTTGTGTTGA TGGCATTTCAG TTGCTGTCAT GGCCTTAAAT
 ACATTTAGTC CTAGGCAATT GGCTTTAGTC ATTTGCCGGA
 TGTAGACTCT AGAGTGCCTG AGGAGCAACG ACTTGGTTAG
 TGAGTTCATA ATTCCAAGTC AATCAGTCTC TTCTTGA ACT
 15 AGGTCTTAAT CTTTATGGAC TAGTGAGAGG ATCTAACTTG
 GGTCTTCTCT TAAAACAAAC TCACATCTAG ATCTGAAATC
 AACTGAGATC ACCCGCTGAA CTAA (SEQ ID NO:21)

20 *Absidia corymbifera* (strain ATCC46773) internal transcribed spacer 2 and adjacent regions.

AAAGTGCGAT AATTATTGCG ACTTGCATTC ATAGTGAATC
 ATCGAGTTCT TGAACGCATC TTGCGCCTAG TAGTCAATCT
 ACTAGGCACA GTTGTTTCAG TATCTGCATC CACCAATCAA
 CTTAACCTTT TGTGTTGAGT TGGAACTGGG CTTCTAGTTG
 25 ATGGCATTTA GTTGCTGTCA TGGCCTTAAA TCAATGTCCT
 AGGTGTTAGA ACATCTAACA CCGGATGGAA ACTTTAGAGC
 GCTTTAAGAG CAGCTTGGTT AGTGAGTTCA ATAATTCCAA
 GCATTAAGTC TTTTAATGAA CTAGCTTTTC TATCTATGGG
 ACACTACTTG GAGAAATCCA AGTAACCTTT AA ACTCCCAT
 30 TTAGATCTGA AATCAACTGA GACCACCCGC TGA ACTTAA (SEQ ID NO:22)

Cunninghamella elegans (strain ATCC42113) internal transcribed spacer 2 and adjacent regions.

35 AAATCGCGAT ATGTAATGTG ACTGCCTATA GTGAATCATC
 AAATCTTTGA AACGCATCTT GCACCTTATG GTATTCCATA
 AGGTACGTCT GTTTCAGTAC CACTAATAAA TCTCTCTCTA

TCCTTGATGA TAGAAAAAAA AAAAATAATT TTTACTGGGC
 CCGGGGAATC CTTTTTTTTT TTTAATAAAA AGGACCAATT
 TTGGCCCAA AAAAAGGGTT GAACTTTTTT TACCAGATCT
 TGCATCTAGT AAAAACCTAG TCGGCTTTAA TAGATTTTAA
 5 TTTTCTATTA AGTTTATAGC CATTCTTATA TTTTAA
 TCTTGGCCTG AAATCAGATG GGATACCCGC TGA ACTTAA (SEQ ID
 NO:23)

10 *Pseudallescheria boydii* (strain ATCC44328) internal transcribed spacer 2 and
 adjacent regions (teleomorph of *Scedosporium apiospermum*).

AAATGCGATA AGTAATGTAA ATTGCAAAAT TCAGTGAATC
 ATCGAATCTT TGAAACGCAC ATTGCGCCCG GCAGTAATCT
 GCCGGGCATG CCTGTCCGAG CGTCATTTC ACCCTCGAAC
 CTCCGTTTC CTTAGGGAAG CCTAGGGTCG GTGTTGGGGC
 15 GCTACGGCAA GTCCTCGCAA CCCCCGTAGG CCCTGAAATA
 CAGTGGCGGT CCCGCCGCGG TTGCCTTCTG CGTAGTAAGT
 CTCTTTTGCA AGCTCGCATT GGGTCCCGGC GGAGGCCTGC
 CGTCAAACCA CCTAACAACT CCAGATGGTT TGACCTCGGA
 TCAGGTAGGG TTACCCGCTG AACTTAA (SEQ ID NO:24)

20 *Pseudallescheria boydii* (strain ATCC36282) internal transcribed spacer 2 and
 adjacent regions (teleomorph of *Scedosporium apiospermum*).

GAAATGCGAT AAGTAATGTG AATTGCAGAA TTCAGTGAAT
 CATCGAATCT TTGAAACGCA CATTGCGCCC GGCAGTAATC
 25 TGCCGGGCAT GCCTGTCCGA GCGTCATTTC AACCTCGAA
 CCTCCGTTTC CTCAGGGAAG CTCAGGGTCG GTGTTGGGGC
 GCTACGGCAA GTCTTCGCAA CCCTCCGTAG GCCCTGAAAT
 ACAGTGGCGG TCCCGCCGCG GTTGCCTTCT GCGTAGAAGT
 CTCTTTTGCA AGCTCGCATT GGGTCCCGGC GGAGGCCTGC
 30 CGTCAAACCA CCTATAACTC CAAATGGTTT GACCTCGGAT
 CAGGTAGGGT TACCCGCTGA ACTTAA (SEQ ID NO:25)

35 *Scedosporium apiospermum* (strain ATCC64215) internal transcribed spacer 2
 and adjacent regions.

GAAATGCGAT AAGTAATGTG AATTGCAGAA TTCAGTGAATC
 ATCGAATCTT TGAACGCACA TTGCGCCCGG CAGTAATCTG
 CCGGGCATGC CTGTCCGAGC GTCATTTC AA CCCTCGAACC

5 TCCGTTTCCT CAGGGAAGCT CAGGGTCGGT GTTGGGGCGC
 TACGGCGAGT CTTCGCGACC CTCCGTAGGC CCTGAAATAC
 AGTGGCGGTC CCGCCGCGGT TGCCTTCTGC GTAGTAAGTC
 TCTTTTGCAA GCTCGCATTG GGTCCCGGCG GAGGCCTGCC
 GTCAAACCAC CTATAACTCC AGATGGTTTG ACCTCGGATC
 AGGTAGGTAC CCGCTGAACT TAA (SEQ ID NO:26)

Scedosporium apiospermum (strain ATCC46173) internal transcribed spacer 2 and adjacent regions.

10 AAATGCGATA AGTAATGTGA ATTGCAGAAT TCAGTGAATC
 ATCGAATCTT TGAACGCACA TTGCGCCCGG CAGTAATCTG
 CCGGGCATGC CTGTCCGAGC GTCATTTCAA CCCTCGAACC
 TCCGTTTCCT CAGGGAAGCT CAGGGTCGGT GTTGGGGCGC
 TACGGCGAGT CTTCGCGACC CTCCGTAGGC CCTGAAATAC
 15 AGTGGCGGTC CCGCCGCGGT TGCCTTCTGC GTAGTAAGTC
 TCTTTTGCAA GCTCGCATTG GGTCCCGGCG GAGGCCTGCC
 GTCAAACCAC CTATAACTCC AGATGGTTTG ACCTCGGATC
 AGGTAGGTAC CCGCTGAACT TAA (SEQ ID NO:27)

20 *Penicillium notatum* (strain ATCC10108) internal transcribed spacer 2 and adjacent regions.

AAATGCGATA CGTAATGTGA ATTGCAAATT CAGTGAATCA
 TCGAGTCTT TGAACGCACA TTGCGCCCCC TGGTATTCCG
 GGGGGCATGC CTGTCCGAGC GTCATTGCTG CCCTCAAGCA
 25 CGGCTTGTGT GTTGGGGCCCC GTCCTCCGAT CCCGGGGGAC
 GGGCCCGAAA GGCAGCGGCG GCACCGCGTC CGGTCCTCGA
 GCGTATGGGG CTTTGTCAACC CGCTCTGTAG GCCCGGCCGG
 CGCTTGCCGA TCAACCCAAA TTTTATCCA GGTTGACCTC
 GGATCAGGTA GGGATACCCG CTGAACTTAA (SEQ ID NO:28)

30

Sporothrix schenckii (strain ATCC14284) internal transcribed spacer 2 and adjacent regions.

GAAATGCGAT ACTAATGTGA ATTGCAGAAT TCAGCGAACC
 ATCGAATCTT TGAACGCACA TTGCGCCCGC CAGCATTCTG
 35 GCGGGCATGC CTGTCCGAGC GTCATTTCCC CCCTCACGCG
 CCCC GTTGCG CGCTGGTGTT GGGGCGCCCT CCGCCTGGCG
 GGGGGCCCC GAAAGCGAGT GGCGGGCCCT GTGGAAGGCT

CCGAGCGCAG TACCGAACGC ATGTTCTCCC CTCGCTCCGG
AGGCCCCCCA GGCGCCCTGC CGGTGAAAAC GCGCATGACG
CGCAGCTCTT TTTACAAGGT TGACCTCGGA TCAGGTGAGG
ATACCCGCTG ACTTAA (SEQ ID NO:29)

5

Contamination precautions

Precautions were taken to avoid possible contamination of PCR samples by following the guidelines of Fujita and Kwok (13, 22). All buffers and distilled water used for PCR assays were autoclaved and fresh PCR reagents were aliquoted prior to use. Physical separation of laboratory areas used to prepare PCR assays and to analyze PCR products, and the use of aerosol-resistant pipette tips, reduced possible cross-contamination of samples by aerosols. Appropriate negative controls were included in each test run, including controls omitting either the primer or the DNA template during PCR assays.

15

Agarose gel electrophoresis

Gel electrophoresis was conducted in TBE buffer (0.1 M Tris, 0.09 M boric acid, 1 mM EDTA, pH 8.4) at 80 V for 1 to 2 hours using gels composed of 1% (w/vol) agarose (International Technologies, New Haven, CT) and 1% (w/vol) NuSieve agar (FMC Bioproducts, Rockland, ME). Gels were stained with 0.5 µg of ethidium bromide (EtBr) per ml of distilled H₂O for 10 minutes followed by three serial washes for 10 minutes each with distilled H₂O.

25

Microtitration plate enzyme immunoassay for the detection of PCR products

Amplicons were detected using species-specific and genus probes labeled with digoxigenin and an all-filamentous fungal probe labeled with biotin in a streptavidin-coated microtiter plate format (13, 34). Ten µl of PCR product was added to each 1.5 ml Eppendorf tube. Single-stranded DNA was then prepared by heating the tubes at 95°C for 5 minutes and cooling immediately on ice. Two-tenths of a ml of hybridization solution [4x SSC (saline sodium citrate buffer, 0.6 M NaCl, 0.06 M trisodium citrate, pH 7.0) containing 20 mM Hepes, 2 mM EDTA, and 0.15% (vol/vol) TweenTM 20] supplemented with 50 ng/ml each of the all-*Aspergillus* biotinylated probe and a species-specific digoxigenin-labeled probe was added to each

35

5 tube containing denatured PCR product. Tubes were mixed by inversion and placed in a water bath at 37°C to allow probes to anneal to PCR product DNA. After 1 hour, 100 µl of each sample was added to duplicate wells of a commercially prepared streptavidin-coated microtitration plate (Boehringer Mannheim, Indianapolis, IN). The plate was incubated at ambient temperature for 1 hour with shaking, using a microtitration plate shaker (manufactured for Dynatech by CLTI, Middletown, NY). Plates were washed 6 times with 0.01 M potassium phosphate buffered saline, pH 7.2, containing 0.05% Tween 20 (PBST). Each well then received 100 µl of horseradish peroxidase-conjugated, anti-digoxigenin Fab fragment (Boehringer Mannheim) diluted 1:1000 in hybridization buffer. After incubation at ambient temperature for 30 minutes with shaking, the plate was washed 6 times with PBST. One hundred µl of a mixture of one volume of 3, 3', 5, 5'-tetramethyl benzidine peroxidase substrate (Kirkegaard and Perry Laboratories, Inc., Gaithersburg, MD) and one volume of peroxidase solution (Kirkegaard and Perry Laboratories) was added to each well and the plate was placed at ambient temperature for 10 minutes for color development. The A_{650nm} of each well was determined with a microtitration plate reader (UV Max, Molecular Devices, Inc., Menlo Park, CA). The absorbance value for the reagent blank, where DNA was absent but replaced with distilled H₂O, was subtracted from each test sample.

Statistical analysis

25 The Student's t test was used to determine differences between sample means. Means are expressed as the mean plus or minus the standard error from the mean. Differences were considered significant when P<0.05.

The following probes were used to detect and distinguish each species.

Table 2
Probe Sequences

PROBES	5' to 3' OLIGONUCLEOTIDE SEQUENCE	
Generic Biotin Probe	5' end-labeled biotinylated probe 5.8S region of rDNA	
B-58	GAA TCA TCG A(AG)T CTT TGA ACG	SEQ ID NO 61
Digoxigenin-probe	5' end-labeled digoxigenin probe ITS2 region of rDNA	
Aspergillus species		
A. flavus 22	GCA AAT CAA TCT TTT TCC	SEQ ID NO 30
A. flavus 23	GAA CGC AAA TCA ATC TTT	SEQ ID NO 31
A. fumigatus	CCG ACA CCC ATC TTT ATT	SEQ ID NO 32
A. niger	GAC GTT ATC CAA CCA TTT	SEQ ID NO 33
A. nidulans	GGC GTC TCC AAC CTT ATC	SEQ ID NO 35
A. terreus	GCA TTT ATT TGC AAC TTG	SEQ ID NO 34
Fusarium species		
F. moniliforme	TCT AGT GAC GGT CTC GCT	SEQ ID NO 49
F. oxysporum	CGT TAA TTC GCG TTC CTC	SEQ ID NO 50
F. solani	CTA ACA CCT CGC AAC TGG AGA	SEQ ID NO 51
Mucor species		
M. circinelloides	AAC ATT TTT GTG AAT AGG ATG	SEQ ID NO 39
M. indicus	CGT GGA TTG AGT GCC GAT	SEQ ID NO 38
M. plumbeus	GAA ACC CTT GAA ATT	SEQ ID NO 37
M. rouxii	GAA TAG GAA TAC TGA GAG	SEQ ID NO 36
M. racemosus	GAA ATC CCT GAA ATT	SEQ ID NO 40
Penicillium species		

Penicillium marneffeii 1	GGG TTG GTC ACC ACC ATA	SEQ ID NO 47
Penicillium marneffeii 2	TGG TCA CCA CCA TAT TTA	SEQ ID NO 48
Penicillium notatum	GAT CAA CCC AAA TTT TTA	SEQ ID NO 46
Rhizopus species		
R. circinans	CTT AGG GTA TCA TTA CTT	SEQ ID NO 42
R. microsporus	CAT ATA ATC TAG GGG TTC	SEQ ID NO 57
R. oryzae	GAG TAT AAT CCA G(CT)A ACT	SEQ ID NO 41
R. stolonifer	CTT GGT ATT ATA ACG ATT	SEQ ID NO 44
Rhizomucor pusillus	TCC TTG AGG GCT TGC ATT	SEQ ID NO 43
Other Genera		
Absidia corymbifera	GTT GCT GTC ATG GCC TTA	SEQ ID NO 55
Cunninghamella elegans 4	TAG TCG GCT TTA ATA GAT	SEQ ID NO 52
Cunninghamella elegans 5	TAT TAA GTT TAT AGC CAT	SEQ ID NO 53
Cunninghamella elegans 6	TAA GTT TAT AGC CAT TCT	SEQ ID NO 54
Pseudallescheria boydii	AAG TCT CTT TTG CAA GCT	SEQ ID NO 45
Sporothrix schoenckii	GAC GCG CAG CTC TTT TTA	SEQ ID NO 56
Genus Probes		
G-ASPERGILLUS	CCT CGA GCG TAT GGG GCT	SEQ ID NO 58
G-FUSARIUM	CCC AAC TTC TGA ATG TTG	SEQ ID NO 59
G-MUCOR	(AC)TG GGG CCT CCC AAA TAA	SEQ ID NO 60

Species-specific probes to the ITS2 region of rDNA for *Aspergillus fumigatus* (SEQ ID NO:32), *A. flavus* (SEQ ID NO:31), *A. niger* (SEQ ID NO:33), *A. terreus* (SEQ ID NO:34), and *A. nidulans* (SEQ ID NO:35) correctly identified each of the respective species ($P < 0.001$), and gave no false-positive reactions with *Rhizopus*, *Mucor*, *Fusarium*, *Penicillium*, or *Candida* species. The *A. flavus* probe also recognized *A. oryzae*, which belongs to the *A. flavus* group. Identification time was reduced from a mean of 5 days by conventional methods to 8 hours.

Table 3
Aspergillus Probes

Fungus	<i>A. fumigatus</i>	<i>A. nidulans</i>	<i>A. niger</i>	<i>A. terreus</i>	<i>A. flavus</i>
<i>A. fumigatus</i> (n=6)	2.197 ± 0.187	0.002	0.000	0.001	0.001
<i>A. nidulans</i> (n=3)	0.001	1.315 ± 0.464	0.002	0.000	0.001
<i>A. niger</i> (n=5)	0.000	0.000	1.242 ± 0.471	0.001	0.003
<i>A. terreus</i> (n=4)	0.001	0.000	0.001	1.603 ± 0.378	0.001
<i>A. flavus</i> (n=6)	0.001	0.001	0.000	0.001	2.043 ± 0.390
<i>A. oryzae</i> (n=2)	0.001	0.002	0.001	0.001	2.445 ± 0.106
<i>A. parasitica</i> (n=1)	0.001	0.002	0.002	0.002	0.051
<i>A. clavus</i> (n=1)	0.005	0.005	0.006	0.005	0.003
<i>C. albicans</i> (n=1)	0.002	0.001	0.002	0.000	0.000
<i>C. parasilosis</i> (n=1)	0.001	0.002	0.002	0.002	0.001
<i>C. glabrata</i> (n=1)	0.001	0.003	0.001	0.001	0.005

C.krusei (n=1)	0.002	0.002	0.002	0.001	0.001
C.tropicalis (n=1)	0.002	0.002	0.001	0.000	0.001
F.moniliforme (n=1)	0.003	0.003	0.001	0.001	0.001
F.solani (n=1)	0.006	0.002	0.001	0.000	0.001
R.oryzac (n=1)	0.001	0.001	0.001	0.001	0.001
M.racemosus (n=1)	0.001	0.002	0.005	0.002	0.000
P.notatum (n=1)	0.001	0.002	0.002	0.002	0.000
Avg±SD negative controls	0.001 ± 0.002	0.001 ± 0.001	0.000 ± 0.002	0.000 ± 0.002	0.002 ± 0.010

Species-specific probes to the ITS2 region of rDNA for *Fusarium oxysporum*, *F. solani*, and *F. moniliforme*, correctly identified each of the respective species ($P < 0.001$), and gave no false-positive reactions with *Blastomyces*, *Apophysomyces*, *Candida*, *Aspergillus*, *Mucor*, *Penicillium*, *Rhizopus*, *Rhizomucor*, *Absidia*, *Cunninghamella*, *Pseudallescheria*, *Sporothrix*, or *Neosartorya*. Empty boxes in Table 4 represent zero probe reactivity.

Table 4
Fusarium Probes

Fungus	F. oxysporum	F. solani	F. moniliforme	Generic Fusarium
F. oxysporum (n=3)	1.40 ± 0.13			1.76 ± 0.27
F. solani (n=5)		1.57 ± 0.07		1.35 ± 0.28

F. moniliforme (n=2)			1.40 ± 0.01	1.34 ± 0.91
Negative control				
Fungus	F. oxysporum	F. solani	F. moniliforme	Generic Fusarium
A.fumigatus				
A.flavus				
A.niger				
A.nidulans				
A.terreus				
A.parasiticus				
A.clavatus				
P.marneffei		0.01	0.01	
P.notatum	0.01	0.01	0.01	
Rhizopus oryzae		0.03	0.01	
Rhizopus microsporus		0.01	0.01	
Rhizopus circinans		0.01	0.01	
Rhizopus stolonifer		0.01	0.01	
Rhizomucor pusillus		0.03	0.02	
M. racemosus				
M. circinelloides				
M. rouxii				
M. plumbeus				
M. indicus				
Absidia corymbifera		0.01	0.01	
Cunninghamella elegans		0.01	0.02	
P. boydii			0.02	
Sporothrix schenckii		0.01	0.01	
C.albicans				
C.tropicalis				
C.krusei				
C.parasilosis				
C.glabrata				

Neosartorya fischeri		0.01		
Blastomyces dermatitidis				
Apophysomyces elegans				
Average of negative controls	0.001 $\pm$ 0.002	0.005 $\pm$ 0.01	0.004 $\pm$ 0.006	

Species-specific probes to various other zygomycetes are presented in Table 5, showing correct identification of each species and no false positives. The exceptions are that the *M. circinelloides* probe hybridized with the *M. rouxii* DNA and the *M. plumbeus* probe hybridized with the *M. racemosus* DNA. However, the *M. rouxii* probe did not hybridize with *M. circinelloides* DNA, nor did the *M. racemosus* probe hybridize with *M. plumbeus* DNA. Therefore, by a process of elimination, each species can be correctly identified. Empty boxes in Table 5 represent zero probe reactivity.

Table 5 *Zygomycetes* Probes

[illegible]

Table 5 Continued

Negative control	D- probes	RMIC	RCIR	RSTOL	RPUS	MRACE	MCIR	MRX	MPLUM	MIND	ABS	CUN
FUNGUS	RORY											
A.fumigatus									0.01	0.02		
A.flavus					0.01					0.05		
A.niger								0.01				
A.nidulans									0.01	0.01		
A.terreus	0.01											
A.parasiticus					0.01					0.03		
A.clavatus										0.02		
P.marneffeii		0.01										
P.notatum										0.03		
F.oxysporum								0.01				
F.solani												
F.moniliforme	0.01			0.01				0.01		0.01		
P.boydii	0.02											
Sporothrix schenckii												
C.albicans												
C.tropicalis												
C.krusei												
C.parasilosis												
C.glabrata												
Neosartorya fischeri		0.01										
Blastomyces dermatitidis												
Apophysomyces elegans												
Average	0.001 ± .004	0.001 ± 0.02	0.000 ± 0.0002	0.000 ±0.003	0.001 ±0.003	0.001 ± 0.002	0.001 ±0.002	0.001 ±0.003	0.003 ±0.005	0.005 ± 0.01	0.001 ±0.001	

Species-specific probes to various other fungi are presented in Table 6, showing correct identification of each species and no false positives. Empty boxes in Table 6 represent zero probe reactivity.

5

Table 6
Pseudallescheria and *Sporothrix* Probes

Fungus	P. boydii	P.marneffeii	P.notatum	Sporothrix schenckii
P. boydii (n=4)	1.65 ± 0.48			
P.marneffeii (n=3)	0.01	1.24 ± 0.12		
P.notatum (n=3)			1.93 ± 0.25	
Sporothrix schenckii (n=3)	0.01			1.94 ± 0.25
Negative control				
Fungus	P. boydii	P.marneffeii	P.notatum	Sporothrix schenckii
A.fumigatus	0.01			
A.flavus				
A.niger				
A.nidulans				
A.terreus				
A.parasiticus				
A.clavatus			0.11	
F.oxysporum		0.10		
F. solani		0.14		
F. moniliforme		0.08		
R. oryzae	0.01			
R. microsporus	0.01			
R. circinans	0.01			

R. stolonifer	0.01			
Rhizomucor pusilus				
M. racemosus		0.04		
M. circinelloides	0.01	0.09		
M. rouxii	0.01			
M. plumbeus		0.05		
M. indicus				
Absidia corymbifera	0.01			
Cunninghamella bertholletiae	0.01			
C.albicans				
C.tropicalis		0.02		
C.krusei				
C.parasilosis				
C.glabrata				
Neosatorya pseudofischeri		0.03		
Blastomyces dermatitidis	0.01			
Apophysomyces elegans	0.01			
Average Negative Controls	0.004 ± 0.002	0.013 ± 0.03	0.002 ± 0.019	0.001 ± 0.002

All of the references mentioned in this Specification may be referred to for further details.

5

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10

15

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37

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: The Government of the United, States of America .
.
- (ii) TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus
Species and Other Filamentous Fungi
- (iii) NUMBER OF SEQUENCES: 61
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Jones & Askew, LLP
 - (B) STREET: 2400 Monarch Tower
 - (C) CITY: Atlanta
 - (D) STATE: Georgia
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 30326
- (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: US 60/045,400
 - (B) FILING DATE: 02-MAY-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Warren, William L.
 - (B) REGISTRATION NUMBER: 36,714
 - (C) REFERENCE/DOCKET NUMBER: 03063-0341WP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (404) 949-2400
 - (B) TELEFAX: (404) 949-2499

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 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: Aspergillus flavus

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

GCTGCCCATC AAGCACGGCT TGTGTGTTGG GTCGTCGTCC CCTCTCCGGG GGGGACGGGC	60
CCCAAAGGCA GCGGCGGCAC CGCGTCCGAT CCTCGAGCGT ATGGGGCTTT GTCACCCGCT	120

38

CTGTAGGCCC GGCCGGCGCT TGCCGAACGC AAATCAATCT TTTTCCAGGT TGACCTCGGA 180
 TCAGGTAGGG ATACCCGCTG AACTTCAA 208

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 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: *Aspergillus fumigatus*

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

AAACTTTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA AGAACGCAGC GAAATGCGAT 60
 AACTAATGTG AATTGCAGAA TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC 120
 CTGGTATTCC GGGGGGCATG CCTGTCCGAG CGTCATTGCT GCCCATCAAG CACGGCTTGT 180
 GTGTTGGGCC CCCGTCCCCC TCTCCCGGGG GACGGGCCCC AAAGGCAGCG GCGGCACCGC 240
 GTCCGGTCCT CGAGCGTATG GGGCTTGTCA CCTGCTCTGT AGGCCCGGCC GCGGCCAGCC 300
 GACACCCAAC TTTATTTTTC TAAGGTTGAC CTCGGATCAG GTAGGGATAC CCGCTGAACT 360
 TAAA 364

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 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: *Aspergillus niger*

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

AAACTTTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA AGAACGCAGC GAAATGCGAT 60
 AACTAATGTG AATTGCAGAA TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC 120
 CTGGTATTCC GGGGGGCATG CCTGTCCGAG CGTCATTGCT GCCCTCAAGC ACGGCTTGTG 180
 TGTGTTGGGTCG CCGTCCCCCT CTCCCGGGGG ACGGGCCCCG AAGGCAGCGG CGGCACCGCG 240

39

TCCGATCCTC GAGCGTATGG GGCTTTGTCA CCTGCTCTGT AGGCCCGGCC GCGCCTGCC 300
 GACGTTATCC AACCATT TTTT TTCCAGGTTG ACCTCGGATC AGGTAGGGAT ACCCGCTGAA 360
 CTTAA 365

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 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: *Aspergillus terreus*

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

AAACTTTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA AGAACGCAGC GAAATGCGAT 60
 AACTAATGTG AATTGCAGAA TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC 120
 CTGGTATTCC GGGGGGGCAT GCCTGTCCGA GCGTCATTGC TGCCCTCAAG CCCGGCTTGT 180
 GTGTTGGGCC CTCGTCCCCC GGCTCCCGGG GGACGGGCCC GAAAGGCAGC GCGGGCACCG 240
 CGTCCGGTCC TCGAGCGTAT GGGGCTTCGT CTTCCGCTCC GTAGGCCCGG CCGGCGCCCC 300
 CCGAACGCAT TTATTGCAA CTTGTTTTTT TTTCCAGGTT GACCTCGGAT CAGGT 355

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 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: *Aspergillus nidulans*

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

AAACTTTCAA CAATGGATCT CTTGGTTCCG GCATCGATGA AGAACGCAGC GAACTGCGAT 60
 AAGTAATGTG AATTGCAGAA TTCAGTGAAT CATCGAGTCT TTGAACGCAC ATTGCGCCCC 120
 CTGGCATTCC GGGGGGCATG CCTGTCCGAG CGTCATTGCT GCCCTCAAGC CCGGCTTGTG 180
 TGTTGGGTCG TCGTCCCCC CCCCAGGGGA CGGGCCCGAA AGGCAGCGGC GGCACCGGTC 240

40

CGGTCCTCGA GCGTATGGGG CTTGGTCACC CGCTCGATTA GGGCCGGCCG GCGGCCAGCC	300
GGCGTCTCCA ACCTTATCTT TCTCAGGTTG ACCTCGGATC AGGTAGGGAT ACCCGCTGAA	360
CTTAA	365

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 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: *Fusarium solani*

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

GAAAATGCGA TAAGTAATGT GAATTGCAGA ATTCAGTGAA TCATCGAATC TTTGAACGCA	60
CATTGCGCCC GCCAGTATTC TGGCGGGCAT GCCTGTTCGA GCGTCATTAC AACCTCAGG	120
CCCCCGGGCC TGGCGTTGGG GATCGGCGGA AGCCCCCTGC GGGCACAACG CCGTCCCCCA	180
AATACAGTGG CGGTCCCGCC GCAGCTTCCA TTGCGTAGTA GCTAACACCT CGCAACTGGA	240
GAGCGGCGCG GCCACGCCGT AAAACACCCA ACTTCTGAAT GTTGACCTCG AATCAGGTAG	300
GAATACCCGC TGAACCTAA	319

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 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: *Fusarium moniliforme*

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

AAATGCGATA AGTAATGTGA ATTGCAAAAT TCAGTGAATC ATCGAATCTT TGAACGCACA	60
TTGCGCCCGC CAGTATTCTG GCGGGCATGC CTGTTCGAGC GTCATTTCAA CCCTCAAGCC	120
CCCGGGTTTG GTGTTGGGGA TCGGCAAGCC CTTGCGGCAA GCCGGCCCCG AAATCTAGTG	180
GCGGTCTCGC TGCAGCTTCC ATTGCGTAGT AGTAAAACCC TCGCAACTGG TACGCGGCGC	240

41

GGCCAAGCCG TTAAACCCCC AACTTCTGAA TGTGACCTC GGATCAGGTA GGAATACCCG 300
CTGAACTTAA 310

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 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: *Mucor rouxii*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC ATCGAGTCTT TGAACGCAAC 60
TTGCGCTCAT TGGTATTCCA ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC 120
CAGCATTTTG TTGAATAGGA ATACTGAGAG TCTCTTGATC TATTCTGATC TCGAACCTCT 180
TGAAATGTAC AAAGGCCTGA TCTTGTTTAA ATGCCTGAAC TTTTTTTTAA TATAAAGAGA 240
AGCTCTTGCG GTAAACTGTG CTGGGGCCTC CCAAATAATA CTCTTTTAA ATTTGATCTG 300
AAATCAGGCG GGATTACCCG CTGAACTTAA 330

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 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: *Mucor racemosus*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC ATCGAGTCTT TGAACGCAAC 60
TTGCGCTCAT TGGTATTCCA ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC 120
CAACTTTTGT TGTATAGGAT TATTGGGGGC CTCTCGATCT GTATAGATCT TGAAATCCCT 180
GAAATTTACT AAGGCCTGAA CTTGTTTAA TGCCTGAACT TTTTTTTAAT ATAAAGGAAA 240
GCTCTTGTA TTTGACTTTGA TGGGGCCTCC CAAATAAATC TCTTTTAAAT TTGATCTGAA 300

ATCAGGCGGG ATTACCCGCT GAACTTAA

328

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 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: *Mucor plumbeus*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC ATCGAGTCTT TGAACGCAAC	60
TTGCGCTCAT TGGTATTCCA ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC	120
CAACTTTTGT TGTATAGGAT TATTGGGGGC CTCTCGATCT GTATAGATCT TGAAACCCTT	180
GAAATTTACT AAGGCCTGAA CTTGTTTAAT GCCTGAACTT TTTTSTAATA TAAAGGAAAG	240
CTCTTGTAAT TGAATTTGAT GGGGCCTCCC AAATAAATCT TTTTSTAATT TGATCTGAAA	300
TCAGGTGGGA TTACCCGCTG AACTTAA	327

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 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: *Mucor indicus*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC ATCGAGTCTT TGAACGCATC	60
TTGCACTCAA TGGTATTCCA TTGAGTACGC CTGTTTCAGT ATCAAAAACA ACCCTTATTC	120
AAAATTCTTT TTTTGAATAG ATATGAGTGT AGCAACCTTA CAAGTTGAGA CATTTTAAAT	180
AAAGTCAGGC CATATCGTGG ATTGAGTGCC GATACTTTTT TAATTTTGAA AAGGTAAAGC	240
ATGTTGATGT CCGCTTTTTG GGCCTCCCAA ATAACTTTTT AAACCTTGATC TGAAATCAGG	300
TGGGATTACC CGCTGAACTT AA	322

43

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 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: *Mucor circinelloides*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC ATCGAGTCTT TGAACGCAAC	60
TTGCGCTCAT TGGTATTCCA ATGAGCACGC CTGTTTCAGT ATCAAAACAA ACCCTCTATC	120
CAACATTTTT GTTGAATAGG ATGACTGAGA GTCTCTTGAT CTATTCTGAT CTCGAAGCTC	180
TTGAAATGTA CAAAGGCCTG ATCTTGTTTG AATGCCTGAA CTTTTTTTAA ATATAAAGAG	240
AAGCTCTTGC GGTAAGCTGT GCTGGGGCCT CCCAAATAAC ACATCTTTAA ATTTGATCTG	300
AAATCAGGTG GGACTACCCG CTGAACTTAA	330

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 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: *Rhizopus oryzae*

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

AGTGCGATAA CTAGTGTGAA TTGCATATTC AGTGAATCAT CGAGTCTTTG AACGCAGCTT	60
GCACTCTATG GTTTTTCTAT AGAGTACGCC TGCTTCAGTA TCATCACAAA CCCACACATA	120
ACATTTGTTT ATGTGGTGAT GGGTCGCATC GCTGTTTTAT TACAGTGAGC ACCTAAAATG	180
TGTGTGATTT TCTGTCTGGC TTGCTAGGCA GGAATATTAC GCTGGTCTCA GGATCTTTTT	240
TTTTGGTTTCG CCCAGGAAGT AAAGTACAAG AGTATAATCC AGTAACTTTC AAACATATGAT	300
CTGAAGTCAG GTGGGATTAC CCGCTGAACT TAA	333

(2) INFORMATION FOR SEQ ID NO:14:

44

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 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: *Rhizopus oryzae*

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

AGTGCGATAA CTAGTGTGAA TTGCATATTC AGTGAATCAT CGAGTCTTTG AACGCAGCTT	60
GCACTCTATG GTTTTTCTAT AGAGTACGCC TGCTTCAGTA TCATCACAAA CCCACACATA	120
ACATTTGTTT ATGTGGTAAT GGGTCGCATC GCTGTTTTAT TACAGTGAGC ACCTAAAATG	180
TGTGTGATTT TCTGTCTGGC TTGCTAGGCA GGAATATTAC GCTGGTCTCA GGATCTTTTT	240
CTTTGGTTCG CCCAGGAAGT AAAGTACAAG AGTATAATCC AGCAACTTTC AAACATATGAT	300
CTGAAGTCAG GTGGGATTAC CCGCTGAACT TAA	333

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 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: *Rhizopus microsporus*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCGTGAATCA TCGAGTCTTT GAACGCAGCT	60
TGCACTCTAT GGATCTTCTA TAGAGTACGC TTGCTTCAGT ATCATAACCA ACCCACACAT	120
AAAATTTATT TTATGTGGTG ATGGACAAGC TCGGTAAAT TTAATTATTA TACCGATTGT	180
CTAAAATACA GCCTCTTTGT AATTTTCATT AAATTACGAA CTACCTAGCC ATCGTGCTTT	240
TTTGGTCCAA CCAAAAACA TATAATCTAG GGGTTCTGCT AGCCAGCAGA TATTTTAATG	300
ATCTTTAACT ATGATCTGAA GTCAAGTGGG ACTACCCGCT GAACTTAA	348

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 349 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: *Rhizopus microsporus*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCGTGAATCA TCGAGTCTTT GAACGCAGCT	60
TGCACTCTAT GGATCTTCTA TAGAGTACGC TTGCTTCAGT ATCATAACCA ACCCACACAT	120
AAAATTTATT TTATGTGGTG ATGGACAAGC TCGGTTAAAT TTAATTATTA TACCGATTGT	180
CTAAAATACA GCCTCTTGT AATTTTCATT AAATTACGAA CTACCTAGCC ATCGTGCTTT	240
TTTGGTCCAA CCAAAAAACA TATAATCTAG GGGTCTGCT AGCCAGCAA TATTTTAATG	300
ATCTTTAACC TATGATCTGA AGTCAAGTGG GACTACCCGC TGAAC TTAA	349

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 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: *Rhizopus circinans*

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

AAATTGCGAT AACTAGTGTG AATTGCATTT TCAGTGAATC ATCGAGTCTT TGAACGCATC	60
TTGCGCTCTT GGGATTCTTC CCTAGAGCAC ACTTGCTTCA GTATCATAAC AAAACCCTCA	120
CCTAATATTT TTTTTTTTAA AAAAAAAAT ATTAGAGTGG TATTGGGGTC TCTTTGGTAA	180
TTCTTTGTAA TTATAAAAGT ACCCTTAAAT GTCATAAACA GGTTAGCTTT AGCTTGCCTT	240
TAAAGATCTT CTTAGGGTAT CATTACTTTT CGTAAATCTT TAATAGGCCT GTCACATAAT	300
TCTACCCTTA AATTTCTTAA ACCTTGATCT GAAGTCAAGT GGGAGTACCC GCTGAACTTA	360
A	361

(2) INFORMATION FOR SEQ ID NO:18:

46

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 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: *Rhizopus circinans*

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

AAATTGCGAT AACTAGTGTG AATTGCATTT TCAGTGAATC ATCGAGTCTT TGAACGCATC	60
TTGCGCTCTT GGGATTCTTC CCTAGAGCAC ACTTGCTTCA GTATCATAAC AAAACCCTCA	120
CCTAATATTT TTTTTTAAAA AAAAAAATA TTAGAGTGGT ATTGGGGTCT CTTTGGTAAT	180
TCTTTGTAAT TATAAAAGTA CCCTTAAATG TCATAAACAG GTTAGCTTTA GCTTGCCTTT	240
AAAGATCTTC TTAGGGTATC ATTACTTTTC GTAAATCTTT AATAGGCCTG TCACATAATT	300
CTACCCTTAA ATTTCTTAAA CCTTGATCTG AAGTCAAGTG GGAGTACCCG CTGAACTTAA	360

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 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: *Rhizous stolinifer*

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

AAAGTGCGAT AACTAGTGTG AATTGCATAT TCAGTGAATC ATCGAGTCTT TGAACGCAAC	60
TTGCACTCTA TGGTTTTCCG TAAAGTACGC TTGCTTCAGT ATCATAAAGA CCCCATCCTG	120
ATTATTATTT TTTTATTAAA ATAATTAATT TTGGAGATAA TAAAAATGAG GCTCTTTCTT	180
TTCTTTTTTT TTTTTTTAAA AAAAAGGGGG GGAAAGGGTC TTTTAAAATG GGCAAATTCT	240
GGGTTTTTTA CTAAACCTGA ACTCCCCCA AAAATTCAAA AAAAAAAAAA TGGGTTTTTAC	300
CAAATTTTTT TTTTTTTTCT CCTTTTGTG TAGTTAATAC TCTATTAAAT TTATTTACTT	360
GGTATTATAA CGATTATGCA AGAAGGGAGA GAACAAAGAA TAATGAAAGA GAGTTTTTAA	420

47

ATAAATTCTT TTTTCATTTT TTCAATCAAT GATCTGAAGT CAAGTGGGAT TACCCGCTGA 480
 ACTTAA 486

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 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: *Rhizomucor pusillus*

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

AAATTGCGAA AAGTAATGCG ATCTGCAGCC TTTGCGAATC ATCGAATTCT CGAACGCACC 60
 TTGCACCCTT TGGTTCATCC ATTGGGTACG TCTAGTTCAG TATCTTTATT AACCCCTAAA 120
 GGTTTATTTT TTGATAAATC TTTGGATTG CGGTGCTGAT GGATTTTCAT CCGTTCAAGC 180
 TACCCGAACA ATTTGTATGT TGTGACCCT TGATATTTC TTGAGGGCTT GCATTGGTAT 240
 CTAATTTTTT ACCAGTGTGC TTCGAGATGA TCAAGTATAA AGGTCAATCA ACCACAAATA 300
 AATTTCAACT ATGGATCTGA ACTTAGATGG GATTACCCGC TGAACCTAA 349

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 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: *Absidia corymbifera*

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

AAAGTGCAT AATTATTGCG ACTTGCATTC ATAGCGAATC ATCGAGTTCT CGAACGCATC 60
 TTGCGCCTAG TAGTCAATCT ACTAGGCACA GTTGTTTCAG TATCTGCAAC TACCAATCAG 120
 TTCAACTTGG TTCTTTGAAC CTAAGCGAGC TGGAAATGGG CTTGTGTTGA TGGCATTGAG 180
 TTGCTGTCAT GGCCTTAAAT ACATTTAGTC CTAGGCAATT GGCTTTAGTC ATTTGCCGGA 240
 TGTAGACTCT AGAGTGCCTG AGGAGCAACG ACTTGTTAG TGAGTTCATA ATTCCAAGTC 300

48

AATCAGTCTC TTCTTGAAC AGGTCTTAAT CTTTATGGAC TAGTGAGAGG ATCTAACTTG	360
GGTCTTCTCT TAAACAAAC TCACATCTAG ATCTGAAATC AACTGAGATC ACCCGCTGAA	420
CTTAA	425

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 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: *Absidia corymbifera*

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

AAAGTGCAT AATTATTGCG ACTTGCATTC ATAGTGAATC ATCGAGTTCT TGAACGCATC	60
TTGCGCCTAG TAGTCAATCT ACTAGGCACA GTTGTTTCAG TATCTGCATC CACCAATCAA	120
CTTAACCTTT TGTGTTGAGT TGGAAGTGGG CTTCTAGTTG ATGGCATTTA GTTGCTGTCA	180
TGGCCTTAAA TCAATGTCCT AGGTGTTAGA ACATCTAACA CCGGATGGAA ACTTTAGAGC	240
GCTTTAAGAG CAGCTTGGTT AGTGAGTTCA ATAATTCCAA GCATTAAGTC TTTTAATGAA	300
CTAGCTTTTC TATCTATGGG ACACTACTTG GAGAAATCCA AGTAACCTTT AAACCTCCAT	360
TTAGATCTGA AATCAACTGA GACCACCCGC TGAACCTAA	399

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 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: *Cunninghamella elegans*

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

AAATCGCGAT ATGTAATGTG ACTGCCTATA GTGAATCATC AAATCTTTGA AACGCATCTT	60
GCACCTTATG GTATTCCATA AGGTACGTCT GTTTCAGTAC CACTAATAAA TCTCTCTCTA	120
TCCTTGATGA TAGAAAAAAA AAAAATAATT TTTACTGGGC CCGGGGAATC CTTTTTTTTT	180

49

TTTAATAAAA AGGACCAATT TTGGCCCAAA AAAAAGGGTT GAACTTTTTT TACCAGATCT	240
TGCATCTAGT AAAAACCTAG TCGGCTTTAA TAGATTTTAA TTTTCTATTA AGTTTATAGC	300
CATTCTTATA TTTTTTAAAA TCTTGGCCTG AAATCAGATG GGATACCCGC TGAACCTAA	359

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 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: *Pseudallescheria boydii*

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

AAATGCGATA AGTAATGTAA ATTGCAAAAT TCAGTGAATC ATCGAATCTT TGAAACGCAC	60
ATTGCGCCCG GCAGTAATCT GCCGGGCATG CCTGTCCGAG CGTCATTTCA ACCCTCGAAC	120
CTCCGTTTCC TTAGGGAAGC CTAGGGTCGG TGTTGGGGCG CTACGGCAAG TCCTCGCAAC	180
CCCCGTAGGC CCTGAAATAC AGTGGCGGTC CCGCCGCGGT TGCCTTCTGC GTAGTAAGTC	240
TCTTTTGCAA GCTCGCATTG GGTCCCGGCG GAGGCCTGCC GTCAAACCAC CTAACAATC	300
CAGATGGTTT GACCTCGGAT CAGGTAGGGT TACCCGCTGA ACTTAA	346

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 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: *Pseudallescheria boydii*

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

GAAATGCGAT AAGTAATGTG AATTGCAGAA TTCAGTGAAT CATCGAATCT TTGAAACGCA	60
CATTGCGCCC GGCAGTAATC TGCCGGGCAT GCCTGTCCGA GCGTCATTTT AACCCTCGAA	120
CCTCCGTTTC CTCAGGGAAG CTCAGGGTCG GTGTTGGGGC GCTACGGCAA GTCTTCGCAA	180
CCCTCCGTAG GCCCTGAAAT ACAGTGGCGG TCCCGCCGCG GTTGCCTTCT GCGTAGAAGT	240

50

CTCTTTTGCA AGCTCGCATT GGGTCCCGGC GGAGGCCTGC CGTCAAACCA CCTATAACTC 300
 CAAATGGTTT GACCTCGGAT CAGGTAGGGT TACCCGCTGA ACTTAA 346

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 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: *Scedosporium apiospermum*

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

GAAATGCGAT AAGTAATGTG AATTGCAGAA TTCAGTGAAT CATCGAATCT TTGAACGCAC 60
 ATTGCGCCCG GCAGTAATCT GCCGGGCATG CCTGTCCGAG CGTCATTTCA ACCCTCGAAC 120
 CTCCGTTTCC TCAGGGAAGC TCAGGGTCGG TGTGTTGGGGCG CTACGGCGAG TCTTCGCGAC 180
 CCTCCGTAGG CCCTGAAATA CAGTGGCGGT CCCGCCGCGG TTGCCTTCTG CGTAGTAAGT 240
 CTCTTTTGCA AGCTCGCATT GGGTCCCGGC GGAGGCCTGC CGTCAAACCA CCTATAACTC 300
 CAGATGGTTT GACCTCGGAT CAGGTAGGTA CCCGCTGAAC TTAA 344

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 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: *Scedosporium apiospermum*

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

AAATGCGATA AGTAATGTGA ATTGCAGAAT TCAGTGAATC ATCGAATCTT TGAACGCACA 60
 TTGCGCCCGG CAGTAATCTG CCGGGCATGC CTGTCCGAGC GTCATTTCAA CCCTCGAACC 120
 TCCGTTTCCT CAGGGAAGCT CAGGGTCGGT GTTGGGGCGC TACGGCGAGT CTTTCGCGACC 180
 CTCCGTAGGC CCTGAAATAC AGTGGCGGTC CCGCCGCGGT TGCCTTCTGC GTAGTAAGTC 240
 TCTTTTGCAA GCTCGCATTG GGTCCCGGCG GAGGCCTGCC GTCAAACCAC CTATAACTCC 300

AGATGGTTTG ACCTCGGATC AGGTAGGTAC CCGCTGAACT TAA

343

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 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: *Penicillium notatum*

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

AAATGCGATA CGTAATGTGA ATTGCAAATT CAGTGAATCA TCGAGTCTTT GAACGCACAT	60
TGCGCCCCCT GGTATTCCGG GGGGCATGCC TGTCCGAGCG TCATTGCTGC CCTCAAGCAC	120
GGCTTGTGTG TTGGGCCCCG TCCTCCGATC CCGGGGACG GGCCCGAAAG GCAGCGGCGG	180
CACCGCGTCC GGTCCTCGAG CGTATGGGGC TTTGTCACCC GCTCTGTAGG CCCGGCCGGC	240
GCTTGCCGAT CAACCCAAAT TTTTATCCAG GTTGACCTCG GATCAGGTAG GGATACCCGC	300
TGAACTTAA	309

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 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: *Sporothrix schenckii*

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

GAAATGCGAT ACTAATGTGA ATTGCAGAAT TCAGCGAACC ATCGAATCTT TGAACGCACA	60
TTGCGCCCGC CAGCATTCTG GCGGGCATGC CTGTCCGAGC GTCATTTCCC CCCTCACGCG	120
CCCCGTTGCG CGCTGGTGTT GGGGCGCCCT CCGCCTGGCG GGGGGCCCCC GAAAGCGAGT	180
GGCGGGCCCT GTGGAAGGCT CCGAGCGCAG TACCGAACGC ATGTTCTCCC CTCGCTCCGG	240
AGGCCCCCCA GGCGCCCTGC CGGTGAAAAC GCGCATGACG CGCAGCTCTT TTTACAAGGT	300
TGACCTCGGA TCAGGTGAGG ATACCCGCTG ACTTAA	336

52

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Aspergillus flavus*

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

GCAAATCAAT CTTTTTCC

18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Aspergillus flavus*

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

GAACGCAAAT CAATCTTT

18

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Aspergillus fumigatus*

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

CCGACACCCA TCTTTATT

18

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Aspergillus niger*

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

GACGTTATCC AACCATTT

18

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Aspergillus terreus*

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

GCATTTATTT GCAACTTG

18

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Aspergillus nidulans*

54

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

GGCGTCTCCA ACCTTATC

18

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 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: *Mucor rouxii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATAGGAAT ACTGAGAG

18

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 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: *Mucor plumbeus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAAACCCTTG AAATT

15

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 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: *Mucor indicus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGTGGATTGA GTGCCGAT

18

(2) INFORMATION FOR SEQ ID NO:39:

(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

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mucor circinelloides*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACATTTTGTG TGAATAGGAT G

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 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: *Mucor racemosus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAAATCCCTG AAATT

15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Rhizopus oryzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAGTATAATC CAGYAACT

18

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: Rhizopus circinans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTAGGGTAT CATTACTT

18

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: Rhizomucor pusillus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCCTTGAGGG CTTGCATT

18

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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:

57

(A) ORGANISM: *Rhizopus stolonifer*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTTGGTATTA TAACGATT

18

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Pseudallescheria boydii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAGTCTCTTT TGCAAGCT

18

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 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: *Penicillium notatum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCAACCCA AATTTTTA

18

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

58

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Penicillium marneffei* 1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGTTGGTCA CCACCATA

18

- (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 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: *Penicillium marneffei* 2

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TGGTCACCAC CATATTTA

18

- (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 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: *Fusarium moniliforme*

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCTAGTGACG GTCTCGCT

18

- (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

59

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGTTAATTCG CGTTCCTC

18

(2) INFORMATION FOR SEQ ID NO:51:

(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

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTAACACCTC GCAACTGGAG A

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 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: *Cunninghamella elegans* 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TAGTCGGCTT TAATAGAT

18

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

60

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella elegans* 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATTAAGTTT ATAGCCAT

18

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 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: *Cunninghamella elegans* 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAAGTTTATA GCCATTCT

18

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 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: *Absidia corymbifera*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTTGCTGTCA TGCCTTA

18

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

61

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Sporothrix schoenckii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
GACGCGCAGC TCTTTTTA

18

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 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: *Rhizopus microsporus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
CATATAATCT AGGGGTTC

18

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
CCTCGAGCGT ATGGGGCT

18

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

62

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCCAACTTCT GAATGTTG

18

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

MTGGGGCCTC CCAAATAA

18

(2) INFORMATION FOR SEQ ID NO:61:

- (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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAATCATCGA RTCTTTGAAC G

21

The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. An isolated nucleic acid probe for identifying a species of *Aspergillus* wherein the probe selectively hybridizing under stringent conditions to the nucleic acid of *Aspergillus flavus* (SEQ ID NO:1), *Aspergillus fumigatus* (SEQ ID NO:2), *Aspergillus niger* (SEQ ID NO:3), *Aspergillus terreus* (SEQ ID NO:4), *Aspergillus nidulans* (SEQ ID NO:5), or a complementary sequence thereof.
2. The isolated nucleic acid probe of Claim 1 capable of selectively hybridizing under stringent conditions with an *Aspergillus flavus* nucleic acid of SEQ ID NO:1, or a complementary sequence thereof.
3. The isolated nucleic acid probe of Claim 1 capable of selectively hybridizing under stringent conditions with an *Aspergillus fumigatus* nucleic acid of SEQ ID NO:2, or a complementary sequence thereof.
4. The isolated nucleic acid probe Claim 1 capable of selectively hybridizing under stringent conditions with an *Aspergillus niger* nucleic acid of SEQ ID NO:3, or a complementary sequence thereof.
5. The isolated nucleic acid probe of Claim 1 capable of selectively hybridizing under stringent conditions with an *Aspergillus terreus* nucleic acid of SEQ ID NO:4, or a complementary sequence thereof.
6. The isolated nucleic acid probe of Claim 1 capable of selectively hybridizing under stringent conditions with an *Aspergillus nidulans* nucleic acid of SEQ ID NO:5, or a complementary sequence thereof.

7. A method of detecting a species of *Aspergillus* in a sample comprising combining the sample with a nucleic acid probe capable of selectively hybridizing under stringent conditions with a nucleic acid of *Aspergillus flavus* (SEQ ID NO:1), *Aspergillus fumigatus* (SEQ ID NO:2), *Aspergillus niger* (SEQ ID NO:3), *Aspergillus terreus* (SEQ ID NO:4), *Aspergillus nidulans* (SEQ ID NO:5), or a complementary sequence thereof, the presence of hybridization indicating the detection of the species in the sample.

8. The method of Claim 7, wherein the probe is capable of selectively hybridizing under stringent conditions with an *Aspergillus flavus* nucleic acid of SEQ ID NO:1, or a complementary sequence thereof.

9. The method of Claim 7, wherein the probe is capable of selectively hybridizing under stringent conditions with an *Aspergillus fumigatus* nucleic acid of SEQ ID NO:2, or a complementary sequence thereof.

10. The method of Claim 7, wherein the probe is capable of selectively hybridizing under stringent conditions with an *Aspergillus niger* nucleic acid of SEQ ID NO:3, or a complementary sequence thereof.

11. The method of Claim 7, wherein the probe is capable of selectively hybridizing under stringent conditions with an *Aspergillus terreus* nucleic acid of SEQ ID NO:4, or a complementary sequence thereof.

12. The method of Claim 7, wherein the probe is capable of selectively hybridizing under stringent conditions with an *Aspergillus nidulans* nucleic acid of SEQ ID NO:5, or a complementary sequence thereof.

13. An isolated nucleic acid probe for identifying a member of a genus selected from the group consisting of *Aspergillus*, wherein the probe selectively hybridizes under stringent conditions to the nucleic acid of SEQ ID NO:58, or a complementary sequence thereof.

14. A method for detecting a member of a genus selected from the group consisting of *Aspergillus*, in a sample comprising combining the sample with a nucleic acid probe capable of selectively hybridizing under stringent conditions to the nucleic acid of SEQ ID NO:58, or a complementary sequence thereof, the presence of hybridization indicating the detection of the respective genus.