
Strain: **E8**

Identified genus: *Fusarium*

ITS sequence:

CCTACTGGGAATCGAGGATGACAGCGGAGGGACATTACCGAGTTTACAACCTCCCAAACCCCTGTGAACATA
CCACTTGTTCCTCGGCGGATCAGCCCGCTCCCGGTAAAACGGGACGGCCCGCCAGAGGACCCCTAAACTC
TGTTTCTATATGTAACCTCTGAGTAAAACCATAAATAAATCAAAACTTTCAACAACGGATCTCTTGGTTCTG
GCATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTT
TGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATTTC AACCTCAAGCACA
GCTTGGTGTGGGACTCGCGTTAATTCGCGTTCCTCAAATTGATTGGCGGTCACGTCGAGCTTCCATAGCGT
AGTAGTAAAACCCCTCGTTACTGGTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGACCTC
GGATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGGAGGAACGAAAGATTCATTATAATT
CTTGT

BLAST query:

>Fusarium oxysporum strain 4099 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MN817702.1 Length: 540

Range 1: 1 to 540 Score:981 bits(531), Expect:0.0, Identities:537/540(99%), Gaps:0/540(0%), Strand: Plus/Plus

Strain: **E9**

Identified genus: *Fusarium*

ITS sequence:

GTCTTGGGGCCCCGGCTGGGACAGCGGAGGGACATTACCGAGTTTACAACCTCCCAAACCCCTGTGAACATA
CCACTTGTTCCTCGGCGGATCAGCCCGCTCCCGGTAAAACGGGACGGCCCGCCAGAGGACCCCTAAACTC
TGTTTCTATATGTAACCTCTGAGTAAAACCATAAATAAATCAAAACTTTCAACAACGGATCTCTTGGTTCTG
GCATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTT
TGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATTTC AACCTCAAGCACA
GCTTGGTGTGGGACTCGCGTTAATTCGCGTTCCTCAAATTGATTGGCGGTCACGTCGAGCTTCCATAGCGT
AGTAGTAAAACCCCTCGTTACTGGTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGACCTC
GGATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAGATAAAACCCCAAAAAAAAA
G

BLAST query:

>Fusarium oxysporum isolate Fox64 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KJ562370.1 Length: 555

Range 1: 14 to 555 Score:983 bits(532), Expect:0.0, Identities:539/542(99%), Gaps:2/542(0%), Strand: Plus/Plus

Strain: **E10**

Identified genus: *Fusarium*

ITS sequence:

TACTAGGGCAATGCGTGGGGGAACAGCGGAGGGACATTACCGAGTTTACAACCTCCCAAACCCCTGTGAAC
ATACCACTTGTTGCCTCGGCGGATCAGCCCGCTCCCGGTAAAACGGGACGGCCCGCCAGAGGACCCCTAAA
CTCTGTTTCTATATGTAACCTCTGAGTAAAACCATAAATAAATCAAAACTTTCAACAACGGATCTCTTGGTT
CTGGCATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAAT
CTTTGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATTTC AACCTCAAGC
ACAGCTTGGTGTGGGACTCGCGTTAATTCGCGTTCCTCAAATTGATTGGCGGTCACGTCGAGCTTCCATAG
CGTAGTAGTAAAAACCCCTCGTTACTGGTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGA
CCTCGGATCAGGTAGGAAATACCC

BLAST query:

>Fusarium oxysporum isolate P45_ITS_G03_010.ab1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MT032691.1 Length: 534

Range 1: 6 to 514

Score:913 bits(494), Expect:0.0, Identities:506/511(99%), Gaps:3/511(0%), Strand: Plus/Plus

Strain: **E11**

Identified genus: *Plectosphaerella*

ITS sequence:

ACAAAAACCAACTGGTTTTGTGACAGCGGAGGGATCATTACTGAGGTACTACACTCTCTACCCTTTGTGAAC
TATTATACCTGTTGCTTCGGCGGCGCCCGCGAGGGTGCCCGCCGGTCTCATCAGAATCTCTGTTTTCGAACC
CGACGATACTTCTGAGTGTTCTTAGCGAACTGTCAAAACTTTTAACAACGGATCTCTTGGCTCCAGCATCGA
TGAAGAACGCAGCGAAACGCGATATGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGC
ACATGGCGCCTTCCAGTATCCTGGGAGGCATGCCTGTCCGAGCGTCGTTTCAACCCTCGAGCCCCCGTGGCC
CGGCG

BLAST query:

>Plectosphaerella cucumerina isolate I652 ITS1_F07_027.ab1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MT032542.1 Length: 519

Range 1: 1 to 345

Score:627 bits(339), Expect:2e-175, Identities:344/346(99%), Gaps:2/346(0%), Strand: Plus/Plus

Strain: **E12**

Identified genus: *Plectosphaerella*

ITS sequence:

AATGTYACGTTGGTGTACCAGCGGAGGTACATTACTGAGTACTACACTCTCTACCCTTTGTGAACATTATACC
TGTTGCTTCGGCGGCGCCCGCGAGGGTGCCCGCCGGTCTCATCAGAATCTCTGTTTTCGAACCCGACGATAC
TTCTGAGTGTTCTTAGCGAACTGTCAAAACTTTTAACAACGGATCTCTTGGCTCCAGCATCGATGAAGAACG
CAGCGAAACGCGATATGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATGGCGC
CTTCCAGTATCCTGGGAGGCATGCCTGTCCGAGCGTCGTTTCAACCCTCGAGCCCCCGTGGCCCCGGCGTTGG
GGATCTGCCACGGCAGGCCCCCTAAACCAGTGGCGGACCCGAAGGCCCTCTCTTTGCGCAGTAGCATCAG
CCTCGCATTTGGGATCCCTCGGCGTCTGCCTCTAAACCCCCACAAGTCCGCTCCGGCGGCACCAAGGTTG
ACCTCGGATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAWTAAGCGGAGGGAA

BLAST query:

>Plectosphaerella cucumerina strain NQ5GI3 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MK183802.1 Length: 597

Range 1: 45 to 595

Score:990 bits(536), Expect:0.0, Identities:546/551(99%), Gaps:1/551(0%), Strand: Plus/Plus

Strain: **E13**

Identified genus: *Pyrenochaeta*

ITS sequence:

GGGGACAGTRCGTTAGTGACCTGCGGAGGTACATTATTGTATAACGGGGGCGGCGAGGGATTGCGCACTT
CGGTGCGCCTTTCTTCCCCGCCCTGTCTGATACTACCCATGTCTTTTGCGTACCAATTGTTTCCTCGGTGGGCT
TGCCCGCCGGTTGGACACTATAAAACCTTTTGTAATTGCAGTCAGCGTCAGAAAAACATAATAATTACAAC
TTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAGTGTAATTGC
AGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTTGGTATTCCATGGGGCATGCCTGTTCG
AGCGTCATTTGTACCCTCAAGCTCTGCTTGGTGTTGGGTGTTTGTCCCGCTTTGCGCGTGGACTCGCCTTAAA
GCAATTGGCAGCCGGCAATCTGGTTATAGAGCGCAGCACATTTTGCGCTTCTTGCCATGGATGTGGGCATCC
ATCAAAGTACATTTTTTTTGTCTTTGACCTCGGGATCAGGTAGGGATAACCCGCTGAAACTTAAGCATATCA
AATAAGCCRGAGGAA

BLAST query:

>Pyrenochaeta sp. strain Py004 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MN537136.1 Length: 608

Range 1: 34 to 607 Score:996 bits(539), Expect:0.0, Identities:568/580(98%), Gaps:9/580(1%), Strand: Plus/Plus

Range 1: 19 to 395 Score:649 bits(351), Expect:0.0, Identities:368/378(97%), Gaps:4/378(1%), Strand: Plus/Plus

Strain: **E16**

Identified genus: *Cadophora*

ITS sequence:

ARTKKGACAATTCAGTTRGTGACCTGCGGGAGGTACATTACTAGAGCAAAGGATAGACAGCGCCCGTGGAG
CTCGCTCCCGGGGCTACCCTACTCCGGTAGGGTTTAGAGTCGTCGAGCCTCTCGAAGAAGCTCGGTCTGAA
CTCCACCCTTGAATAAACTACCTTTGTTGCTTTGGCGGGCCGCCTCGTGCCAGCGGCTTCGGCTGTTGAGTG
CCCGCCAGAGGACCACAACCTCTTGTCTTTAGTGATGTCTGAGTACTATATAATAGTTAAACTTTCAACAACG
GATCTCTTGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCRGT
GAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGGGGGCATGCCTGTTTCGAGCGTCATTA
TAACCACTCAAGCTCTCGCTTGGTATTTGGGGGTTCGCGGWTTTCGCGGYCCCTAAAAATCAATKGGRRGGT
GCCCTGTWCGGCTCTRCRSCGTAATAATAMATCCTTCGSSKTTTGGATTCCGGGTAAGGTAATAAWTTWG
GCSAAAAAACCCTTAATTGTTTTTAAAAAGGWTGGAACCTTCGGGAAAWAAGGTAAAAAATAARCCAA
GSTGAAAACCTTTAARSMATAATWAAWAAAAAAMGGARAGAGGAAAAGARARRAGGAAAGAAGAKGTTA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG
GAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG
AWAAGAGAAAGAAAAAAGAAAAAARGKAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG
GAAAAAGAGGAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
WAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

BLAST query:

>Cadophora orchidicola voucher JS242014 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KY271867.1 Length: 630

Range 1: 23 to 528 Score:833 bits(451), Expect:0.0, Identities:493/514(96%), Gaps:9/514(1%), Strand: Plus/Plus

Strain: **E17**

Identified genus: *Colletotrichum*

ITS sequence:

AGAARCARWYCGTTGGTGACCAGCGGAGGGTACATTACTGAGTACTACACTCTCTACCCCTTTGTGAACCTAT
TATACCTGTTGCTTCGGCGGGCGCCCGCGAGGGTGCCCGCCGGTCTCATCAGAATCTCTGTTTTCGAACCCGA
CGATACTTCTGAGTGTTCTTAGCGAACTGTCAAACTTTTAACAACGGATCTCTTGGCTCCAGCATCGATGA
AGAACGCAGCGAAACGCGATATGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
TGGCGCCTTCCAGTATCCTGGGAGGCATGCCTGTCCGAGCGTCGTTTCAACCCTCGAGCCCCCGTGGCCCCG
CGTTGGGGGATCTGCCCCACGGCAGGCCCTAAACCAGTGGCGGACCCGAAGGGCCCTTCTCCTTTGCGCA
AGWAAAMAAYAARCCTACGCATTGAGGWTGCCRTCGGGGAGAACCATGCCCTCTWAAGACCGCRCCCAC
AAAGGGAWAAGTTACRAGRAGAAWMCCRAAGGKTTAGAYWCTWCMGRATCMAAGKTA

BLAST query:

>Colletotrichum pisi isolate OTU560 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: GU934514.1 Length: 563

Range 1: 12 to 425 Score:741 bits(401), Expect:0.0, Identities:414/419(99%), Gaps:5/419(1%), Strand: Plus/Plus

Strain: **S1**

Identified genus: *Notophoma*

ITS sequence:

CCTATAGGCTTTTCGTAGGTGACTGCGGAGGACATTACCTAGAGTTGCGGGCTTTGCCTGCCATCTCTTACCCA
TGTCTTTTGAGTACCTTCGTTTCCTCGGCGGGTCCGCCCCGCCGATTGGACAAAACCTTAAACCCTTTGTAATTG
AAATCAGCGTCTGAAAAAACTTAATAGTTACAACCTTTCAACAACGGATCTCTTGTTCTGGCATCGATGAA
GAACGCAGCGAAATGCGATAAGTAGTGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACAT
TGCGCCCCCTTGGTATTCCATGGGGCATGCCTGTTTCGAGCGTCATTTGTACCTTCAAGCTTTGCTTGGTGTGG
GTGTTTGTCTCGCCTCTGCGCGCAGACTCGCCTCAAAAACGATTGGCAGCCGGCGTATTGATTTCGGAGCGCA
GTACATCTCGCGCTTTGTAGTCTCAACGACGACGTCGAAGAGAGTACTTTTTTCACTCTTGACCTCGGATCAG
GTAGGGATACCCGCTGAACCTTAAGCATATCAATTAAGCGGAGAGAATCCCCTTTTTTTTTTCAAAAAATAG

BLAST query:

>Nothophoma quercina isolate R49 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MT420644.1 Length: 542

Range 1: 3 to 540 Score:948 bits(513), Expect:0.0, Identities:532/540(99%), Gaps:6/540(1%), Strand: Plus/Plus

Strain: **S2**

Identified genus: *Penicillium*

ITS sequence:

CMWWMCAGKGRGGYCTCTGGGTACCTCCACCCGYWTTATCGACCTTMTTGCTTCGGTGGTTCGMCTCT
CCGCCGGCGGGTGGCTATTCATGATGCTTTRATTACRACATCCCTTATTAATTCACACCCACCCCCCCTAG
CACKATACTTTTTTAATTTCTTCCCCCTCACTCAAAAATTACCATAACAACTCAAACACCTCCCCCTCCCCCT
CCCTTCCCTKCCTTTCCCCCCCCCACTTATCTTAAACATTAAACAACCAKCCCACACCAACCCCCCKCCC
ATCCRCCCCCCCCCTCKKAMARRTAATTTCTTAATMTTWATYTARCATAAARMAAASMCGATAAAAAACA
CAAAATAATAAATTTAAAAAATTSTTAATAAAAAAAAAGKACCCCCCGCCGKTCACACCTCCTAAKTAA
AATAACWCCCCTCACCCCTCCTYCCATMCTTTTCTTSATTTYTTCTCTCCCTCCTGCCCCGMSAGACGCYCA
TTCCCAGGAWCTTACGAWTGAGGGCCTCKGGGTCCTCCACGCGTTTATGWACTGTTGCTCGGGGGCGCCC
GGYCGCGGGGGGCTCGCCCCGGCCCCGCCGCAAAACATGAAGCGCCGAGAMGCGTCTGGCAWTACTAAA
AGTAAACTTCACAGGTACCTGGTTCGCTCATCAWAACCGSAATGSYTARCAKGTGAATGCRAATCGKGAAC
CMGTCTTGAAGCCMTGATTCCSSYATCGGGGGGKAGCGGRAAATTKSCTCTYCTSTKMGRGGGGWWCCWG
ACCATAAAGSCAGCSCWCCTAAATKTGAGWTCAACMTCTGTCRCGTTGTAKKTCACCTTTTYYSTGWGTCY
YGTSTGKWSIGWCCGGACTTTMATCAAKGGGGGAATTCACCTSTSTGTTTCATCTGTGCR

BLAST query:

>Penicillium lanosum strain 2# 10-2 No.110411-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: JX536388.1 Length: 525

Range 1: 12 to 117 Score:73.4 bits(80), Expect:2e-08, Identities:86/107(80%), Gaps:12/107(11%), Strand: Plus/Plus

Strain: **S3**

Identified genus: *Curvularia*

ITS sequence:

AAAACCTGTTTCGTAAGTGACCTMGC GGAGGGTACATTACACAATACAATATGAAGGCCCGTAACACGGCTGG
ATTATTTTATTACCCTTGTCTTTTGCGCACTTGTGTTCCTGGGCGGGTTTCGCCCCGCCACCAGGACCACACC
ATAAACCTTTTTTATGCAGTTGCAATCAGCGTCAGTACAACAAATGTAAATCATTTACAACCTTTCAACAACG
GATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAGTGTGAATTGCAGAAATTCAGT
GAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTTCGAGCGTCATTT
GTACCCTCAAGCTTTGCTTGGTGTGGGCGTTTTTTTGTCTTTGGTTATGCCAAAGACTCGCCTTAAAACGAT
TGGCAGCCGGCCTCCTGGTTTCGCAGCGCAGCACATTTTTCGCTTGAATCAGCAATAGAGGGCGGCACT
CCATCAAGACACTTTTTTTCACGTTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCATATCAAT
AAGCGGAGG

BLAST query:

>Curvularia inaequalis strain 4Lss1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: KC897660.1 Length: 577

Range 1: 1 to 576 Score:1037 bits(561), Expect:0.0, Identities:572/577(99%), Gaps:2/577(0%), Strand: Plus/Plus

Strain: **S4**

Identified genus: *Curvularia*

ITS sequence:

ATWTWACAGTTCGTTAGTGTAMCTGCGGAGGTACATTACACAATACAATATGAAGGCCCGTGACACGGCTG
GATTATTTTATTACCCTTGTCTTTTGCGCACTTGTGTTCCTGGGCGGKTTTCGCCCCGCCACCAGGACCRC
CCATAAACCTTTTTTATGCAGTTGCAATCAGCGTCAGTACAACAAATGTAAATCATTTACAACCTTTCAACA
CGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAKCGAAATGCGATACGTASTGTGAATTGCAGAAATTCAG
TGAATCATCSAATCTTTGAACGSACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTTCGAGCGKCATT
GTACCCTCAAGCTTTGCTTGGTGTGGGCGTTTTTTTGTCTTTGGTTATGCCAAAGACTCGCCTTAAAACGAT
TGGCAGCCGGCCTCCTGGTTTCGCAGCGCAGCACATTTTTCGCTTGAATCAGCAATAKAGGGCGGCACT
CCATCAAGACACTTTTTTTCACGTTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCATATCATT
AGCGGAGGAA

BLAST query:

>Curvularia inaequalis 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: AF313409.1 Length: 605

Range 1: 33 to 605 Score:992 bits(537), Expect:0.0, Identities:558/573(97%), Gaps:1/573(0%), Strand: Plus/Plus

Strain: **S5**

Identified genus: *Curvularia*

ITS sequence:

AGCATTCGTAAGTGTACCTGCGGAGGTACATTACCGAKCGAGATTCTCTGATTCACCTCCCWCCCGTGTTTAT
TGTCCCTTGTGCTTCSGCGCTTGKGTCCCGGGCGGGGGTTCGCCCCGCGMCCCCGACCACCCRTCCGCCT
TTTTTACTTGTGTGCTGCAGCGTCTTGACAWCTGAGTMAATCATTACTATTTCACAACCGATCTCTTGKYTC
TGGSWTCSAKGAWSAAYGAAGARMAMTGGAWAYGYAATGYGAATTGYRAAWTTCAGAGAAYCATCRAAY
CTTTGAACKYWCAATTGCGCCCTGTGSCATTCGRAAKGSCATGCCTGTTCSAGCGYCATTTGTACCCTGCAAGC
CYTTGCTTGGTGTGGGCGTGTTTTTTGTCTKTCSGYTATGCCCAAAGGACTMSCCTTCCAACRAKTGGCAG
CCGGMCTCCTGGYGKSCASCRCAGCACRTTTTTTGYGCTTGAATCATSAATAGASGGCGGCACTTCRTCAA
KACACTTTTTAYTTCWYGYTGTACCTCRSCATCGAGRTCAGGGTATACCMTGCTGCAACTKTAAGTCATAT
CAWATAMAGCTGGAASSGAAAGGAA

BLAST query:

>Curvularia inaequalis isolate F2-3-3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KX349453.1 Length: 559

Range 1: 59 to 558

Score:380 bits(421), Expect:7e-101, Identities:385/519(74%), Gaps:24/519(4%), Strand: Plus/Plus

Strain: **S6**

Identified genus: *Aspergillus*

α -actin sequence:

GGGRRWCCTYSRRMWGTTTTTCGTAAGTCCAACCAAAATCCCCCACAAGATCCCTCACAAKGGCAACCCTT
CCCCTCCTCCKGGGAAGTCATTCCCACCAACCCTTGCGTCAGCCCCCTCGGCCAAGCTGGGGTTGGTCGGAG
AATTTGCCACTTTGGACGTCGAGTGGAATTGACCATCAAAAATCCAAATACTGACCAAAAATCCATAGCCTC
CATTGTCTGGTCTGTCCTCCCGTCACCAKGGGWAAATATCCCCTTGTTCTCTCACTGTTTCTCGGCCTTGACCTGGC
GTCGTTGCTCTATGCGCTGTTTAAACGCATCGCAAGCATTCTTGCAAAATTGTCTTCCARAAAATAACGC
AATGCTCCAGTATCAKGATKGGTATGGGCCAGAAGAAGCTCGWAAACTTTTKGTTCTGTYMCTMTTTAAATA
TCTMCTMTTTAAACYTTTTYATAATTGCTTATATTCTATAAAATAKATAAATAAKCCAATCAAGTCAKMAAA
AAAAAMMAATAWATAATAATTTYTTTTTTTTTYTTGTTAKTTATTATACTTATTTTTATTTATTTMAWACATTMA
AACTWATTYMATTTTTTTKATTTTTWTWTWTWATCWAAATTAATACTCCATCAACCATMTTATYTAATT
ATTKATATATTTAKTTTWGTTTTTAAATCCTATATTTTCCTTCRTTSTTTTTYTYTTKRTSTGTTSTCGTCTATYA
YTCCTCATTCTAWTTATAACTCTTCTTTCCTTCTTTTTTYTTTTTTTAAATTCACKATTKWTWTYARATCAR
AYMCATATTTTCAMACTAATATATTCTTTCATTCTRTTTTTCAKTTTCTTTYCTCATTCTCAKTGATTTTCCATC
TSMAATTSTCTCTTTGCGTGSCTTCCCTTGTTTATCCTSCACTTCTCSTKTGTTATTTCTTTTTTCTCTCYKTC
TSTGTSTACACAATAGRTGATGTAARTRKCTTTATTTCACTCCTCCASAATCAWAACGTTCTCAAMATTAKTAT
TCAGAATCTTCACAKSTCGTSKT

BLAST query:

>Aspergillus udagawae strain CBS DTO_283-D3 actin gene, partial cds

Sequence ID: KY808536.1 Length: 705

Range 1: 493 to 539 Score:80.5 bits(43), Expect:2e-10, Identities:45/47(96%), Gaps:0/47(0%), Strand: Plus/Plus

Strain: **S7**

Identified genus: *Fusarium*

ITS sequence:

GAACGACGGACTCGTGTTGTGACAGCGGAGGACATTACCGAGTTTACACTCCCCAAACCCCTGTGAACATACC
ACTTGTTGCCTCGGCGGATCAGCCCGCTCCCGGTAAAACGGGACGGCCCGCCAGAGGACCCCTAAACTCTG
TTTCTATATGTAACCTCTGAGTAAAACCATAAAATAAATCAAAACTTTCAACAACGGATCTCTTGTTCTGGC
ATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTG
AACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATTTC AACCCCTCAAGCACAG
CTTGTTGTTGGGACTCGCGTTAATTCGCGTTCCTCAAATTGATTGGCGGTCACGTCGAGCTTCCATAGCGTA
GTAGTAAAACCCCTCGTTACTGGTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGACCTCG
GATCAGGTAGGAATACCCGCTGAACTTAAGCATATCATAAGCGGAGGAATCCCCCAATACTTCATTTATTT
TTT

BLAST query:

>Fusarium oxysporum isolate Fox64 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene,
partial sequence

Sequence ID: KJ562370.1 Length: 555

Range 1: 13 to 555 Score:966 bits(523), Expect:0.0, Identities:538/544(99%), Gaps:6/544(1%), Strand: Plus/Plus

Strain: **S8**

Identified genus: *Fusarium*

ITS sequence:

ATTCCCTACCTGGATCCAAGGGTCACATTCAGAAAGTTGGGGTTTACGGCGTGGCCGCGACGATTACCAGTAA
CGAGGGTTTTACTACTACGCTATGGAAGCTCGACGTGACCGCCAATCAATTTGGGGAACGCGATTTGACTCG
CGAGTCCCAACACCAAGCTGGGCTTGAGGGTTGAAATGACGCTCGAACAGGCATGCCCCGCCAGAATACTG
GCGGGCGCAATGTGCGTTCAAAGATTCATGATTCCTGAATTCTGCAATTCACATTACTTATCGCATTTTGCT
GCGTTCTTCATCGATGCCAGAACCAAGAGATCCGTTGTTGAAAGTTTTGATTTATTTATGGTTTACTCAGAA
GTTACATATAGAAACAGAGTTTAGGGGTCCTCTGGCGGGCCGTCCCCGGGTACGG

BLAST query:

>Fusarium verticillioides isolate FM2 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MK790042.1 Length: 679

Range 1: 259 to 667 Score:717 bits(388), Expect:0.0, Identities:404/411(98%), Gaps:4/411(0%), Strand: Plus/Minus

Strain: **S9**

Identified genus: *Penicillium*

ITS sequence:

GACRGTCTKAAGGTGACCTGCGGAGGWCTTACCGAGCGAGRITCCTCTGARKTCMACCYTCCMMCCCCG
KTGKTTTWTGTCGAMCYTGTTGCTTCGGCGGGCCCCGCTCACGGCCGCCGGGGGGCTTCTGCCCTCTGGCCC
GCGCCCGCCGAAGACACCWTTGAMCGCTGWCTGAARATTGCAGTCTGAGCTATTAGCTAAATAAGTTAAA
ACTTTCAGCAACGGATCTCTKGGTCCGGCATCRATGAAAAACGC

BLAST query:

>Penicillium restrictum strain GZU-BCEC393-3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: GU565105.1 Length: 573

Range 1: 1 to 239 Score:311 bits(168), Expect:1e-80, Identities:215/244(88%), Gaps:7/244(2%), Strand: Plus/Plus

Strain: **S10**

Identified genus: *Fusarium*

ITS sequence:

AACAAGTTCGTTGGTGACCAGCGGAGGGTACATTACCGAGTTTACAACCTCCCAAACCCCTGTGAACATACCT
ATACGTTGCCTCGGCGGATCAGCCCCGCGCCCTGTAAAAAGGGACGGCCCGCCGAGGACCCTAAACTCTGT
TTTTAGTGGAATTCTGAGTAAACAAACAAATAAATCAAACTTTCAACAACGGATCTCTTGTTCTGGC
ATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTG
AACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATTTCACCCCTCAAGCTCAGC
TTGGTGTGTTGGGACTCGCGGTAACCCGCGTTCCCCAAATCGATTGGCGGTCACGTCGAGCTTCCATAGCGTAG
TAATCATACACCTCGTTACTGGTAATCGTCGCGGCCACGCCGTAAACCCCAACTTCTGAATGTTGACCTCG
GATCAGGTAGGAATACCCGCTGAACCTTAAGCATATCATTAAGCGGGAGGAAA

BLAST query:

>Fusarium sp. isolate DSM100287_DF16_RLCS18 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MT453272.1 Length: 1136

Range 1: 30 to 585 Score:979 bits(530), Expect:0.0, Identities:549/557(99%), Gaps:5/557(0%), Strand: Plus/Plus

Strain: **S11**

Identified genus: *Fusarium*

ITS sequence:

GRWAYSSGRGTTTWMCTCCCAAACCCCTGTGAACATACCACTTGTTCCTTCGGCGGATCAGCCCCGCTCCCG
GTAAAACGGGACGGCCCCGCCAGAGGACCCCTAAACTCTGTTTCTATATGTAACCTCTGAGTAAAACCATAA
ATAAATCAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCAAAATGCGATAA
GTAATGTGAATTGCAGAATCAKTGAATCATCGAATCTTTGAACGCACATTGCGCCCCGCCAGTATTCTGGCG
GGCATGCCTGTTCKAGCGTCATTTCAACCCTCAAGCACAGCTTTGTGTGGGATTTKATTTAATTCTTGTTC
TYATATTGATTGGATTTTTATTTTATWAMMTAYAGTTAYASCAAACTTTTTTTACTTTTATYTTTTTCTTTTY
TTCTTCTTTTAACTACTCCTRTWATWWTTTCTATTTTTTTTTTCA

BLAST query:

>*Fusarium oxysporum* f. sp. *lycopersici* strain FWC81 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KC478641.1 Length: 561

Range 1: 55 to 410 Score:599 bits(324), Expect:5e-167, Identities:344/356(97%), Gaps:0/356(0%), Strand: Plus/Plus

Strain: **S12**

Identified genus: *Fusarium*

ITS sequence:

AWWTWACGTTTCGTTGGTGTACCAGCGGAGGGTACATTACCGAGTTTACAACCTCCCAAACCCCTGTGAACAT
ACCTATACGTTGCCTCGGCGGATCAGCCCGCGCCCTGTAAAAAGGGACGGCCCGCCGAGGACCCTAAACT
CTGTTTTTAGTGGAACCTTCTGAGTAAAACAAACAATAAATCAAAACTTTCAACAACGGATCTCTTGGTTC
TGGCATCGATGAAGAACGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATC
TTTGAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATTTCAACCCTCAAGCT
CAGCTTGGTGTGGGACTCGCGGTAACCCGCGTTCCCCAAATCGATTGGCGGTACAGTCGAGCTTCCATAGC
GTAGTAATCATACACCTCGTTACTGGTAATCGTCGCGGCCACGCCGTAAAACCCCAACTTCTGAATGTTGAC
CTCGRATCAGGTAGGAAATACCCGCTGAACTTWAAGCATATCAATWAAGSSGGRAGGAA

BLAST query:

>*Fusarium equiseti* isolate Fequi20 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KJ562376.1 Length: 558

Range 1: 14 to 558 Score:957 bits(518), Expect:0.0, Identities:540/551(98%), Gaps:6/551(1%), Strand: Plus/Plus

Strain: **S13**

Identified genus: *Penicillium*

ITS sequence:

AAGGGWMATTACCGAGCGAGATTCTCTGATTCAACCTCCCACCCGTGTTTATTGTACCTTGTTCCTTCGGCG
GGCCCGCCTCACGGCCCGCGGGGGGCATCTGCCCCGGGCCCCGCGCCCGCCGAAGACACCTTGAACCTCTGT
ATGAAAATTGCAGTCTGAGTCTAAATATAAATTATTTAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT
CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAA
CGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCCGCTT
GTGTGTTGGGTCTCGTCCCCCTTCCCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT
CGAGCGTATGGGGCTTTGTACCCGCTCTGTAGGCCCGCGCGGCGCTTGCCGATCAACCAAAAACCTTT

BLAST query:

>*Penicillium fellutanum* strain CBS 118477 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MT309667.1 Length: 900

Range 1: 159 to 650

Score:891 bits(482), Expect:0.0, Identities:490/493(99%), Gaps:3/493(0%), Strand: Plus/Plus

Strain: **S14**

Identified genus: *Penicillium*

ITS sequence:

GRGGCAGTACGCAAGTGACCTGCGGAGGTACATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCCCACCC
GTGTTTATCGTACCTTGTGCTTCGGCGGGCCCGCTCACGGCCGCGGGGGGCTTCTGCCCTCTGGCCCGC
GCCCCGCCGAAGACACCATTGAACGCTGTCTGAAGATTGCAGTCTGAGCAATTAGCTAAATAAGTTAAACT
TTCAACAACGGATCTCTTGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGC
AGAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCG
AGCGTCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGTCTCTCTCCCGGGGGACGGGCCCCGAA
AGGCAGCGGMGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTCACCCGCTCTTGTAGGCCCGGMC
GGCGCTTGMCRAMACATCAAATCTTTTTTCCRGGWTGACCTCGGATCARGWAAGGGATACCCCGCTTGAA
CATTAAARCATATCMAAWAAAGCGAGARGGAAA

BLAST query:

>Penicillium philippinense strain CBS 623.72 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MH860600.1 Length: 833

Range 1: 103 to 680 Score:950 bits(514), Expect:0.0, Identities:562/588(96%), Gaps:11/588(1%), Strand: Plus/Plus

Strain: **S15**

Identified genus: *Fusarium*

ITS sequence:

AAACATTTCGTTGGTGACTAGCGGAGGGTACATTACCGAGTTTCACTCCCGRCCCCTGTGACTACCTAKACGTT
GCCTCGGGGGRTCASCCCGCGCCCGTAMAAAGGGACGGCCCGCCGAGGACCCCTAAACTCTGTTTTTAG
TGGAACCTCTGAGTAAACAAACAAATAAATCAAACTTTCAACAACGGATCTCTTGTTCTGGCATCGAT
GAARAACGCAGCAAAATGCGATAAGTAATGTGAATTGCARAATTCAGTGAATCATCGAATCTTTGAACGCA
CATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTGAGCGTCATTTCACCCTCAAGCTCAGCTTGGTG
TTGGGACTCGCGGTAACCCGCGTTCCCCAAATCGATTGGCGGTCACGTCGAGCTTCCATAGCGTAGTAATCA
TACACCTCGTTACTGGTAATCGTCGCGGCCACGCCGTAAACCCCAACTTCTGAATGTTGACCTCGGATCAG
GTAGGAATACCCGCTGAAACTTAAGCATATCATTAAARGCGGGAGGAA

BLAST query:

>Fusarium sp. NRRL 45996 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: GQ505760.1 Length: 1130

Range 1: 16 to 558 Score:898 bits(486), Expect:0.0, Identities:525/546(96%), Gaps:7/546(1%), Strand: Plus/Plus

Strain: **S16**

Identified genus: *Fusarium*

ITS sequence:

AACAGTTCGTTAGTGACTAGCGGAGGTCTTACCGAGYGTGCKTTCCTCCCGAYCTCCTGCGCCCACCCCTGTTCCG
TTGCCCCGGGGGYCTCCCCGCGCCCGYAMAARGGGACGGCCCGCCCGAKGACCCCTAAACTCTGTTTTT
AGTGGAACCTCTGAGTAAACAAACAAATAAATCAAACTTTCAACWACGGATCTCTTGTTCTGGCATC
GATGAARAACGRCGAWAAKGCATAAGTAATGTGAATTGCARAATTCAGTGAATCRKCGAATCTTTGAA
CGCACATTGCGCCCGCCAGTWTCTGGCGGGCATGCCTGTTGAGCGTCATTTCRACCTCAAGCTCARCTT
GGTGTGTTGGGACTCGCGGTAACCKCGTTCCCCRAATCGATTGSCGGTCACGTCGAGCTTCCATAGCGTAGTA
ATCATACACCTCGTTACTGGTAATCGTCGCGGCCACGCCGTAAACCCCAACTTCTGAATGTTGACCTCGGA
TCAGGTAGGAATACCCGCTGAACCTTAAGCATATCATTAAAGCGGAGGAA

BLAST query:

>Fusarium sp. strain RS-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MT150615.1 Length: 528

Range 1: 30 to 513 Score:771 bits(417), Expect:0.0, Identities:455/484(94%), Gaps:0/484(0%), Strand: Plus/Plus

Strain: **S17**

Identified genus: *Penicillium*

ITS sequence:

TTKTTKACAATTTCGCAGTGACCTGCGGTAGGTACATTACCGAGCGAGAATTCTCTGATTCAACCTCCCACCC
GTGTTTATTGTACCTTGTGCTTCGGCGGGCCCCGCTCACGGCCGCCGGGGGGGCATCTGCCCCGGGCCCCGC
GCCCCGCCGAAGACACCTAGAACTCTGTATGAAAATTGCAGTCTGAGTCTAAATACAAATTATTTAAAACCTT
CAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAG
AATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAG
CGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTCGTCCCCCTTCCCGGGGGGACGGGGCCCGAAA
GGCAGCGGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTTGTACCCGCTCTGTAGGCCCGGGCCGGC
GCTTGCCGATCAACCAAACTTTTTTCCAGGTTGACCTCGGAWCAAGGTAGGGATACCCGCTRAACTTAAG
CATAATCAATAAAGCGGRAGGAAA

BLAST query:

>Penicillium sp. P10-15b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KT354993.1 Length: 592

Range 1: 16 to 592 Score:1005 bits(544), Expect:0.0, Identities:568/580(98%), Gaps:4/580(0%), Strand: Plus/Plus

Strain: **S18**

Identified genus: *Penicillium*

ITS sequence:

TAWTWAWACARTCGTAGTGACCTGCGGAGGTACATTACCGAGCGAGAATTCTCTGATTCAACCTCCCACCC
GTGTTTATTGTACCTTGTGCTTCGGCGGGCCCCGCTCACGGCCGCCGGGGGGGCATCTGCCCCGGGCCCCGC
GCCCCGCCGAAGACACCTTGAACCTCTGTATGAAAATTGCAGTCTGAGTCTAAATATAAATTATTTAAAACCTT
CAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAG
AATTCAGTGAATCATCRAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAG
CGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTCGWCCCMCTTCCCGGARAGGACRGGGMCCG
AAAS

BLAST query:

>Penicillium sp. P10-16c internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KT354994.1 Length: 593

Range 1: 14 to 431 Score:715 bits(387), Expect:0.0, Identities:408/420(97%), Gaps:4/420(0%), Strand: Plus/Plus

Strain: **S19**

Identified genus: *Fusarium*

ITS sequence:

GRRWYWWKRRTTTYACTTRCAAACCCCTGTGAACATACCACTTGTTGCCTCGGCGGATCAGCCCGCTCCCG
GTAAAACGGGACGGCCCCGCCAGAGGACCCCTAAACTCTGTTTCTATATGTAACCTCTGAGTAAAACCATAA
ATAAATCAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCAAAATGCGATAA
GTAATGTGAATTGCAGAAATCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCGCCAGTATTCTGGCG
GGCATGCCTGTTCKAGCGTCATTTCACCCCTCAAGCACAKCTTGGTGTGGGACTCKCGTTAATTCKCGTTC
CTCAAATTGAWTGGCGGTCACGTCKAGCTTCCATAGCGTAKTAGTAAAACCCCTCKTTACTGGTAATCGTCKC
GGCCACRCCGTTAATCCCCAACTTCTGAATGTTGACCTCKGATCATGTAGGAATACCTGCTGAACCTTATKCAT
ATCAATTAGCGGARGTAGTA

BLAST query:

>Fusarium oxysporum isolate Ginrarsnl_1 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MN055701.1 Length: 578

Range 1: 74 to 574 Score:845 bits(457), Expect:0.0, Identities:482/501(96%), Gaps:0/501(0%), Strand: Plus/Plus

Strain: **S20**

Identified genus: *Penicillium*

ITS sequence:

ARGAGCAGTGCGCAGTGACCTGCGGAGGTACATTACCGAGCGAGAATTCTCTGATTCAACCTCCCACCCGTG
TTTATTGTACCTTGTTGCTTCGGCGGGCCCCGCCCTACGGCCCGCGGGGGGCATCTGCCCCCGGGCCCCGCGCC
CGCCGAAGACACCTTGAACCTCTGTATGAAAATTGCAGTCTGAGTCTAAATATAAATTATTTAAAACCTTTCAA
CAACGGATCTCTTGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCARAAT
TCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGRGGMATGCCTGTCCGAGCGT
CATTGCTGMCCTCAAGCCCGGCTTGTGTGTTGGGTCTCGTCCCCCTTCCACRGGAAARAACRGRMMCCCC
AAA

BLAST query:

>Penicillium canescens strain HSP207 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MK543250.1 Length: 562

Range 1: 1 to 395 Score:697 bits(377), Expect:0.0, Identities:387/395(98%), Gaps:1/395(0%), Strand: Plus/Plus

Strain: **S21**

Identified genus: *Paraphoma*

ITS sequence:

TSSRRAAGGWMWTACCTTTTCATGCAGAAGAGTTGAGATGGTTGAGTATCTCGCCTCTCAATTCTCGCTGTAT
TTTACCCTTGTTTTTCTCATACTATTATTTCCCTCGGCAGGCTCGCCTGCCGGGTGAAACAACCTTCAAACCTGT
TTAATTTTCAATCAGCGTCTGAACAAATTAATAATTACAACCTTTCAACAACGGATCTCTTGGTTCTGGCATC
GATGAAGAACGCAGCGAAATGCGATAAGTAGTGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAAC
GCACATTGCGCCCCCTTGGTATTCCATGGGGCATGCCTGTTTCGAGCGTCATTGTACCTTCAAGCTCTGCTTGG
TGTTGGGTGTTTGTCTTGTCTAGTGGCGGGACTCGCCTCAAAGTAATTGGCAGCCAGTGTTTTGGTTTTG
AAGCGCAGCACAAGTCGCGATTCAAGTCTATACGCTAGTTTCCACAAGTCTTTTATCACTTTTGACCTCGGAT
CAGGGT

BLAST query:

>Paraphoma radicina genomic DNA sequence contains ITS1, 5.8S rRNA gene and ITS2, culture collection UTHSC:DI16-209

Sequence ID: LT796835.1 Length: 587

Range 1: 55 to 553 Score:915 bits(495), Expect:0.0, Identities:498/499(99%), Gaps:1/499(0%), Strand: Plus/Plus

Strain: **S22**

Identified genus: *Penicillium*

ITS sequence:

AAACARTACGTAAGTGACCTGCGGAGGTACATTACCGAGCGAGAATTCTCTGATTCAACCTCCCACCCGTGT
TTATTGTACCTTGTTGCTTCGGYGGGYCCGCCTACGGCCGTCGGGGGKGCTGTCTCCGGTTCCKTGCCCGS
CKAGACMCCTTGAACCTCTGTWTGAAAATTGCWKGCTGAGTCTAAMTATRAMTTATTTAAWACTTTCAWC
MAMSGATCWCTTGGMTMCGGCTTSGATGAAGAACSCAKSRAAATGSSATACRWAAGTGAATTGCAGAAT
WCAKKGAAWCATCRAGKCTTTGAACGCWCATTGCGCCCCCTGGTATTCCGGGGGGAATGCCTGTCCGAGC
GTCRTTGMTGCCCTCATWRCCGGCTTAKGYTTTGAGGACTCGAACCCCAAWCCAGAAAA

BLAST query:

>Penicillium sp. P10-16c internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KT354994.1 Length: 593

Range 1: 14 to 387 Score:435 bits(235), Expect:1e-117, Identities:315/374(84%), Gaps:3/374(0%), Strand: Plus/Plus

Strain: **S23**

Identified genus: *Penicillium*

ITS sequence:

GRAAACARTGAGTAGTGACCTGCGGAGGTACATTACCGAGCGAGAATTCTCTGATTCAACCTCCCACCCGTG
TTTATTGTACCTTGTTGCTTCGGCGGGCCCCGCCCTCACGGCCCGCGGGGGGCATCTGCCCCCGGGCCCCGCGCC
CGCCGAAGACACCTTGAACCTCTGTATGAAAATTGCAGTCTGAGTCTAAATATAAATTATTTAAAACCTTTCAA
CAACGGATCTCTTGTTCCGGCATCGATGAAGAACGCAGMGAAATGCGATACGTAATGTGAATTGCAGAAT
TCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGACCGAGCGT
CATTGCTGCCCTCGAGCCCCGGCTTGAGAACAAAARGAATAAATSAAAAATTCCCGGGAGGAAAC

BLAST query:

>Penicillium sp. P10-16c internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KT354994.1 Length: 593

Range 1: 13 to 388 Score:656 bits(355), Expect:0.0, Identities:369/376(98%), Gaps:2/376(0%), Strand: Plus/Plus

Strain: **S24**

Identified genus: *Aspergillus*

calmodulin sequence:

CAYSRRRCYKKWAWWWGAAAWWTTTGTGTTGTMCGGTTTCGAAAACCTTGAAAGCCTCTCGGATTTCCTCC
TCGGAGTCGGTGTCCTTCATCTTTCTGGCCATCATTGTGAGGAACCTCTGATATATTTTTTTTGAGTCAGTGATC
TGCCCAATATCCTGTAAGCCTAGAGGTTGTATCGTGAGTATATACCTGGGAAATCAATGGTGCCGTTGTTGTC
GGCGTCAACCTCGTTGATCATGTCCTGGAGTTCAGACTCGGAGGGGTTCTGCCCCGAGCGAGCGCATCACAG
TGCCGAGTTCCTTGTTGGTAATCTGGCCTAATCGCATTACACATTATCTATACCAGGTTAATTGATGGTGCT
AAATATTATGGGATAATCGAGGCTGAGCGTATGCWAWAACTTTGCCGGATTGGGTGGGTTGCACYTTTTAT
CTCTTTACTTTTCCWGTTCATAGCTGATTTTGTATTWTTTTTTWTTTTTTTTATM

BLAST query:

>Aspergillus pseudodeflectus partial CaM gene for calmodulin, isolate CCF 4965

Sequence ID: LT558760.1 Length: 752

Range 1: 140 to 539 Score:671 bits(363), Expect:0.0, Identities:389/402(97%), Gaps:3/402(0%), Strand: Plus/Minus

Strain: **S25**

Identified genus: *Fusarium*

ITS sequence:

GAWYSRRGTWYYAMTTCCAAACCCCTTGTGACATACCTATAACGTTGCCTCGGCGGGCGCCCGTCTCCCCGTA
AAACGGGAGCGGCCCGCCAGAGGAAAACCAAACTCTTGTTTTAGAAGTATCTTCTGAGTAACAAAAATAA
TCAATTAAAACCTTCAACAACGGATCTCTTGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGT
AATGTGAATTGCAGAAATCAGTGAATCATCRAATCTTTGAACGCACATTGCGCCCCGCCAGTACTCTGGCGG
GCATGCCTGTTTCGAGCGTCATTCAACCTCWAGCCCCATCGGTTTGGTTTTTTGTWTCATTTTMTAATATT
AATTCCC

BLAST query:

>Fusarium sp. BDS-2017a strain CGMCC3.17370 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Sequence ID: KX790415.1 Length: 527

Range 1: 59 to 375 Score:562 bits(304), Expect:5e-156, Identities:313/318(98%), Gaps:2/318(0%), Strand: Plus/Plus

Strain: **S26**

Identified genus: *Penicillium*

ITS sequence:

TGGWGCAGTCGCAGTGACCTGCGGGAGGtaCatTACCGAGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGT
GTTTATCGTACCTTGTTGCTTCGGCGGGCCCCGCCTCACGGCCGCCGGGGGGCTTCTGCCCTCTGGCCCGCGC
CCGCCGAAGACACCATTGAACGCTGTCTGAAGATTGCAGTCTGAGCAATTAGCTAAATAAGTTAAAACCTTT
CAACAACGGATCTCTTGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAG
AATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAG
CGTCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGTCCTCCTCCCGGGGGACGGGCCCCGAAAG
GCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTCGTCACCCGCTCTTGTAGGCCCGGCCGCGC
GCTTGCCGACACATCAATCTTTTTTCCAGGTTGACCTCGGATCAGGTAGGGATAACCCGCT

BLAST query:

>Penicillium sp. isolate AM038-P9T4R 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene,
partial sequence

Sequence ID: KT264414.1 Length: 581

Range 1: 10 to 557 Score:989 bits(535), Expect:0.0, Identities:544/548(99%), Gaps:1/548(0%), Strand: Plus/Plus
