Supplementary Information for:

Increased prevalence of indoor *Aspergillus* and *Penicillium* species is associated with indoor flooding and coastal proximity: a case study of 28 moldy buildings

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SI Table 1: PA prevalence in each building sampled for this study. ID, Building Identification Numberused in this study; State, U.S. state in which the sampled buildings are located; F vs. NF, whether mold growth was due to indoor flooding (F) or other dampness issues (NF); RES (Y/N), whether the buildings are used for residential (Y) or non-residential purposes (N); C vs. NC, whether buildings are located in coastal (C) or a non-coastal (NC) location and Asp-Pen (%), percent prevalence of Asp-Pen.

ID	State	F vs. NF	RES (Y/N)	C vs. NC	Asp-Pen (%) *(n / total colonies)*
1	NJ	F	Y	C	87 (25/29)
2	NJ	F	Y	C	92 (20 /22)
3	NJ	F	Y	C	97 (36/37)
4	NJ	F	Y	C	81 (13/16)
5	NJ	F	Y	C	88 (23/26)
6	SC	F	N	C	84 (16/19)
7	SC	F	N	C	93 (26/28)
8	SC	F	N	C	83 (19/23)
9	SC	F	N	C	82 (27/33)
10	SC	F	N	C	86 (25/29)
11	NC	F	N	NC	63 (12/19)
12	NC	F	N	NC	70 (16/23)
13	NC	F	Y	NC	76 (13/17)
14	SC	F	Y	NC	81 (22/27)
15	SC	F	Y	NC	79 (15/19)
16	SC	NF	Y	C	48 (10/21)
17	SC	NF	Y	C	45 (14/31)
18	SC	NF	N	C	43 (10/23)
19	SC	NF	N	C	49 (16/33)
20	SC	NF	N	C	46 (11/24)
21	SC	NF	N	C	38 (12/32)
22	SC	NF	Y	NC	45 (13/29)
23	SC	NF	Y	NC	20 (5/25)
24	NC	NF	Y	NC	29 (5/17)
25	NC	NF	Y	NC	31 (8/26)
26	SC	NF	Y	NC	27 (6/22)
27	NC	NF	N	NC	18 (5/28)
28	DC	NF	N	NC	22 (5/23)

SI Fig 1. NJ phylograms of the strains that were identified in the study (generated from ITS2 sequence data). The ITS2 sequences were searched against the Accugenix fungal library database using the BLAST algorithm and proprietary software to determine the closest library reference matches to the unknown sequence. These reference library entries entered in the phylogenetic analysis pipeline with a pairwise alignment, percent difference and genetic distance calculations. Once the evolutionary distance measurements were calculated, the Neighbor Joining tree was constructed using proprietary software and the identification of the isolates from the phylogenetic tree were inferred to the genus level (for all isolates) and to the species level (for most isolates). The genera are displayed in the order of their prevalence.
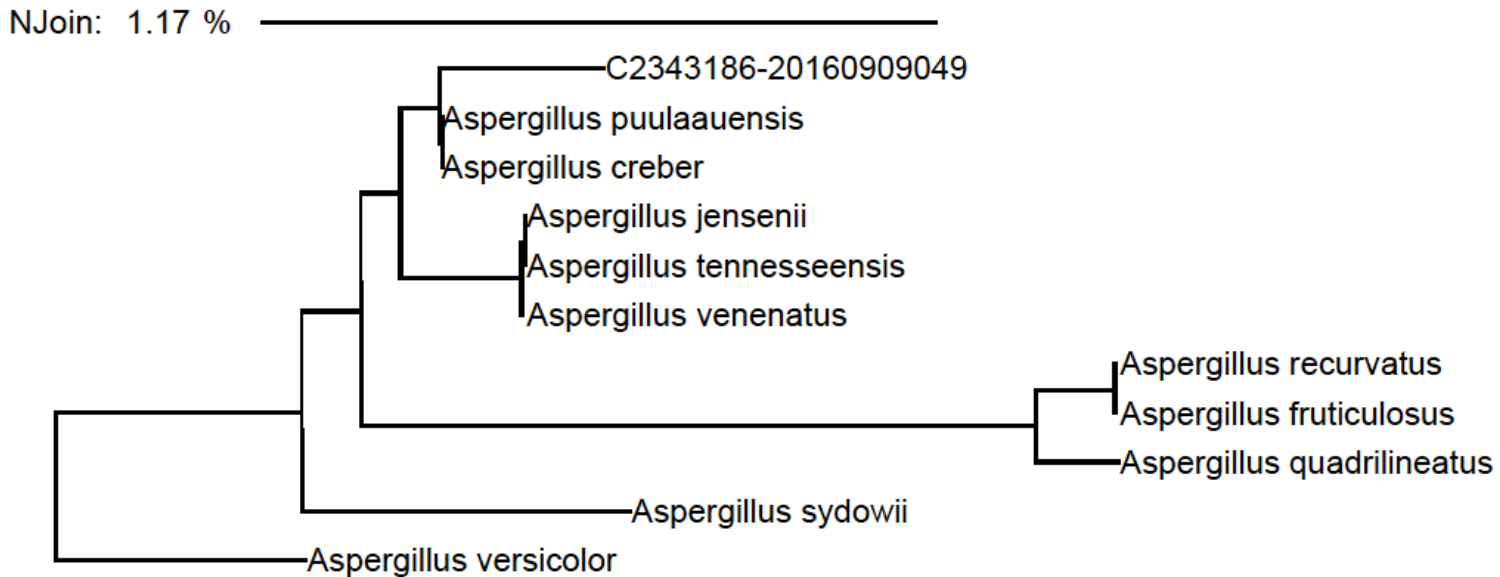
Identification: **Aspergillus creber / puulaauensis**

Confidence Level: **Species***

*The Unknown matches two or more closely related species.

Sequence Alignment

Alignment: 352 C2343186-20160909049
0.28 % 352 Aspergillus puulaauensis
0.28 % 352 Aspergillus creber
0.57 % 352 Aspergillus jensenii
0.57 % 352 Aspergillus tennesseensis
0.57 % 352 Aspergillus venenatus
1.14 % 353 Aspergillus sydowii
1.42 % 352 Aspergillus versicolor
1.70 % 354 Aspergillus recurvatus
1.70 % 353 Aspergillus quadrilineatus
1.70 % 354 Aspergillus fruticulosus

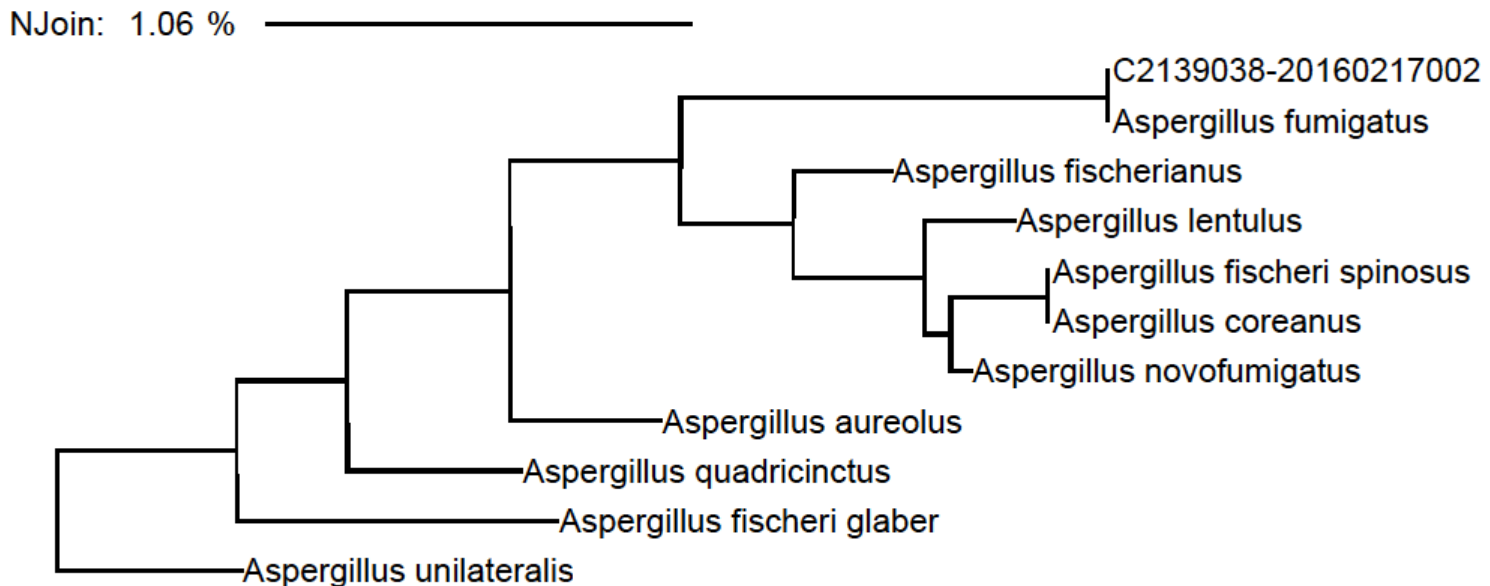## Neighbor Joining Tree

NJoin: 1.17 %

Identification: **Aspergillus flavus flavus / Aspergillus oryzae oryzae**

Confidence Level: **Species***

*The Unknown matches two or more closely related species.

Sequence Alignment

Alignment: 354 C2138022-20160210139
0.00 % 354 Aspergillus flavus flavus
0.00 % 354 Aspergillus oryzae oryzae
0.85 % 352 Aspergillus novoparasiticus
1.13 % 356 Aspergillus parasiticus
1.13 % 356 Aspergillus mottae
1.41 % 356 Aspergillus caelatus
1.41 % 356 Aspergillus tamarii
2.26 % 358 Aspergillus nomius
4.83 % 352 Aspergillus leporis
5.13 % 351 Aspergillus heteromorphus

Neighbor Joining Tree

NJoin: 3.06 %

Identification: **Aspergillus   fumigatus**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 353 C2139038-20160217002
0.00 % 353 Aspergillus fumigatus
1.43 % 349 Aspergillus fischerianus
1.72 % 349 Aspergillus lentulus
2.01 % 349 Aspergillus fischeri spinosus
2.01 % 349 Aspergillus coreanus
2.01 % 348 Aspergillus novofumigatus
2.27 % 355 Aspergillus unilateralis
2.27 % 353 Aspergillus aureolus
2.27 % 355 Aspergillus quadricinctus
2.27 % 357 Aspergillus fischeri glaber

Neighbor   Joining   Tree

NJoin: 1.06 %

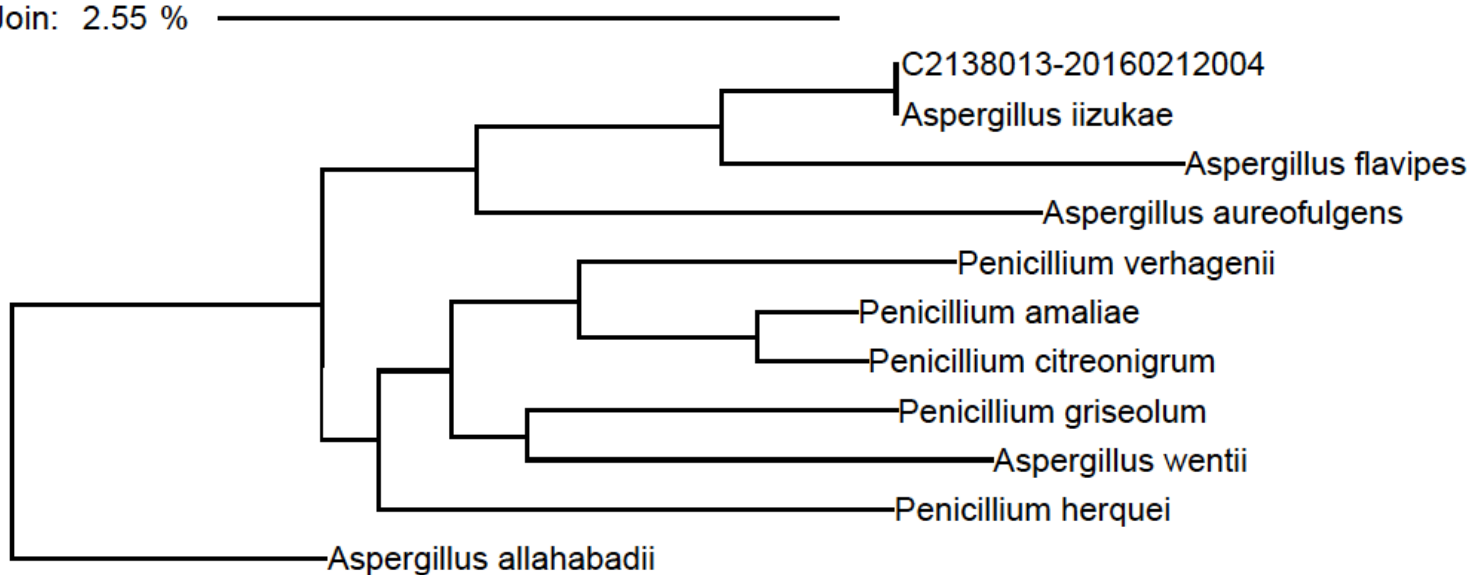Identification: **Aspergillus   iizukae**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 348 C2138013-20160212004
 0.00 % 348 Aspergillus iizukae
 2.61 % 345 Aspergillus flavipes
 4.02 % 354 Aspergillus aureofulgens
 4.60 % 352 Penicillium verhagenii
 4.60 % 353 Penicillium herquei
 4.89 % 354 Aspergillus allahabadii
 4.89 % 352 Penicillium griseolum
 4.89 % 353 Penicillium amaliae
 4.89 % 355 Penicillium citreonigrum
 4.89 % 351 Aspergillus wentii

Neighbor Joining Tree

NJoin: 2.55 %

C2138013-20160212004
Aspergillus iizukae
Aspergillus flavipes
Aspergillus aureofulgens
Penicillium verhagenii
Penicillium amaliae
Penicillium citreonigrum
Penicillium griseolum
Aspergillus wentii
Penicillium herquei
Aspergillus allahabadii

Identification: **Aspergillus jensenii / tennesseensis / venenatus**

Confidence Level: **Species***

*The Unknown matches two or more closely related species.

Sequence Alignment

Alignment: 352 C2138018-20160212005
0.00 % 352 Aspergillus venenatus
0.00 % 352 Aspergillus jensenii
0.00 % 352 Aspergillus tennesseensis
0.28 % 352 Aspergillus creber
0.28 % 352 Aspergillus puulaauensis
0.85 % 353 Aspergillus sydowii
1.14 % 352 Aspergillus versicolor
1.70 % 354 Emericella desertorum
1.70 % 354 Aspergillus nidulans
1.70 % 354 Aspergillus recurvatus

Neighbor Joining Tree

NJoin: 1.12 %

C2138018-20160212005
Aspergillus venenatus
Aspergillus jensenii
Aspergillus tennesseensis
Aspergillus creber
Aspergillus puulaauensis
Emericella desertorum
Aspergillus recurvatus
Aspergillus nidulans
Aspergillus sydowii
Aspergillus versicolor
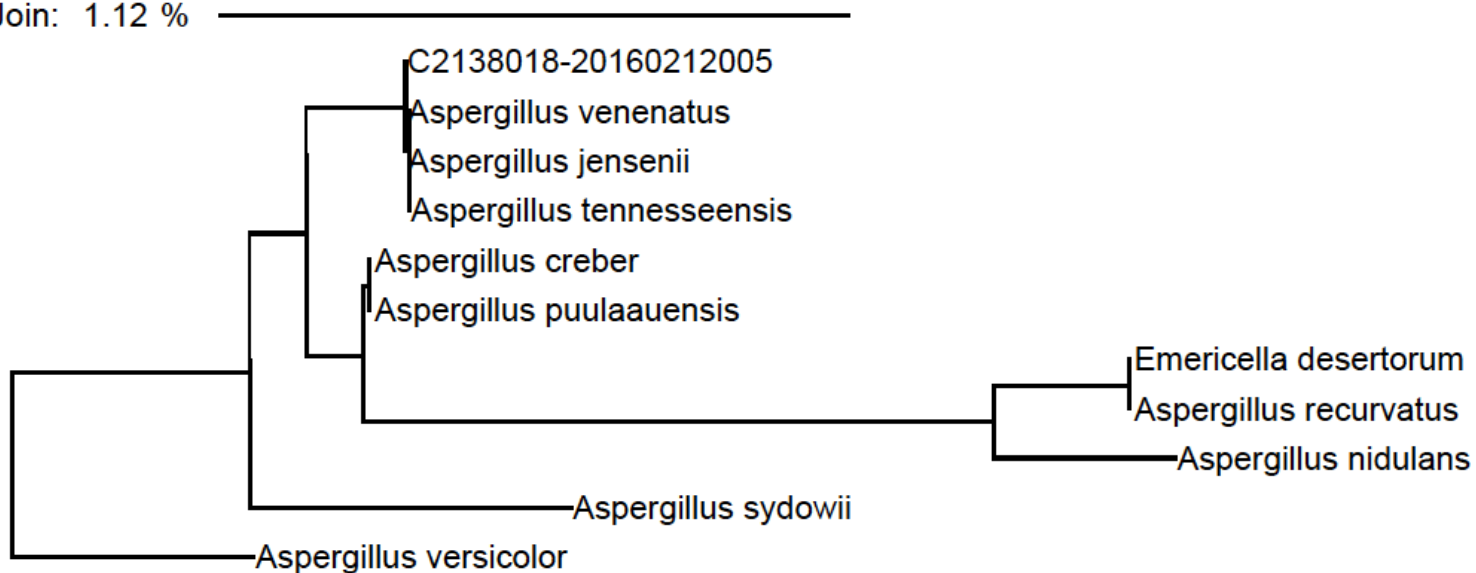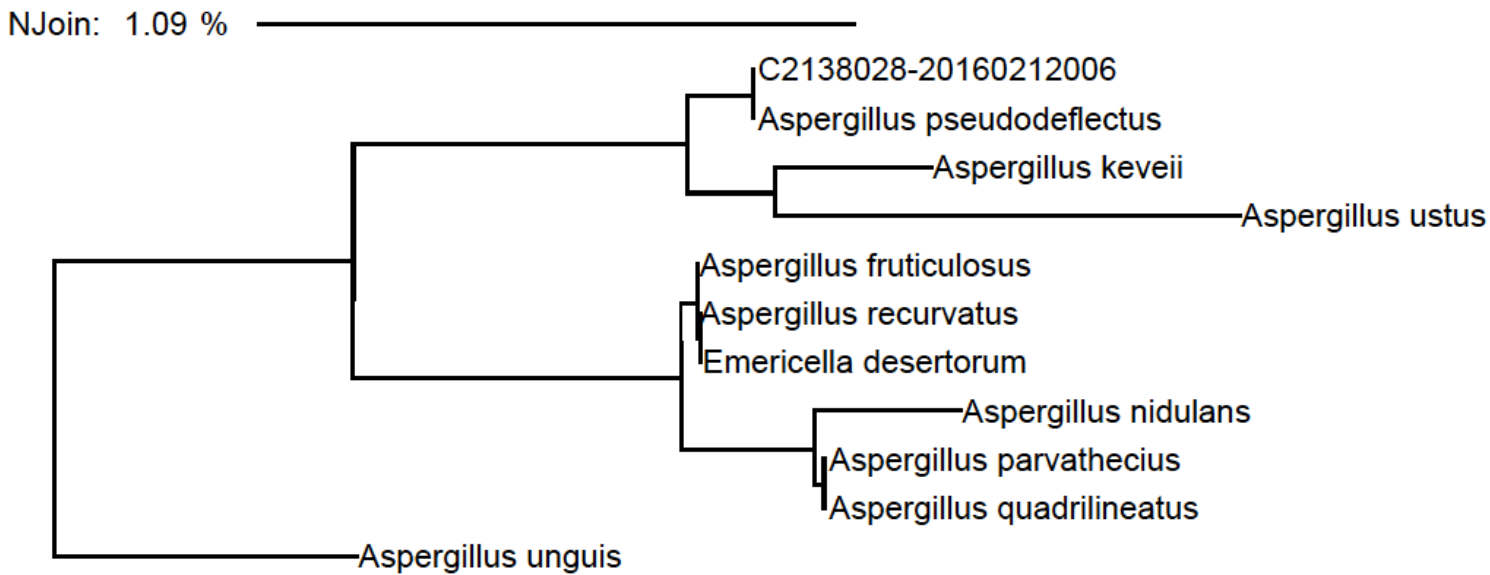
Identification: **Aspergillus pseudodeflectus**

Confidence Level: **Species**

Sequence Alignment

Alignment: 355 C2138028-20160212006
0.00 % 355 Aspergillus pseudodeflectus
0.56 % 355 Aspergillus keveii
1.13 % 357 Aspergillus ustus
1.41 % 354 Aspergillus fruticulosus
1.41 % 354 Aspergillus recurvatus
1.41 % 354 Emericella desertorum
1.69 % 354 Aspergillus nidulans
1.70 % 353 Aspergillus parvathecius
1.70 % 353 Aspergillus quadrilineatus
1.70 % 352 Aspergillus unguis

Neighbor Joining Tree

NJoin: 1.09 %

Identification: **Aspergillus sydowii**

Confidence Level: **Species**

Sequence Alignment

Alignment: 353 C2138016-20160212004
 0.28 % 353 Aspergillus sydowii
 0.57 % 352 Aspergillus tennesseensis
 0.57 % 352 Aspergillus venenatus
 0.57 % 352 Aspergillus creber
 0.57 % 352 Aspergillus puulaauensis
 0.57 % 352 Aspergillus jensenii
 1.14 % 352 Aspergillus versicolor
 1.70 % 354 Emericella desertorum
 1.70 % 354 Aspergillus recurvatus
 1.70 % 354 Aspergillus fruticulosus

Neighbor Joining Tree

NJoin: 1.35 %

C2138016-20160212004
Aspergillus sydowii
Aspergillus tennesseensis
Aspergillus venenatus
Aspergillus jensenii
Aspergillus creber
Aspergillus puulaauensis
Emericella desertorum
Aspergillus recurvatus
Aspergillus fruticulosus
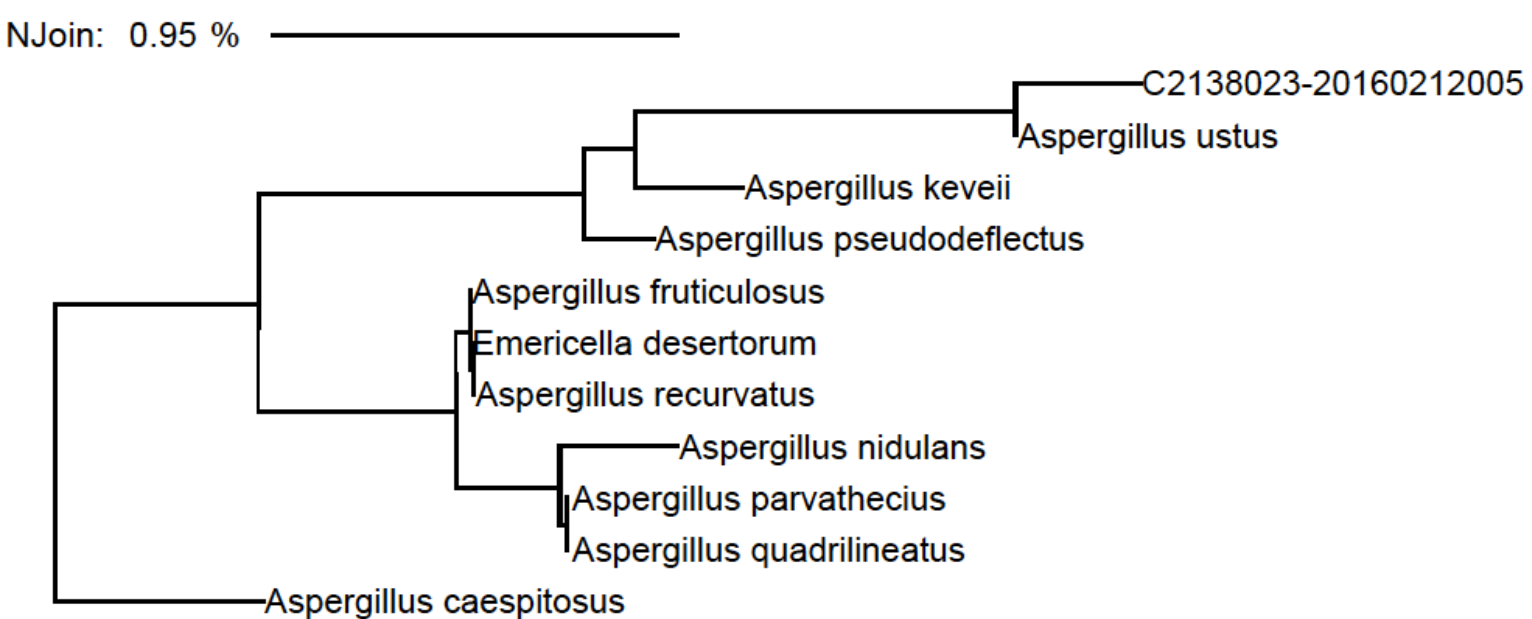Aspergillus versicolor
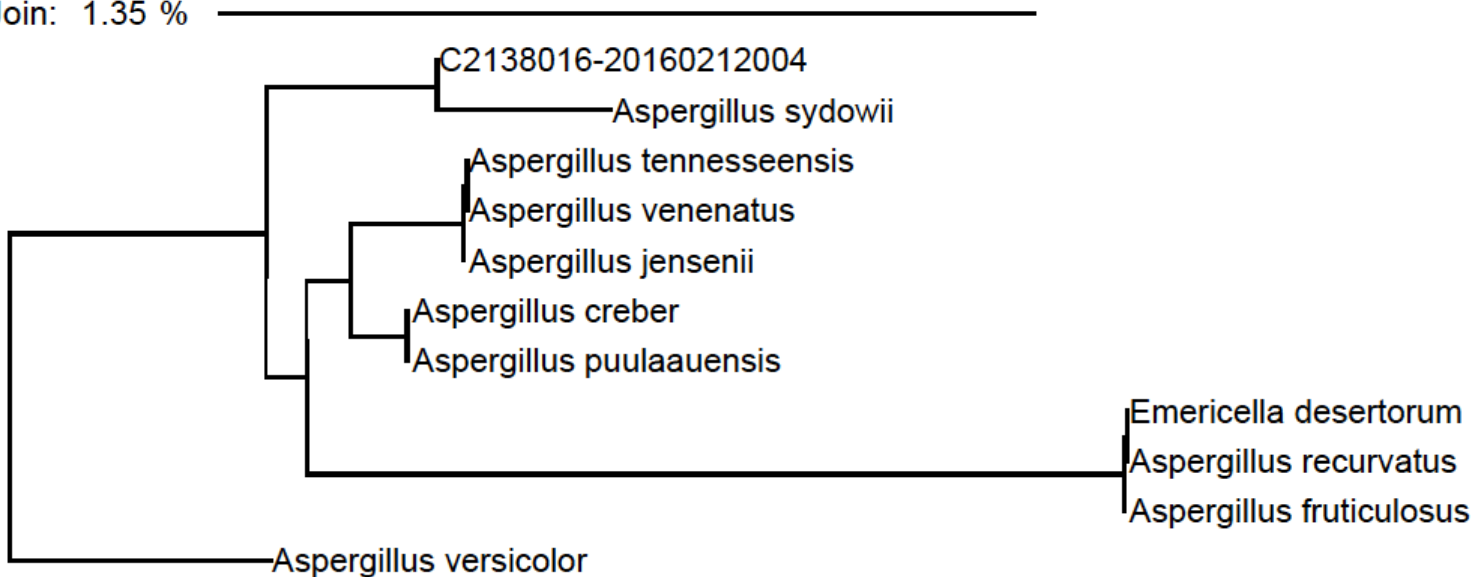
Identification: **Aspergillus ustus**

Confidence Level: **Species**

Sequence Alignment

Alignment: 357 C2138023-20160212005
 0.28 % 357 Aspergillus ustus
 1.41 % 355 Aspergillus keveii
 1.41 % 355 Aspergillus pseudodeflectus
 2.54 % 354 Aspergillus fruticulosus
 2.54 % 354 Emericella desertorum
 2.54 % 354 Aspergillus recurvatus
 2.82 % 354 Aspergillus nidulans
 2.83 % 353 Aspergillus parvathecius
 2.83 % 353 Aspergillus quadrilineatus
 3.12 % 353 Aspergillus caespitosus

Neighbor Joining Tree

NJoin: 0.95 %

C2138023-20160212005
Aspergillus ustus
Aspergillus keveii
Aspergillus pseudodeflectus
Aspergillus fruticulosus
Emericella desertorum
Aspergillus recurvatus
Aspergillus nidulans
Aspergillus parvathecius
Aspergillus quadrilineatus
Aspergillus caespitosus

Identification: **Aspergillus   versicolor**
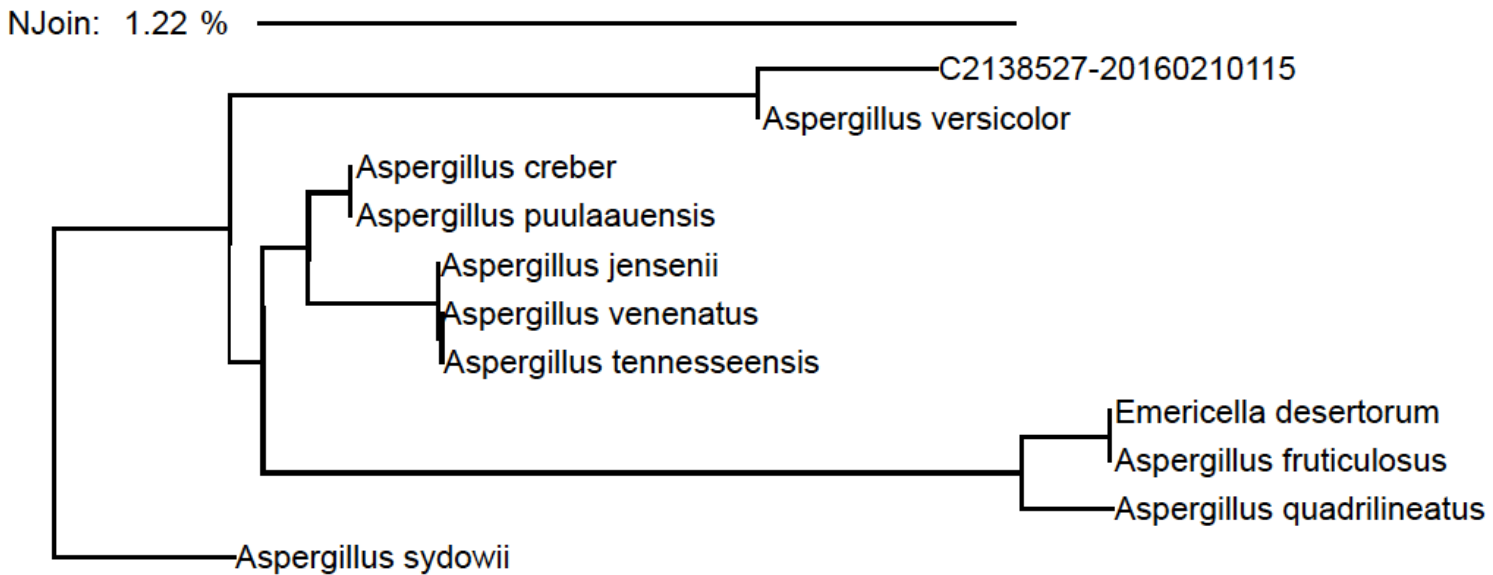
Confidence Level: **Species**

Sequence Alignment

Alignment: 353 C2138527-20160210115
 0.28 % 352 Aspergillus versicolor
 1.42 % 352 Aspergillus creber
 1.42 % 352 Aspergillus jensenii
 1.42 % 352 Aspergillus venenatus
 1.42 % 352 Aspergillus puulaauensis
 1.42 % 352 Aspergillus tennesseensis
 1.70 % 353 Aspergillus sydowii
 2.55 % 354 Emericella desertorum
 2.55 % 353 Aspergillus quadrilineatus
 2.55 % 354 Aspergillus fruticulosus

Neighbor Joining Tree

NJoin: 1.22 %

Identification: **Penicillium   oxalicum**

Confidence Level: **S p e c i e s**

Sequence   Alignment

Alignment: 354 C2139036-20160217001
0.00 % 354 Penicillium oxalicum
2.27 % 353 Penicillium reticulisporum
2.27 % 353 Penicillium mariae-crucis
2.82 % 355 Penicillium janthinellum
2.84 % 352 Penicillium simplicissimum
2.84 % 352 Penicillium rolfsii
3.11 % 355 Penicillium brasilianum
3.12 % 353 Penicillium boreae
3.39 % 355 Penicillium daleae
3.40 % 353 Penicillium ochrochloron

Neighbor   Joining   Tree

NJoin: 1.61 %
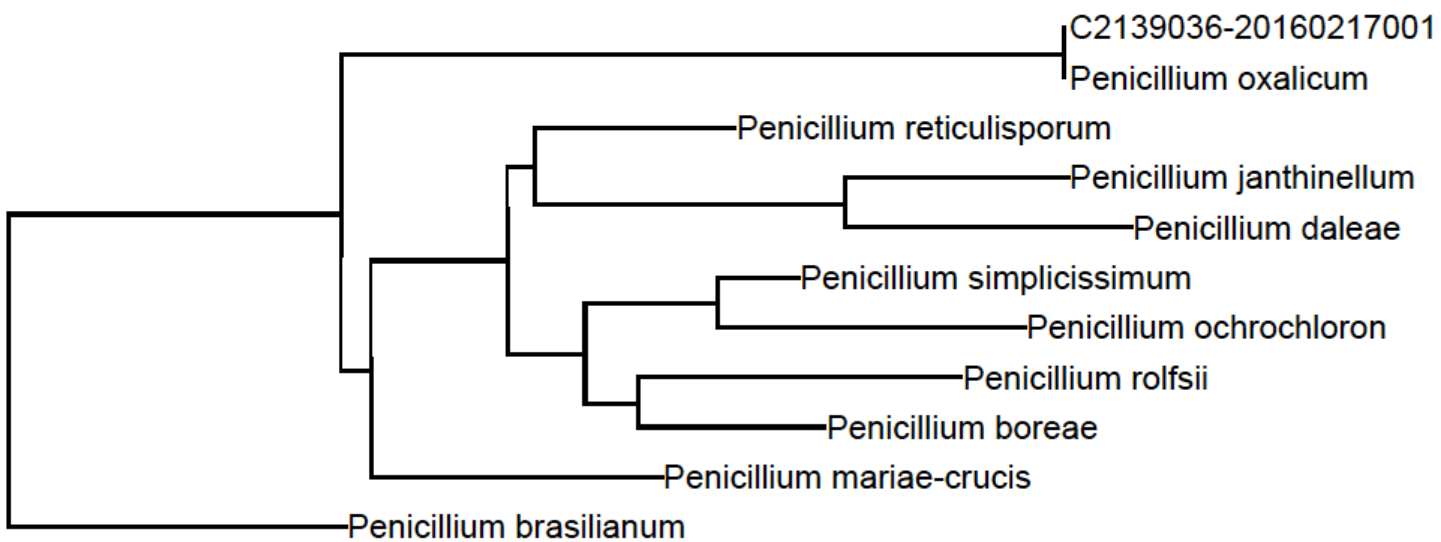
Identification: **Penicillium chrysogenum / flavigenum**

Confidence Level: **Species***

*The Unknown matches two or more closely related species.

Sequence Alignment

Alignment: 350 C2138024-20160212006
0.00 % 350 Penicillium flavigenum
0.00 % 350 Penicillium chrysogenum
0.29 % 350 Penicillium melanoconidium
0.29 % 350 Penicillium nalgiovense
0.29 % 350 Penicillium rubens
0.29 % 351 Penicillium flavigenum clade 1
0.29 % 350 Penicillium cyclopium
0.29 % 350 Penicillium griseofulvum
0.57 % 350 Penicillium viridicatum
0.57 % 351 Penicillium caseifulvum

Neighbor Joining Tree

NJoin: 0.29 %

C2138024-20160212006
Penicillium flavigenum
Penicillium chrysogenum
Penicillium melanoconidium
Penicillium nalgiovense
Penicillium viridicatum
Penicillium caseifulvum
Penicillium cyclopium
Penicillium griseofulvum
Penicillium flavigenum clade 1
Penicillium rubens
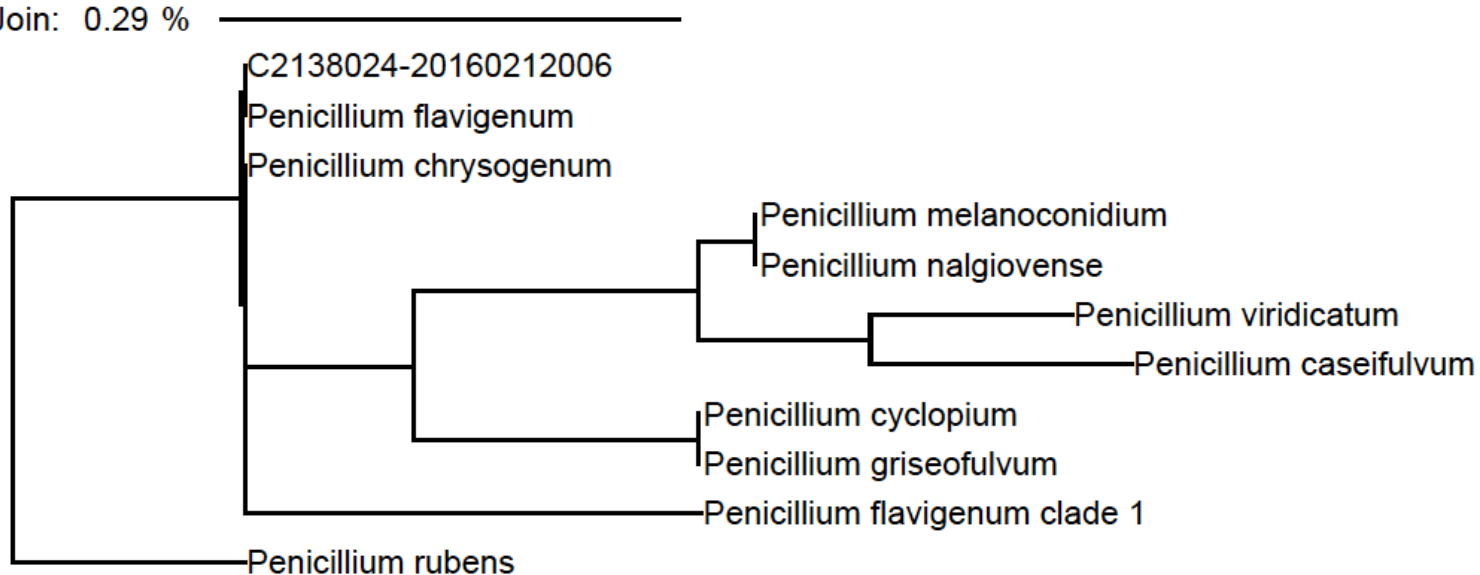
Identification: **Penicillium   citrinum**

Confidence Level: **Species**

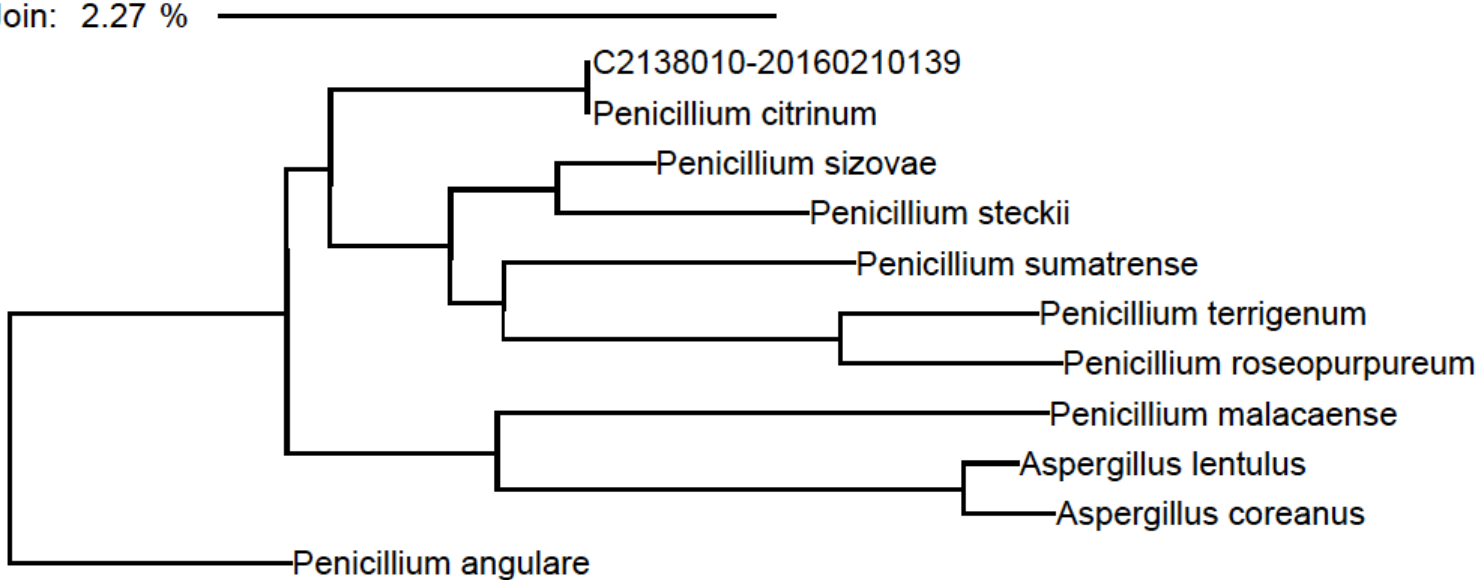## Sequence   Alignment

Alignment: 354 C2138010-20160210139
0.00 % 354 Penicillium citrinum
1.69 % 357 Penicillium sizovae
2.82 % 360 Penicillium steckii
3.39 % 358 Penicillium sumatrense
3.69 % 352 Penicillium angulare
4.00 % 350 Penicillium malacaense
4.24 % 356 Penicillium terrigenum
4.24 % 355 Penicillium roseopurpureum
4.30 % 349 Aspergillus lentulus
4.30 % 349 Aspergillus coreanus

Neighbor Joining Tree

NJoin: 2.27 %

C2138010-20160210139
Penicillium citrinum
Penicillium sizovae
Penicillium steckii
Penicillium sumatrense
Penicillium terrigenum
Penicillium roseopurpureum
Penicillium malacaense
Aspergillus lentulus
Aspergillus coreanus
Penicillium angulare
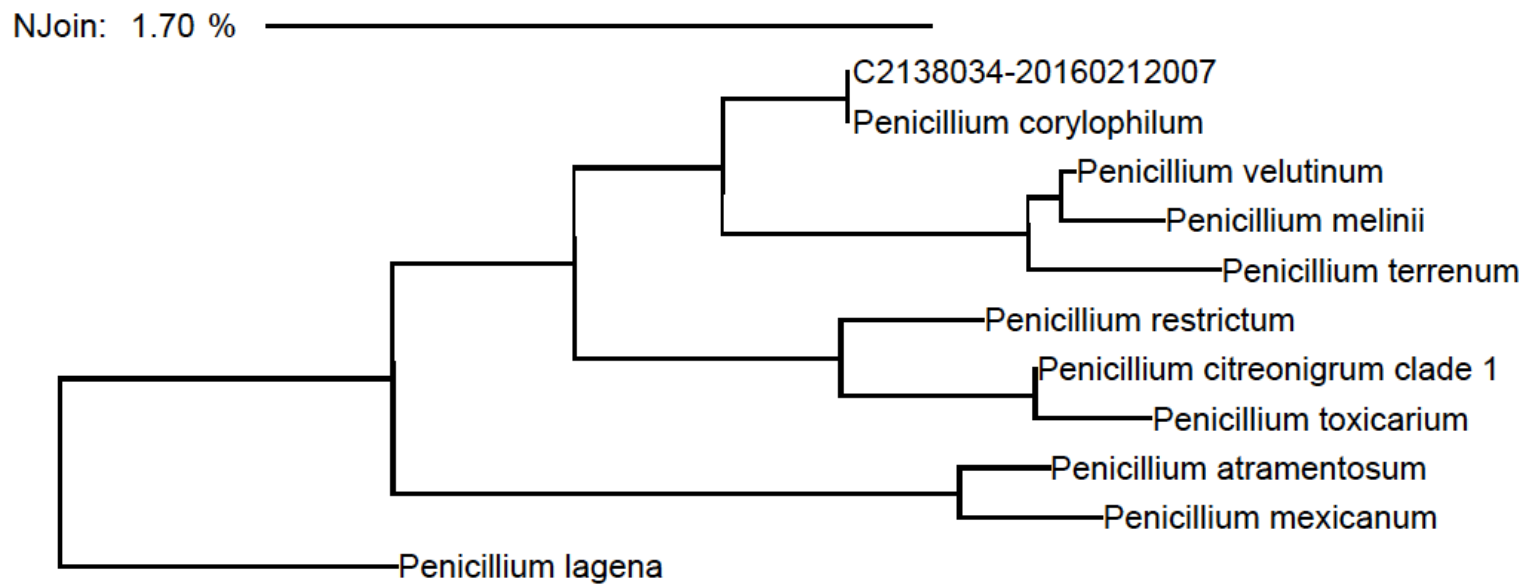
Identification: **Penicillium   corylophilum**

Confidence Level: **Species**

Sequence Alignment

Alignment: 351 C2138034-20160212007
0.00 % 351 Penicillium corylophilum
1.14 % 351 Penicillium velutinum
1.42 % 351 Penicillium melinii
1.71 % 352 Penicillium terrenum
1.99 % 351 Penicillium restrictum
2.30 % 348 Penicillium citreonigrum clade 1
2.56 % 352 Penicillium lagena
2.57 % 350 Penicillium atramentosum
2.58 % 349 Penicillium mexicanum
2.59 % 348 Penicillium toxicarium

Neighbor Joining Tree

NJoin: 1.70 %

- C2138034-20160212007
- Penicillium corylophilum
- Penicillium velutinum
- Penicillium melinii
- Penicillium terrenum
- Penicillium restrictum
- Penicillium citreonigrum clade 1
- Penicillium toxicarium
- Penicillium atramentosum
- Penicillium mexicanum
- Penicillium lagena

Identification: **Penicillium   crustosum**
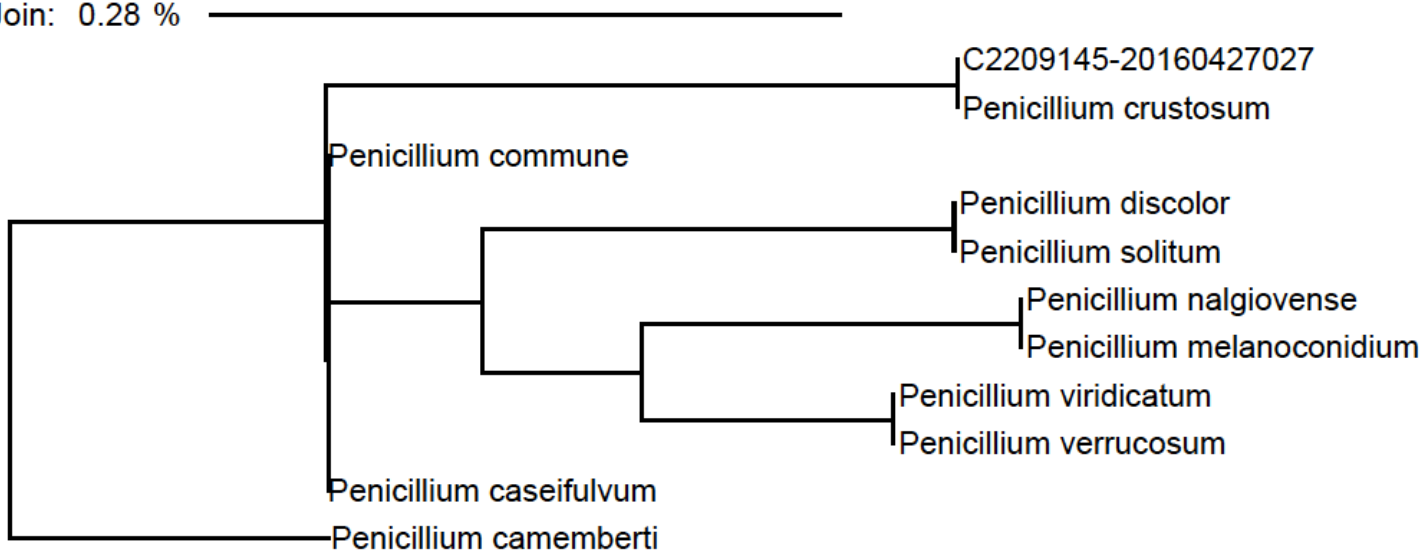
Confidence Level: **S p e c i e s**

Sequence   Alignment

Alignment: 351 C2209145-20160427027
0.00 % 351 Penicillium crustosum
0.28 % 351 Penicillium commune
0.28 % 351 Penicillium caseifulvum
0.57 % 351 Penicillium discolor
0.57 % 351 Penicillium solitum
0.57 % 351 Penicillium camemberti
0.57 % 350 Penicillium nalgiovense
0.57 % 350 Penicillium viridicatum
0.57 % 350 Penicillium verrucosum
0.57 % 350 Penicillium melanoconidium

Neighbor Joining Tree

NJoin: 0.28 %

C2209145-20160427027
Penicillium crustosum
Penicillium commune
Penicillium discolor
Penicillium solitum
Penicillium nalgiovense
Penicillium melanoconidium
Penicillium viridicatum
Penicillium verrucosum
Penicillium caseifulvum
Penicillium camemberti

Identification: **Penicillium glabrum**

Confidence Level: **Species**

Sequence Alignment

Alignment: 346 C2209166-20160427029
0.00 % 346 Penicillium glabrum
1.16 % 344 Penicillium spinulosum
2.89 % 346 Penicillium hirayamae
3.18 % 352 Penicillium verhagenii
3.47 % 349 Penicillium thomii
3.47 % 350 Penicillium adametzii
3.47 % 353 Penicillium amaliae
3.76 % 349 Penicillium lividum
3.77 % 345 Aspergillus neoniveus
4.05 % 355 Penicillium citreonigrum

Neighbor Joining Tree

NJoin: 2.23 %

C2209166-20160427029
Penicillium glabrum
Penicillium spinulosum
Penicillium verhagenii
Penicillium adametzii
Penicillium amaliae
Penicillium citreonigrum
Penicillium thomii
Penicillium lividum
Penicillium hirayamae
Aspergillus neoniveus
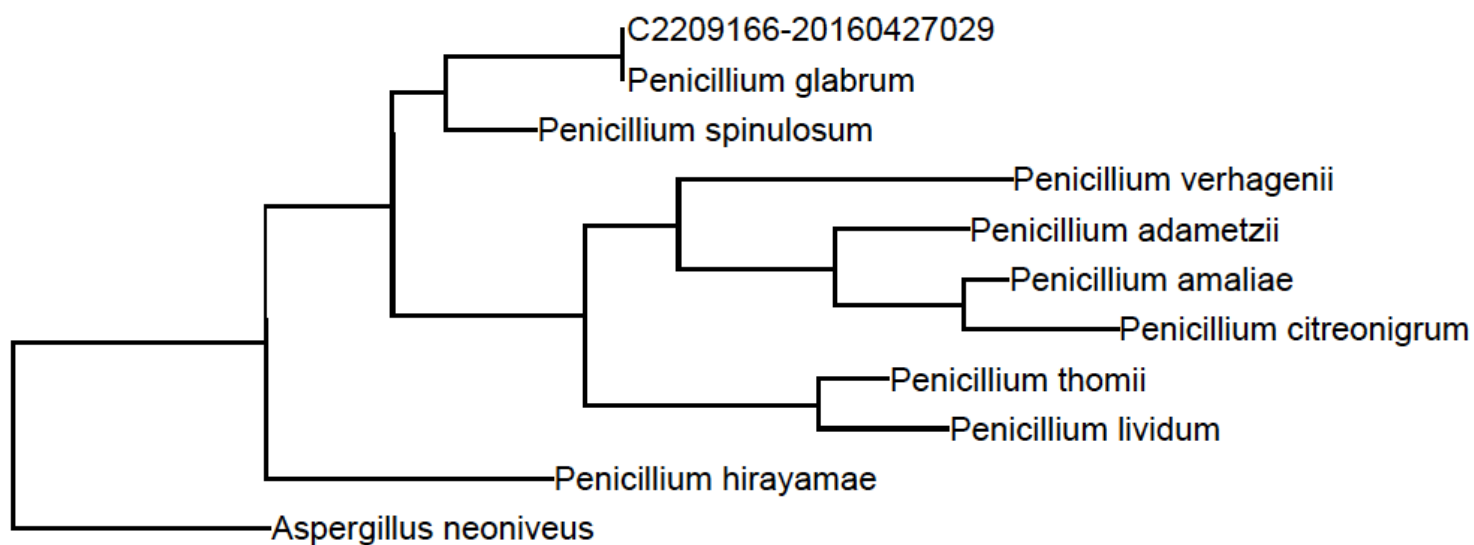
Identification: **Penicillium janthinellum**

Confidence Level: **Species**

Sequence Alignment

Alignment: 355 C2343197-20160909051
0.00 % 355 Penicillium janthinellum
1.13 % 355 Penicillium daleae
1.42 % 353 Penicillium reticulisporum
1.70 % 353 Penicillium mariae-crucis
1.98 % 353 Penicillium boreae
1.99 % 352 Penicillium simplicissimum
2.55 % 353 Penicillium ochrochloron
2.56 % 352 Penicillium rolfsii
2.82 % 354 Penicillium oxalicum
3.66 % 355 Penicillium dravuni

Neighbor Joining Tree

NJoin: 2.90 %

C2343197-20160909051
Penicillium janthinellum
Penicillium daleae
Penicillium reticulisporum
Penicillium boreae
Penicillium rolfsii
Penicillium simplicissimum
Penicillium ochrochloron
Penicillium mariae-crucis
Penicillium oxalicum
Penicillium dravuni
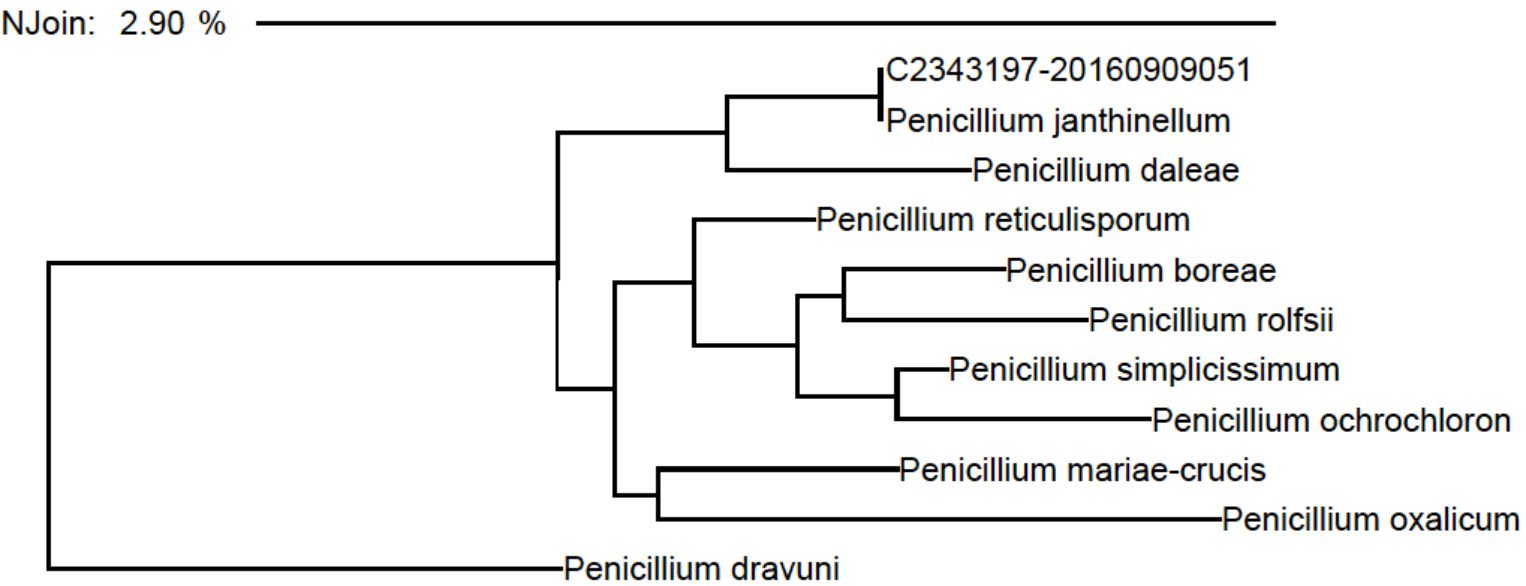
Identification: **Penicillium   macrosporum**
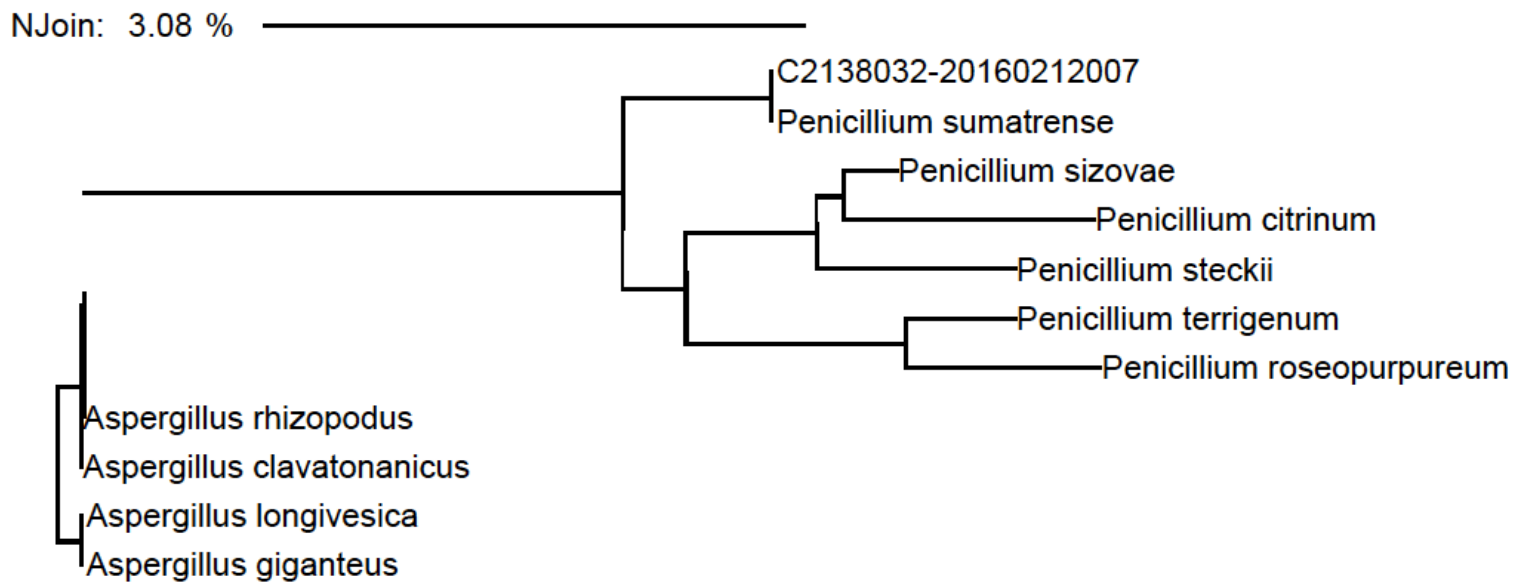
Confidence Level: **Species**

Sequence   Alignment

Alignment: 342 C2138027-20160212006
0.29 % 341 Penicillium macrosporum
0.58 % 342 Penicillium calidicanium
0.58 % 342 Penicillium pinophilum
0.58 % 342 Penicillium aculeatum
0.88 % 342 Penicillium verruculosum
0.88 % 341 Penicillium marneffei
0.88 % 339 Talaromyces(Penicillium) flavus flavus
1.17 % 342 Penicillium primulinum
1.75 % 344 Penicillium purpurogenum
1.75 % 344 Penicillium guizhouanum

Neighbor   Joining   Tree

NJoin: 1.02 %

C2138027-20160212006
Penicillium macrosporum
Penicillium calidicanium
Penicillium aculeatum
Penicillium primulinum
Penicillium verruculosum
Penicillium pinophilum
Penicillium marneffei
Talaromyces(Penicillium) flavus flavus
Penicillium guizhouanum
Penicillium purpurogenum
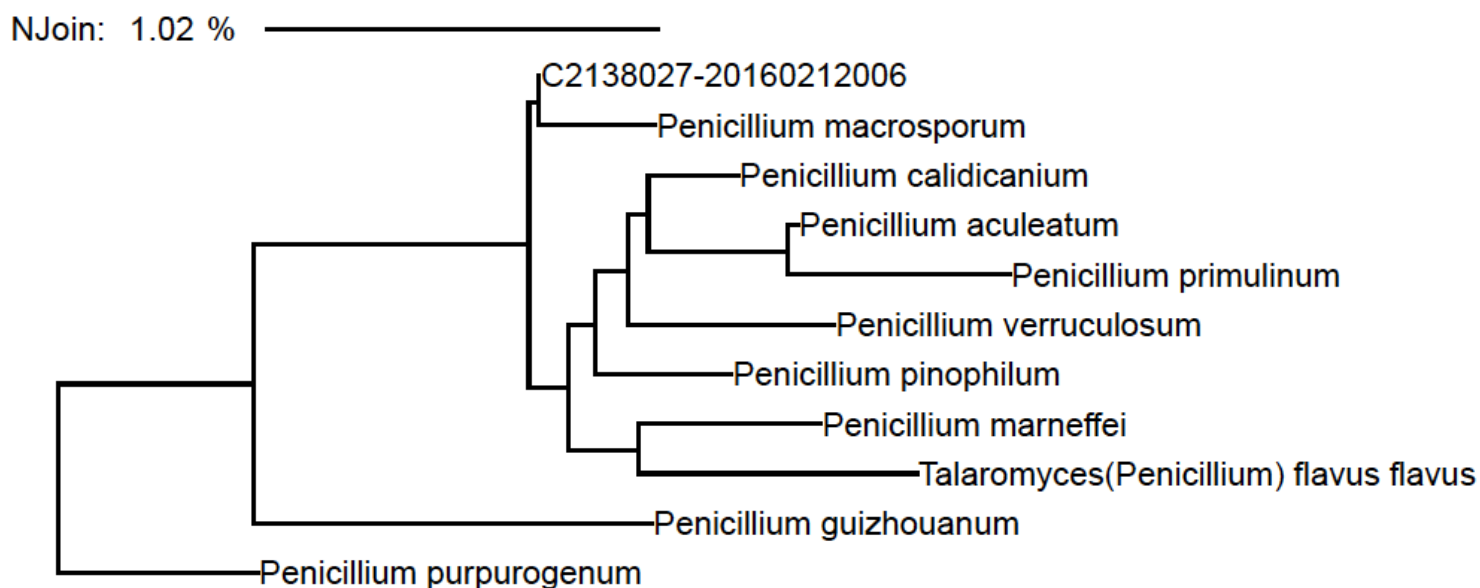
Identification: **Penicillium   rubens**

Confidence Level: **Species**

Sequence Alignment

Alignment: 350 C2138030-20160212006
 0.00 % 350 Penicillium rubens
 0.29 % 350 Penicillium chrysogenum
 0.29 % 350 Penicillium flavigenum
 0.57 % 350 Penicillium griseofulvum
 0.57 % 350 Penicillium cyclopium
 0.57 % 350 Penicillium glandicola
 0.57 % 350 Penicillium melanoconidium
 0.57 % 350 Penicillium nalgiovense
 0.57 % 351 Penicillium flavigenum clade 1
 0.86 % 350 Penicillium viridicatum

Neighbor Joining Tree

NJoin: 0.45 %

C2138030-20160212006
Penicillium rubens
Penicillium chrysogenum
Penicillium flavigenum
Penicillium flavigenum clade 1
Penicillium melanoconidium
Penicillium nalgiovense
Penicillium viridicatum
Penicillium griseofulvum
Penicillium cyclopium
Penicillium glandicola
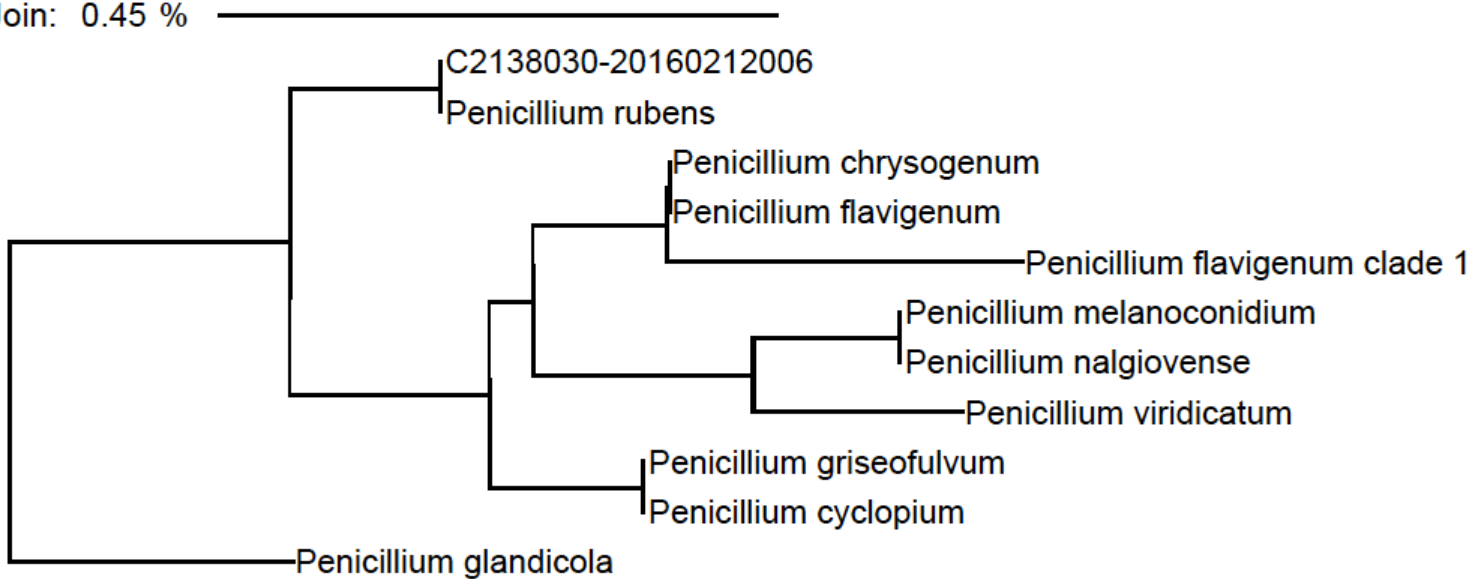
Identification: **Penicillium   sumatrense**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 358 C2138032-20160212007
 0.00 % 358 Penicillium sumatrense
 2.52 % 357 Penicillium sizovae
 2.79 % 360 Penicillium steckii
 3.37 % 356 Penicillium terrigenum
 3.39 % 354 Penicillium citrinum
 3.93 % 356 Aspergillus clavatonanicus
 3.93 % 356 Aspergillus rhizopodus
 3.94 % 355 Penicillium roseopurpureum
 4.21 % 356 Aspergillus longivesica
 4.21 % 356 Aspergillus giganteus

Neighbor Joining Tree

NJoin: 3.08 %

C2138032-20160212007
Penicillium sumatrense
Penicillium sizovae
Penicillium citrinum
Penicillium steckii
Penicillium terrigenum
Penicillium roseopurpureum
Aspergillus rhizopodus
Aspergillus clavatonanicus
Aspergillus longivesica
Aspergillus giganteus

Identification: **Penicillium   toxicarium**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 349 C2209161-20160427029
 0.29 % 348 Penicillium toxicarium
 0.57 % 348 Penicillium citreonigrum clade 1
 0.86 % 351 Penicillium restrictum
 1.72 % 351 Penicillium meridianum
 2.58 % 351 Penicillium corylophilum
 2.58 % 350 Penicillium decumbens
 2.58 % 351 Penicillium melinii
 2.87 % 352 Penicillium terrenum
 2.87 % 351 Penicillium velutinum
 3.15 % 350 Penicillium atramentosum

Neighbor   Joining   Tree

NJoin: 1.96 %
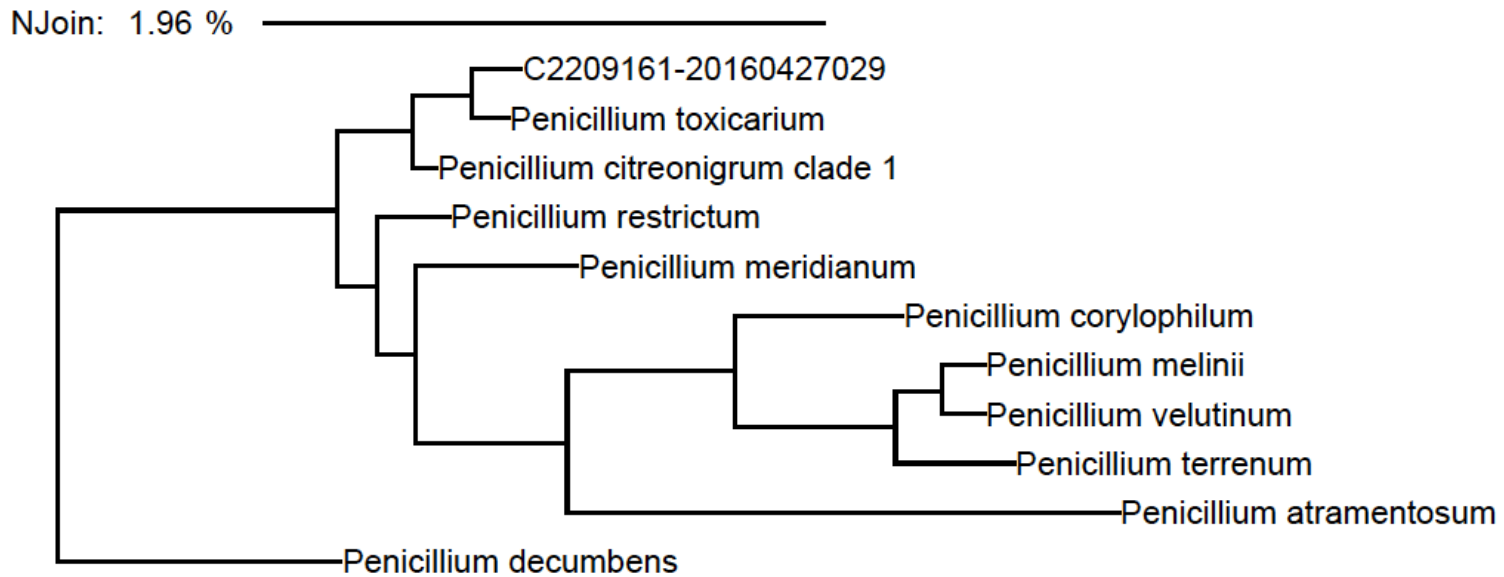
Identification: **Penicillium   verruculosum**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 342 C2209167-20160427030
0.29 % 342 Penicillium verruculosum
0.58 % 342 Penicillium aculeatum
0.58 % 342 Penicillium calidicanium
0.58 % 342 Penicillium pinophilum
0.88 % 341 Penicillium marneffei
0.88 % 341 Penicillium macrosporum
1.17 % 342 Penicillium primulinum
1.46 % 344 Penicillium dangeardii
1.47 % 339 Talaromyces(Penicillium) flavus flavus
1.75 % 343 Penicillium purpurogenum clade 2

Neighbor   Joining   Tree

NJoin: 1.46 %

C2209167-20160427030
Penicillium verruculosum
Penicillium aculeatum
Penicillium primulinum
Penicillium purpurogenum clade 2
Penicillium calidicanium
Penicillium pinophilum
Penicillium marneffei
Talaromyces(Penicillium) flavus flavus
Penicillium macrosporum
Penicillium dangeardii
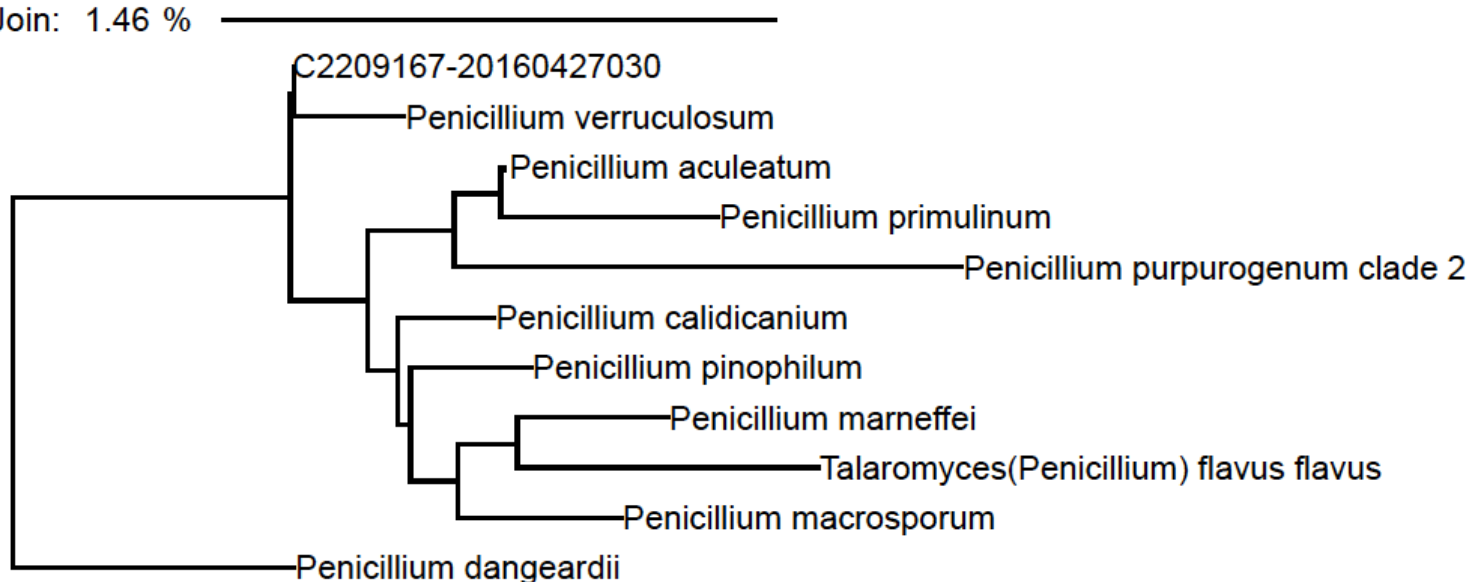
Identification: **Penicillium   sp.**

Confidence Level: **Genus**

Sequence   Alignment

Alignment: 342 C2138025-20160212006
 0.29 % 342 Penicillium calidicanium
 0.29 % 342 Penicillium pinophilum
 0.58 % 342 Penicillium verruculosum
 0.59 % 341 Penicillium macrosporum
 0.59 % 341 Penicillium marneffei
 0.88 % 342 Penicillium aculeatum
 1.18 % 339 Talaromyces(Penicillium) flavus flavus
 1.46 % 342 Penicillium primulinum
 1.75 % 344 Penicillium dangeardii
 2.05 % 344 Penicillium guizhouanum

Neighbor   Joining   Tree

NJoin: 1.71 %

C2138025-20160212006
Penicillium pinophilum
Penicillium calidicanium
Penicillium aculeatum
Penicillium primulinum
Penicillium verruculosum
Penicillium dangeardii
Penicillium marneffei
Talaromyces(Penicillium) flavus flavus
Penicillium macrosporum
Penicillium guizhouanum
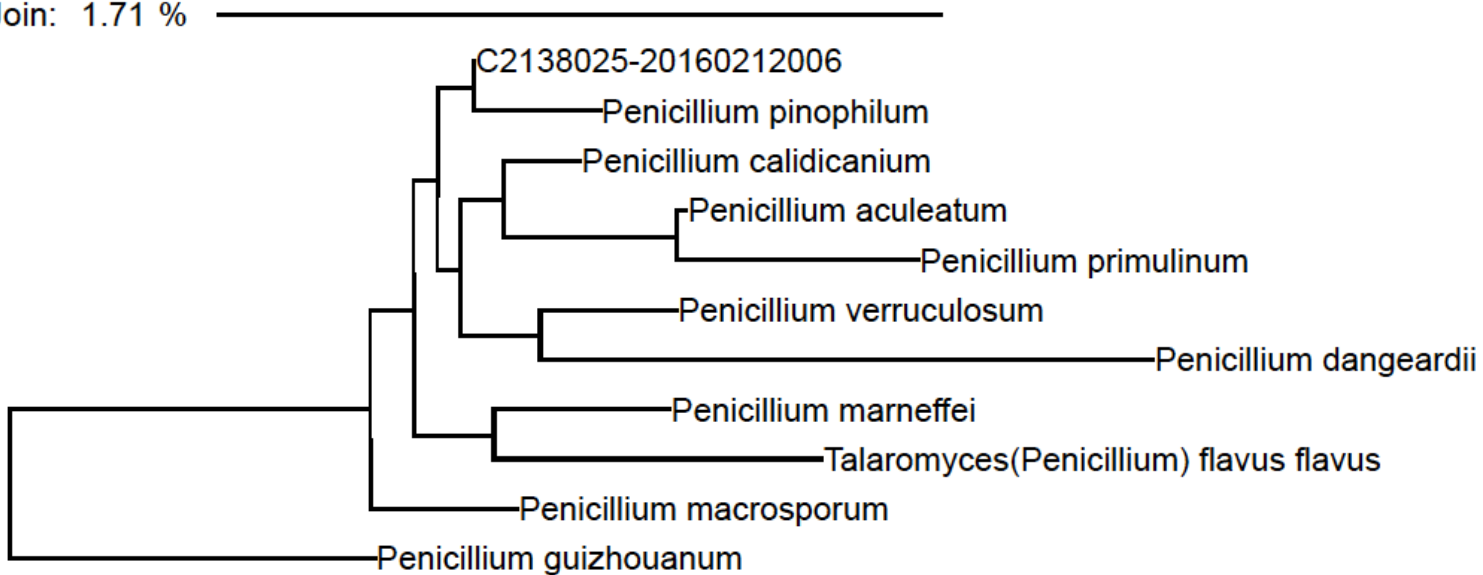
Identification: **Cladosporium cladosporioides / herbarum**

Confidence Level: **S p e c i e s ***

*The Unknown matches two or more closely related species.

Sequence Alignment

Alignment: 336 C2209160-20160427029
0.30 % 336 Cladosporium cladosporioides clade 1
0.60 % 336 Cladosporium cladosporioides
0.60 % 336 Cladosporium herbarum
0.89 % 336 Cladosporium tenuissimum
0.89 % 336 Cladosporium aphidis
0.89 % 336 Cladosporium grevilleae
0.89 % 336 Cladosporium langeronii
1.79 % 336 Cladosporium velox
2.98 % 337 Cladosporium sphaerospermum
2.98 % 337 Cladosporium halotolerans

Neighbor Joining Tree

NJoin: 0.83 % ─────────────────

C2209160-20160427029
Cladosporium cladosporioides clade 1
Cladosporium cladosporioides
Cladosporium herbarum
Cladosporium grevilleae
Cladosporium langeronii
Cladosporium tenuissimum
Cladosporium aphidis
Cladosporium velox
Cladosporium sphaerospermum
Cladosporium halotolerans
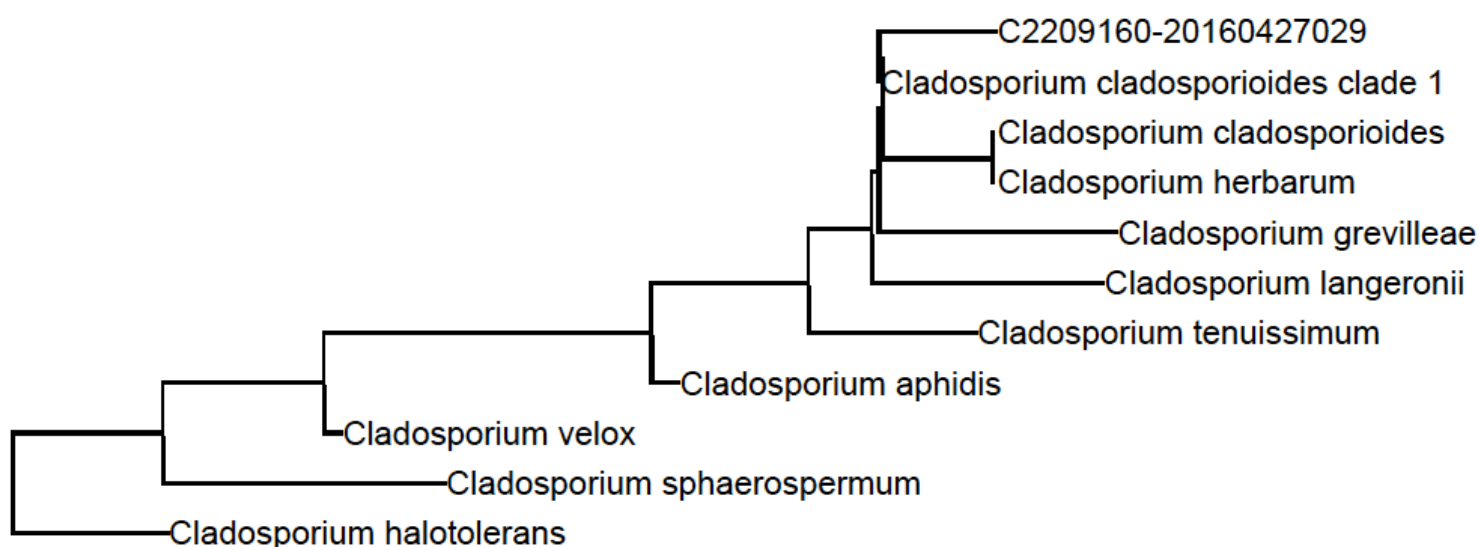
Identification: **Cladosporium   halotolerans**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 337 C2138031-20160212007
0.00 % 337 Cladosporium halotolerans
1.19 % 336 Cladosporium velox
1.48 % 337 Cladosporium sphaerospermum
2.08 % 336 Cladosporium aphidis
2.68 % 336 Cladosporium tenuissimum
2.68 % 336 Cladosporium cladosporioides clade 1
2.98 % 336 Cladosporium langeronii
2.98 % 336 Cladosporium cladosporioides
2.98 % 336 Cladosporium herbarum
3.27 % 336 Cladosporium grevilleae

Neighbor   Joining   Tree

NJoin: 0.82 % ——————————
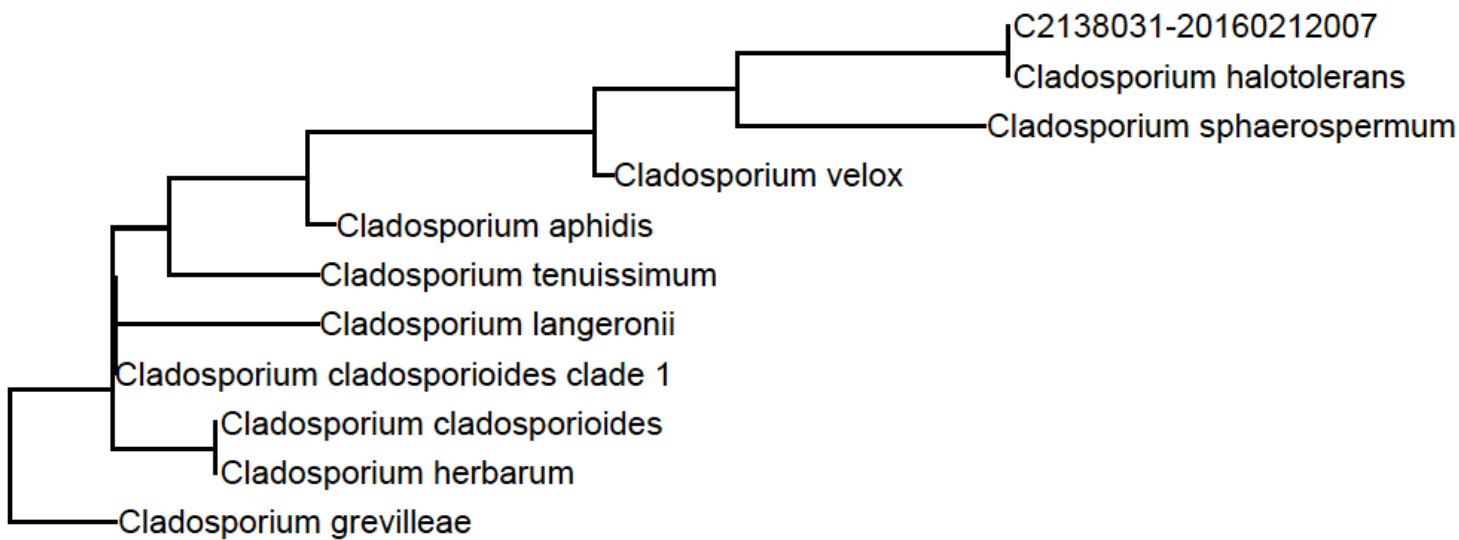
Identification: **Toxicocladosporium   irritans**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 338 C2343177-20160909043
 0.00 % 338 Toxicocladosporium irritans
 6.21 % 339 Verrucocladosporium dirinae
 6.21 % 341 Rachicladosporium cboliae
 6.23 % 337 Cladosporium halotolerans
 6.82 % 337 Cladosporium sphaerospermum
 6.85 % 336 Cladosporium velox
 6.85 % 336 Cladosporium aphidis
 7.14 % 336 Cladosporium tenuissimum
 7.44 % 336 Cladosporium langeronii
 7.44 % 336 Cladosporium cladosporioides clade 1

Neighbor Joining Tree

NJoin: 3.64 %
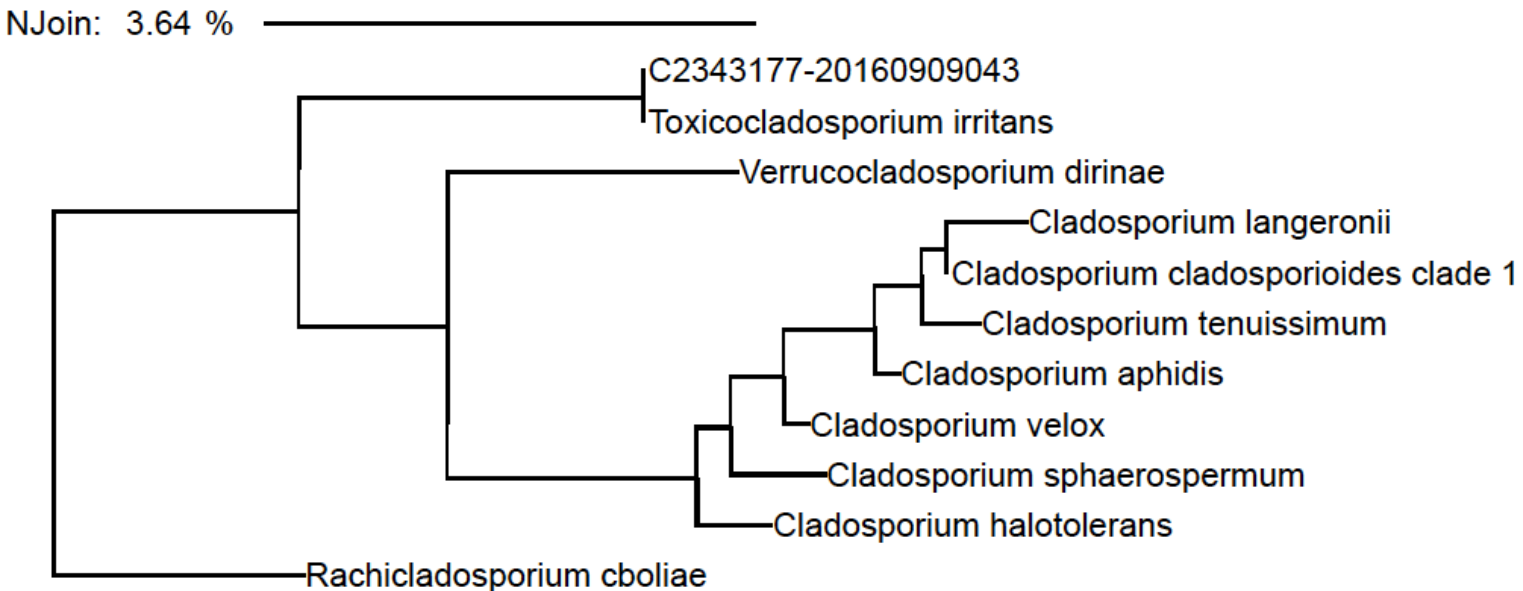
Identification: **Epicoccum   nigrum**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 343 C2209159-20160502024
0.00 % 343 Epicoccum nigrum clade 2
0.88 % 342 Phoma zeae-maydis
1.17 % 342 Phoma pomorum
1.17 % 342 Epicoccum nigrum clade 1
1.46 % 343 Phoma negriana
1.46 % 343 Phoma eucalyptica
1.46 % 343 Phoma draconis
1.46 % 342 Ascochyta rabiei
1.46 % 342 Phoma rumicicola
1.46 % 342 Phoma huancayensis

Neighbor   Joining   Tree

NJoin: 0.77 %

C2209159-20160502024
Epicoccum nigrum clade 2
Phoma zeae-maydis
Phoma draconis
Phoma rumicicola
Phoma pomorum
Epicoccum nigrum clade 1
Phoma huancayensis
Ascochyta rabiei
Phoma eucalyptica
Phoma negriana
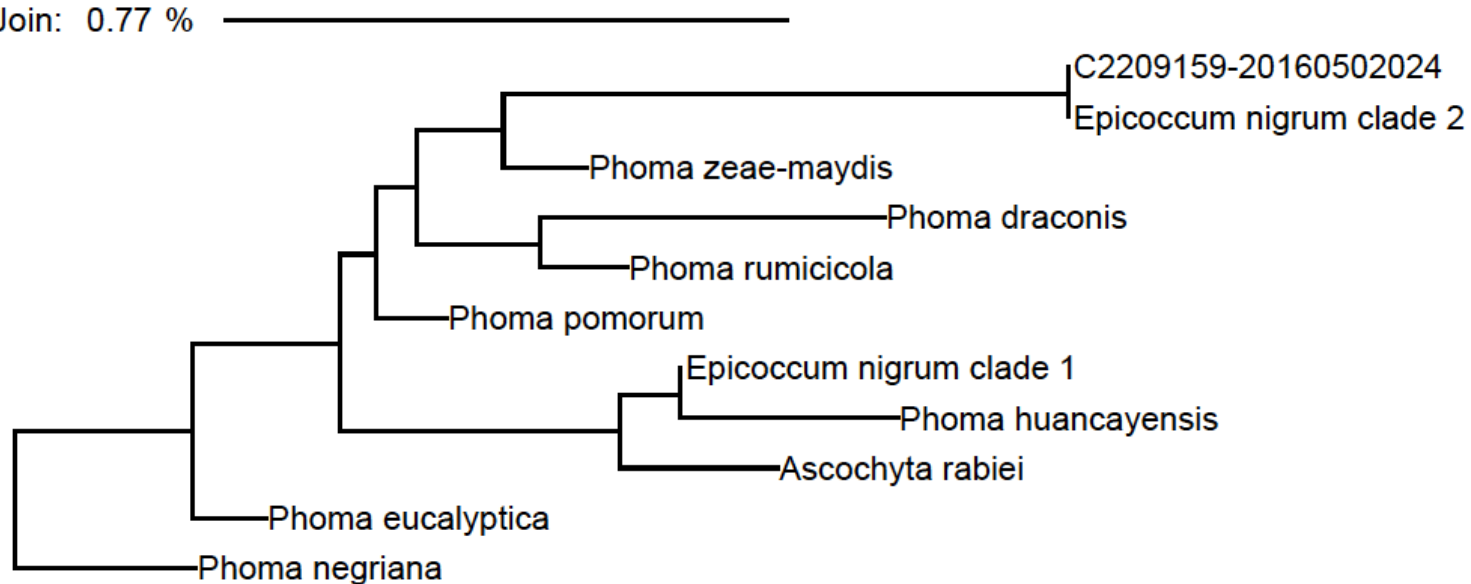
Identification: **Epicoccum   sorghi**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 334 C2138033-20160212007
 0.00 % 334 Epicoccum sorghi
 2.69 % 342 Didymella urticicola
 2.69 % 342 Phoma huancayensis
 2.69 % 342 Epicoccum nigrum clade 1
 2.99 % 342 Phoma glomerata
 2.99 % 342 Phoma pomorum
 2.99 % 342 Didymella phacae
 2.99 % 342 Phoma eupyrena
 2.99 % 342 Ascochyta rabiei
 3.29 % 342 Coniothyrium pyrinum

Neighbor Joining Tree

NJoin: 2.47 %

C2138033-20160212007
Epicoccum sorghi
Didymella urticicola
Phoma huancayensis
Epicoccum nigrum clade 1
Didymella phacae
Coniothyrium pyrinum
Ascochyta rabiei
Phoma eupyrena
Phoma glomerata
Phoma pomorum
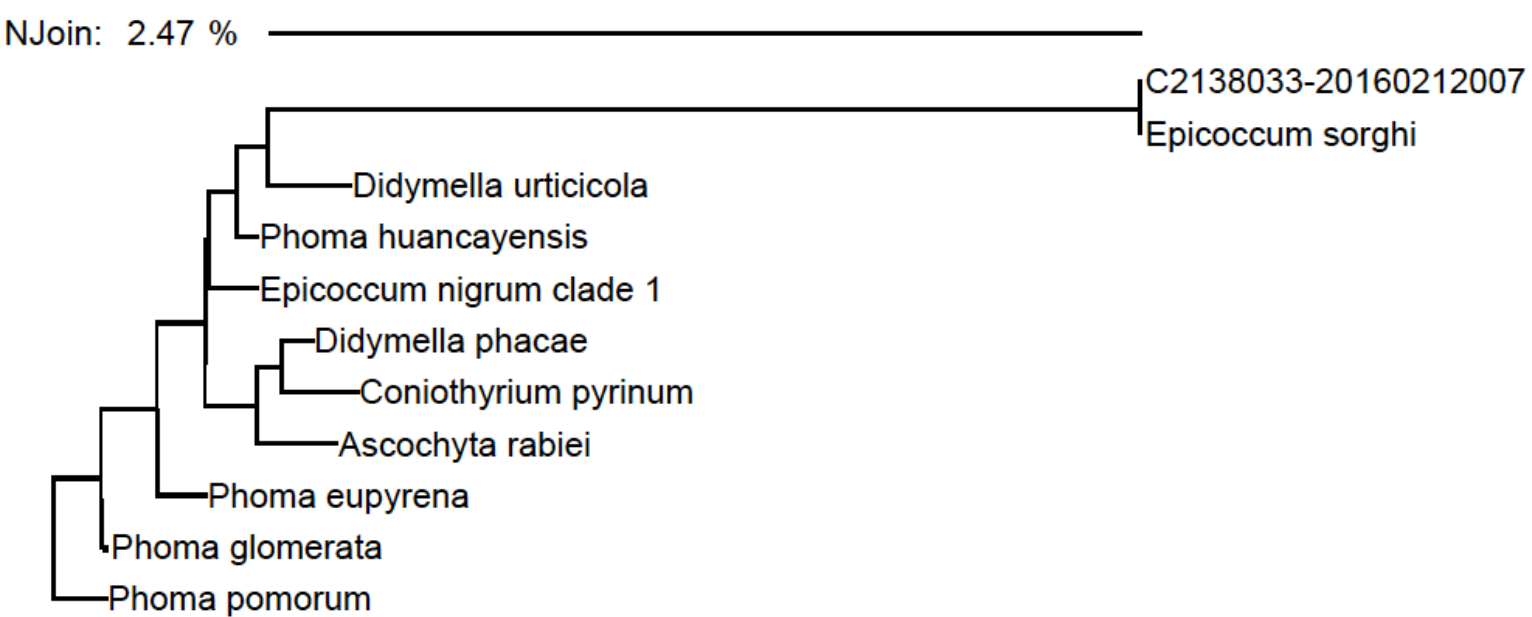
Identification: **Bipolaris papendorfii**

Confidence Level: **Species**

Sequence Alignment

Alignment: 345 C2209170-20160425109
0.00 % 345 Bipolaris papendorfii
3.77 % 349 Bipolaris spicifera
3.77 % 346 Bipolaris ravenelii
4.06 % 350 Bipolaris perotidis
4.06 % 349 Curvularia lunata clade 1
4.06 % 347 Curvularia protuberata
4.06 % 350 Bipolaris australiensis
4.35 % 349 Bipolaris miyakei
4.93 % 352 Curvularia lunata clade 2
5.22 % 348 Curvularia sichuanensis

Neighbor Joining Tree

NJoin: 2.73 %
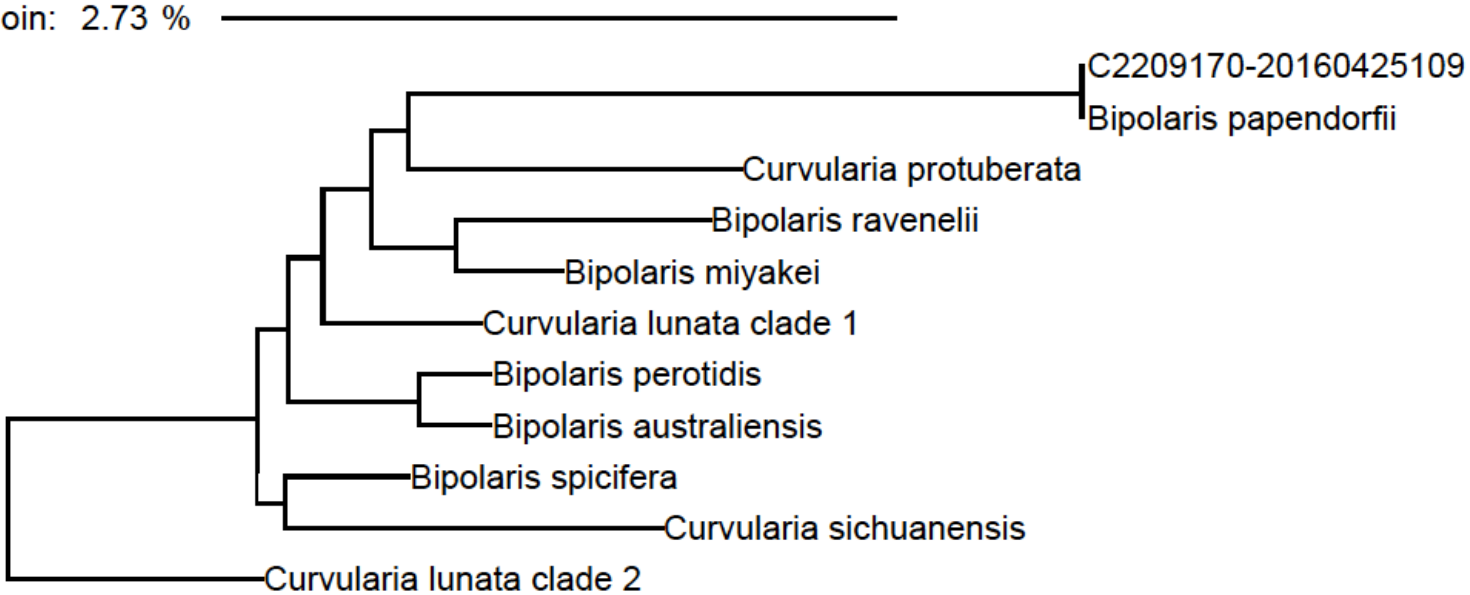
Identification: **Bipolaris   spicifera**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 349 C2139042-20160217001
 0.00 % 349 Bipolaris spicifera
 1.43 % 349 Curvularia lunata clade 1
 1.72 % 350 Bipolaris perotidis
 1.72 % 349 Bipolaris miyakei
 1.72 % 350 Bipolaris australiensis
 2.01 % 348 Curvularia sichuanensis
 2.58 % 353 Curvularia gladioli
 2.58 % 352 Curvularia lunata clade 2
 2.59 % 347 Curvularia affinis
 2.88 % 347 Curvularia protuberata

Neighbor   Joining   Tree

NJoin: 1.96 %

C2139042-20160217001
Bipolaris spicifera
Curvularia lunata clade 1
Bipolaris miyakei
Bipolaris perotidis
Bipolaris australiensis
Curvularia protuberata
Curvularia sichuanensis
Curvularia gladioli
Curvularia affinis
Curvularia lunata clade 2
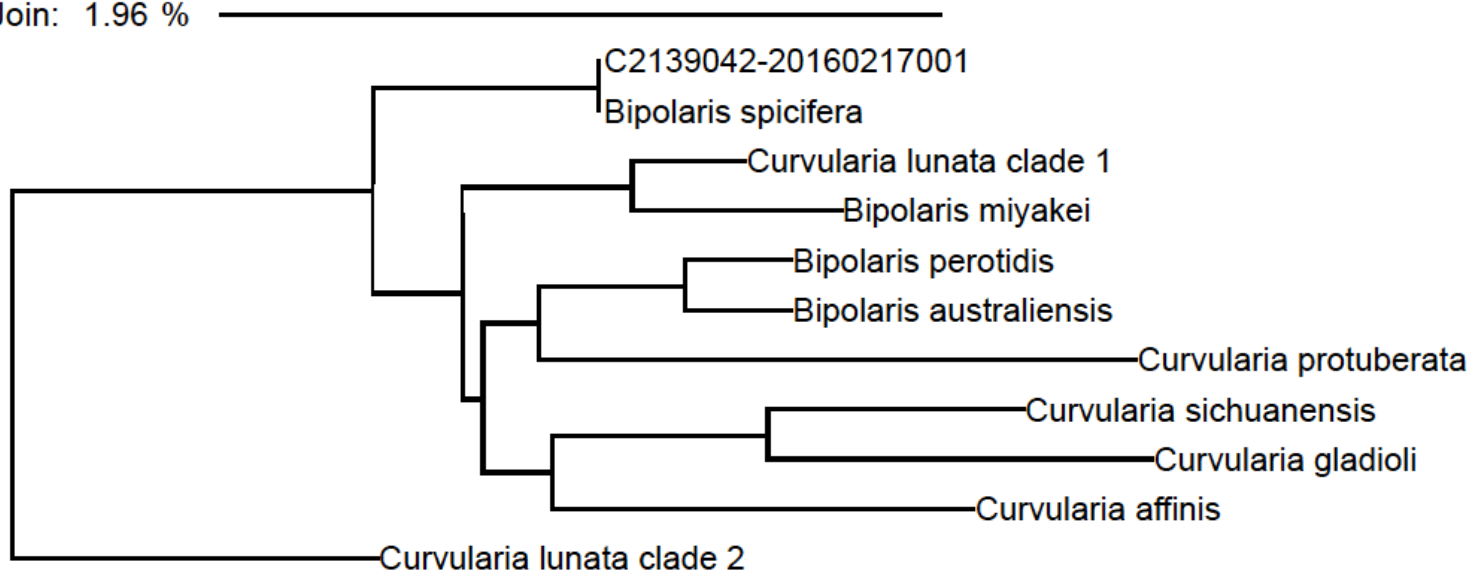
Identification: **Chaetomium globosum**

Confidence Level: **Species**

Sequence Alignment

Alignment: 341 C2138017-20160212005
0.00 % 341 Chaetomium globosum
1.47 % 341 Chaetomium rectangulare
1.76 % 342 Chaetomium angustispirale
1.76 % 340 Chaetomidium fimeti
1.76 % 340 Chaetomium cristatum
2.35 % 341 Chaetomium grande
2.35 % 340 Chaetomium undulatulum
2.36 % 339 Chaetomium subaffine
2.93 % 342 Chaetomium iranianum
3.52 % 342 Chaetomium gangligerum

Neighbor Joining Tree

NJoin: 1.47 %

C2138017-20160212005
Chaetomium globosum
Chaetomium rectangulare
Chaetomium angustispirale
Chaetomidium fimeti
Chaetomium grande
Chaetomium gangligerum
Chaetomium cristatum
Chaetomium subaffine
Chaetomium undulatulum
Chaetomium iranianum
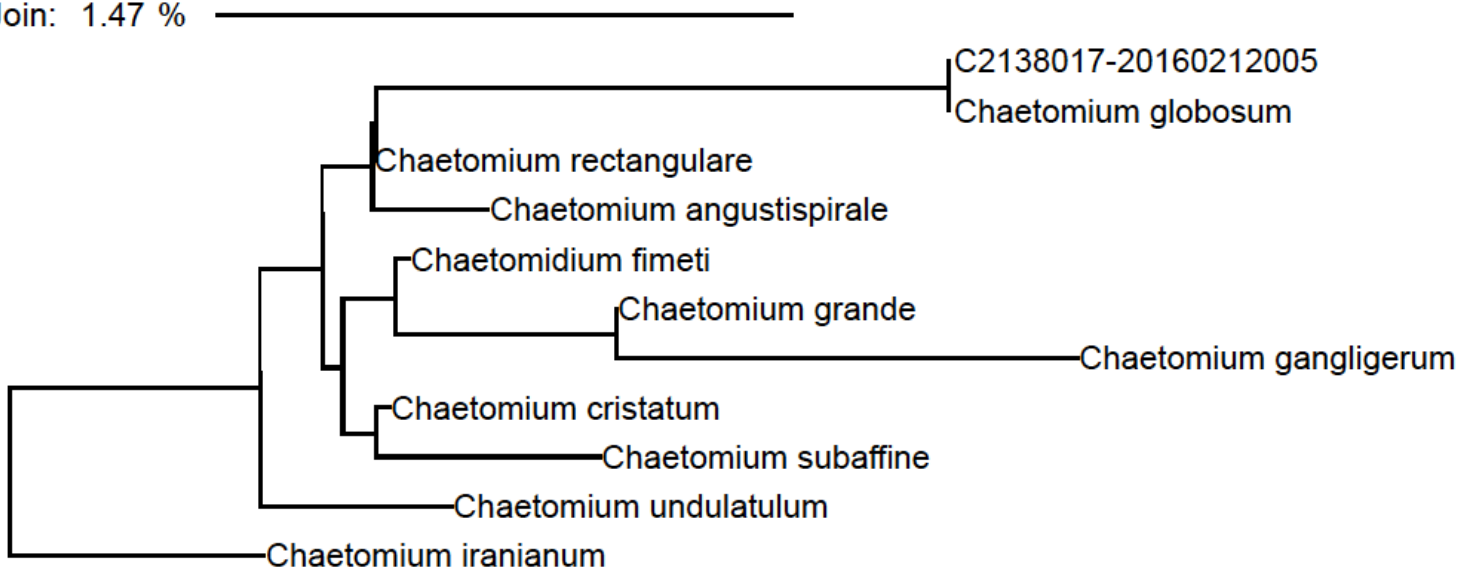
Identification: **Chaetomium   grande**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 341 C2343189-20160909050
0.00 % 341 Chaetomium grande
0.59 % 340 Chaetomidium fimeti
0.88 % 341 Chaetomium rectangulare
0.88 % 340 Chaetomium cristatum
1.17 % 342 Chaetomium gangligerum
1.17 % 342 Chaetomium angustispirale
1.18 % 339 Chaetomium subaffine
1.47 % 341 Chaetomium carinthiacum
1.47 % 343 Chaetomium deceptivum
1.47 % 341 Chaetomium truncatulum

Neighbor   Joining   Tree

NJoin: 0.70 % ——————————————
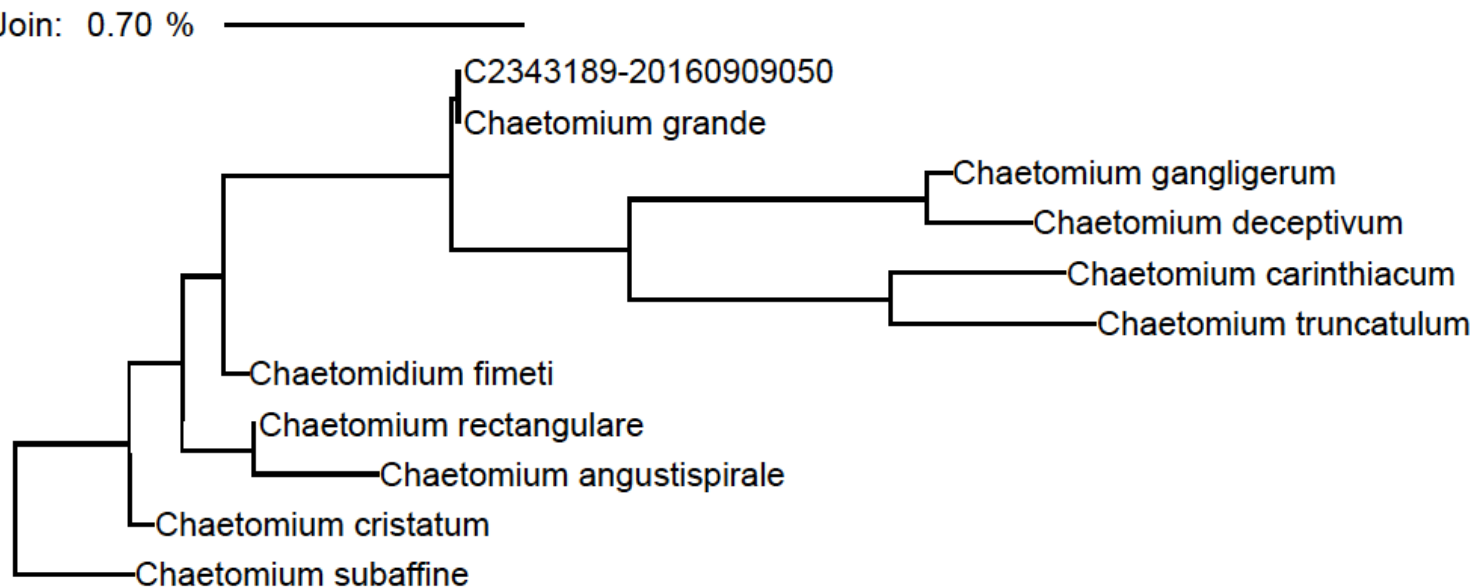
Identification: **Trichoderma citrinoviride / reesei**

Confidence Level: **Species***

*The Unknown matches two or more closely related species.

Sequence Alignment

Alignment: 354 C2209168-20160427030
0.00 % 354 Trichoderma citrinoviride
0.00 % 354 Trichoderma reesei
0.28 % 354 Trichoderma saturnisporum
0.28 % 355 Trichoderma longibrachiatum
1.13 % 356 Hypocrea orientalis
2.26 % 355 Trichoderma virens
2.54 % 361 Trichoderma parceramosum
2.55 % 353 Trichoderma phyllostachydis
2.83 % 353 Trichoderma brevicompactum
3.39 % 354 Trichoderma longipile

Neighbor Joining Tree

NJoin: 1.74 %

C2209168-20160427030
Trichoderma citrinoviride
Trichoderma reesei
Trichoderma saturnisporum
Trichoderma longibrachiatum
Hypocrea orientalis
Trichoderma virens
Trichoderma phyllostachydis
Trichoderma longipile
Trichoderma brevicompactum
Trichoderma parceramosum
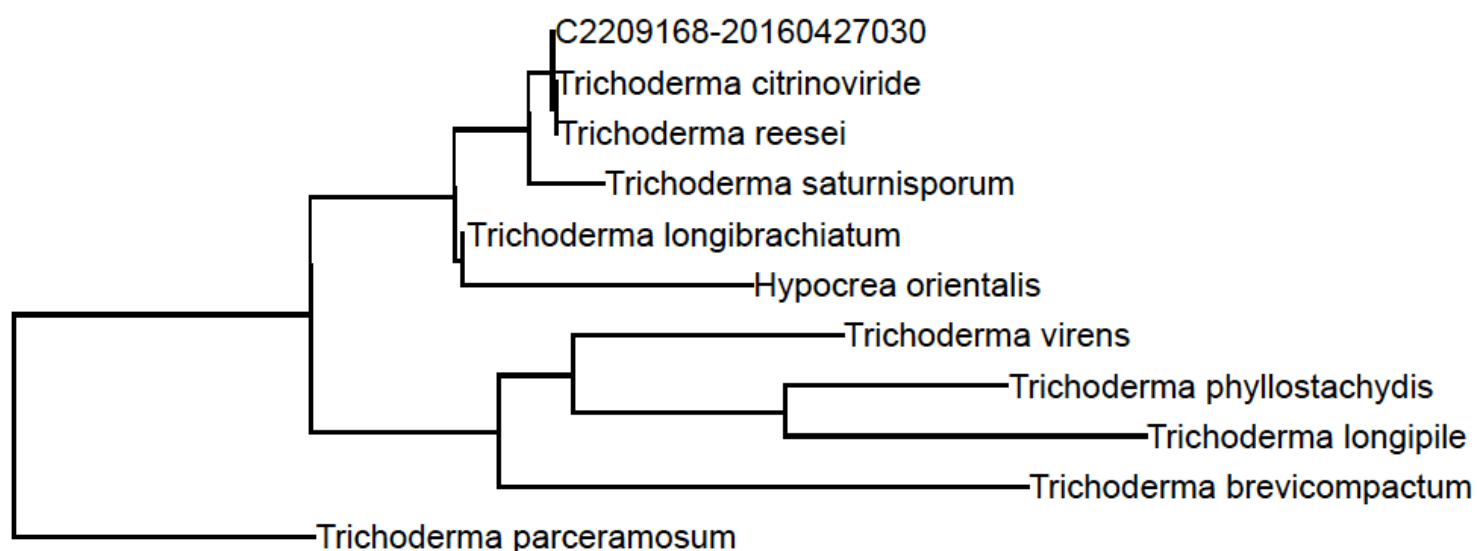
Identification: **Trichoderma   longibrachiatum**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 355 C2139045-20160211091
 0.00 % 355 Trichoderma longibrachiatum
 0.28 % 354 Trichoderma citrinoviride
 0.28 % 354 Trichoderma reesei
 0.56 % 354 Trichoderma saturnisporum
 0.85 % 356 Hypocrea orientalis
 1.97 % 355 Trichoderma virens
 2.25 % 361 Trichoderma parceramosum
 2.27 % 353 Trichoderma phyllostachydis
 2.55 % 353 Trichoderma brevicompactum
 3.11 % 354 Trichoderma spirale

Neighbor Joining Tree

NJoin: 1.74 %
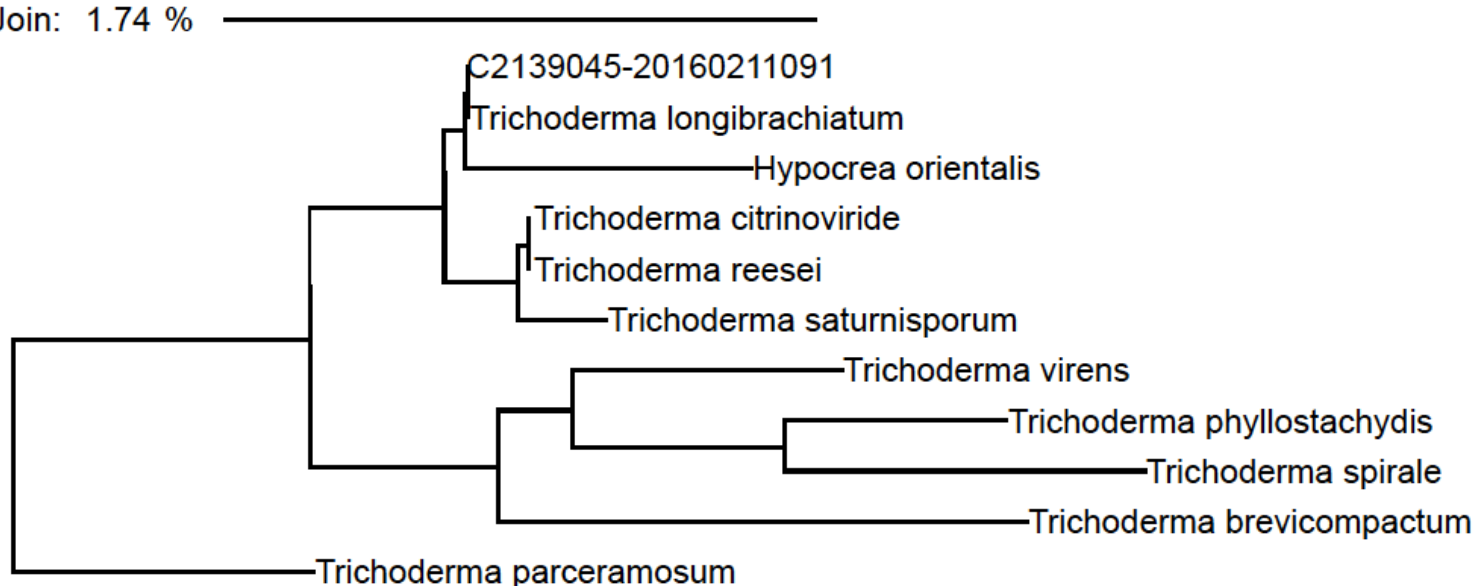
Identification:　**Fusarium　tricinctum**

Confidence Level:　**Species**

Sequence　Alignment

Alignment:　353 C2209158-20160427028
 0.00 % 353 Fusarium tricinctum
 1.14 % 351 Fusarium avenaceum
 2.83 % 354 Fusarium avenaceum nurragi
 5.38 % 353 Fusarium chlamydosporum
 6.84 % 351 Fusarium proliferatum
 7.18 % 348 Fusarium lateritium
 8.22 % 357 Fusarium solani phaseoli
 8.62 % 348 Nectria cucurbitula
 8.78 % 353 Fusarium merismoides acetilereum
 8.80 % 341 Paracremonium inflatum

Neighbor　Joining　Tree

NJoin: 5.09 %

C2209158-20160427028
Fusarium tricinctum
Fusarium avenaceum
Fusarium avenaceum nurragi
Fusarium chlamydosporum
Fusarium lateritium
Fusarium proliferatum
Nectria cucurbitula
Paracremonium inflatum
Fusarium merismoides acetilereum
Fusarium solani phaseoli
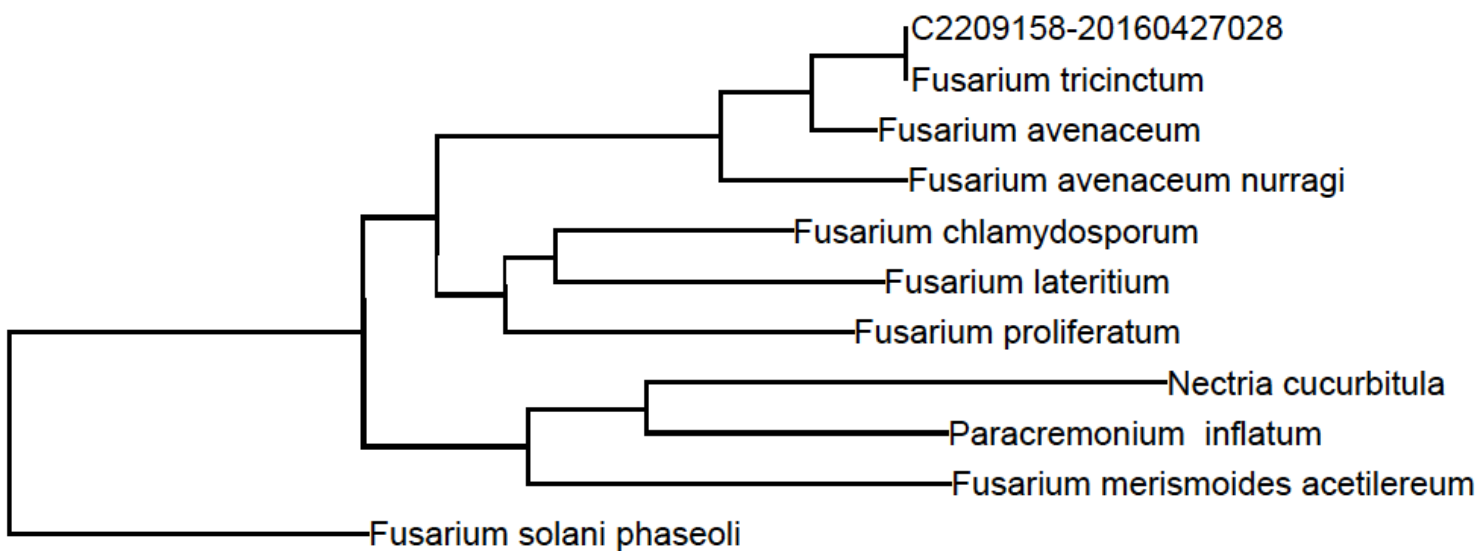
Identification: **Galactomyces   geotrichum**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 245 C2209153-20160504042
 2.45 % 246 Galactomyces geotrichum
 4.90 % 245 Galactomyces candidus
15.98 % 244 Geotrichum klebahnii
17.96 % 247 Dipodascus tetrasporeus
18.03 % 244 Geotrichum cucujoidarum
18.67 % 241 Geotrichum fermentans
23.50 % 234 Candida oslonensis
23.63 % 237 Candida hollandica
24.03 % 233 Candida galli
24.03 % 233 Candida alimentaria

Neighbor   Joining   Tree

NJoin: 10.14 %
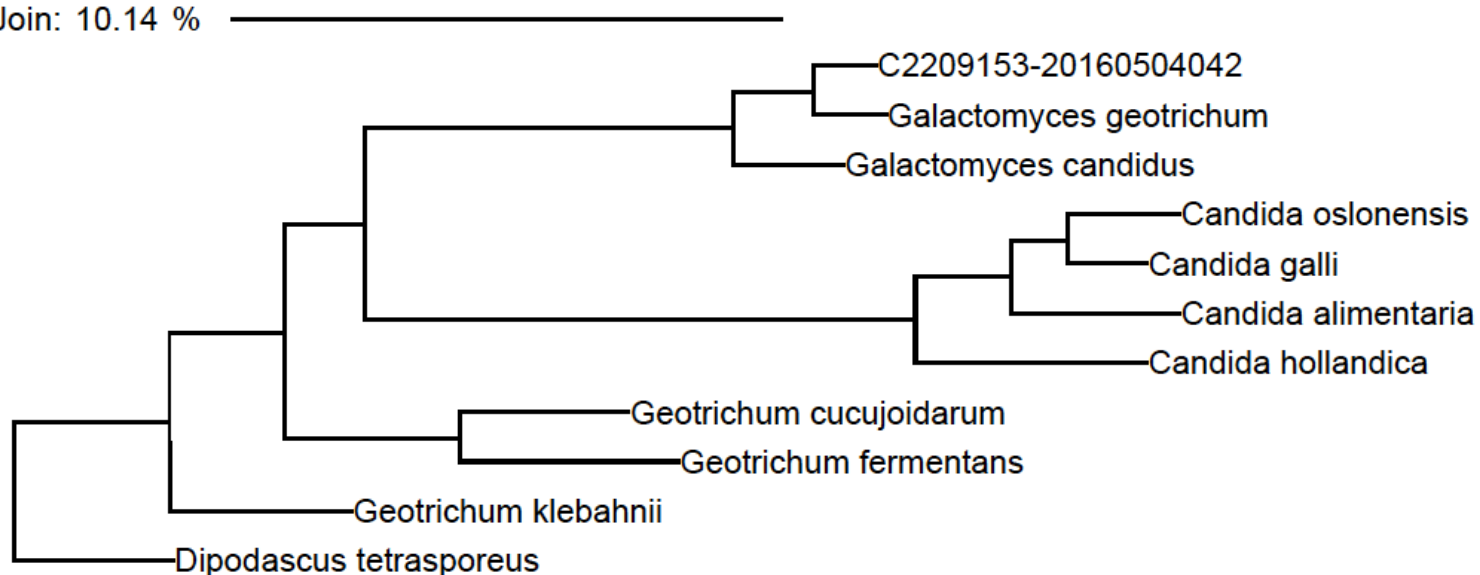
Identification: **Microsphaeropsis   arundinis**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 339 C2209156-20160427028
0.00 % 339 Microsphaeropsis arundinis
2.36 % 340 Paraconiothyrium africanum
2.36 % 340 Paraphaeosphaeria viridescens
2.65 % 341 Paraconiothyrium fuckelii
2.65 % 340 Paraconiothyrium brasiliense
2.65 % 340 Paraconiothyrium variabile
2.65 % 341 Paraphaeosphaeria verruculosa
2.65 % 341 Paraphaeosphaeria parmeliae
2.95 % 340 Paraconiothyrium hawaiiense
3.54 % 340 Paraconiothyrium archidendri

Neighbor   Joining   Tree

NJoin: 1.45 % ────────────────────

C2209156-20160427028
Microsphaeropsis arundinis
Paraconiothyrium africanum
Paraconiothyrium variabile
Paraconiothyrium archidendri
Paraconiothyrium brasiliense
Paraconiothyrium hawaiiense
Paraconiothyrium fuckelii
Paraphaeosphaeria verruculosa
Paraphaeosphaeria parmeliae
Paraphaeosphaeria viridescens
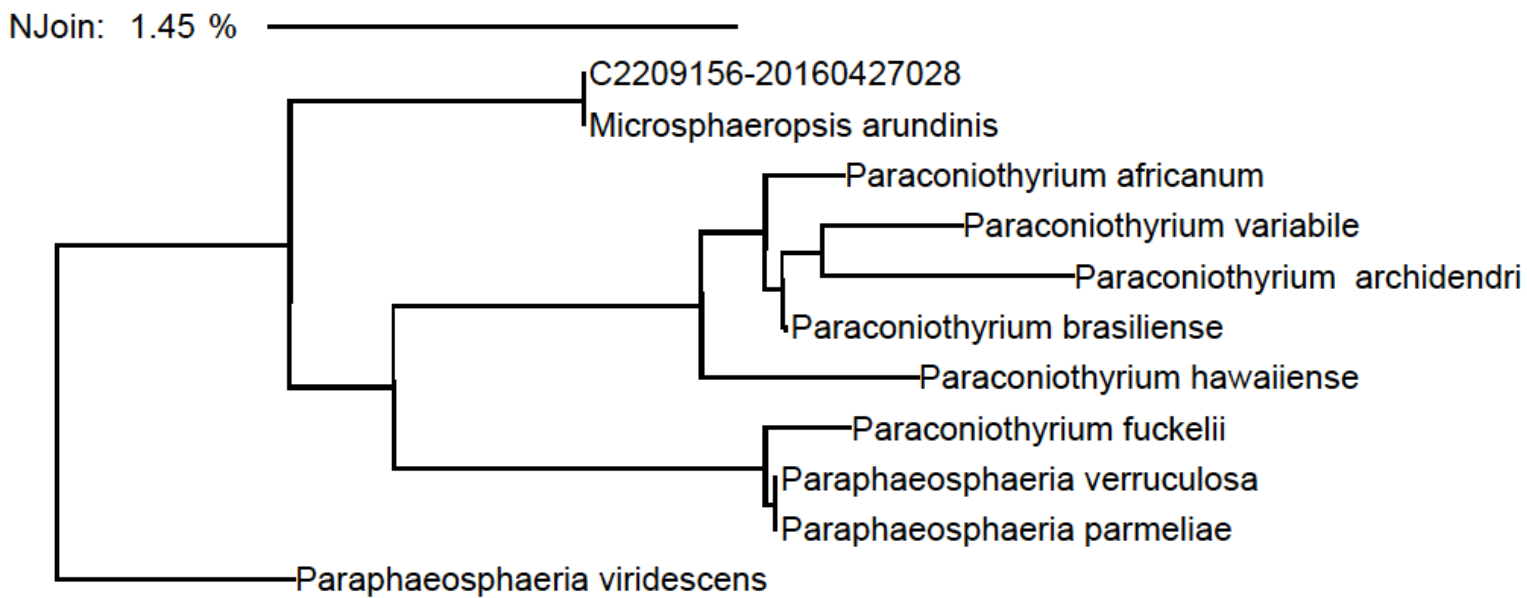
Identification: **Neurospora sitophila / tetrasperma**

Confidence Level: **Species***

*The Unknown matches two or more closely related species.

Sequence Alignment

Alignment: 337 C2343181-20160909049
0.00 % 337 Neurospora sitophila
0.00 % 337 Neurospora tetrasperma
0.30 % 337 Neurospora crassa
0.59 % 337 Sordaria tomentoalba
1.19 % 338 Sordaria alcina
1.19 % 338 Neurospora discreta
1.19 % 338 Neurospora terricola
1.49 % 336 Sordaria fimicola
7.12 % 338 Zopfiella longicaudata clade 1
7.42 % 338 Zopfiella latipes

Neighbor Joining Tree

NJoin: 6.30 %

C2343181-20160909049
Neurospora sitophila
Neurospora tetrasperma
Neurospora crassa
Sordaria tomentoalba
Sordaria alcina
Sordaria fimicola
Neurospora discreta
Neurospora terricola
Zopfiella longicaudata clade 1
Zopfiella latipes
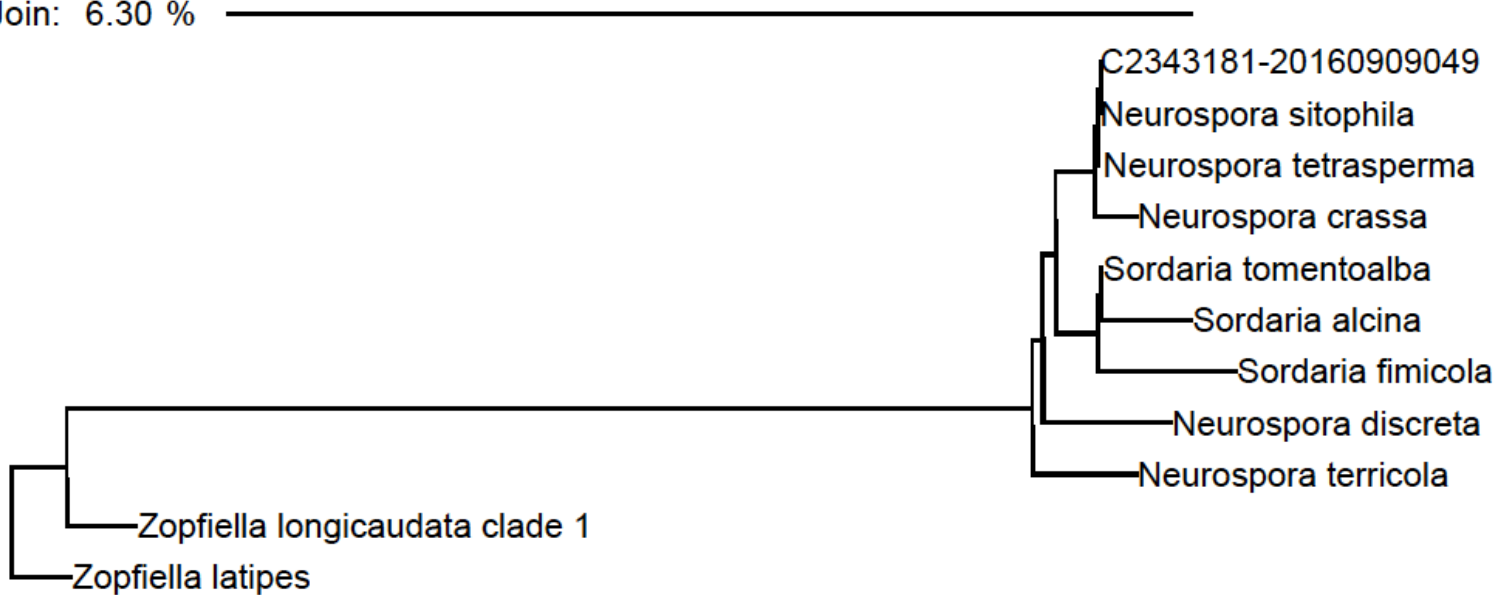
Identification: **Paecilomyces   lilacinus**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 349 C2138014-20160212004
 0.29 % 348 Paecilomyces lilacinus
 5.73 % 353 Chaunopycnis alba
 5.73 % 350 Chaunopycnis pustulata
 5.73 % 355 Metarhiziopsis microspora
 5.75 % 348 Elaphocordyceps ophioglossoides
 6.49 % 339 Tolypocladium inflatum
 8.62 % 348 Haptocillium sinense
10.03 % 349 Lecanicillium fusisporum
10.03 % 355 Nalanthamala vermoesenii
10.32 % 351 Lecanicillium kalimantanense

Neighbor Joining Tree

NJoin: 6.49 %
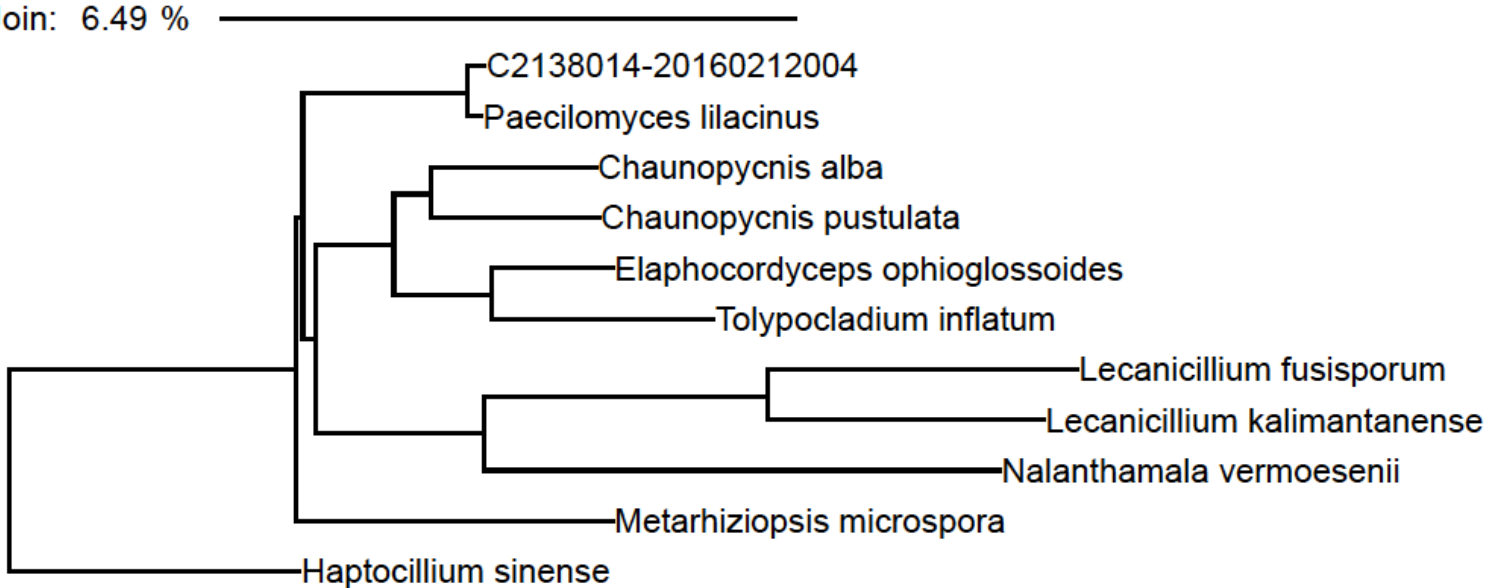
Identification: **Paecilomyces   variotii**

Confidence Level: **S p e c i e s**

Sequence   Alignment

Alignment: 367 C2138015-20160212004
 0.27 % 367 Paecilomyces variotii clade 1
 2.75 % 364 Paecilomyces brunneolus
 4.42 % 362 Paecilomyces saturatus
 4.42 % 362 Paecilomyces fulvus
 4.51 % 355 Paecilomyces variotii
 4.97 % 362 Paecilomyces niveus
 5.85 % 359 Paecilomyces divaricatus
 6.59 % 364 Paecilomyces formosus
 9.94 % 352 Penicillium lagena
 10.20 % 353 Aspergillus fumigatus

Neighbor Joining Tree

NJoin: 4.55 %

C2138015-20160212004
Paecilomyces variotii clade 1
Paecilomyces brunneolus
Paecilomyces saturatus
Paecilomyces niveus
Paecilomyces fulvus
Paecilomyces formosus
Paecilomyces divaricatus
Penicillium lagena
Aspergillus fumigatus
Paecilomyces variotii
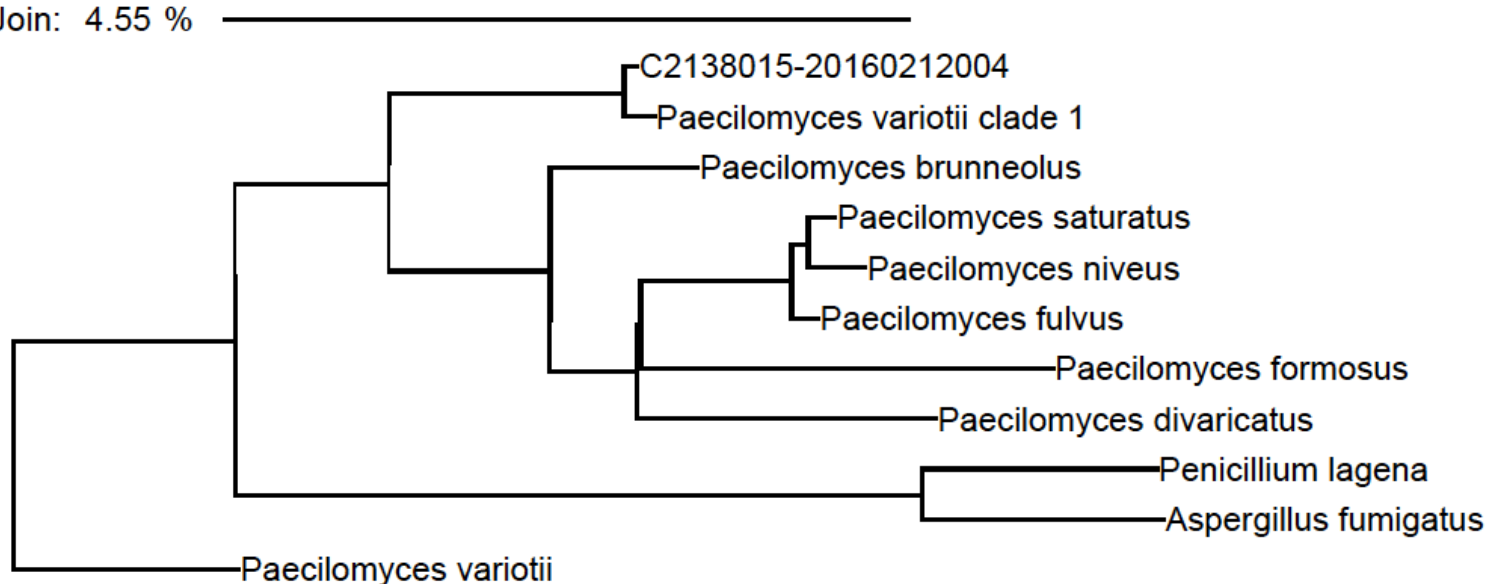
Identification: **Pithomyces   atro-olivaceus**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 343 C2209169-20160427030
0.29 % 343 Pithomyces atro-olivaceus
1.17 % 343 Pithomyces sacchari
3.23 % 341 Pithomyces chartarum
3.53 % 340 Paraconiothyrium brasiliense
3.53 % 340 Paraconiothyrium variabile
3.53 % 340 Paraconiothyrium africanum
3.81 % 341 Camarosporium leucadendri
3.82 % 340 Paraconiothyrium archidendri
4.08 % 343 Letendraea cordylinicola
4.11 % 341 Camarosporium mamanes

Neighbor Joining Tree

NJoin: 2.14 %

C2209169-20160427030
Pithomyces atro-olivaceus
Pithomyces sacchari
Paraconiothyrium archidendri
Paraconiothyrium variabile
Paraconiothyrium brasiliense
Paraconiothyrium africanum
Camarosporium leucadendri
Camarosporium mamanes
Letendraea cordylinicola
Pithomyces chartarum
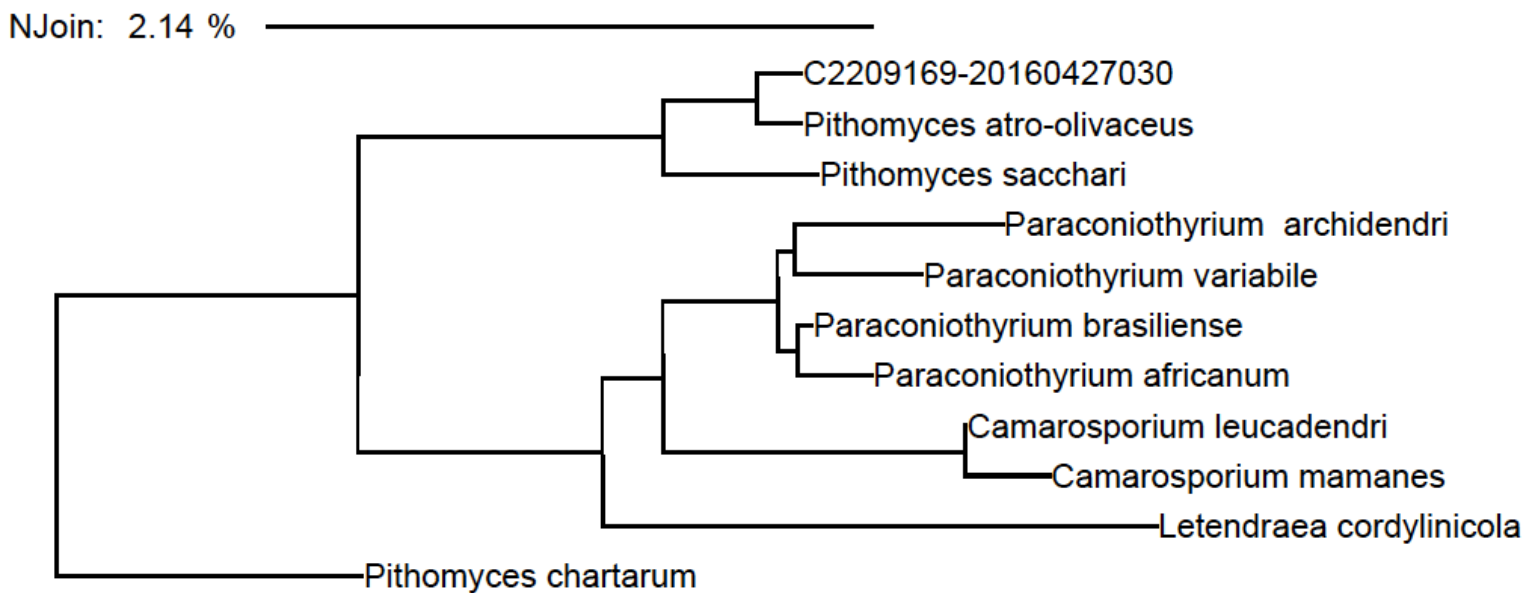
Identification: **Schizophyllum sp.**

Confidence Level: **Genus**

Sequence Alignment

Alignment: 427 C2209149-20160425109
 0.47 % 428 Schizophyllum commune
 1.17 % 428 Schizophyllum radiatum
 5.18 % 425 Schizophyllum fasciatum
23.89 % 449 Fistulina pallida
23.94 % 401 Mycena pura
24.16 % 385 Gloeoporus pannocinctus
25.06 % 395 Phellinus tuberculosus
25.51 % 392 Pleurotus djamor
25.58 % 391 Panellus stipticus
25.58 % 387 Pleurotus ostreatus

Neighbor Joining Tree

NJoin: 15.03 %

C2209149-20160425109
Schizophyllum commune
Schizophyllum radiatum
Schizophyllum fasciatum
Pleurotus djamor
Pleurotus ostreatus
Gloeoporus pannocinctus
Mycena pura
Panellus stipticus
Phellinus tuberculosus
Fistulina pallida
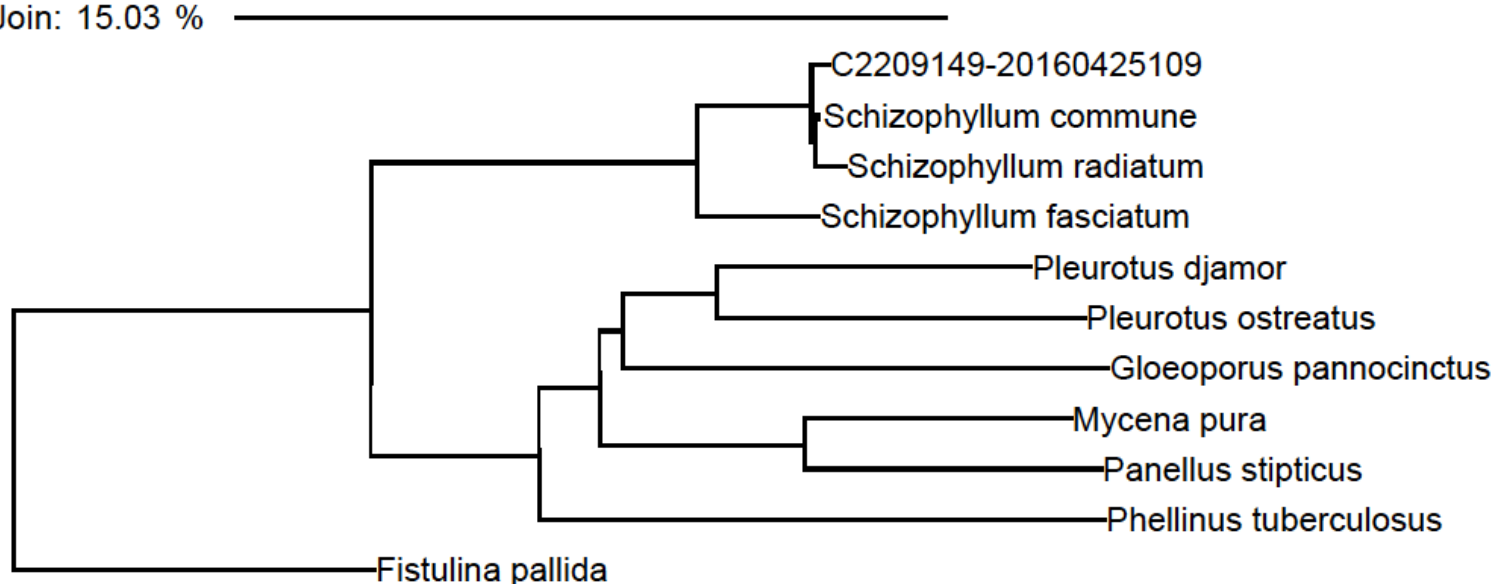
Identification: **Trametes   lactinea**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 384 C2209162-20160427029
 0.00 % 384 Trametes lactinea
 6.30 % 381 Trametes polyzona
 6.35 % 378 Trametes hirsuta
 6.60 % 379 Trametes maxima
 6.61 % 378 Trametes membranacea
 6.77 % 384 Trametes cinnabarina
 6.81 % 382 Lenzites betulina
 6.99 % 379 Trametes versicolor
 7.03 % 385 Lenzites warnieri
 7.07 % 382 Trametes elegans

Neighbor   Joining   Tree

NJoin: 3.93 %

C2209162-20160427029
Trametes lactinea
Trametes polyzona
Trametes maxima
Trametes elegans
Lenzites warnieri
Trametes hirsuta
Trametes versicolor
Trametes membranacea
Lenzites betulina
Trametes cinnabarina
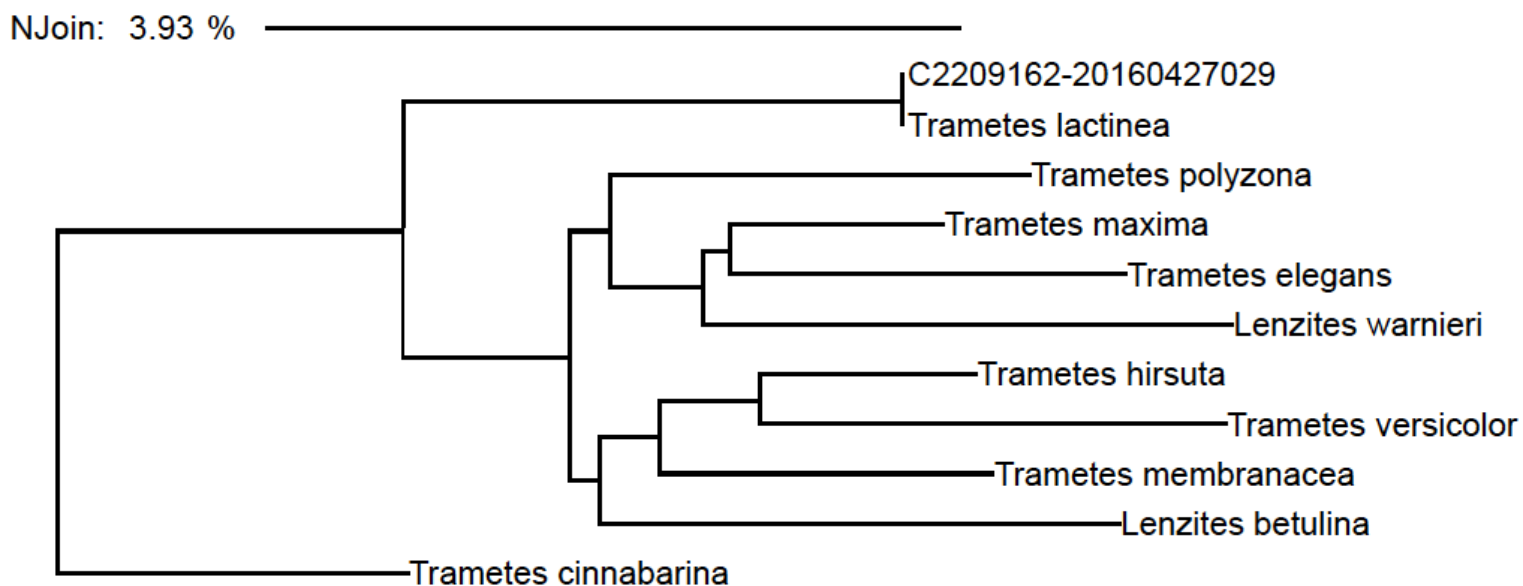
Identification: **Trametes   versicolor**

Confidence Level: **Species**

Sequence   Alignment

Alignment: 378 C2209163-20160427029
0.40 % 379 Trametes versicolor
3.44 % 378 Trametes hirsuta
5.29 % 378 Trametes membranacea
5.82 % 379 Trametes maxima
6.08 % 381 Trametes polyzona
6.61 % 382 Lenzites betulina
6.61 % 384 Trametes lactinea
7.41 % 382 Trametes elegans
7.94 % 385 Lenzites warnieri
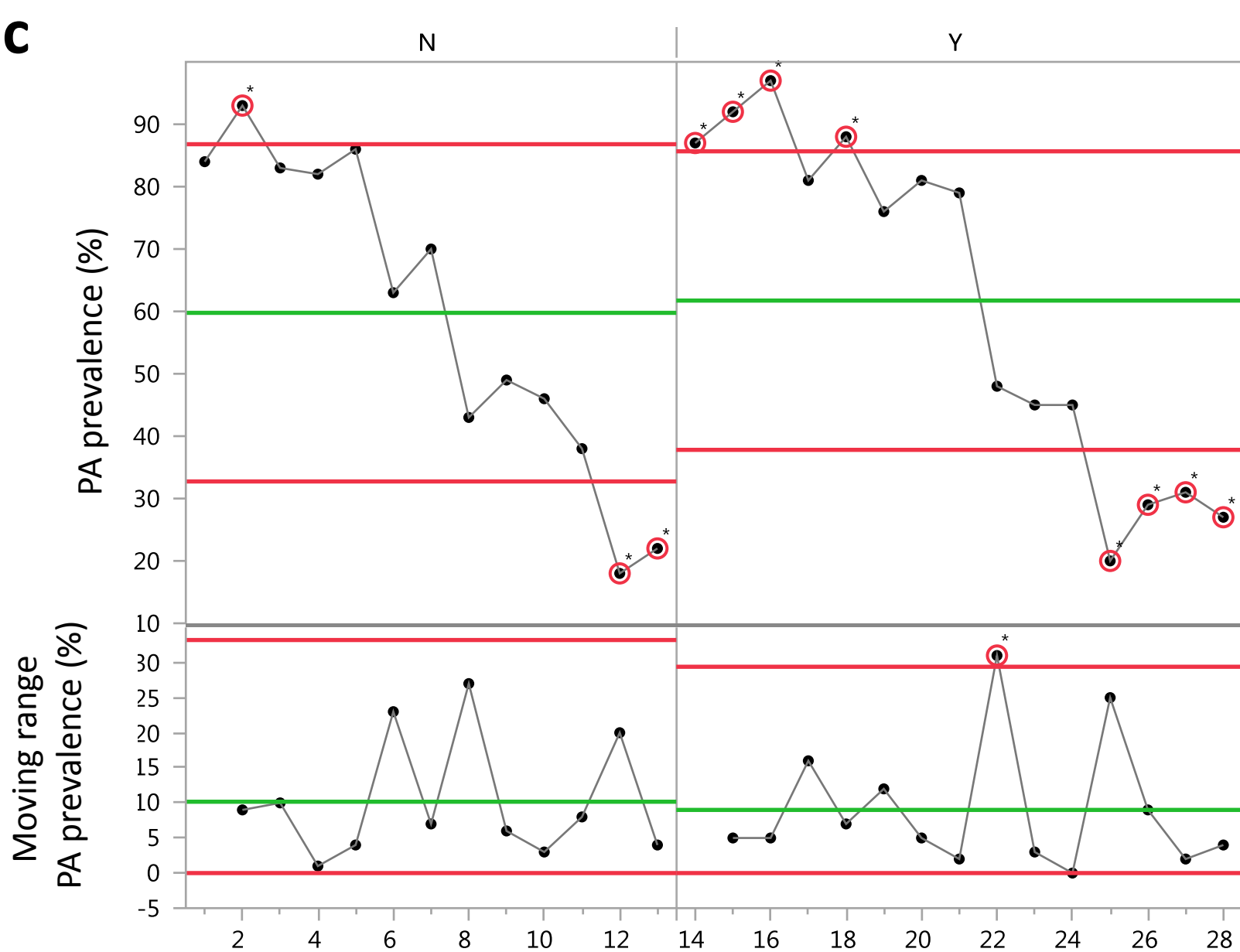7.94 % 380 Tinctoporellus epimiltinus

Neighbor   Joining   Tree

NJoin: 4.95 %

SI Figure 2. Individual and Moving Range (I and MR) Charts comparing **(a)** PA prevalence in buildings with indoor flooding (F) as primary issue of dampness *versus* buildings with non-flood dampness issues (NF) **(b)** buildings located in a coastal zone (within 100 Km from shoreline) and non-coastal zones and **(c)** residential (Y) and non-residential (N) buildings. Numbers in the X- axis correspond to the building demonstrating the individual PA percent prevalence.