

EndoPhytic Fungi of Potato for ExoPlantMedicine & Beyond ...

SUPPLEMENTARY TABLE S1

For Report-Submission to NLM-NCBI

USDA-ARS-GIFVL

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.

4/28/2024

TGATTATGGGNCGGGAATTCCTCTGG
AAGTAAAGTCGAACNAGTTGATCTCCCGCACTTCGGGAAGCCTTT
GCAGCTGGAAACAGTAGCAAAACGACGTTAAATAATCATGGCCTCATGCA
AGTCAGCATTTTGCTGGCAACACTTCGAATTCGGGGGAACCTCTAGAGGC
CTTTTACACCAACTAGCTGGGAACCGGCTAGAGGCTCTGGGGAACCT
ACAGGGTATGGTACAGTGAAGGATGATCAACAGCGTTAGTGAATG
GGCAATCCGACGGAAGCTCTGCTGTTGATGGTATTTGAAGCTCTATG
CCCTGGTATATCTTCGAGACAGCCAAACATGGGGGAGCCTTACAGACTAA
GTGGAAAGTGGTGGGGTATTACGTGCTCTGTTAAGATATATGCGAGCC
CCTTTGGAACTCTGGGGATGAAGTACTGCAGATGTAGAAGAGGGTATT
CTTTTCTACAGACGTGCTCTCATATAGCTGTTCCGTAGGTGAACCTGCG
GAAGGATCATACACTCACTAGTTACTACTGCAAGGGGGCTCTTATGTC
TGATAGCGGCAAGCTGATGAGACGCTGGCTCTTTACCGACCTGCTCT
TTTGGTACCCATGTTCTCTGGGAGCGCTGCTGCGGATTTGACCCCAAC
TATAACCTTTTAAATGTCAATCAGCGCTCGAAAACTAATTATTACAA
CTTTCAACACGGATCTCTGTTGCTGGCATCGATGAAGACGACGAGGAA
ATGCGATAGTATGTGAATTCGAGAACTCAGTGATGATGAATCTTTG
AAGCAGCATTTGGCCCTTGGTATTCATGGGGATGCTGCTTCGAGCGT
CATTTGTAACCTCAAGCTTGGCTGGGCTGGGTGTTGCTCACTCT
GCGTTTGGACTCGCTTAAACCATTTGGAGCGAGTGTTTGGCGGTGAA
GGCGGGCAGACGTGCGATTCACNNAACGGTCTCTCCCTAAGCTCTT
TATCAGTTTGAACCTCAGTATGGGATACCCGCACTTAAAGCAT

Phaeosphaeria avenaria 18S ribosomal RNA gene, partial sequence, ITS1, 5.8S ribosomal RNA gene, and ITS2, complete sequence, and 26S ribosomal RNA gene, partial sequence
Sequence ID: U77357.1 Length: 865 Number of Matches: 1

Range 1: 1 to 569		GenBank		GenBank		* (Accession)		Accession	
Start	End	Start	End	Start	End	Start	End	Start	End
953	855(514)	953	855(514)	953	855(514)	953	855(514)	953	855(514)
Query	512	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	571	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	571	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	571	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	571
Seq:ct	1	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	60	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	60	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	60	TCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	60
Query	572	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	631	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	631	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	631	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	631
Seq:ct	61	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	120	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	120	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	120	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	120
Query	632	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	691	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	691	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	691	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	691
Seq:ct	121	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	180	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	180	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	180	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	180
Query	692	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	751	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	751	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	751	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	751
Seq:ct	181	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	240	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	240	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	240	AATTCCTAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	240
Query	752	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	811	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	811	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	811	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	811
Seq:ct	241	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	300	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	300	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	300	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	300
Query	812	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	871	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	871	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	871	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	871
Seq:ct	341	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	400	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	400	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	400	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	400
Query	872	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	931	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	931	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	931	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	931
Seq:ct	361	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	420	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	420	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	420	TGTTAGCTGTATAGCGAGCTGATGAGGAGCTGGCTCTTTTACCGACCTTCT	420
Query	932	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	991	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	991	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	991	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	991
Seq:ct	421	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	480	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	480	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	480	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	480
Query	992	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1051	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1051	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1051	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1051
Seq:ct	481	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	540	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	540	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	540	TTTGGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	540
Query	1052	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1111	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1111	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1111	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	1111
Seq:ct	541	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	600	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	600	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	600	CAGTATGAGTGAAGCTCGGAAGATCATTAACCTAGTATTTACTTGAAGAGGAG	600

↑ LOCUS PAU77357 569 bp DNA linear PLN 08-APR-2003

4/28/2024

11

4/28/2024

TEF Parastagonospora avenae DQ677885

Parastagonospora nodorum isolate LDN03-Sn4 chromosome 19, complete sequence

Sequence ID: [CP022818.1](#) Length: 1125282 Number of Matches: 1

Range 1: 623893 to 624491 [GetRank](#) [Graphics](#) [Full Match](#) [Previous Match](#)[illegible]

↑ LOCUS CP022818 1125282 bp DNA linear PLN 23-AUG-2017

USDA-ARS-GIFVL
↓ LOCUS 639 bp DNA linear PLN 23-APR-2024

DEFINITION Nemanla delonici voucher MFLU 19-2124 translation elongation factor 1-alpha (TEF1) gene, partial cds.

ACCESSION

VERSION

KEYWORDS

SOURCE Nemanla delonici

ORGANISM Nemanla delonici

Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;

Sordariomycetes; Xylariomycetidae; Xylariales; Xylariaceae;

Nemanla.

REFERENCE 1 (bases 1 to 639)

AUTHORS Unpublished

TITLE Unpublished

JOURNAL Unpublished

FEATURES Location/Qualifiers

source 1..639
/organism="Nemanla delonici"
/mol_type="genomic DNA"
/isolation_source="stems"
/db_xref="taxon:2924959"
/country="USA: Maryland"
/lat_lon="39.026, -76.925"
/collection_date="2021"
/PCR_primers: "fwd1_seq: GAYTTTCATCAAGAATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCACRTTGTG
fwd1_name: Ef13, fwd1_seq: gtaaaagccagGAYTTCATCAAG, rev1_name: Er13, rev1_seq: caggaagactatgacGAGCTTGAADCCRAC"

ORIGIN
1 TTANNNTCTCAGCTGCTGGTGGTCATCTGACGGACTTGACTTCAGTGGTGACCATGGA
61 GGGAGCGAAGTAACGACCATACCGGGCTTGAGTTCACCGCTCTCGATAGCGGCGACAGG
121 GACCGTGCATAACCGCGACTTGTAACATCTCTGGAGGGGACAGCGAGGGGCTTGTC
181 GTTGGGACGCTTGGGCTCTCGATGGCATCAATGGCGTCGAGGAGAGTCTTGCACATAAT
241 CTGGGACCTTGGGGGAGCTCTTCCAGCCCTTGATACAGGAGCGTTCTGGTGGAC
301 GTCAGCATGTTGTGCGCGTTGAACACGAGATGGGGGACAAAGGCAACGCTGGTGGGGTT
361 GAAACGACCTCTTGATGAAGGAAGAGGTCTCTTGCACATCTCGTTGAACGAGCCTC
421 GGACCATTAGCGGATTCATCTTGTGTATGGGCAAAATGAGTTGCTTGACACGAGGGGT
481 GAAGCGGAGGAGAGCGTCTACGGGCTCGGATCTTGGGATCTGAGATACGAGCTCGAATCT
541 ACCAGTACCGGACGAATGATGAGAATGGCGAGTCCGCTTGGGAGGTACCCGTAATCAT
601 GTTCTTGATGAATCCCGCGGNNNNNNNNNAANNNNNNA
//

4/28/2024

Commented [CT4]: Waiting for associated GenBank number for these ... after submission to the NLM and review from by such ... Applies to two lines up for blank script next to locus, as well

Commented [CT5]: To Mark all as such

USDA-ARS-GIFVL

Supplementary Table S1. ITS region sequences from isolated fungi.

Blintze-2Xylariaceae.sp. LC431575

4/28/2024

ANTGANTAGCGCCGGGAATTCGCCCTT
TCTTCCGCTTATTGATGCTTAAGTTCAGCGGGATTCTCACTCACTGATCC
GAGGTCAACCTATACATTGGGGGGTGTTTTACGCGAGGGCGCGGGCTTA
GGCTACAGCGCATGTGTAAAAGCTACTACGCTGAGAGTGTAAACCGGCT
CCGCGCATGCTCTTGGGGGAGTACGGGACAGGGGTCCGATAGGTCCTCAAC
GCTAAGCAACTAGGGCTTAAGGGTTGAAATGACGCCGGAACGAGCATGCC
CACCAGAACTAGTGGGCGCAATGTGCGTTCAAGAGTTCGATGATTCAC
TGAATTCGCAATTCACATTAATCTGATGCTTCCGCTGCTTCTTGATCG
ATGCGAGAACGAGAGATCCGTTGTTGAAGTTTAACTGATTTAGTTAT
CTTTGTTACAGAGTCTAATGCTATATAAACAGAGTTTCGGGGGCGCTC
GGCAGGTTTCGCTACAGGGGTAGGGCGGCGCTCGCGAGGCAACGAGA
GGATGTTTCACATGGGTTCCGAGAGTTTGTAGAACCTATATAGATCCCT
CCGCTGGTTACCAACGGAGACTTGTATGAGCTTTTACTCTCAAGGGGCG
AATTCGTTAAACCTGACGAGACTGCTCTTATGAGGGGTAAATTCGA
GCTTGGCGTAATCATGTCATAGCTGTTCTCGGNNNGNNNATTATCTCT
NCTNCTATCCATATTGC

Xylariaceae sp. MYA0703 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence

Sequence ID: LC431575.1 Length: 593 Number of Matches: 1

Score	Expect	Identical	Gaps	Strand
1068.884(578)	0.0	588/593(99%)	0/593(0%)	Plus/Minus
Query 249	TCTTCCGCTTATTGATGCTTAAGTTCAGCGGGATTCTCACTCACTGATCCAGGTCAAC	89		
ShJct 593	TCTTCCGCTTATTGATGCTTAAGTTCAGCGGGATTCTCACTCACTGATCCAGGTCAAC	534		
Query 99	TATGATTTGGGGGTTTTCGAGAGAGGCTCGAGTGAAGTTCAGGCGATGTCTAA	349		
ShJct 533	TATGATTTGGGGGTTTTCGAGAGAGGCTCGAGTGAAGTTCAGGCGATGTCTAA	478		
Query 159	AGCTATGATGTTGAGTTTACAGAGGCTTCGAGTGAAGTTCAGGCGATGTCTAA	389		
ShJct 475	AGCTATGATGTTGAGTTTACAGAGGCTTCGAGTGAAGTTCAGGCGATGTCTAA	414		
Query 219	GGATTCGGTGGCTTCGAGAGGCTGAGTGAAGTTCAGGCGATGTCTAA	269		
ShJct 413	GGATTCGGTGGCTTCGAGAGGCTGAGTGAAGTTCAGGCGATGTCTAA	354		
Query 279	GAGGATGCTCCAGCAGATGCTGGGCGAGTCTCGTCAAGATTTCGATGATTCAC	329		
ShJct 253	GAGGATGCTCCAGCAGATGCTGGGCGAGTCTCGTCAAGATTTCGATGATTCAC	294		
Query 339	TGAATTCGATGATTCATTAATGATGATTCGATGATTCGATGATTCGATGATTCAC	389		
ShJct 293	TGAATTCGATGATTCATTAATGATGATTCGATGATTCGATGATTCGATGATTCAC	234		
Query 299	CAGAGATCCGTTTGAAGTTTTCAGTGAAGTTCGATGATTCGATGATTCGATGATTCAC	449		
ShJct 233	CAGAGATCCGTTTGAAGTTTTCAGTGAAGTTCGATGATTCGATGATTCGATGATTCAC	174		
Query 459	GCTATATAAAGAGGTTTCGAGGCGCTGAGGAGTTTCGATGATTCGATGATTCGATGATTCAC	509		
ShJct 373	GCTATATAAAGAGGTTTCGAGGCGCTGAGGAGTTTCGATGATTCGATGATTCGATGATTCAC	314		
Query 519	GCTTCTCGAGGAGCAGAGGATTTTACATGATGATTCGATGATTCGATGATTCGATGATTCAC	569		
ShJct 313	GCTTCTCGAGGAGCAGAGGATTTTACATGATGATTCGATGATTCGATGATTCGATGATTCAC	54		
ShJct 53	AGTATGCTTCTGCTGTTTCTACAGCGAGGCTTTTACAGGCTTTTACCTTCT	1		

↑ LOCUS LC431575 593 bp DNA linear PLN 27-MAR-2020

USDA-ARS-GIFVL Supplementary Table S1. ITS region sequences from isolated fungi.

4/28/2024

↓ LOCUS 748 bp DNA linear PLN 23-APR-2024

DEFINITION Xylariaceae sp. MYA0703

ACCESSION

VERSION

KEYWORDS

SOURCE Xylariaceae sp.

ORGANISM Xylariaceae sp.

Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;

Sordariomycetes; Xylariomycetidae; Xylariales; Xylariaceae.

REFERENCE

AUTHORS Unpublished

TITLE Unpublished

JOURNAL Unpublished

FEATURES Location/Qualifiers

source 1..748

/organism="Xylariaceae sp."

/mol_type="genomic DNA"

/isolation_source="stems"

/host="Solanum tuberosum "Bintje"

/db_xref="taxon:1881983"

/country="USA:Maryland"

/lat_lon="39.026, -76.925"

/collection_date="2021"

/PCR_primers="fw1_name: ITS1, fwd1_seq:tcgttagtgaactcggg; rev1_name: ITS4, rev1_seq: tcctccgcttattgatgc"

"fwd2_name: M13-ITS1, fwd2_seq: gtaaaacggcagctcgtagtgaaac, rev2_name: M13R-ITS4, rev2_seq: caggaaacagctagactcctccgtattatg"

Gene <1..>748

/gene="18S rRNA, ITS1, 5.8S rRNA, ITS2, and 28S rRNA"

mRNA <1..>748

/gene="18S rRNA, ITS1, 5.8S rRNA, ITS2, and 28S rRNA"

/product="Xylariaceae sp. MYA0703"

CDS <1..>748

/gene="18S rRNA, ITS1, 5.8S rRNA, ITS2, and 28S rRNA"

/product="Xylariaceae sp. MYA0703"

ORIGIN

1 ANTGANTTAGCGCGCGGAATTCGCCCTTCTCCCGCTTATGATGCTTAAGTTCAAC
61 GGGTATTACTTACCTGATCCGAGGTCAACCTATACATGGGGGGTGTTTTACGGCAGGGCG
121 CGGGGCTTAGCTACAGCGGATGTGTAAGAAGCTACTACGCTGAGAGTGTAAACCGGCTC
181 CGCCACTGACTTTGGGGAGCTACGGGACAGGCTCGGTAGGCTCCCAACGCTAAGCACT
241 AGGGCTAAGGGTGAATGACGCCCGACACAGGATGCCACACAGATACTGGTGGGCGC
301 AATGTGCGTTCAAGATTGCGATGATTCCTGAATTCGCAATTCACATTACTATCGAT
361 TTGCTGCGTCTTTCATCGATGCCAGAACCAAGAGATCCGTGTTGAAGTTTAACTGA
421 TTTAGTATCTTTGTTTCAGAGGTCTAATGCTATATAAAGAGAGTTTCGGGGCGCGTCG
481 GCAGTCTTCGGCTACGAGGGTAGGGCGGCCCTCCCGAGGCAAGCAGAGATGTTTCA
541 ATGGGTTCCGGAGTTGTTGAGAACTCTATAATGATCCCTCCCGCTGGTTCACCAACGGAGA
601 CTTTGATGACACTTTTACTCCAAGGGCGAATTCGTTAAACCTCGAGACTAGTCTCT
661 TAGTGAGGGTAAATCTGAGCTTGGCGTAATCATGTGTCATGCTGTTCTCGGNNNGTNN
721 ATTCTATCTNCTNCTATTCATATTGTC

Commented [TCTRA6]: Should Strain be in the Definition? Applies to all given samples here

Commented [TCTRA7]: May you please provide primers? Under the given Table 1, 'Endophyte isolation from...' there is only Phaeosphaeria and Nemanis spp. Listed... what primers are to be used with Xylariaceae? ITS, TEF, Both?

Commented [CT8R7]: ITS

USDA-ARS-GIFVL

Supplementary Table S1. ITS region sequences from isolated fungi.

4/28/2024

TEF 1 Arcopilus aureus MG890137

TGNTCNCGNNGNNCCCTCGGTGAGCTGCTCGTGGTGCACTCTC
GACGGACTTGACTTCAGTGGTGACGTTGGAGGGAGCGAAGGTGACGACCA
TGCCGGGCTTCAGGATACCAAGTCTCATACGCGCCACAGGGACAGTGGCG
ATACCGCGATCTTGTACACTCTCGAGGGGAGAGCGAGGGGCTGTCTC
GGTGGGGCGCTTGGGGGGCTCAATGGCTGATGGCCCTCAAGGAGGGTCT
TGCCAGTGGCTTGCCACCTTGATCTCTTCTCCAGCCCTTGACCAA
GGAGCGTCTTGGTGGCTCGAGCATGTTGTCTGGCGTGGAGCCGAGAT
GGGAGCAAGGCAACGGCTCTGGGGTGTAGCGACCTCTTGATGATGAT
TGGAGGTCTCTTGATGATCTCTGTAAGCGGTTCTCAACCACTGGGCG
GTGTCCATCTTGTGATGGGACGATGAGCTGCTTCACCCAGGGGTGA
GGCGAGCAGAGCGTGTCTACGAGTGTGGCCATCTTGGAGATACACGCT
CGAACTCACAGTGGCGGACGATGATGAGATAGCGAGTGGGCTGG
GAGGTACCAAGTATCATGTTCTGTGATGATCTGGGCGCTGTTTAAAAA
ANNNAAGTCCAGCATCTCCGGGTCTCGAGCGGCTCCACTTGTGACA
AAACACGATGCGCTGCACGCCCACTGCGCGCCAGCAGCAAGTGTCTC
GCGGCTCTGGGCACTCTGGCTCCGAGCGGCCACCAAGATGATGGG
CCGTCAATGCTTGGCGGCGACGTGATCATGTTCTTGANAAATCGTNG
CCAGCTTTAGANNCGAGGTGACGGGNNNGATTNNNNNAAGCTANN
AANGNNNCTATGCAANTNTGNNNTGCGTGNNGANGTGGGTCCCGNN
NNGNAGTCCAGGAATGATGNNCCG

Arcopilus aureus isolate E1 translation elongation factor 1a (tef1) gene, partial cds

Sequence ID: MG890137.1 Length: 910 Number of Matches: 1

Range 1: 1 to 913 GenBank OpenBLAST

Score	Expect	Identical	Score	Strand	% Identical
1046.184(366)	0.0	975/972(99%)	5/972(1%)	Plus/Minus	
Query 14	CCCTCGGTGACCTCTGCTGCTGATCTCGACCGAGCTTGACTTCAGTGGTGA	73			
Sbjct 14	CCCTCGGTGACCTCTGCTGCTGATCTCGACCGAGCTTGACTTCAGTGGTGA	73			
Query 74	GGAGCGAGGTGAGAGCTTGGGGGCTCAATGGCTGATGGCCCTCAAGGAGGGTCT	129			
Sbjct 14	GGAGCGAGGTGAGAGCTTGGGGGCTCAATGGCTGATGGCCCTCAAGGAGGGTCT	129			
Query 134	AGAGTGGGCTGAGAGCTTGGGGGCTCAATGGCTGATGGCCCTCAAGGAGGGTCT	102			
Sbjct 403	AGAGTGGGCTGAGAGCTTGGGGGCTCAATGGCTGATGGCCCTCAAGGAGGGTCT	102			
Query 154	GTGGGGGCTTGGGGGCTCAATGGCTGATGGCTGAGAGGAGGTCTGGCGTGGC	253			
Sbjct 352	GTGGGGGCTTGGGGGCTCAATGGCTGATGGCTGAGAGGAGGTCTGGCGTGGC	253			
Query 254	TTGGCAGCTTGATCTCTCTTCCAGCCCTTATACCAAGAGGTCTTGGTGGCTG	313			
Sbjct 332	TTGGCAGCTTGATCTCTCTTCCAGCCCTTATACCAAGAGGTCTTGGTGGCTG	279			
Query 314	ATCATTTTTCCTCGGTGGAACCGGAGATGAGGAGCAAGGAGGTCTTGGTGGCTG	373			
Sbjct 312	ATCATTTTTCCTCGGTGGAACCGGAGATGAGGAGCAAGGAGGTCTTGGTGGCTG	213			
Query 374	CGGAGCTCTTGATGAGGTGGAGGTCTCTTGGTGGCTTGGTGGAGGGTCTGGAAC	433			
Sbjct 312	CGGAGCTCTTGATGAGGTGGAGGTCTCTTGGTGGCTTGGTGGAGGGTCTGGAAC	153			
Query 414	CAGTGGGCGCTCTCATCTTGTGATGGGAGAGTGGCTTCTTCAACCTCAGGCTGAG	493			
Sbjct 152	CAGTGGGCGCTCTCATCTTGTGATGGGAGAGTGGCTTCTTCAACCTCAGGCTGAG	93			
Query 494	GGGAGCAGAGCTCTTCAACCTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG	553			
Sbjct 92	GGGAGCAGAGCTCTTCAACCTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG	33			
Query 554	GTGGGGGCTTGGGGGCTCAATGGCTGATGGCTGAGAGGAGGTCTGGCGTGGC	585			
Sbjct 32	GTGGGGGCTTGGGGGCTCAATGGCTGATGGCTGAGAGGAGGTCTGGCGTGGC	2			

USDA-ARS-GIFVL Supplementary Table S1. ITS region sequences from isolated fungi.

↓ LOCUS 743 bp DNA linear PLN 16-APR-2024

DEFINITION Arcopilius aureus isolate ATT218

ACCESSION

VERSION

KEYWORDS

SOURCE Arcopilius aureus

ORGANISM Arcopilius aureus

Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiaceae;
Arcopilius.

REFERENCE 1 (bases 1 to 743)

AUTHORS Unpublished

TITLE Unpublished

JOURNAL Unpublished

FEATURES Location/Qualifiers

source 1..743
 /organism="Arcopilius aureus"
 /mol_type="genomic DNA"
 /isolation_source="stems"
 /host="Solanum microdontum"
 /db_xref="taxon:79815"
 /country="USA:Maryland"
 /lab_inov="39-026, -76-925"
 /collection_date="2021"
 /PCR_primers="fw1_name: ITS1, fw1_seq: tcctggtgaacctgagg, rev1_name: ITS4, rev1_seq: tcttcgcttatgtatgc,
 fw2_name: M13-ITS1, fw2_seq: gtaaaaggcagctcgtagtggaac, rev2_name: M13R-ITS4, rev2_seq: (caggaacagtagtactcctgcttatgt)
 fw3_name: E1, fw3_seq: GAYTTCACAGAACATGAT, rev3_name: E5, rev3_seq: GAGCTTGAADCRACRTTGTG
 fw4_name: E1f3, fw4_seq: gtaaaaggcagGAYTTCACAG, rev4_name: E1f3, rev4_seq: caggaacagtagtgcGAGCTTGAADCRAC"

Gene <1..>743
 /gene="contains 18S ribosomal RNA, internal transcribed
 spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
 2, and 28S ribosomal RNA"

mRNA <1..>743
 /gene="contains 18S ribosomal RNA, internal transcribed
 spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
 2, and 28S ribosomal RNA"
 /product="Arcopilius aureus isolate ATT218"

CDS <1..>743
 /gene="contains 18S ribosomal RNA, internal transcribed
 spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
 2, and 28S ribosomal RNA"
 /product="Arcopilius aureus isolate ATT218"

ORIGIN

1 ACCCTCACTAAAGGACTAGTCTCGAGGTTAAACGAATTCGCCCTGGGAAGTAAAGT
61 CGTAACAAGGTCTCGTTGGTGAACACGGAGGGATCATACAGAGTTGCAAACTCCC
121 CAAACCATTTGTGGACGCTACCTTTAAAGCTTGCTCGGCGGGCGGCCGCTCCCTGGAA
181 AGCCCTGTGTGGCCCGGGGGTGGAGCCCCCGGCCCTCGCGGGGGCGCCCGCC
241 GAGGATACCAACTCTTGATTATTATAGGCTCTCTGAGTCTCTGTACTGAATAAGTCA
301 AAACTTTCAACACGGATCTCTTGTTCTGGCATCATGATGAAGAAGCAGCGAAATGCGAT
361 AAGTAATGTGAATTGCAAGATTCAGTGAATCATCGAATCTTTGAACGACATCTGGCCCG
421 CAGATATTGGCGGGGATGCTCTGTTGAGGTCATATTCAACATCAAGCCAGGCTTG
481 TGTGGGGGACCTGGCGGCCGAGCGCTGAAATCAGTGGCGGCTTCGCTGCACCC
541 GAGCGTAGTAGCAATATCTCGCTCAGGGCGTCTGCGGGCGCCGGCGTTAAAGCTCC
601 TTCTGGCAACACCAAGGTTGACCTCGGATCAGGTAGGAAAGACCGCTCGAATTAAGCAT
661 ATCATACGCGGAGGAAGGGCGAATTCGGCGCCGCTAAATCAITTCGCCCTATAGTGA
721 GTCGTATTACCAATCACTGGCCG
//

4/28/2024

USDA-ARS-GIFVL

Supplementary Table S1. ITS region sequences from isolated fungi.

↓ Solanum microdontum-2, Cladosporium cladosporioides MT466517

GGGCGATTGAATTTACGGCGCGGAATTCGCCCTT
GGAAGTAAAGTCGTAAACAAGGTCTCCGTAGGTGAACCTGCGGAGGATC
ATTACAGTGACCCCGGTCTAACACCGGGATGTTCTAACCTTTGTTG
TCCGACTCTTGCTCTCGGGGCGACCTGCTTACGGCGGGGCTCCGG
GTGGGACTTCAAACTTTGGCTAACTTGGAGCTTGAGTAAACCTAATT
AATAAATTAACCTTTAAACACGGATCTCTTGTTCTGGCATCGATGAA
GAACGAGCGAAATGCGATAGTAACTGTAATTCGAGAATTCAGTGAATC
ATCGAATTTGAACGACATCTGCGCCCTGGTATTCCGGGGGGCATGC
CTGCTCGAGGCTATTTCACCACTCAAGCTCGCTTGTTTGGGCAACG
CGGTCCGCCGCGTCTCAATCGACCGGCTGGGTCTCTGTCCCTAAG
CGTTGTGGAACTATTGCTAAAGGGTGTTCGGAGGCTACGCCGTAAAA
CAACCCATTCTAAGGTTGACTCGGATCAGGTAGGATACCCCTGAA
CTTAGCATCATTAAGCGGAGAAAGGCGGAATCGTTTAACTTGA
GGATAGTCCCTTAGTGAGGTTAATTCGAGCTGGCGTAATCATGTGT
CATAGCTGTTCTCGAGG

4/28/2024

select all 100 sequences selected		GetBark	Graphics	Distance tree of results	MSA Viewer				
Description		Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident %	Acc. Len	Accu
☒	Cladosporium sp. strain CH10187 small subunit ribosomal RNA, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300333
☐	Cladosporium trawickiiCladosporium trawickii CH10142 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300021
☐	Cladosporium cladosporioides strain CH10144 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300346
☐	Cladosporium sp. strain CH10152 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	820	CF300345
☒	Cladosporium sp. strain CH10152 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300345
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300342
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1000	62%	0.0	100.00%	821	CF300341
☐	Cladosporium sp. strain CH10151 small subunit ribosomal RNA, gene, partial sequence, internal transcribed spacer 1	Cladosporium sp.	1000	1					

LOCUS 635 bp DNA linear PLN 23-APR-2024
DEFINITION Exserohilum rostratum strain LWI chromosome 7.
ACCESSION
VERSION
KEYWORDS
SOURCE Exserohilum rostratum
ORGANISM Exserohilum rostratum
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Dothideomycetes; Pleosporomycetidae; Pleosporales; Pleosporineae;
Pleosporaceae; Exserohilum.
REFERENCE 1 (bases 1 to 635)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..635

/organism="Exserohilum rostratum"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Kennebec'
/db_xref="taxon:165983"
/country="USA:Maryland"
/lat_lon="39.026,-76.925"
/collection_date="2021"
PCR_primers="fwd1_name: Ef, fwd1_seq: GAYTTCATCAAGACATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCMRCTTGTG
fwd2_name: Ef13, fwd2_seq: gtaaaagccagGAYTTCATCAAG, rev1_name: Ef13, rev1_seq: caggaacagctatgacGACGTTGAADCCAC

ORIGIN

1 NAGGNACCTCTCTGTNANGTGCTCTCGGTGATCTCTCGTGGACTTGACGTANGTGGGAAC
61 ACCTTCTTGGGCAAGGTGGGACCATACCAAGCTTGATGATACCGGTCTCGACACGAC
121 GACGGGAACCGTGCCAATACCAACAATCTGTAGACATCTGGAGGGGAAGACGGAGGGG
181 CTGTGCGTAGGACGGCTGGGAGGGTCSATGGCGCTCAATGGCTCAAGGAAGGCTCTTACC
241 AGTGGCTTGGGCTTGATCTCTCTCCCAACCTTGACACGGGGGACAGTTGCTGAGGGC
301 CTGATCATCTGTCTCGTGAACCGGGATGGGACGAAGGGGAACGTGCTGGGGGTT
361 GTAGCCGACCTCTTGATGAAGTTGGAGGTCTCTCTGATGATCTCTGGTAACGGCTCTC
421 AGACCACTTGGGTGTCCATCTGTTGATGGGACGATGAGCTGCTGACACGAGGGGT
481 GTAGGCAAGCAGGGGCTGCTCACGGGTCTGACCATCTTGGAGATACACGACCTCGAATC
541 ACCAGTACCGGCGCGATGATGAGATAGGCGAGTCTGGCCTGGGAGGTACCAAGTATCAT
601 GTTCTTGATAAACTCGGNNNTTTTTAAAAA
//

Commented [CT11]: Please see previous comment-question on what to do in scenarios-accessions-samples when the whole chromosome is sequenced, seems as if it is too long to put in this document-report-table so have been using _ as a placeholder

Kennebec2 Cladosporium cladosporioides MT466517

TGATTTAGCGCCGCGAATTCGCCCTTGGAA
AGTAAAGTCGTAAACAGGTCTCCGTAGGTGAACCTCGGGAGGATCAT
ACAAGTGAACCCCGTCTAACACCGGGATGTTCTAAACCTTTGATGTC
GACTCTGTGCTCCGGGGCCACCTGCTTCGGGCGGGGCTCCGGGGT
GACACTCAAACTTCTGTGTACTTGGCAGTCTGGATAACTTAATTAAT
AAATTAATACTTTAAACACGGATCTCTGGTCTGGCATCGATGAAGA
CGACGGAATGCGATAAGTAATGTAATTGAGAATTCAGTGAATCATC
GAATCTTGAAACGACATTCGCCCCCTGGTATTCGGGGGGCATGCTG
CTCGAGGCTGATTCACCACTCAAGCTCTGTTGATTGGGCAACGGGG
TCCGCGGCTGCTCAATCGAACCGGCTGGTCTCTGCTCCCTAAGCTG
TGTGGAACCACTTCGTAAGGGGTGTCGGGAGGCTACGCCGTAACAA
CCCATTTCTAAGGTTCACCTCGGATGAGTGAAGGATACCCGCTGAACCT
AGGCATATCATAGCGGAGGAAGGGGAATTCGTTAAACCTGCGAGAC
TAGTCCCTTTAGTAGGGTTAATCTGAGCTGGCGTAATCATGTGCATA
GCTGGGTTTCTCTGAG

Cladosporium sp. strain CN136B7 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: DP596126.1 Length: 821 Number of Matches: 1

Range: 1: 75 to 631					* PROBABILITIES	
Score	Expect	Identical	Gaps	Strand		
1031 bits(588)	0.0	97.1(97.7)(99%)	1/977(0%)	Plus/Plus		
Query: 28	GGAACTAAAGTGTGAGAGACTCTCTGAGGACCTCGGAGGACATTCAGATC			87		
Seq1: 75	GGAACTAAAGTGTGAGAGACTCTCTGAGGACCTCGGAGGACATTCAGATC			338		
Query: 88	ACCCGCTTAACTCAACGAGATGTCAGACCTTTGATCTCGGCTCTCTGAGTGG			347		
Seq1: 335	ACCCGCTTAACTCAACGAGATGTCAGACCTTTGATCTCGGCTCTCTGAGTGG			394		
Query: 348	GGGAGGCTGCTCTTCTGGGAGGGGCTCGGAGGCTACGCCGTAACAA			287		
Seq1: 395	GGGAGGCTGCTCTTCTGGGAGGGGCTCGGAGGCTACGCCGTAACAA			254		
Query: 288	CAGTCTGAGTAACCTTAACTATAAATAAATTTTAAACAGGATCTCTTGGTTGG			267		
Seq1: 255	CAGTCTGAGTAACCTTAACTATAAATAAATTTTAAACAGGATCTCTTGGTTGG			334		
Query: 288	CATCTGAGGAGGCGGCAAGTGGGATGAGTATCTGAATTCAGATTCAGTAACT			537		
Seq1: 315	CATCTGAGGAGGCGGCAAGTGGGATGAGTATCTGAATTCAGATTCAGTAACT			374		
Query: 328	ATCGATCTTTGAGGAGATTCGCTCTCTGATTCCTGGGAGGATCTCTCTGAG			387		
Seq1: 375	ATCGATCTTTGAGGAGATTCGCTCTCTGATTCCTGGGAGGATCTCTCTGAG			434		
Query: 288	GTGATTTGAGGATTCAGGCTCTCTGATTCCTGGGAGGATCTCTCTGAG			447		
Seq1: 435	GTGATTTGAGGATTCAGGCTCTCTGATTCCTGGGAGGATCTCTCTGAG			494		
Query: 468	ATCGAGGCTGGGTCTCTCTCTGAGGCTCTGAGGATTCAGGATTCAGGATTC			587		
Seq1: 495	ATCGAGGCTGGGTCTCTCTCTGAGGCTCTGAGGATTCAGGATTCAGGATTC			554		
Query: 588	CGGAGGATTCGCTGAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG			567		
Seq1: 565	CGGAGGATTCGCTGAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG			614		
Query: 568	ACCCGCTTAACTCAACGAGATGTCAGACCTTTGATCTCGGCTCTCTGAGTGG			683		
Seq1: 615	ACCCGCTTAACTCAACGAGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG			651		

LOCUS DP596126 821 bp DNA linear PLN 01-SEP-2023

Commented [CT12]: This matching sequence from NCBI does not have a matching GenBank # to the given sample... the given GenBank # matches to an older and shorter sample ... ?

Commented [CT13R12]: Please see comment below for quality assurance of biological determination of the strain for accuracy of the entry in NLM

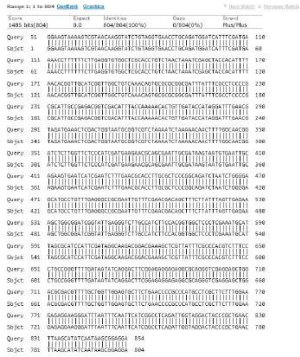
Commented [CT14R12]: Possibly cladosporioides or pseudocladosporioides? As the species ...

USDA-ARS-GIFVL
↓ LOCUS 838 bp DNA linear PLN 23-APR-2024
DEFINITION Cladosporium sp. isolate CAR_T3L3C15 translation elongation factor 1-alpha (EF1a) gene, partial cds.
ACCESSION
VERSION
KEYWORDS
SOURCE Cladosporium sp.
ORGANISM Cladosporium sp.
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Dothideomycetes; Dothideomycetidae; Cladosporiales;
Cladosporiaceae; Cladosporium.
REFERENCE 1 (bases 1 to 988)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..838
/organism="Cladosporium sp."
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Kennebec'"
/db_xref="taxon:1207700"
/country="USA: Maryland"
/lat_lon="39.026, -76.925"
/collection_date="2021"
/PCR_primers="fwd1_name: Ef, fwd1_seq: GAYTTCATCAAGAATCATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCMRCTTGTC
fwd2_name: EF13, fwd2_seq: gtaaaagccagGAYTTCATCAAG, rev1_name: EF13, rev1_seq: caggaacgctagcGACGTTGAADCCAC
cgc <1..>838
/gene="EF1a"
mRNA <1..>838
/gene="EF1a"
/product="translation elongation factor 1-alpha"
cds <1..>838
/gene="EF1a"
/codon_start=2
/product="translation elongation factor 1-alpha"
ORIGIN
1 CNVGGGNNANNTCGCGAGCTGCTCGTGTCATCTCGACGGACTTGACCTCGTGGTG
61 ACACCCGCGGGGCGGAGGTGACGACTTGGCCCTTGATGTGATCCAGTCGACACCA
121 CCACAGGAACCCGTCCGATACCCGGAATCTTGATGACATCTGGAGGGGAAGACGAGG
181 GGCTTGTCACTGGGACGGCTGGGGGGGTGATGGCCTCAATGGCTCGAGGAGGGTCTTG
241 CGGTGGCTTAGCCTTGTGCTCTCTCTCCAACTTGTACAGGGGCAAGTTGGTGAG
301 ACCTCATGATGTTGTACCTTGAACCGGAGATGGGGACGAGGGACAGCTGTGGGG
361 TTGAAGCGACCTTCTTGTGAACCGGAGGTCTCCTTGATGATCTCTCGTGAACGGGCC
421 TCAGACCACTTGGTGGTGCATCTTGTGTATGGCAACAATGAGTCTTGACACCAAG
481 GTGTAGGCGAAGAAGCGCTGCTACGGGCTGACCGCTCTGGAGATACCGCTCCACAC
541 TCACAGTACCGGGGGCAATGATGAAGTGGCGAGCTCTGCCCGGAGGTACCAAGTATC
601 ATGNTCTAGATGANNCTGCCNNNTNTTANAAAGCTCCAATCTCTCTGCTCTCAAT
661 GGCATGACCTTGTGTACGAAGACACAATACGCTTGACACCGACCTGGCGGGGAGGAG
721 CAAGTGCCTCCTGTTCTGGGGATCTGTCCGCTGCTGGCGCAACGANNATGATGGCGCG
781 TCCATGGAGGAGCAGCATGATCTGTTCTGATGNAATCGNNNNNNNTTNNNN

USDA-ARS-GIFVL
Kennebec-3 Moesziomyces aphidis isolate E24790 MK267771

TTACCTCCTCAAGGGACTAGTCTGCGAGGTTTAAAC
CGAATTCGGCTTGGGAAGTAAAGTCGTAACAAGGTATCTGTAGGTGAAC
CTGCAGATGGATCTTTCGATGAAACCTTTTCTTGAGGTGTGGCTCG
CAGCTGTCTAACCTAAATCGAGCTACCACTTTTAAACAGGTTGTCATCGGT
TGGCTGTCAAAAGTCCGCGGGGGGATTTATTTCGCTCTCCCGCGCATTCG
CCGAGACGGTGCACATTTACCAAAAACACTGTTGATACCATAGGATTGA
ACGTAGATGAAACTCGACTGGTAATCGGTGCTCTAAATCTAAAAACAA
CTTTGGACACGGATCTCTTGCTCTCCATCGATGAGAGAACGAGCGAA
TTGGGATAGTAATGTGATTCGAGAGATGAATCTCGCAATCTTTGAACG
CACCCTGGCTCCCGGAGATCTAATCTGGGGAGCATGCCTGTTTGAAGGG
CCGCGAATTGTTTGAACGACAGCTTCTTATTATTGTTGAGAAAGCTGGC
GGATCGGATTGAGGGGTCTTGCCATCTCCACGGTGGCTCTCGAAATG
CATTAGCGATCATTGATAGGGGAAGACGGGCGAAGCTGTTATTTCG
CCACGCTTTCCTCCCGGGTTTGAATAATCAGGACTTCGAGAGGA
GAGGCGCAGGGTCGAGGAGCTGGACGCGAGCTTTGCTGGTTGGAGTGCT
TCTGAACCCCGCATGCTCGTCTTTTGGAAAGAGAGGAGGATTAA
TTTCATTCACTGGCTCAGATGGGTAGGACTACCCGCTGAATCTAGCA
TATCAATAAGCGGAGGAAGGGCGAATTGGCGCGCGCTAAATCAATTCTG
CCCTATAGTGAGTGATTACAATTCACTGGCGG

Moesziomyces aphidis isolate E24790, ITS 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: MK267771.1 Length: 804 Number of Matches: 1



↑ LOCUS MK267771 804 bp DNA linear PLN 12-DEC-2018

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.
4/28/2024
LOCUS 921 bp DNA linear PLN 16-APR-2024
DEFINITION Moesziomyces aphidis isolate E24790
ACCESSION
VERSION
KEYWORDS
SOURCE Moesziomyces aphidis
ORGANISM Moesziomyces aphidis
Eukaryota; Fungi; Dikarya; Basidiomycota; Ustilaginomycotina;
Ustilaginomycetes; Ustilaginales; Ustilaginaceae; Moesziomyces.
REFERENCE 1 (bases 1 to 921)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source
1..921
/organism="Moesziomyces aphidis"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Kennebec'"
/db_xref="taxon:84754"
/country="USA-Maryland"
/lat_lon="39.026,-76.925"
/collection_date="2021"
/PCR_primers="fwd1_name: ITS1, fwd1_seq: tccgtaggtaacctggg, rev1_name: ITS4, rev1_seq: tctccgcttattgatgc, fwd2_name: M13-ITS1, fwd2_seq: gtaaaacggcagctcgttagtgaacc, rev2_name: M13R-ITS4, rev2_seq: (caggaaacagctatgacctccgcttattgatg)
Gene
1..921
/gene="contains small subunit ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"
mRNA
1..921
/gene="contains small subunit ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"
/product="Moesziomyces aphidis isolate E24790"
CDS
1..921
/gene="contains small subunit ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"
/product="Moesziomyces aphidis isolate E24790"
ORIGIN
1 TTACCCCTCAATAAGGGACTAGTCTCGAGGTTTAAACGAATTCGCCCTTGAAGTAAAA
61 GTCGTAACAAGGTATCTGTAGGTGAACCTCGAGATGGATCATTTGATGAAAACCTTTT
121 TCTTGAGGTGTGGCTCGACCTCTTAACTAAATCGAGCTACACATTTTAAACGGTGT
181 CATCGGTTGGCTGTCAAAAGTGGCGCGCGGCGATTATTTCGGCTCCCCGCGATGTGCG
241 AGACGGTGCACATTACCAAAAACACTGTTGATACCATAGGATTGAACGTAGATGAAC
301 TCGACTGGTAATGGCGCTGTCTAAATCTAAAAACAACTTTGGCAACGGATCTCTTGCT
361 TCCCTCATCATGAGAGACACGCGAATTCGATGAATTAATGTGAATTCGAGAAGTGAAT
421 CATGAATCTTTGAAGCACCTTGCCTCTCCGCGAGATCTAATCTGGGGAAGCATGCTGT
481 TTGAGGGCCGGAATTGTTTGAACGACAGCTTTCTATTATTAGTTGAGAAGCTGGCGGA
541 TCGGTATTGAGGGTCTTGCATCTTCCAGGTGGCTCLCTCGAATTCATTAGCGCATCC
601 ATTGCAATGGCAAGCGAGCAAGCTGTTATTTCGCCACCTCTTCTCTCGCGGTT
661 TTGATAATATCAGGACTTCGAGAGGAGAGGCGCAGGGTCTGAGGAGCTGGACGCCAGCT
721 TTGCTGGTTGGAGTGTCTTGAACCCGCCCATGCCCTGCTCTTTGGGAAGAGGGAAGG
781 GATTTAATTTCAATTCATCGGCTCAGATTGGTAGGACTACCCGCTGAACCTTAAGCATAT
841 CAATAAGCGAGGAAGGGCGAATTCGCGCGCGCTAAATTCATTTCCCTTATAGTGAGT
901 CGTATTACAATTCATCGGCG
//

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.
4/28/2024
TEF Moesziomyces rugulosus KP323133

CGNGGANACCCCTCGGAGGACCTCGTGGTCATCTCGACCGACTTCGCTCGGTGGTGACGTTGGAG
GGGGAAACCGTGGACGACCATGCCGCCCTTGATGACACCGGTCTGCACACGCCGACGGCACAGTTCGGA
TACCGCCGATCTTGAGACGCTCTGGAGNGNGCNGGGTGAAGNNGCTTGCTGGTGGGGCGGAGGGGG
CTCGATGGTGCGATGGGCTGGAGAGGGCTCTCGCGTGACCTTGGCGGCTTGCTCGCTGGCTCCAG
CCCTCTAGCCAGGCATCTCTGGTGGGCTCGATCATGTTCTGCCGTCGACGCGAGATGGGGACGA
AGGCGACGGTCTGGGGTGTAGCCACCTCTTGATAAAGTTGGAGGTCTCTTGACAATCTGTTGAA
GCGGTCTCGGAGTACTTGTTGGTGTTCATCTTGTTGACGGCGACGATAGCTGACCGACACCGAGGGGTG
AAGGAGAGAGGGGTGCTCGCGGCTCTGGCGCTCTGGAGATACATCTCAAAATCACCGGGTACC
ACGAGCATGATGAGGATGGCGAGTCGGCTCGGAGGTACCGGTGATCATGTTCTTGATGAATCTGG
NNCTTTTAAAAAGCCANNGTGGAGCCTGGTGAATGTCCACATTNNGGCGGTTTTTGCCTGATCT
CTGGATNMACGACANNANCCGNNGATGCANNGTTGAAGTACTCCGAGAACANNTTGTGATGAGGAN
NAAGTAGGGATAGCATCTAGCAGATGTGANNCAATGAGANNCTAGANNCTGGAGGCTGCTGAGA
ANCTGATGATNTCGCTTNCGACNNACAGACACAAATCTNNGCANNNGTCTACGNTNNGTCTTGAG
GCNNNNNNCTGCGGTTNNGATCCNNNTGTNNGCCANAATGCAAAATCCGTAATAGTCCCTGAAGNNTG

Moesziomyces rugulosus strain CBS 170.88 translation elongation factor 1-alpha (tef1) gene, partial cds
Sequence ID: KP323133.1 Length: 1034 Number of Matches: 1

Score	Expect	Identical	Query	Match
1588.184(97.1)	0.0	606/624(97%)	8/924(1%)	PhageMug
Query 1	CGGGAACCCCTCGGAGGACCTCGTGGTCATCTCGACCGACTTCGCTCGGTGGTGACGTTGGAG			68
Seq1: 634	CGGGGAGACCCCTCGGAGGACCTCGTGGTCATCTCGACCGACTTCGCTCGGTGGTGACGTTGGAG			575
Query 61	CGTTGGAAAGGGGCAAAAGTGGAGACCTGCGGCCCTTGATGACGACGTTCTCGACACCGG			120
Seq1: 574	CGTTGGAGGGGGCAAAAGTGGAGACCTGCGGCCCTTGATGACGACGTTCTCGACACCGG			515
Query 121	CGAGCGGCGACATTTCCGATACCGCGGATCTTGATGAGATCTCGAGAGGAGGAGGAGGAGG			180
Seq1: 514	CGAGCGGCGACATTTCCGATACCGCGGATCTTGATGAGATCTCGAGAGGAGGAGGAGGAGG			457
Query 181	GAGGCTTCTCGTGGGGGCGAGGGGGGCTCGATGGGCTCGATGGCTCGAGAGGGGCTCT			240
Seq1: 454	GA-GCTTCTCGTGGGGGCGAGGGGGGCTCGATGGGCTCGATGGCTCGAGAGGGGCTCT			398
Query 241	TGCGGTGACCTTGCGGGCTTGCTCTCGGCTCCGACCTTTATACAGGCGATCTCTCT			300
Seq1: 397	TGCGGTGACCTTGCGGGCTTGCTCTCGGCTCCGACCTTTATACAGGCGATCTCTCT			338
Query 301	TGCTGGGTGATGATGTTCTGCGCTGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG			240
Seq1: 337	TGCTGGGTGATGATGTTCTGCGCTGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG			278
Query 361	TGGGGTTAGCGCGCTCTTGATGAATGGAGGCTCTTGATGATCTCGTGGAGG			420
Seq1: 277	TGGGGTTAGCGCGCTCTTGATGAATGGAGGCTCTTGATGATCTCGTGGAGG			218
Query 421	GCTCTCGAGTACTTGCTGGTGGTCTGCTTGATGGGAGGAGTCACTGACGCGACGAC			480
Seq1: 217	GCTCTCGAGTACTTGCTGGTGGTCTGCTTGATGGGAGGAGTCACTGACGCGACGAC			158
Query 481	CGAGGGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG			540
Seq1: 157	CGAGGGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG			88
Query 541	CAAAATCAACGGATACGACGAGGATGAGGATGGGAGGAGGAGGAGGAGGAGGAGGAGG			600
Seq1: 97	CGAA-CTCAAC-GGATACGACGAGGATGAGGATGGGAGGAGGAGGAGGAGGAGGAGG			46
Query 601	GATGATGATGTTCTTGATGAATC 634			
Seq1: 39	GATGATGATGTTCTTGATGAATC 16			

LOCUS KP323133 1034 bp DNA linear

Commented [CT17]: See page 62; repeat?

Commented [CT1817]: Or same EndoPathogen in different cultivar hosts? Former being 'Kennebec' and latter being 'Pontiac' ...

Commented [CT1917]: Leaning towards the latter determination...

4/28/2024

```

gene      <1..978
          /gene="tef1"
mRNA      <1..978
          /gene="tef1"
          /product="translation elongation factor 1-alpha"
CDS       <1..978
          /gene="tef1"
          /product="translation elongation factor 1-alpha"

```

Colletotrichum siamense strain T1 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: [KY421040.1](#) Length: 582 Number of Matches: 1

↑ LOCUS KY421040 582 bp DNA linear PLN 27-NOV-2017

↑ LOCUS KY421040 582 bp DNA linear PLN 27-NOV-2017

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.
4/28/2024
LOCUS 831 bp mRNA linear PLN 23-APR-2024
DEFINITION Colletotrichum gloeosporioides translation elongation factor EF-1 alpha (GCG54_00009205), partial mRNA.
ACCESSION
VERSION
KEYWORDS
SOURCE Colletotrichum gloeosporioides
ORGANISM Colletotrichum gloeosporioides
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Hypocreomycetidae; Glomerellales; Glomerellaceae;
Colletotrichum; Colletotrichum gloeosporioides species complex.
REFERENCE 1 (bases 1 to 831)
AUTHORS Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..831
/organism="Colletotrichum gloeosporioides"
/mol_type="mRNA"
/isolation_source="stems"
/hosts="Solanum tuberosum 'Kennebec'"
/db_xref="taxon:474922"
/country="USA-Maryland"
/dat_jon="39-026,-76-925"
/collection_date="2021"
/PCR_primers=""fwd1_name: Ef, fwd1_seq: GAYTTCATCAAGACATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCRACRTTGTG
"twd2_name: Ef13, fwd2_seq: gtaaaacggcagGAYTTCATCAAG, rev1_name: Er13, rev1_seq: caggaaacagtatgacGACGTTGAADCCRAC
ORIGIN
1 CTCTTGAGCTGCTGCTGGTGCTCTCGCCGACTTGACGTCAGTGGTGACATTGGCTGGA
61 GCCCAGGTGACCAACATGCGCGGCTTGAGGATACAGGTCTCGATACGGCCGACACANAC
121 AGTGGCAATACCACTCTGTAGACATCTGGAGGGGAGACCGAGGGGCTGTGCGGT
181 GGGACGCTTGGGGGGCTCGATGGAGTCAATGGCTCCAGAGAGGGTCTTGGCGTGACCTT
241 GCCACCTTGCCTCTCTCCAGCCTTGTACCAAGAAGGCTTGGTGGTGGGGGACG
301 CATGTGTGTGCGGTGGAGCGCGACATGGGGACGAGGCAACCGCTCTGGGGTTGTAGCC
361 GAAGCTCTTGATGAGTGTGAGGCTCTCTTGATGATCTCTGGTACGGTCTCAACCA
421 CTTGGTGGTGTCCATCTGTGTTATGCGACNACATCGCTTGACACCCAGGCGTAGGC
481 NAGCANATCGTGCTCACGGGCTCGGCATCTGGAGATACCAACCCGAACTACACAGT
541 ACCGGCAGCGATGATGAGGATAGCGACGTCGGCTGGGAAGTACCANTGATCATGTTCTT
601 GATANNKCTNCCCTCTTTTANANNAAAAAACCCCACTCTNCGGGGNKCCGCAATG
661 AGCNTCGNNCNTTTNTNAAAAAANAACNTNTNGCTNGACACCNCTNTGGC
721 GGGCGAGCANCGTGTGCTACGGTCTCTGGGNATCTGANCTCAGANCGGCGACNACNAN
781 NTGGCAGCTCCATGTTGGCGGCACAGTATCATGTTCTTGNNNNAANGT

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.
4/28/2024
Kennebec-5 Fusarium oxysporum MT507289

CATTACCGAGTTTACAACCTCCAACCCCTGTGAACAT
ACCACCTGTTGCTCGGCGGATCAGCCCGTCCCGTAACGGGACGGC
CCGCCAGAGGACCCCTAACTCTGTTCTATATGTAACTCTGAGTAA
CCATAAATAAATCAAACTTTCAACAACGATCTCTTGCTCTGGCATCG
ATGAGGAGACGAGCAAAATGGCGATAAGTAATGTGAATTGGAGATTTCAGT
GAATCATGAACTTTGAAGCACAATTGCGCCCGCAGTATTCTGGCGGG
CATGCTGTTCGAGCGTATTTC AACCTCAAGCACAGCTTGGTGTGGG
ACTCGGTTAATTCGGCTTCCCAATTAATTGGCGGTACGTCGAGCTT
CCATAGCGTAGTGTAAACCCCTGGTACTGGTAATCGTCGGGGCAGCG
CGTTAAACCCCAACTCTGATGTTGACCTCGATCAGGTAGGAATACCC
GCTGAACCTTAGCATATCAATAGCGGAGGAGTCATAGCTGGTTTCTCTG

Fusarium oxysporum isolate cymbidium 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: MT907289.1 Length: 619 Number of labels: 1

Range 1: 94 to 344		Query	GenBank	F (94% ID) A (90% ID)	
GenBank	Expert	Identities	Gap	Score	
963 hah[221]	6.0	528/531(99%)	2/531(0%)		Plus/Plus
Query	1	CATTACCGAGTTTACAACCTCCAACCCCTGTGAACAT			68
Sbjct	64	CATTACCGAGTTTACAACCTCCAACCCCTGTGAACAT			123
Query	61	CCGCCAGAGGACCCCTAACTCTGTTCTATATGTAACTCTGAGTAA			119
Sbjct	124	CCGCCAGAGGACCCCTAACTCTGTTCTATATGTAACTCTGAGTAA			188
Query	128	ATGAGTCTGATGAGTGTAAACCCCTGGTACTGGTAATCGTCGGGGCAGCG			179
Sbjct	184	ATGAGTCTGATGAGTGTAAACCCCTGGTACTGGTAATCGTCGGGGCAGCG			249
Query	188	CGTTAAACCCCAACTCTGATGTTGACCTCGATCAGGTAGGAATACCC			239
Sbjct	244	CGTTAAACCCCAACTCTGATGTTGACCTCGATCAGGTAGGAATACCC			303
Query	248	AUTCATGGAATCTTTGAAGCACAATTGCGCCCGCAGTATTCTGGCGGG			288
Sbjct	304	AUTCATGGAATCTTTGAAGCACAATTGCGCCCGCAGTATTCTGGCGGG			363
Query	308	GAGCGTGATTGACCCCTCAAGCAGACTTGGTCTTGGAGTGGGTAATTGGGTTCC			359
Sbjct	364	GAGCGTGATTGACCCCTCAAGCAGACTTGGTCTTGGAGTGGGTAATTGGGTTCC			423
Query	368	CCAAATTAATGGGGGTGAGTGGAGTTCATAGCGTACTAAACCCCTGGTACTG			410
Sbjct	424	CCAAATTAATGGGGGTGAGTGGAGTTCATAGCGTACTAAACCCCTGGTACTG			483
Query	428	GTAACTGTGGGGCAGCGGCTTAAACCCCAACTCTGAACTTTGAGCTTGGATGAGTA			470
Sbjct	484	GTAACTGTGGGGCAGCGGCTTAAACCCCAACTCTGAACTTTGAGCTTGGATGAGTA			543
Query	488	GGAAATACCCCTGAACCTTAAGCATATCAATAGCGGAGGAGTATAGTACT			529
Sbjct	544	GGAAATACCCCTGAACCTTAAGCATATCAATAGCGGAGGAGTATAGTACT			594

LOCUS MT907289 619 bp DNA linear PLN 26-AUG-2020

4/28/2024

VERSION
KEYWORDS
SOURCE *Fusarium oxysporum*
ORGANISM [Fusarium oxysporum](#)
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae;
Fusarium; *Fusarium oxysporum* species complex.

REFERENCE 1 (bases 1 to 538)

AUTHORS Unpublishe

TITLE Unpublished

JOURNAL Unpublishe

FEATURES	Location
----------	----------

FEATURES	Location, Quantity
source	1, 538

```

/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Kennebec'"
/db_xref="taxon:3530"
/country="USA:Maryland"
/dat_lens="39,026, -76,925"
/collection_date="2012"
/pca_primers=fwd1_name: ITS1, fwd1_seq: tccgatggatgcacgcr, rev1_name: ITS4, rev1_seq: tccctcgattatgatgc,
fwd2_name: M13-ITS1, fwd2_seq: gtaaaacggcgcctcctggatgac, rev2_name: M13R-ITS4, rev2_seq: (gagaagcaactatgctacctctctctgattgatt)
fwd3_name: ITS1, fwd3_seq: gatttcatcaaaacacatgatt, rev3_name: r, rev3_seq: GACGCTGATGACCAATCTGTTC
fwd4_name: ITS1, fwd4_seq: gtaaaacggcgcctcctggatgac, rev4_name: ITS1, rev4_seq: GAGaaacactatgctacctctctgattgatt
fwd5_name: ITS1, fwd5_seq: gtaaaacggcgcctcctggatgac, rev5_name: ITS1, rev5_seq: GAGaaacactatgctacctctctgattgatt

```

Gene <1..538
/gene=" contains small subunit ribosomal RNA, internal
transcribed spacer 1, 5.8S ribosomal RNA, internal
transcribed spacer 2, and large subunit ribosomal RNA

mRNA
<1>.538
/gene="contains small subunit ribosomal RNA, internal
transcribed spacer 1, 5.8S ribosomal RNA, internal
transcribed spacer 2, and large subunit ribosomal RNA"
/product="Fusarium oxysporum"

CDS
 <1..538
 /gene="contains small subunit ribosomal RNA, internal
 transcribed spacer 1, 5.8S ribosomal RNA, internal
 transcribed spacer 2, and large subunit ribosomal RNA"
 /product="Fusarium oxysporum"

ORIGIN

1 CATTCAGCGCTGACCTATCCCCAACCTGGTGGTAAACACCACTGTTGTCCTGGCGGAGG
 61 AGCCAGGCTCCCGGTAAACAGGAGCGGCCGCGACAGAGAGGCTAAACTCTTCTTATCA
 121 TGTAACTCTCGAGTAAACCAATAAAATAACAACTTTCACAAACGGATCTGTTGGTTC
 181 TGGCATCGTAGGAAGACGACGAGAAATCGCGTAAGATGTAATGGTAATTCGCAAGATTCAGT
 241 ATCATCGAATCTTGTAAGCACTATCGGCCCGCGAGTATCTTGGCGAGGACGCTTCGTG
 301 CGGCTCATCTCAACCTCAAGCAGCACTGGTGTTGGGACGTGGGTAATTCGCTGCTCG
 361 AAGCAATGATGGGCGTGCTAGCTGAGCTTCATAGCTAGTAGTAAACCTCGCTACTGGC
 421 TAATCTCGGGGACGACCTGTAAACCACCACTCTGAATGGTGACTCGGGATCAGGATG
 481 AAGATACCGGTGCAATTAAGCATCAATAAGCGGAGGAGTCATAGCTGTTTCTTCCTG

4/28/2024

TEF *Fusarium oxysporum* MN329697

AGCTGGCTCAGTGAAGCTCGTGGTGCTGCTCG
 AGCGACTGACTTGACGTGGTGCATGGTGAAGGAAGCAAGGTACACGACAT
 ACCAGGCTGTATGACACCAAGCTTCGATAGCGGCGAAGGAACGGTCTTCA
 TACCACTCATCTGTGATAGATCGATGGGAGAGCGGAGGGGCTGTCA
 AGCGAGCATCTGGGGGCTGCGATCGATCAATGGCTCGTGAAGAGGGGTTT
 GCGAGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
 GCGATCTGGTGAGGGGGTAAGCATTTGTCACGCTGGAAGACCGAGATG
 GGGGGAAGACGACAGCTCGGGGGTGTGACGCACTCTGTGTAAGA
 GGGGCTCTTAAATGATGTCTGTAAGGGGCTGACAGCATCTGTAAGG
 TGTCCATCTGTGATGGCGACCAATGAGGTTTGACACAGAGGGGTGATG
 GCAGAAAGAGCGTGCTCAAGGTTGGCATCTTGGAGATACACCGCTG
 CACTGACCAAGTACCGCGGCAATGAGTAAGATGGCGCATCTGCGGCTGGG
 CAGTGGATGATCTGTGTGATGAGTACGGGGGGTTCGAA
 AAG

Fusarium oxysporum Fo47 chromosome VI

Sequence ID: [CP052043.1](#) Length: 4390638 Number of Matches: 1

Sequence ID: [CP002043.1](#) | Length: 4300836 | Number of markers: 1

Range	Start	End	Accession	Quality	RefSeq Match
Range 1	15083532	to 15084747	NC_017047	100	99.99999999999999
Seq 1	15083532	15083532	NC_017047.1	100	99.99999999999999
Seq 2	15083533	15083533	NC_017047.1	100	99.99999999999999
Seq 3	15083534	15083534	NC_017047.1	100	99.99999999999999
Seq 4	15083535	15083535	NC_017047.1	100	99.99999999999999
Seq 5	15083536	15083536	NC_017047.1	100	99.99999999999999
Seq 6	15083537	15083537	NC_017047.1	100	99.99999999999999
Seq 7	15083538	15083538	NC_017047.1	100	99.99999999999999
Seq 8	15083539	15083539	NC_017047.1	100	99.99999999999999
Seq 9	15083540	15083540	NC_017047.1	100	99.99999999999999
Seq 10	15083541	15083541	NC_017047.1	100	99.99999999999999
Seq 11	15083542	15083542	NC_017047.1	100	99.99999999999999
Seq 12	15083543	15083543	NC_017047.1	100	99.99999999999999
Seq 13	15083544	15083544	NC_017047.1	100	99.99999999999999
Seq 14	15083545	15083545	NC_017047.1	100	99.99999999999999
Seq 15	15083546	15083546	NC_017047.1	100	99.99999999999999
Seq 16	15083547	15083547	NC_017047.1	100	99.99999999999999
Seq 17	15083548	15083548	NC_017047.1	100	99.99999999999999
Seq 18	15083549	15083549	NC_017047.1	100	99.99999999999999
Seq 19	15083550	15083550	NC_017047.1	100	99.99999999999999
Seq 20	15083551	15083551	NC_017047.1	100	99.99999999999999
Seq 21	15083552	15083552	NC_017047.1	100	99.99999999999999
Seq 22	15083553	15083553	NC_017047.1	100	99.99999999999999
Seq 23	15083554	15083554	NC_017047.1	100	99.99999999999999
Seq 24	15083555	15083555	NC_017047.1	100	99.99999999999999
Seq 25	15083556	15083556	NC_017047.1	100	99.99999999999999
Seq 26	15083557	15083557	NC_017047.1	100	99.99999999999999
Seq 27	15083558	15083558	NC_017047.1	100	99.99999999999999
Seq 28	15083559	15083559	NC_017047.1	100	99.99999999999999
Seq 29	15083560	15083560	NC_017047.1	100	99.99999999999999
Seq 30	15083561	15083561	NC_017047.1	100	99.99999999999999
Seq 31	15083562	15083562	NC_017047.1	100	99.99999999999999
Seq 32	15083563	15083563	NC_017047.1	100	99.99999999999999
Seq 33	15083564	15083564	NC_017047.1	100	99.99999999999999
Seq 34	15083565	15083565	NC_017047.1	100	99.99999999999999
Seq 35	15083566	15083566	NC_017047.1	100	99.99999999999999
Seq 36	15083567	15083567	NC_017047.1	100	99.99999999999999
Seq 37	15083568	15083568	NC_017047.1	100	99.99999999999999
Seq 38	15083569	15083569	NC_017047.1	100	99.99999999999999
Seq 39	15083570	15083570	NC_017047.1	100	99.99999999999999
Seq 40	15083571	15083571	NC_017047.1	100	99.99999999999999
Seq 41	15083572	15083572	NC_017047.1	100	99.99999999999999
Seq 42	15083573	15083573	NC_017047.1	100	99.99999999999999
Seq 43	15083574	15083574	NC_017047.1	100	99.99999999999999
Seq 44	15083575	15083575	NC_017047.1	100	99.99999999999999
Seq 45	15083576	15083576	NC_017047.1	100	99.99999999999999
Seq 46	15083577	15083577	NC_017047.1	100	99.99999999999999

↑ LOCUS CP052043 4300638 bp DNA linear PLN 21-JUN-2023

Commented [TCTRA24]: Whole chromosome was isolated-sequenced-updated-etc. in 2023 ... closer whole non match reported instead; what is best to do in this scenario?

4/28/2024

ORIGIN

1 AGANATATCTAGAGTTTGGGGCTTGCCACGTGCTTACCATCATTTTGGTAATAC
61 TACGTTTCTCTCGTGGGCTGCGCCCGCGGTCAGTGGACATTAATCAATCTGACGTGTAATAC
121 TACGCTGTCGAAAGCAATAATGTATACACTTACCAACGGCATCTTGCTTGTCGCAAT
181 CGATGAAGAAGACGACCAATGTCAGTTGATGTTGAATTCGAGCAATTCGAGTGAACATCAT
241 TGGTTTCTGAAGCAGCATATGCGGCCGCTGGTATGATGCTGAGCAATCTGCTTGAGTCAAT
301 TGGTCTGCTGCTGCTGCTGGTGGTGGTGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
361 CTTCTAAACCAATCGACGCGCGGTATTTGTTCCGAGCGACATCATCTCCGCTGTTCTG
421 ACTCATACGACGCTGCAAAAGTCTGCTGCTGCTTGCACCTGTCGATCGATGCAATGAGTGGGA
481 TCCGCGAAGATCATTAAGCATCAATAACGGGGAAGCATATGCTAGTCTGTTTCCGTCATAAA
541 GCGGGAAGCTCATATCTGTTGGGGAATAAGGGGGAAGGAATCATATTTTTCGCGG

Commented [CT28R27]: ITS

4/28/2024

[illegible][illegible]

↑ LOCUS FJ449999 831 bp DNA linear PLN 16-DEC-2008

Commented [TCTRA30R29]: Kennebec-7 *Chaetopyrena* penicillate ON712593, from second update of table

4/28/2024

4/28/2024

Colletotrichum fioriniae isolate Cf.60.014.DDPP translation elongation factor EF-1 (EF-1) gene, complete cds
Sequence ID: KU847413.1 Length: 2388 Number of Matches: 1

[illegible]

USDA-ARS-GIFVL
LOCUS 840 bp DNA linear PLN 23-APR-2024
DEFINITION Colletotrichum florinae isolate CT.60.D14.DDPP translation elongation factor EF-1 (EF-1) gene, complete cds.
ACCESSION
VERSION
KEYWORDS
SOURCE Colletotrichum florinae
ORGANISM Colletotrichum florinae
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Hypocreomycetidae; Glomerellales; Glomerellaceae;
Colletotrichum; Colletotrichum acutatum species complex.
REFERENCE 1 (bases 1 to 840)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..840
/organism="Colletotrichum florinae"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Kennebec'"
/db_xref="taxon:710243"
/country="USA:Maryland"
/lat_lon="39.026, -76.925"
/PCR_primers="fwd3_name: Ef, fwd3_seq: GAYTTCAAGAACATGAT, rev3_name: Er, rev3_seq: GACGTTGAADCCRACRTTGTG
"fwd4_name: Ef13, fwd4_seq: gtaaaagccgagGAYTTCATCAAG, rev4_name: Er13, rev4_seq: caggaacagctatgacGACGTGAADCCRAC"
ORIGIN
1 C N N G G G A G A C C T C N G T A A G C T G C T G T G G T G C A T C T G A C G G A C T T G A C T C T G G T G A C
61 A T T G G C G G G G C G A A G G T G A C C A C C A C T G C C G G C T T G A T G T C A C C G A T C T G A T A C G G C
121 G A C G G G A C T G T T C C A A T A C C A C C G A T C T T G A G A C A T C T G G A G G G A A G A C G G A N G G G
181 C T T G T C G T G G G A C G C T T G G G G T G T C G A T G G C G T C A A T G G C C T C A G A A G G G T C T T G C C
241 G G T G A C T G C C A C T C T G G T C C T C T C C A T C C T T G T A C A C G G A G C G T G G T G G T
301 G G G G C A N G C A T G T T G T G C C G T G A A C C G G A G A T G G G G A C A A G G C A C A G T C T T G G G
361 G T T G A G C C A A C T T C T T G A T A C C C A G A G G T C T C T T G A T G A T C T C T G T A A C G G G C
421 C T C G G A C C A C T T G G T G G N T C A T C T T G T G A T G G C G A C T A C G C T G C T G A C C A A G
481 G G T G T A G G C A A G C A C T G T G C T C T G G G T C T G G C A T C T T G G A T A C A G C T C T A A
541 C T C A C A A C A C C G G C N G C G A T G A G A A T A C A C A G T C G G C T G G G A G T A C C G G T A A T
601 C A T G T T C T G A N N N N C G N C C N C T N T T T N N N A N A A A A A A A A C C C A A A T T T C T N
661 G G G G G T C T C A N A N N G G G C T C C A A C C T T G T T G A N A A A A A N A N A N A N T N T T C G N A N
721 N N C N A N C N A N G N G A A N N C N A N G N G N N A C N N G T C C N G G G C A T G G C C G
781 T C N G A N C N A C G A C N A T G A T G G C A C G T C A T G T T G G G C A C N G T A T C A T G T C T G A N G A
//

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.
Kennebec-10 Pestalotiopsis sp. JQ341112

CNTTATAGAGTTTCTTAAATCCCAACCATGT
GAACCTACCTTTTGTGCTGGCAGAGTTATAGGCTCTCTATAGCTG
CTGCCGGTGACCATTAACCTCTGTTATTTATGTAATCGAGCGCTCT
ATTTAATAAGTCAAACTTTCAACAACGGATCTCTGGTCTTGGCATCG
ATGAAAACGCAAGCGAATGCGATAACTAATGTGAATTGACAGATTACGT
GAATCATGAACTCTTGAAGCACATGCGCCCAATAATTCTAGTGGG
CATGCTGTTCGAGCGTCATTCAACCTTAAGCTAGCTTAGTGTGGG
AATCTACTCTCTTAGAGAGTTGTAGTTCTCTGAATAACACCGCGGATTG
TAGTATCTCTGAAGCTAGTAATTTTTTTCTCTTTGGTAAGTGCTAT
NACTCCCGGCGCTAAACCCCAATTTTGTGGTGACCCCGATCAGG
CAGGAATACCCCGAGCTTAACGATATCAGAAATGTGAANNAGCCCAATC
TGGGTCCTGAANTATATAAGAAACAATGAAAAATGGAAGGNGAGNCGN
GCNNA

Pestalotiopsis sp. D6WS 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: JQ341112.1 Length: 566 Number of Matches: 1

Range 1: 56 to 346 GenBank Clade(s)					T (Total Matches) + T (Total Mismatches)	
Score	Expect	Identities	Gaps	Simple		
841 bits(453)	0.0	492/511(96%)	0/511(0%)	PhyloPlus		
Query 3	TTATAGAGTTTTCTAAATCCCAACCATGTGAACCTACCTTTTGTGCTGGCAGAG	62				
Seq1 56	TTATAGAGTTTTCTAAATCCCAACCATGTGAACCTACCTTTTGTGCTGGCAGAG	115				
Query 63	TTATAGAGTTTTCTAAATCCCAACCATGTGAACCTACCTTTTGTGCTGGCAGAG	122				
Seq1 116	TTATAGAGTTTTCTAAATCCCAACCATGTGAACCTACCTTTTGTGCTGGCAGAG	175				
Query 123	CTGAACCTCTTATTTTAAATCCCAACCATGTGAACCTACCTTTTGTGCTGGCAGAG	182				
Seq1 176	CTGAACCTCTTATTTTAAATCCCAACCATGTGAACCTACCTTTTGTGCTGGCAGAG	235				
Query 183	GAATCATGAACTCTTGAAGCACATGCGCCCAATAATTCTAGTGGG	242				
Seq1 236	GAATCATGAACTCTTGAAGCACATGCGCCCAATAATTCTAGTGGG	295				
Query 242	AATCTACTCTCTTAGAGAGTTGTAGTTCTCTGAATAACACCGCGGATTG	302				
Seq1 296	AATCTACTCTCTTAGAGAGTTGTAGTTCTCTGAATAACACCGCGGATTG	355				
Query 303	TTGACACCTTAAGCTAGCTAGTGTGGGAATCTAGCTCTTAGAGAGTTGATTC	362				
Seq1 356	TTGACACCTTAAGCTAGCTAGTGTGGGAATCTAGCTCTTAGAGAGTTGATTC	415				
Query 363	TGAATACCAAGCGGAGTTGTGATATCTCTGAACCTAGTAAATTTTTTCTCTTTC	422				
Seq1 418	TGAATACCAAGCGGAGTTGTGATATCTCTGAACCTAGTAAATTTTTTCTCTTTC	475				
Query 473	GTAACTGTATTAATCTCCCGGGGCAACCCCAATTTTGTGGTGAACCCGATCAG	480				
Seq1 476	TAACTGTATTAATCTCCCGGGGCAACCCCAATTTTGTGGTGAACCCGATCAG	533				
Query 483	GCAGGAATACCCCGAGCTTAACGATATCAGAAATGTGAANNAGCCCAATC	540				
Seq1 536	GCAGGAATACCCCGAGCTTAACGATATCAGAAATGTGAANNAGCCCAATC	593				

↑ LOCUS JQ341112 566 bp DNA linear PLN 06-DEC-2015

USDA-ARS-GIFVL
↓ LOCUS 588 bp DNA linear PLN 06-DEC-2015
DEFINITION *Pestalotiopsis* sp. **D6WS**
ACCESSION
VERSION
KEYWORDS
SOURCE *Pestalotiopsis* sp. D6WS
ORGANISM *Pestalotiopsis* sp. [D6WS](#)
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Xylariomycetidae; Xylariales; Sporocadaceae;
Pestalotiopsis;
REFERENCE 1 (bases 1 to 588)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..588
/organism="Pestalotiopsis sp. D6WS"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Kennebec'"
/db_xref="taxon:[1233915](#)"
/country="USA:Maryland"
/lat_lon="39.026, -76.925"
/collection_date="2021"
/PCR_primers="fwd1_name: ITS1, fwd1_seq: tcgtagtgaaactggg, rev1_name: ITS4, rev1_seq: tctccgtctattgatgc, fwd2_name: M13-ITS1, fwd2_seq: gtaaacggcagtcgtagtgaacc, rev2_name: M13R-ITS4, rev2_seq: (caggaacagctgactctccgtcttgatgc)
Gene
 <1..>588
 /feature="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
mRNA
 <1..>588
 /feature="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
 /product="Pestalotiopsis sp. D6WS"
CDS
 <1..>588
 /feature="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
 /product="Pestalotiopsis sp. D6WS"
ORIGIN
1 CNTTATAGAGTTTCTAAACTCCCAACCACTGAACTTACCTTTGTTGCTCGGCAGA
61 AGTTATAGGCTTCTTATAGCTGCTCGGTGACATTAACACTCTGTATTATTATGA
121 ATCTGAGGCGCTCTATTTAATGAAGTCAAACTTTCAMCAACGGATCTCTGGTTGCGCA
181 TCGATGAAAAACGAGCGAAATGCGATAAGTAATGTGAATTGCGAATTCAGTGAATCAT
241 CGAATCTTTGAACGCACATTGCGCCATTAAATATCTAGTGGGCATGCTGTTGAGCGT
301 CATTTCAACCTTAAGCTAGCTAGTGTGGGAATCACTACTCTTCAAGGAGTGTAGTT
361 CCTGAAATACCAACGGCGATTGTGATGATCCTCTGAACGATAGTAATTTTTTCTCTTT
421 TGGTAAGTGCTATNACTCCCCGCGCTAAACCCCATTTTGTGTGGACCCCGATC
481 AGGCAAGGAATACCGCGAGCTTAACGATATCAGAAATGTGANNAGCCCAATCTGGGTC
541 TGAANTATATAAGGAACACATGAAATGGAAGNGGAGNGGNCNNA
//

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.
[TEF](#) *Pestalotiopsis* fici [XM-007831532](#)

AGTGCACTCT
AGACGGACTTGACCTCAGTGGTGACGTTGGAGGGAGGAAGGTAAACGACC
ATACCGGGCTTGATGGTACCGGTCTCGATACGGCCGACGGGCACTGTGCC
AATACCACTGATCTTETAACATCTCGAGGGGAAGACGAGGAGGGCTTGT
CGGTAGACGGCTAGGGGGGTTGATGGCGTCAATGGCTGGGAAGAGGGCTC
TTGCCCTCTCTTGACACCTTGACCTCTCTTCCAGCCCTTGATACCA
GGGAAGCGTTGGTGCTCTCTCAACATGTTGTACCGCTTGAACCGGAGA
TGGGACGAGAAGGACACCTCTGGGTTGTAGCAACCTTGTGATGAAG
TTGGAGGCTCTCTGATGATCTCTGTAAACGGGCTCGAACCACTTGGC
AGTGTCATCTCTGTTGATGGGACGATGAGCTGCTTGACACCGAGGGTGA
AAGCGAGCAGAGCGTGCTACGAGTCTGGCATACTTGGAGATACAGCC
TCGAATCAACGATCCGGCGCAATGATGAGAAATGGCGAGTGGCCTG
GGAAGTACCAATATCATGTTCTTGTGAATCNNNNNNTTTTTTAAAAAA
AAAAAANAATTTGGGGGGCCNAGGGGGCANCNCCTTTGTNAACNAA
AACANNCCCTTTTGGTATCCCAACNTGGGGGGGNGAACACCAAGNTGCT
CAGGGNNNGGGGACCTGACCTCTGAAAGCGCCGACCAATGATGGCC
CGTCCATGTTGGCGGGNCCAGTGATCATGTCTTGATGAATNTGCC
GCCTTTANAAAA

Neopestalotiopsis hyperici isolate CC.HK04 translation elongation factor 1-alpha (TEF) gene, partial cds
Sequence ID [PP496594.1](#) Length: 1279 Number of Matches: 1

Range 1: 315 to 605					T (nt) (nt) a (nt) (nt) (nt)	
Score	Access	Ident	Gap	Score		
18S1.18k(18S)	S1	999 (99.99%)	0 (0%)	7967 (99%)		
Query: 2	GTGCATCTGAGAGGACTTGAACCTCACTGCTGACCTTGGAGGGAGGAAGGTAAACGACC	61				
Sbjct: 315	GTGCATCTGAGAGGACTTGAACCTCACTGCTGACCTTGGAGGGAGGAAGGTAAACGACC	373				
Query: 62	TACCGGGCTTGATGGTACCGGTCTCGATACGGCCGACGGGCACTGTGGAGATACAGCC	121				
Sbjct: 374	TACCGGGCTTGATGGTACCGGTCTCGATACGGCCGACGGGCACTGTGGAGATACAGCC	433				
Query: 122	TCTTGTAAACATCTTGAGGGGAGAGCGAGGGGCTTGTGGTGAAGAGGCTACGGGGGT	181				
Sbjct: 434	TCTTGTAAACATCTTGAGGGGAGAGCGAGGGGCTTGTGGTGAAGAGGCTACGGGGGT	493				
Query: 162	TGATGGCTCAATGGCTTGAGAGAGGCTTGGCTTCTCTTGACACCTTGACCTCTCT	241				
Sbjct: 494	TGATGGCTCAATGGCTTGAGAGAGGCTTGGCTTCTCTTGACACCTTGACCTCTCT	553				
Query: 242	TCTTCCAGGCTTGTACCAAGAGGCTTGTGGTCTCTCCAACTGTGTACCTGATG	301				
Sbjct: 554	TCTTCCAGGCTTGTACCAAGAGGCTTGTGGTCTCTCCAACTGTGTACCTGATG	613				
Query: 362	AACCGAGTGGAGGAGAGAGAGGCTTGGGTTGTACCACTCTTGTGGTGGT	421				
Sbjct: 614	AACCGAGTGGAGGAGAGAGAGGCTTGGGTTGTACCACTCTTGTGGTGGT	673				
Query: 362	TGGAGTCTCTTGTGATCTCTTGAAGGGGCTGGAGCACTTGGCACTGTGGTGGT	421				
Sbjct: 674	TGGAGTCTCTTGTGATCTCTTGAAGGGGCTGGAGCACTTGGCACTGTGGTGGT	733				
Query: 422	TCTTGTAGGAGAGCTGAGCTGCTTGACACGAGGCTGAAGGAGAGAGGCTGCTAC	481				
Sbjct: 734	TCTTGTAGGAGAGCTGAGCTGCTTGACACGAGGCTGAAGGAGAGAGGCTGCTAC	793				
Query: 482	GAGCTTGGGCTCTTGAGATACAGGCTCGAATCACTGATACGGGAGGAGTGTG	541				
Sbjct: 794	GAGCTTGGGCTCTTGAGATACAGGCTCGAATCACTGATACGGGAGGAGTGTG	853				
Query: 542	GATBGGCAGTGGGCTTGGAGATACAGGCTCGAATCACTGATACGGGAGGAGTGTG	601				
Sbjct: 854	GATBGGCAGTGGGCTTGGAGATACAGGCTCGAATCACTGATACGGGAGGAGTGTG	903				

↑ LOCUS PP496594 1279 bp DNA linear PLN 15-APR-2024

Commented [TCTRA33]: Higher percent identity E value, but shorter query length; is this the accurate genera-species-accession?

Neopestalotiopsis hyperici, instead of Pestalotiopsis fici ?

USDA-ARS-GIFVL
↓ LOCUS 823 bp DNA linear PLN 23-APR-2024
DEFINITION Neopetalotripsiopsis hyperici [isolate CC-HK04 translation elongation factor 1-alpha (TEF) gene, partial cds.
ACCESSION
VERSION
KEYWORDS
SOURCE Neopetalotripsiopsis hyperici
ORGANISM Neopetalotripsiopsis hyperici
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Xylariomycetidae; Xylariales; Sporocadaceae;
Neopetalotripsiopsis.
REFERENCE 1 (bases 1 to 823)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..823
/organism="Neopetalotripsiopsis hyperici"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Pontiac'"
/db_xref="taxon:3015324"
/country="USA,Maryland"
/lat_lon="39.026, -76.925"
/collection_date="2021"
/PCR_primers=fwd3_name: Ef, fwd3_seq: GAYTTTCATCAAGAATGAT, rev3_name: Er, rev3_seq: GACGTTGAADCCRCRRTGTG
fwd4_name: Ef13, fwd4_seq: gtaaaacggcagGAYTTCATCAAG, rev4_name: Er13, rev4_seq: caggaaacagctgacGACGTTGAADCCRAAC"
misc_feature
1..823
/gene="TEF"
mRNA
1..823
/gene="TEF"
/product="translation elongation factor 1-alpha"
CDS
1..823
/gene="TEF"
/product="translation elongation factor 1-alpha"
ORIGIN
1 AGTGCATCTCAGACGACTTGACCTCAGTGGTGACGTTGGAGGGGACGGAAGGTAACGACC
61 ATACCGGGCTTGATGGTACCGTCTCGATACGGCCGACGGGCACTGTGCCAATACACCG
121 ATCTTGTAAACATCTCTGAGGGGAAGACGGAGGGGCTGTGCGTAGACGCGCTAGGGGGG
181 TTGATGGGCTGAATGGCTCGAGAGGGGCTTGGCTCTCTTCTTGACACCTTGACCTCC
241 TTCTCCGACCCCTTGTACCGAAGCGTTGGTGTCTCTTCCAACATGTTGTCAACGGTG
301 AAACCGGAGATGGGGACGAAGGGAACCTCTTGGGGTTGTAGCCAACCTCTTGATGAAG
361 TTGAGAGTCTCTTGTATGATCTCTTGTAAACGGGCTTCGACCACTTGGCAGTGTCAATC
421 TTGTTGATGGCAGCAGTGGCTGCTTGACACGAGGGGTGAAGCGAGGAGAGAGTGCTCA
481 CGAGTCTGGCCATCTCTGGAGTACAGCCCTGCAATCACCAGTACCGGCGGCAATGATG
541 AGAATGGCGCAGTCCGCTGGGAAGTACAGTAATCATGTTCTTGTGAATCNNNNNTT
601 TTTTMAAAAAAANAANAATTTCCGGGGGCCCCNAGGGGGGCGANNCCTTTGTNAACNAAA
661 AACANNCTTTTTGTCCACATGNTGGGGGGAACACCAAGNTGCTCAGGGGNNNG
721 GGGCANCTGACCTTCGAAAGCGGCGNCAACAATGATGGCCCCGTCCATGTTGGCGGNC
781 CAGTGATCATGCTCTTGATGAAATNGCGGCTCTTTANAAAA
//

Commented [CT34]: As relating to the next comment-question, this (P.f.) is shorter in sequence length than the closest induced match (N.h.) ... N.h. would be the correct determination?
Commented [TCTRA35]: Neopetalotripsiopsis hyperici or Pestalotripsiopsis fici ? Which is the accurate Genera and species to put?

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.
F. Pontica Cladosporium cladosporioides KC464337
NATTGATTAGCGCCCGGAATCGCCCTTGCT
CCATTATTGATGGGACTCCCAACGGGAATCTGATACATGAACGAGGTC
AACCAACCCCGGTGTAAACACCGGGATGTTCTAAACCCCTTGTTGTCGAG
TCTGTTGCTCTCCGGGGGACCTGCTTCCGAGAGGGGCTCCGGGCGAAC
ACTTCAAACTCTTGATATCTTGGCCCACTGAGTAACCTTAATTAACAAA
TTAAAACTTTTAAACAACGGATCTCTTGGCTCTGGCATCGATGAAGAAGCG
GGCGAAATGCGATAAGTAATGTGAATTGAGAAATTCAGTGAATCATCTAA
TCTTGAACGACATTCGCGCCCTGGGATTCAGGGGGGGAATGCTGTTTC
GAGCGTATTACCAACTCAAGCCCTGGTTGTATTGGGCAACGGCGTCC
GACGCGNAACTCAATCGACCGAGCCCGCTTCTAATCCCTCAAGCCCC
ONNNAACATTACTCAAAAGGGTGTTCGGTAGGGGAACATCCCGAGGTTA
GACCGCTGTACACTTATCATGATATTCGCGAGGNTACTACTGATATC
TTGTTTACTACTTTAGCTACGAAGGGGAATTTCTTTNATTTTGTGTTT
TTTTTTCTTTTGTAGTGATTATC

Cladosporium cladosporioides strain Fg138 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: KC464337.1 Length: 500 Number of Nucleotides: 1

Range 1: 26 to 452		GenBank		GenBank		* Local BLAST		+ Protein BLAST	
Score	Expect	Identical	Query	Score	Expect				
599.1446(24)	4e-166	2932/425(69%)	Query	2/4296(0%)	Phen/Plus				
Query 89	ACCCCGGTGTAAACACCGGGAATCTGAAGCCCTTTGTTCGAGATCTTTGCTCTCGG	140	Seq1c 26	ACCCCGGTGTAAACACCGGGAATCTGAAGCCCTTTGTTCGAGATCTTTGCTCTCGG	85				
Query 149	GGGAAATGCGATAAGTAATGTGAATTGAGAAATTCAGTGAATCATCTAA	200	Seq1c 86	GGGAAATGCGATAAGTAATGTGAATTGAGAAATTCAGTGAATCATCTAA	145				
Query 209	CTTGTGAACGACATTCGCGCCCTGGGATTCAGGGGGGGAATGCTGTTTC	260	Seq1c 146	CTTGTGAACGACATTCGCGCCCTGGGATTCAGGGGGGGAATGCTGTTTC	205				
Query 269	GAGCGTATTACCAACTCAAGCCCTGGTTGTATTGGGCAACGGCGTCC	320	Seq1c 206	GAGCGTATTACCAACTCAAGCCCTGGTTGTATTGGGCAACGGCGTCC	265				
Query 329	ATCTTGTAAACATCTCTGAGGGGAAGACGGAGGGGCTGTGCGTAGACGCG	380	Query 369	CTCTTGTAAACATCTCTGAGGGGAAGACGGAGGGGCTGTGCGTAGACGCG	440				
Query 389	TTGATGGGCTGAATGGCTCGAGAGGGGCTTGGCTCTCTTCTTGACACCT	440	Seq1c 326	TTGATGGGCTGAATGGCTCGAGAGGGGCTTGGCTCTCTTCTTGACACCT	385				
Query 449	ATGAGCGAGGCGCCCGCTTCTAATCCCTCAAGCGCGGGAATTCATCAT	500	Seq1c 386	ATGAGCGAGGCGCCCGCTTCTAATCCCTCAAGCGCGGGAATTCATCAT	445				
Query 509	TTCCGTAAG 517								
Seq1c 444	TTTTTTT 452								

↑ LOCUS KC464337 500 bp DNA linear PLN 13-JAN-2016

USDA-ARS-GIFVL
LOCUS 660 bp DNA linear PLN 16-APR-2024
DEFINITION Cladosporium cladosporioides strain Fg138
ACCESSION KC464337
VERSION KC464337.1
KEYWORDS
SOURCE Cladosporium cladosporioides
ORGANISM Cladosporium cladosporioides
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Dothideomycetes; Dothideomycetidae; Cladosporiales;
Cladosporiaceae; Cladosporium.
REFERENCE 1 (bases 1 to 660)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..660
/organism="Cladosporium cladosporioides"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Ponitac'
/db_xref="taxon:29917"
/country="USA:Maryland"
/lat_lon="39.026, -76.925"
/collection_date="2021"
/PCR_primers="fw1_name: ITS1, fwd1_seq: tcctgtagtgaacctggg, rev1_name: ITS4, rev1_seq: tcctccgtattgatgac,
fw2_name: M13-ITS1, fwd2_seq: gtaaaacggcagctcgtagtgaaac, rev2_name: M13R-ITS4, rev2_seq: caggaaacagctagctactcctcgcttatg
fw3_name: E1, fwd3_seq: GAYTTCATCAAGACATGAT, rev3_name: E5, rev3_seq: GAGCTTGAADCRACRTTGTG
fw4_name: E13, fwd4_seq: gtaaaacggcagGAYTTCACAA, rev4_name: E13, rev4_seq: caggaaacagctatgacGAGCTTGAADCCRA"

Gene <1..>660
/gene=" contains small subunit ribosomal RNA, internal
transcribed spacer 1, 5.8S ribosomal RNA, internal
transcribed spacer 2, and large subunit ribosomal RNA"

mRNA <1..>660
/gene=" contains small subunit ribosomal RNA, internal
transcribed spacer 1, 5.8S ribosomal RNA, internal
transcribed spacer 2, and large subunit ribosomal RNA"
/product=" Cladosporium cladosporioides strain Fg138"

CDS <1..>660
/gene=" contains small subunit ribosomal RNA, internal
transcribed spacer 1, 5.8S ribosomal RNA, internal
transcribed spacer 2, and large subunit ribosomal RNA"
/product=" Cladosporium cladosporioides strain Fg138"

ORIGIN
1 NATTGATTAGCGGCCGGAATTCGCCCTTGCTCCATTATGATGGGACATCCCAACG
61 GGAATCTGTACATGAACCGAGGTCAACACCCCGGTGAACCAACCGGATGTTCAATAC
121 CTTTGTGTGCCGACTCTGTGCTTCGGGGGCAACCTGCCTTCGGACGAGGGCTCCGGGGC
181 GAACATCTTCAACTCTTGATCACTTGGCCACTGAGTAACTTAATACAAATTAA
241 CTTTATCAACGATCTCTTGGCTCGGATCGATGAAGACCGCGCAATGCGGATAAG
301 TAATGTGAATTGCAGAATTCAAGTGAATCATCTAATCTTTGAACGCACATTCGCGCCCTG
361 GGAATTCAGGGGGGAATGCTGTTGAGCGTCAATTCACCACTCAAGCTTCGCTGGTATT
421 GGGCAACCGGCTCGACGGNACTCAATGACCGAGCCCGCTTAACTCCCTAAG
481 CCCCNNAACTATTCACTAAAGGGGTTCGGTAGGGAACATCCCGAGGTATGACCGG
541 TCTCACTTATCATGATCACTCCGAGGNTACTACTGATATCTGTTTACTTATTAGC
601 TTACGAAGGGGAATTTCTTNNATTTTGTGTTTTTTTTTTCTTTTTTGAGTGTATTAC
//

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.

4/28/2024

CTCGCGAGCTGCTGTGGTGATCTCGAC
GGACTTGACCTGGTGGTACACCCGCGGGGGCGAAGGTGACGACCTTC
CGCCCTTGATGTACCACTCTCGACACCAACGACGACCGTCCGATA
CCACGATCTGTAGACATCTCGAGGGGGAACGACGAGGGGCTTGTGGT
GGGACGCTGGGGGGGCTGATGGGCTCANTGGCTCGAAGGAGGGTCTTC
NNNNTGGCCTAGCCTTGGTCTCTCTCCAAACCTTGACAGGGGCA
GTTGGTGAGACGCTCCATGATGTTGTACCGTTGAAGCCGAGATGGGCA
CCAGGGAACGTCGTGGGGTTGAAGCCACCTCTTGATGAACCGAG
GTCCTCTTGATGATCTCTTGGTAGGGGCTCAACCACTTGGTGGTGT
CATCTGTTGATGGCAACATGAGCTGCTTGACACCAAGGGTGTAGGCGA
GAAGAGCGTGCTACGGGTCTGACCGTCTTGGAGATACCGGCTCCAAC
TCACNNGTACCAAGCGCATATGATAGAAATNGCGAGTCTCCCGGAGG
TACCCCTGATCATGTTCTGANAATCAACCCCTTTTATAAAAA
ACCCCAACATCTCTTGCCCCANTGNNNCNACTTTGTTAAAAA
ACACAATACGCTTGACACCGACCTGGCGGGCGAGGAGCAAGTGTCTCT
GGTCTGGGGCATCTGCTGCTGCTGGCGCAACGCAATGATGGCGCGCT
CCATGGAAGCAGCACAGTATGATGTTCTNATATGNCNCCCCCTTT

Cladosporium sp. isolate CAR_T3L3C15 translation elongation factor 1- α (EF1 α) gene, partial cds
Sequence ID: MN054936.1 Length: 988 Number of Matches: 1

Range 1: 1 to 988		Unifast	Unifast	Y Test Match & Percent Match	
Score	Expect	Identities	Score	Expect	PhyloP
924.186(29)	0.0	98.8(990/54%)	2.960(29)	0.000000	—
Query: 1	CTCGCGAGCTGCTGTGGTGATCTCGAC	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 568	CTCGCGAGCTGCTGTGGTGATCTCGAC	98.8(990/54%)	2.960(29)	0.000000	—
Query: 61	GGACATCTTCAACTCTTGATCACTTGG	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 528	GGACATCTTCAACTCTTGATCACTTGG	98.8(990/54%)	2.960(29)	0.000000	—
Query: 121	CGCCCTTGATGTACCACTCTCGACAC	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 478	CGCCCTTGATGTACCACTCTCGACAC	98.8(990/54%)	2.960(29)	0.000000	—
Query: 181	GAACATCTTCAACTCTTGATCACTTGG	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 438	GAACATCTTCAACTCTTGATCACTTGG	98.8(990/54%)	2.960(29)	0.000000	—
Query: 241	TAAATGTGAATTGCAGAATTCAAGTGA	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 359	TAAATGTGAATTGCAGAATTCAAGTGA	98.8(990/54%)	2.960(29)	0.000000	—
Query: 361	GGAATTCAGGGGGGAATGCTGTTGAG	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 299	GGAATTCAGGGGGGAATGCTGTTGAG	98.8(990/54%)	2.960(29)	0.000000	—
Query: 341	CTTCTTGATGATGATGATGATGATGAT	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 278	CTTCTTGATGATGATGATGATGATGAT	98.8(990/54%)	2.960(29)	0.000000	—
Query: 401	TGAGTGTGCTCACTTGTGATGATGAT	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 378	TGAGTGTGCTCACTTGTGATGATGAT	98.8(990/54%)	2.960(29)	0.000000	—
Query: 481	GAGAGAGCTGCTGAGGAGCTGAGGAG	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 119	GAGAGAGCTGCTGAGGAGCTGAGGAG	98.8(990/54%)	2.960(29)	0.000000	—
Query: 541	CAGGAGAGCTGCTGAGGAGCTGAGG	98.8(990/54%)	2.960(29)	0.000000	—
Seq1: 9	CAGGAGAGCTGCTGAGGAGCTGAGG	98.8(990/54%)	2.960(29)	0.000000	—

LOCUS MN054936 988 bp DNA linear PLN 12-FEB-2020

Commented [CT36]: Highest match on NLM-NCBI does not have a species listed with it; cladosporioides or oxysporum?

4/28/2024

REFERENCE 1 (bases 1 to 971)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished

```

gene      <1..>971
          /gene="tef1"
mRNA      <1..>971
          /gene="tef1"
          /product="translation elongation factor 1-alpha"
CDS       <1..>971
          /gene="tef1"
          /product="translation elongation factor 1-alpha"

```

11

Commented [CT44]: type_material vs isolation_source?
Which terminology prevails?

↓ Pontiac-4 *Didymella bellidis* MN274965

Sequence ID: [MN274965.1](#) Length: 700 Number of Matches: 1

↑ LOCUS MN274965 700 bp DNA linear PLN 07-DEC-2019

↑ LOCUS MN274965 700 bp DNA linear PLN 07-DEC-2019

4/28/2024

↓ LOCUS 692 bp DNA linear PLN 24-APR-2024

DEFINITION Ceratobasidium sp. isolate C662 SV9 translation elongation factor 1-alpha (tef1) gene, partial cds.

ACCESSION

VERSION

KEYWORDS

SOURCE Ceratobasidium sp.

ORGANISM Ceratobasidium sp.

Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;

Agaricomycetes; Cantharellales; Ceratobasidiaceae; Ceratobasidium.

REFERENCE 1 (bases 1 to 692)

AUTHORS Unpublished

TITLE Unpublished

JOURNAL Unpublished

FEATURES Location/Qualifiers

source 1..692

/organism="Ceratobasidium sp."

/mol_type="genomic DNA"

/isolation_source="stems"

/host="Solanum tuberosum 'Pontiac'"

/db_xref="taxon:1768090"

/country="USA-Maryland"

/lat_lon="39.026, -76.925"

/collection_date="2021"

/PCR_primers= fwd1, fwd1_seq: GAYTTCACTAAGACATGAT, rev1_name: Er, rev1_seq: GACGTTAADCRCRATTGTG

fwd2_name: Ef13, fwd2_seq: gtaaaacggcagGAYTTCAACAAG, rev2_name: Er13, rev2_seq: caggaacagctatgacGCGTTGAADCCRC"

/notes="genotype: SV9"

miscfeatures <1..>992

gene="tef1"

miscfeatures join<1..67,117..211,258..470,519..655,708..>942

gene="tef1"

/product="translation elongation factor 1-alpha"

miscfeatures join<1..67,117..211,258..470,519..655,708..>942

gene="tef1"

/product="translation elongation factor 1-alpha"

ORIGIN

1 TCTACGAGCTGCTCTGGTGCATTTCTACGA
61 CTTGACTTCAGTGGTCACATTGGAAGAGCCAACGAGACGACATGCCGG
121 CTTTGATGACACGAGTCTCGACGACCGACGGGCACTGTGCCCTAACAC
181 CGATATTGTACACATCTCGACAGGGGCACTGATGGGCTGTGCCAGGGA
241 CGGACAGGGGGCTCAATGGATCNATGACATCNGGAGGGTCTTCCCTTG
301 ACGGAACCGGCTTGGACTCTTGGTCCACCTTGAACACGGGATGCA
361 CTGTGGGTGGCTTCAAAAAGCATGTTAAATGGACGACGAGTCTTGTATGT
421 GGTGCGCGCTCTTACGACATGTCCTCCGCGCCGCAANTGGGACCA
481 AAGCCACCTGGTGGGGTGTAAACCACTTCTGGATAGTTGGGAGTT
541 TCCTTTGACATTTCTTGAACCGGCTCGTCCCTGGAATGGAATCC
601 ATACATGTCCAATACCAATTACAAATGACCTACCTGTGGTGTGCCCTC
661 TTGTGACCCACACATNANTGACACACACACCGAGGGTGAAGACNAGAN
721 AACTGTGCNAGTCTGGGACATCTTGGAGATACNCGCTTCAATTGNC
781 CANTACCCANCCATGATTAAAGATAGCGAATCCGCGNAGANAGTCCA
841 GTGANCATGTT
//

Commented [CT52]: Should this be here? Please let me know, thanks.

Commented [CT53]: Should this be included here?

Colletotrichum acutatum MH931266

GGGCGGATTGATTAGCGCCCGGAATTCGCCCT
TTCTCTCGCTTATTGATGCTTAAGTTCAGCGGGTATCTCACTGATC
CGAGGTCAACCTGTAAGAATTGGGGGTTAACGGCAAGAGTCCCTCCG
GATCCAGTGCAGACGTTAGTTACTACGCAAGAGGCTCCGGGAGGGT
CCGCACTACCTTTAAGGCGCACCTGGCGGTGGGGCCCCAAGCAAG
CGGTGCTTGAGGGTTGAAATGACGCTCGAACAGCATGCTCGCAGAATG
CTGGGAGCGCAATGTGCGTTCAAAGATTGATGATCACTGAATCTGC
AATCACTACTTATCGGATTCCTGCTGCTTCATCATGATCCAGAGAC
CAAGAGATCGTGTAAAGTTTAAATATTCTTGTGTCGCTCAGAA
GAGACGTGTGTAAATAGAGTTTGTTTCTCCGCGGGGCGCCCGTCCC
CGTGGTGGGGGCGCGCCCGGAGGGGAGGCCCGGAGAGGCTCCCGCTG
CCCGCCGAGCAACGTTAGGTAGTCTGTCACAAAGGTTATAGAGCGGTAA
CTCAGTAATGATCCCTCCGCTGGTTCACCTCGGAGAGCTTTATGCACT
TTTACTTCAAGGGCGAATTCGTTAAACCTCGAGGACTAGTCCCTTTA
GTGAGGGTTAATCTGACCTGGCATAATCTGCTCATACGTTTNTCT

Colletotrichum acutatum isolate TS 12.1.2 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: MH931266.1 Length: 826 Number of Matches: 1

Range 5: 594 to 803 Colletotrichum acutatum					FIND MATCHES > EXCLUDED MATCHES	
Gene	Expect	(position	Gene	(score	PhyloHit	
1122 kb(107)	0.0	609/610(99%)		5/16(31%)		
Query 34						85
Sbjct 1603						744
Query 34						153
Sbjct 743						804
Query 354						213
Sbjct 483						824
Query 214						273
Sbjct 623						561
Query 274						333
Sbjct 563						581
Query 334						393
Sbjct 563						444
Query 354						453
Sbjct 441						304
Query 454						513
Sbjct 383						324
Query 514						573
Sbjct 323						264
Query 574						633
Sbjct 263						204
Query 634						
Sbjct 263						194

LOCUS 826 bp DNA linear PLN 16-APR-2024
DEFINITION Colletotrichum acutatum isolate TS 12.1.2
ACCESSION
VERSION
KEYWORDS
SOURCE Colletotrichum acutatum
ORGANISM Colletotrichum acutatum
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Hypocreomycetidae; Glomerellales; Glomerellaceae;
Colletotrichum; Colletotrichum acutatum species complex.
REFERENCE 1 (bases 1 to 826)
AUTHORS TBD
TITLE TBD
JOURNAL TBD
FEATURES Location/Qualifiers
source 1..826
/organism="Colletotrichum acutatum"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Pontiac'"
/db_xref="taxon:27357"
/country="USA-Maryland"
/lat_lon="39.026, -76.925"
/collection_date="2021"
/PCR_primers="fwd_name: ITS5, fwd_seq: gtagtaaaagctgtaacagg, rev_name: ITS4, rev_seq: tccctcgcttatgatgc"
Gene <1..>826
/gene=" contains small subunit ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"
mRNA <1..>826
/gene=" contains small subunit ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"
/product="Colletotrichum acutatum isolate TS 12.1.2"
CDS <1..>826
/gene=" contains small subunit ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"
/product="Colletotrichum acutatum isolate TS 12.1.2"
ORIGIN
1 GGGGCGATTGATTAGCGGCGCGGAATTCGCCCTTCTCTCGCTTAATGATGCTTAAG
61 TTCAGCGGGTATTCCTACATGCTCCGAGGTCAACCTGTAAAGAATTTGGGGGTTAACGG
121 CAAGAGTCCCTCCGGATCCAGTGCAGAGCTTAGTTACTACGCAAGGAGGCTCCGGGA
181 GGGTCCGCACATACCTTAAGGCGCCACGCTGGCGCTGGGGCCCCAAMACCAAGCGGTG
241 TTGAGGGTTGAATGACGCTGCAACGAGCATGCTGCAGAAATGCTGGCGAGCGCAATG
301 GCGTTCAAGATTCGATGATTCACTGAATTCGAATTCACATTACTATCGCATTTCCG
361 TGCCTTCTCATGATGCCAGAACAGAGAGATCGTTGTTGTTAAAGTTTAAATATTGCT
421 TTGTCACACTCAAGAGAGCTGTTGAATAGATTTGGTTCTTCCCGCGGGCGGCCCG
481 TCCCGTGGTGGGGCGCGCGCGGAGGGAGGCGGCCGAGAGGCTTCCCTGCGCCCG
541 GAAGCAACGGTTAGCTAGCTTCAAAAGGGTTATAGAGCGGTAACCTAGTAATGATCCCT
601 CCGCTGGTCACTACGAGGAGCTTGTACGACTTTTACTTCCAAGGGGGAATTCGTTA
661 AAACCTCGAGGACTAGTCCCTTAGTGAGGGTAAATCTGAGCTTGGCATAATCATGTC
721 ATANCTGTTTNC
//

Commented [CT54]: When possible, may you please provide primers for this sample (Colletotrichum acutatum isolate TS 12.1.2)? Under Table 1 'Endophyte isolation...' there is no ITS or TEF primers associated with this fungi ...

Commented [CT55R54]: ITS?

GGGCGNANTGANTTTAGCGGCCGGAATTCGCCCTTC
CTCCGCTTATTGATGCTTAAGTTTACGGGGTATCCCTACCTGATCGGA
GGTCAAAAGTTGAAAAAGGCTTAATGGATGCTAGACCTTTGCTGATAG
AGAGTGGGACTTGTGCTGGCTCCGAACCAAGTACGGCGGCTGCCAATTA
CTTTAAGGCGAGCTTCTGCAAAAGCTAGAGCAAGAGCGCCCAACCAAG
CAAGCTTGAGGGTACAAATGACGCTGCAACAGGATGCCCTTTGGAATA
CCAAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACTGAATTCG
AATTCACACTACTATGCGATTCTGCTGGCTTCTCATGATGCCAGAAC
CAAGAGATCCGTTGTGAAAGTTGTAATATTATTGTTACTGACGCGTG
ATTGCAATTACAAAGGTTTATGTTTCTCTAGTGGTGGGCGAACCCACC
AAGGAACCAAGATGCAAAAGCAAGGGTGTAATATTCAAGCAAGGCT
GTAACCCGAGAGGTCCAGCCCGCTTCATATTGTTGTATGATCCCTC
CGAGGTTCACTACGAGAGCTTGTACGACTTTTACTCCGAGGGCGA
ATTGCTTAAACCTCGAGGACTAGTCCCTTAGTGAGGGTAAATCTGAG
CTTGGCGTAATCATGTCATANNNTGTTTCTCTGA

Alternaria angustiovoidea isolate BMS 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: MK910060.1 Length: 600 Number of Matches: 1

Range 1: 2 to 599		GenBank	Graphics	* Best Match * Previous Match	
Score	Expect	Identical	Gaps	Strand	
1105 bits(598)	0.0	598/598(100%)	0/598(0%)	Plus/Minus	
Query 34	TTTCTCCGCTTATTGATGCTTAAGTTTACGGGGTATCCCTACCTGATCGGATCGA				93
Subject 599	TTTCTCCGCTTATTGATGCTTAAGTTTACGGGGTATCCCTACCTGATCGGATCGA				540
Query 94	AAGTTGAAAAAGGCTTAATGGATGCTAGACCTTTGCTGATAGAGAGTGGACTTGTGC				153
Subject 539	AAGTTGAAAAAGGCTTAATGGATGCTAGACCTTTGCTGATAGAGAGTGGACTTGTGC				480
Query 154	TGCGCTCGAAACCAAGTACGGCGCGCTGCCAATTACTTTAAGGCGAGTCTCCAGCAAGCT				213
Subject 479	TGCGCTCGAAACCAAGTACGGCGCGCTGCCAATTACTTTAAGGCGAGTCTCCAGCAAGCT				420
Query 214	AGAGACAAAGAGGCCCAACACCAAGCAAGCTTGAGGGTACAAATBACGCTCGAACAGGCA				273
Subject 419	AGAGACAAAGAGGCCCAACACCAAGCAAGCTTGAGGGTACAAATBACGCTCGAACAGGCA				360
Query 274	TGCCCTTTGGAATACCAAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACTGAAT				333
Subject 359	TGCCCTTTGGAATACCAAGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACTGAAT				390
Query 334	CTGCAATTCACTACTTATCGCATTTCTGCTGGTTCTTCATCGATGCCAAGCAAGAG				393
Subject 299	CTGCAATTCACTACTTATCGCATTTCTGCTGGTTCTTCATCGATGCCAAGCAAGAG				240
Query 394	ATCGGTTGTGAAGTTGTAAATTAAATTTGTTTACTGAGCTGATTCGATTCAGAAAG				453
Subject 239	ATCGGTTGTGAAGTTGTAAATTAAATTTGTTTACTGAGCTGATTCGATTCAGAAAG				180
Query 454	GTTTATGTTTCTTCTAGTGTGGGCGAACCCCAAGGAAACCAAGAGTACGCAAAAGAC				513
Subject 179	GTTTATGTTTCTTCTAGTGTGGGCGAACCCCAAGGAAACCAAGAGTACGCAAAAGAC				120
Query 514	AAGGGTGAATAATTACGCAAGGCTGTAAACCCGAGAGGTTCCAGCCCGCTTCAATTTTG				573
Subject 119	AAGGGTGAATAATTACGCAAGGCTGTAAACCCGAGAGGTTCCAGCCCGCTTCAATTTTG				60
Query 574	TGTAATGATCCCTCCGAGGTTCACTACGAGAGCTTGTACGACTTTTACTTCCAA				631
Subject 59	TGTAATGATCCCTCCGAGGTTCACTACGAGAGCTTGTACGACTTTTACTTCCAA				2

Commented [CT56]: Perhaps Alternaria angustiovoidea, as the Genera-species? This was the closest identity match in the NLM that had a Genera-species, and the second closest identity match overall; almost all other identical matches at the top of the ranges were Alternaria spp. ...

USDA-ARS-GIFVL
↓ LOCUS **MT881830** 783 bp DNA linear PLN 24-APR-2024
DEFINITION Biscogniauxia mediterranea strain 18PLE008 translation initiation factor 1 alpha (TEF1a) gene, partial cds.

ACCESSION
VERSION
KEYWORDS
SOURCE Biscogniauxia mediterranea
ORGANISM Biscogniauxia mediterranea
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Xylariomycetidae; Xylariales; Xylariaceae;
Biscogniauxia.

REFERENCE 1 (bases 1 to 783)

AUTHORS Unpublished

TITLE Unpublished

JOURNAL Unpublished

FEATURES Location/Qualifiers

source 1..783
/organism="Biscogniauxia mediterranea"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum 'Pontiac'"
/db_xref="taxon:97377"
/country="USA:Maryland"
/lat_lon="39 02N, -76 92W"
/collection_date="2021"
PCR_primers=fwd1_name: Ef, fwd1_seq: GAYTTCATCAAGACATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCRCRTTGTG
fwd2_name: Ef13, fwd2_seq: gtaaacggcagGAYTTCATCAAG, rev2_name: Ef13, rev2_seq: caggaaacagctatgacAGCTTGAADCCRAAC"

gene <1..>783
/gene="TEF1a"
mRNA <1..>783
/gene="TEF1a"
/product="translation initiation factor 1 alpha"
CDS <1..>783
/gene="TEF1a"
/codon_start=1
/product="translation initiation factor 1 alpha"

ORIGIN
1 GANCTCCGTGAGCTGCTCGTGGTCATCTCAACGGACTTGACTTCAGTGGTGACGGCAGC
61 AGGAGCGAAGGTACACGACATACCGGGCTTGAGAACACCACTCTCGATACGGCGACGGG
121 CACAGTTCATACACCACTCTGTGAGACATCTGAAGGGGGAAGACGAGAGCTCTC
181 GGTAGCGTCTGGGGGGCTCAATCGAGTCAATGGCTCAAGCAGGGCTTACACGATAC
241 CTGGCCACCTTGTTCTCTCTCTCCAGCCCTGTACCAAGGGGAGTTGGTAGAGGAGT
301 CAACATGTTGTACCGTTGAACACAGAGATGGGACGAAGGCAACGGTCTTGGGGTTGTA
361 TCGCATCTTCTGTAGAGTGGAGGCTCTCTGTAGATATTGGTGAACGGCTCTCGGA
421 CCACTGGTGGTGTCATCTGTTGATGGCGACGATGAGCTGTGACCAAGGGTGTA
481 GGCAAGCAGGGGTGCTCACGGGTCTGGCCATCTGGAGATACCAAGCTCGAACTCGA
541 AGTACCAAGCAATGATGAGAAATGGACAGTGGCCTCGGAAGTACCAAGTAAATCATGTT
601 TCTGNNNNNNNGGGTTTTTAAAAAATAAAAAAATAAAAAAATTTGGGGGNNCCCTTA
661 AGGGCCATCTTTTTTGNNAAAAAAATTTTTTAAAAACACCGACTGGGGGNN
721 AAAAAAANAANCTCTCGGTGGGGGGGNCNTCAAACTNNNGAGGGGNCNCAACAATA
781 ATA
//

4/28/2024

Commented [CT59]: This hasn't been included typically, should it be? Applies to all samples here.

Commented [CT60R59]: Seems as if such is more applicable when the whole chromosome is sequenced; you obviously now more, in this area, just let me know for greater script and biological accuracy as time moves forward; thanks

USDA-ARS-GIFVL
Supplementary Table S1. ITS region sequences from isolated fungi.

Pontiac-8 Coniochaeta sp. KF367565

4/28/2024

GANITAGCGGCCGGAATTCGCCCTTTC
CTCCGCTATTGATATGCTTAAGTTCAGCGGGTATTCTACCTGATCCGA
GGTCAACCTTGAGTTAAAGATGGTCTTTAACGGCAGGAGCGCGCCGCAAC
GTCTCTAGCGAGATAAATGAATACTACGCTCGGAGTTGTAGCGAGCCCGC
CATCTCTTTACGGGCTCATCGCACCCCTAGGGGCCCAACACCAAGAGAGG
GCTTAGGGGTTGAAATGACGCTCGAACAGGCGATGCCGCTAGAGTACTAG
CGGGGCAATGTGCTTCAAGATTTCGATGATTCAGTAATTCGGAATT
CACATTAATTATCGATTTCGGTGGCTTCTCATCGATGCAGAACCAAG
AGATCCGTTGTGAAGTTTTAACTATTGTTTTTACTCAGAGATGCC
ACTATAACAGAGTTTCGTACTCCGGCGGGCGCCCACTCCGGAG
AGGCGGGGCTCGCGGCCCGCTGAGAGAGGCGCGCCCGCAAGCAACT
TGGACAGATTCGCGATGGTTTTAAGTAGCTTTCGGCTTCTAATAATGAT
CCCTCCGCTGTTCAACAGCGAGACCTTGACGACTTTTACTCCAGG
GGCGAATTCGTTAACTCGAGGACTAGTCCCTTGTAGTGGGGTTAATT
CTGAGCTGGCGTAATCATGGTCATANNNGTTTTTCTCTGA

Coniochaeta sp. 6 BPO-2013 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: KF367565.1 Length: 749 Number of Matches: 1

Score	Expect	Identical	Query	Subject
1185 bits (100)	0.0	100.0 (100%)	0/0 (0%)	Plus/Minus
Query 25	TTTTCTCCGCTATTGATATGCTTAAGTTCAGCGGGTATTCTACCTGATCCGA			84
Sbjct 634	TTTTCTCCGCTATTGATATGCTTAAGTTCAGCGGGTATTCTACCTGATCCGA			575
Query 85	CTTTGAATTAAGATGTTCTTTAAACGCAAGACGCGCCGCAACTTCTACGAGATTA			144
Sbjct 574	CTTTGAATTAAGATGTTCTTTAAACGCAAGACGCGCCGCAACTTCTACGAGATTA			535
Query 145	TGAATTACTACCTTGAATTTATAGCAAGCCCGCACTTCTTCAAGGGCTATCGGAG			204
Sbjct 514	TGAATTACTACCTTGAATTTATAGCAAGCCCGCACTTCTTCAAGGGCTATCGGAG			465
Query 205	GTAAAGGCGCAAGCAAGCAAGGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA			254
Sbjct 454	GTAAAGGCGCAAGCAAGCAAGGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA			395
Query 265	CCTCAGATTAAGTAAAGGCAATGTTCTTCAAGATTCGATGTTACTGATTTTC			324
Sbjct 394	CCTCAGATTAAGTAAAGGCAATGTTCTTCAAGATTCGATGTTACTGATTTTC			335
Query 325	AATTGAGATTAAGTAAAGGCAATGTTCTTCAAGATTCGATGTTACTGATTTTC			384
Sbjct 354	AATTGAGATTAAGTAAAGGCAATGTTCTTCAAGATTCGATGTTACTGATTTTC			275
Query 385	GTGTTGAAGTTTAACTATTGTTTCTTCAAGATTCGATGTTACTGATTTTC			444
Sbjct 274	GTGTTGAAGTTTAACTATTGTTTCTTCAAGATTCGATGTTACTGATTTTC			215
Query 445	TGTAAGTTCGCGGGGCGCGCACTTCCGAGAGGCGCGCGCGCGCGCGCGCGCGCG			504
Sbjct 314	TGTAAGTTCGCGGGGCGCGCACTTCCGAGAGGCGCGCGCGCGCGCGCGCGCGCG			155
Query 505	AGAGGCGCGCGCGCGCGCACTTCCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCG			564
Sbjct 154	AGAGGCGCGCGCGCGCGCACTTCCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCG			95
Query 565	CTTCTAATTAAGTTCCTCCGTTTCAACAGGAGGCTTTTACGATTTTACCTTTT			624
Sbjct 94	CTTCTAATTAAGTTCCTCCGTTTCAACAGGAGGCTTTTACGATTTTACCTTTT			35
Query 625	C 625			
Sbjct 34	C 34			

↑ LOCUS KF367565 749 bp DNA linear PLN 10-SEP-2013

Commented [CT61]: Should the Genera be Aureobasidium sp, and not Coniochaeta sp? They both have the same identity match (99.83%) in the NLM but the former is a longer sequence length (852 > 749).

Commented [CT62R61]: Please see comment below, as per species determination, for the latter, if such is accurate - right determination ...

4/28/2024

```

VERSION
KEYWORDS
SOURCE Coniochaeta deborreae
ORGANISM Coniochaeta deborreae
    Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
    Sordariomycetes; Sordariomycetidae; Coniochaetales;
    Coniochaetaceae; Coniochaeta.
REFERENCE 1 (bases 1 to 856)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES             Location/Qualifiers
    source             1..856
                        /organism="Coniochaeta deborreae"
                        /mol_type="genomic DNA"
                        /isolation_source="Stems"
                        /hosts="Solanum tuberosum 'Pontac'"
                        /db_xref="taxon:2823762"
                        /country="USA, Maryland"
                        /lat_lon="38.026, -76.923"
                        /collection_date="2021"
                        /primers="fw1_name: Ef, fwd1_seq: GAYTTCATCAAGACATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCRACRTGTC
                        /fwd2_name: Ef13, fwd2_seq: gtaaaagccagGAYTTCATCAAG, rev2_name: Er13, rev2_seq: caggaaacacatgacGAGGTTGAADCCRAC"
Note
    <1..856
    /gene="tef1b"
mRNA
    <1..856
    /gene="tef1b"
    /product="translation elongation factor 1-alpha"
CDS
    <1..856
    /gene="tef1b"
    /product="translation elongation factor 1-alpha"

```

1 AGCGTCGGCGACGTCTGGTGTCATCTGCAGGCGATCTTCAGTGGTCAGCTTGGG
 6 ACAGGACGGAGCGAGCGACATACACGGGTCGTGTATACAGCTGTACAGCGGCGAGGAG
 11 TTGCGGACGCTGGGGGGCTGACGTGGCTGCTTACAGGCGCTTCGAGAAGGCTCTTCGACGAT
 16 CTTCGACCTCTTCCTCTTGACCAACCTCTTCACAGGCGAGCTGGTGCGAGGGGGA
 21 AGCATCATCTGTCGGCTTACCGGAGTCGGAGTACCGGCAAGAACGAGCTCTGGGGTGTT
 26 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
 31 CACTTCGACGTCAGTCTGGCTGTATATGGGCTATGGGCTATGGGCTATGGGCTATGGG
 36 GCTGCTGAGGACGGTGCTCAGATGAGCGATCTGGGATACAGCTCGGATGAGGAGTGA
 41 GAGTCACCGGACGATGATGAGGATAGGCACATCGGCTGGGAGATCTACGATGATCATTT
 46 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
 51 CCGAAGANNNNNTCAATCTGTCCAAACNNNNCAAGCTCTCCCTNNATACGATCTACAG
 56 GCGGACGAGACGATCTGCGGCTGTGGGAGCTGACATCGACGAGGCGGCGGACGACAT
 61 NNNNNNNNNTTCAATCTGTACGGGACNNNNATCTTCTTCTTNNAAAGCGGCGGNNNN
 66 //

↓ Purple Majesty-1 *Phlebiopsis flavidoalba* MN856290

CATTAATGAGGTTTGGNNGGGTTAGCTGGGCTCATAC
 GGGGCGATGTGCACGGCTGCGTCACTCACTTCAACCTCTGCACATT
 TTGATAGTCGTGCAAGAGTCGGATCTTTCAGGAAGTCTGACTGGAGAAA
 ACCTTATCGTCTGTTTACCAACAAGCTCGAGTTAGATAGATTATCTG
 TGCTTAACGAGCTATTTACCAACAGTCAAGTCAAGCTCTGGCTGGCT
 TTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 CAGTGAATCATCTGAATCTTGAAGCAGCTGGCTGCTGCTGATATCCG
 GGGAGGACGCTGTTTGGAGCTGTGAAGGATCTCAACTCTAATAACTT
 TGTCTACAAGAGCTGGACCTGGAGGCTGTGCTGGCTGCTGCTGACGTG
 TTGCTATCTGAAATGAGCTGCTGAATTAATAGATGCTGCTGGTGTTG
 AATATCTATCTCGGCCGTAGCTGGGAAGTACTGTGAAGAGCTAACGCT
 TAAGTCGCTTCAAGAGCAATTAACCTGCACTTTTGACTCTCAACATCAG
 GTAGGATACCTCCGTAACCTAAGCATCATTAATACGGCGAGGAGCATAG
 TTTGTTCTTCCNCGA

Sequence ID: [MN856290.1](#) Length: 662 Number of Matches: 1

[illegible]

↑ LOCUS MN856290 662 bp DNA linear PLN 25-DEC-2019

USDA-ARS-GIFVL Supplementary Table S1. ITS region sequences from isolated fungi.

4/28/2024

LOCUS 653 bp DNA linear PLN 23-APR-2024
DEFINITION Phlebiopsis flavidoolba strain WZ-144

ACCESSION
VERSION
KEYWORDS
SOURCE Phlebiopsis flavidoolba
ORGANISM Phlebiopsis flavidoolba

Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
Agaricomycetes; Polyporales; Phanerochaetaeae; Phlebiopsis.

REFERENCE 1 (bases 1 to 653)

AUTHORS Unpublished

TITLE Unpublished

JOURNAL Unpublished

FEATURES Location/Qualifiers

source

1..653

/organism="Phlebiopsis flavidoolba"

/mol_type="genomic DNA"

/isolation_source="stems"

/host="Solanum tuberosum 'Purple Majesty'"

/db_xref="taxon:467968"

/country="USA-Maryland"

/lat_lon="39.026,-76.925"

/collection_date="2021"

/PCR_primers="fw1_name: ITS1, fwd1_seq: tcctgtagtgaacctggg, rev1_name: ITS4, rev1_seq: tccctcgcttattgatgc,

fwd2_name: M13-ITS1, fwd2_seq: gtaaaacggcctgcttagtgtaacc, rev2_name: M13R-ITS4, rev2_seq: caggaaacagctatgactcctcgcttattgat

fwd3_name: Ef, fwd3_seq: GAYTTCATCAAGAACATGAT, rev3_name: Ef, rev3_seq: GACGTTGAADCCRACRTTGTG

fwd4_name: Ef13, fwd4_seq: gtaaaagccgagGAYTTCATCAAG, rev4_name: Ef13, rev4_seq: caggaaacagctatgacGAGTTGAADCCRAC"

Gene <1..>653

/gene="contains small subunit ribosomal RNA, internal

transcribed spacer 1, 5.8S ribosomal RNA, internal

transcribed spacer 2, and large subunit ribosomal RNA"

mRNA <1..>653

/gene="contains small subunit ribosomal RNA, internal

transcribed spacer 1, 5.8S ribosomal RNA, internal

transcribed spacer 2, and large subunit ribosomal RNA"

/product=" Phlebiopsis flavidoolba strain WZ-144"

CDS <1..>653

/gene="contains small subunit ribosomal RNA, internal

transcribed spacer 1, 5.8S ribosomal RNA, internal

transcribed spacer 2, and large subunit ribosomal RNA"

/product=" Phlebiopsis flavidoolba strain WZ-144"

ORIGIN

1 CATTATCGAGTTTGGNNGGTTGTAGCTGGCCTATACGGGCGCATGTGCAGCGCTGGCTC
61 ATTCACCTCTCAACCTCTGTGCACTTATTGTAGATCGGTGACAGGCTCGAGTCTTTGAC
121 GAGTCTTCTGACTGGAAACACCTTTCTAGTGTTTTACCACAAAGCTTCAGTTATAGAATG
181 TTTATCTGGGTATACAGCATCTTTATACAACTTTGAGCAAGGATCTCTTGGCTCTCGCA
241 TCGATGAGAGACCGACGAACTGGATAGTAATGTAATTCGAGTAATTCAGTGAATCAT
301 CGAATCTTTGAAAGCACTTGGCGCTCCCTGGTATTCCGGGGAGCATGCGTGTTTGAGTGT
361 CATGGAATTCACACTCTTAATACTTTTTGTATCAAGAGCTTGGACTTGGAGCGCTGTG
421 CTGGGCTGCTGTTTCACTGGCTCTCTGAATGCAATGAGCTGGAATTAATAGATCGCT
481 TCGGTGTGTAATTTATCTGCGCGCTAGTGTGAGAGTACTGATAGCTTTAGCGCTCTAA
541 TCGTCTCTACGGGCAATTAACCTGACTTTTGTACCTCAATCAGGTAGGATACCC
601 GCTGAACCTAAGCATATCAATAACGGGAGGAGTATAGNNNNNTTTCCCNNGA
//

Commented [CT66]: This is the first of the two
Phlebiopsis flavidoolba; the 1st on Table 1 "Endophyte
isolation..." has the site as greenhouse and the second has
the site as field. Would this be the sample corresponding to
the greenhouse, correct? Would you like site/location noted
in the source section (applies to all given samples here)?

USDA-ARS-GIFVL

Supplementary Table S1. ITS region sequences from isolated fungi.

4/28/2024

TEF Phlebiopsis flavidoolba OQ954494

NGGANCCTGCTCGAGCTGCTCGTGGTGCACTCGA

CGGACTTGACTCAGGTGGTCACACCGAGGGGGGGAAGGTGACGACCAT

ACCGCGCTTGATGATACAGATCTCGACACGACGACGGGACCGTGCCTAA

TACACCAATCTTETAGACATCTCTGAGGGGGAGAGCGGAGGGGCTTGTG

GAGGACGGACGGGGGGCTCGGCGCTCGATGCACTGAGGAGGGGCTCTT

ACCTTGGACAAACACCCCTTGGTCTCTTGGTCAAGCCTTGTACATG

GCATGCTGGGGGGTAAAGTCAGACAATGTCACGAATGAGATTCTGCAGC

AAGTACTTGGAGGACTCTTCAACATGTTGTACCGCGACGACGAGAGA

TGGGACGACGACGCGACCGCTTGGGGTGTATGCGGACCTCTTGTATGAAG

GTGGAAGTCTCTTAACGATTTGTTGAAACGGTCTCGCTCACTGTAA

ATTTGTTGATTACCAAAACGGAATCTATGATAAAACGTACCTTG

GTGGTCTCATCTTGTACGCGGACGATAGCTGCTGACACCGAGGGT

GAAAGCAAGGAGAGCGGGCTCGCGGGTCTGGCACTCTTGGAGATACGAG

CCTCGAECTCACGGTACACCGCAATGATGAGGATGGCGCAATCGGCC

TGGGAGGTACCAAGTATGATGTTCTTAAACNCGCCTTGTATTAATAA

AAAAAATAAAAGTCAACNNITTCATATTTTGTNNCACAAATNN

GGGGTCTTNCCTCGCNGNNNCAAGTCGNNNNCCATGATTTNNNGAA

TGTTCNCGCCCTCAAGTGTAAATAANNNCAAAAGTCGGGATTTCCN

NGTGCACANNCTCNGGCTCTCGGGGCCNAAATTTGGTCAACCTTG

GTNNNTAAAAAANNCCNNNCTNNNGATTCGAAACNNGGGGTGCGANCN

NCANITTTCTTCTTNNNNATTTNNNNNTTNGTACGGGAANNNNNNAA

TAAANNNGTGCATTNNNNNNNNNNNNNTTT

Phlebiopsis flavidoolba isolate SH52 translation elongation factor 1-alpha (TEF) gene, partial cds

Sequence ID: OQ954494.1 Length: 1066 Number of Matches: 1

Score	Expect	Identical	Similar	Score	Expect
11.8 (18.6) (E05)	0.0	0.45 (66.9) (27%)	1.96 (6.1%)	Phlebiopsis	---
Query: 6	CCCTGCTCGAAGCTCTGCTGCTGATCTCGAGGACTTGAAGTTCAGGACGAC	85			
Subject: 605	CCCTGCTCGAAGCTCTGCTGCTGATCTCGAGGACTTGAAGTTCAGGACGAC	607			
Query: 66	00000000000000000000000000000000000000000000000000000	125			
Subject: 606	00000000000000000000000000000000000000000000000000000	547			
Query: 126	CACCGTGCAGTACCAAGTCTTGTAGATGCTCTGAGGAGGCTCTTACCTTGC	185			
Subject: 546	CACCGTGCAGTACCAAGTCTTGTAGATGCTCTGAGGAGGCTCTTACCTTGC	487			
Query: 186	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	245			
Subject: 486	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	427			
Query: 246	AACACCACTCTTGTCTCTTGTCTGAGGCTCTTACATGATGATCTGAGGAGGCT	305			
Subject: 426	AACACCACTCTTGTCTCTTGTCTGAGGCTCTTACATGATGATCTGAGGAGGCT	367			
Query: 248	CGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	369			
Subject: 394	CGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	397			
Query: 368	TGTGAGGCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	425			
Subject: 396	TGTGAGGCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	247			
Query: 426	TGTGAGGCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	485			
Subject: 348	TGTGAGGCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	167			
Query: 486	AATTTTGTGAGTACCAATACCAATCTATGATAAAGGACTCTGAGGAGGCT	545			
Subject: 186	AATTTTGTGAGTACCAATACCAATCTATGATAAAGGACTCTGAGGAGGCT	127			
Query: 546	ATCTTTTGAAGGAGGAGTCTGAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAG	605			
Subject: 126	ATCTTTTGAAGGAGGAGTCTGAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAG	67			
Query: 606	TGCGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	665			
Subject: 66	TGCGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT	7			
Query: 666	ATGAGG 671				
Subject: 6	ATGAGG 1				

LOCUS OQ954494 1066 bp DNA linear PLN 22-AUG-2023

↓ LOCUS 1072 bp DNA linear PLN 24-APR-2024
DEFINITION Phlebiopsis flavidolba isolate SH52 translation elongation factor
1-alpha (TEF) gene, partial cds.
ACCESSION
VERSION
KEYWORDS
SOURCE Phlebiopsis flavidolba
ORGANISM Phlebiopsis flavidolba
Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
Agaricomycetes; Polyporales; Phanerochaetaceae; Phlebiopsis.
REFERENCE 1 (bases 1 to 1072)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..1072
/organism="Phlebiopsis flavidolba"
/mol_type="genomic DNA"
/isolation_source="stems"
/host="Solanum tuberosum "Purple Majesty"
/db_xref="taxon:467948"
/country="USA:Maryland"
/primers= fwd1_name: Ef, fwd1_seq: GAYTTCATCAAGAACATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCRACRTTGT
fwd2_name: Ef13, fwd2_seq: gtaaaagccagGAYTTTCATCAAG, rev2_name: Er13, rev2_seq: caggaaacgcatgacGACGTTGAADCCRAC"
CDS
mRNA
CDS

ORIGIN
1 NCGANCCCTGCTCGAGCTGCTCGTGGTGATCTCGACGACTTGACCTGACCTGAGTGGTCACA
61 CCGAGCGGGGCGAGGATGACGACCCATACCGCCGTTGATGATACCAAGTCTGACACGACCG
121 ACGGGCACCCTGCCAATACCACCAATCTTGATGACATCTGGAGGGGAGACGGAGGGCG
181 TTGTCGAGGGGACGAGCGGGGGCTGATGGCCTGATGGCATCGAGGAGGGCTCTACCC
241 TTGACACACACCCTTGCTGCTGCTGGCTCAAGCCTTGATCCATGCTCATGCTGGGGGGT
301 AAGTCACAGCAATGTCACGAATGATGATTTGACAGCAAGTACTTTGGAGACTCTCTCAA
401 CATGTTGTACCGTGCAGCGGAGATGGGGAACGACCGCTTGGGGTTGTAGCC
461 GACCTCTTGATGAAGGTGGAAAGTCTCTTAACGATTTCGTTGAACGGTCTCGTCCA
521 CTGTAAATTTGTTGGATGACCAATACGGAATCTGATATAAACATACCTTGGTGG
581 TGTCATCTTGTGGACGGCGACGATGAGTGCCTTGACACGAGGCTGAGGCAAGGAGAG
641 CGGGCTCGGGGCTTGGGCATCTTGGAGATACCAAGCTCGAATCCACCGTACCGTACCGG
701 CAATGATGAGGATGGCGCAATCGGCTTGGGAGGTACCAAGTATCATGTTCTNAAANNCNG
761 CCNNTGTTTATATAAAAAAATAAAGATCAACNNNTTCACTATTGTTNNACN
821 AATNNNGGGGTTCTTCCGTCGNCNNNACCAAGTCGNNNNCCATGATTNNNGAATTGT
881 TNCNGCCCTCAAAAGTTGAATTAANNNACAAAGTCGCGATTTCNNNGTCGACANNCTC
941 NNGCATCTCTGGGGCCCAAAATTTGGTCAALCTCTGGTNNNTAAANNNCCNNNCTN
1001 NTGATCCGAACNNGGGTGGGACNCAANTGTCCTTNCNCTNNNANNNNNNNNTNN
1061 GTAGCGGAANNNNNAATAAANNNCNNGTCCATTNNNNNGNNNNNNNTTTT
//

Commented [CT67]: Same as the below comment?

Commented [CT68]: Should this be here? I've seen on a few other samples but was wondering whether to include or not?

Commented [CT69R68]: As per, previous comment, this seems more applicable when the whole chromosome is sequenced or near whole(y) sequenced,

CATTATCGAGTTTTCGCGGGTTGTAGCTGGCTCATAC
GGGGCATGTGCAGCGCTGGCTCATCACTTCAACCTCTGTGCACATTAT
TGTAGATCGGTGACAAGGTCGAGTCTTTCACGAGTCTTGACTGGAA
ACCTTCTAGGTTTTTACACAACCGCTCAGTATAGAAATGTTATCTG
GDTATACGGATCTTTATACACTTTCAGCGACGGATCTCTTGGCTCG
CATCGATGAAGAACGACGGAATGCGATAAGTAATGTGAATGCAGAAT
TCAGTGAATCATCGAATCTTTGAACGACCTTGCCTCCCTGATTCG
GGGAGCATGCTGTTGGAGTGCATGGAATCTCAACTCTTAATACTTT
TTGATCAAGAGCTTGGACTTTGGAGGCTTGTGCTGGCTCTGCTCAAGTC
GGCTCCTCTGAATGATTGCTGAATTAATGATGATGCTTCTGGTG
ATAATTATCTGCGCGTAGTCGTAAGTACTTGATACGTTTACGCTTCT
ATGCTCTTCAAGGGCAATTAACCTGACTTTTGGACTCAATCAG
GTAGGACTACCGCTGAACCTTAAGCATCAATAGCGGAGGATCATAG

Phlebiopsis flavidolba strain WZ-144 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: MN856290.1 Length: 662 Number of Matches: 1

Range: 1: 28 to 661 GenBank: U000063					% IDENTITY		Phlebiopsis flavidolba	
Score	Expect	Identical	Gaps	Strand				
115.03 Mb (28)	0.0	629/629 (100%)	2/572 (0%)					
Query: 1	CATTATCGAGTTTTCGCGGGTTGTAGCTGGCTCATAC	GGGGCATGTGCAGCGCTGGCTCATCACTTCAACCTCTGTGCACATTAT						
Seq1: 20	CATTATCGAGTTTTCGCGGGTTGTAGCTGGCTCATAC	GGGGCATGTGCAGCGCTGGCTCATCACTTCAACCTCTGTGCACATTAT						
Query: 60	CATCGATGAAGAACGACGGAATGCGATAAGTAATGTGAATGCAGAAT	TCAGTGAATCATCGAATCTTTGAACGACCTTGCCTCCCTGATTCG						
Seq1: 80	CATCGATGAAGAACGACGGAATGCGATAAGTAATGTGAATGCAGAAT	TCAGTGAATCATCGAATCTTTGAACGACCTTGCCTCCCTGATTCG						
Query: 120	CGAGTCTTGCATGGAAGAACTTTTACGCTTTCACGAGTCTTGACTGGAA	ACCTTCTAGGTTTTTACACAACCGCTCAGTATAGAAATGTTATCTG						
Seq1: 140	CGAGTCTTGCATGGAAGAACTTTTACGCTTTCACGAGTCTTGACTGGAA	ACCTTCTAGGTTTTTACACAACCGCTCAGTATAGAAATGTTATCTG						
Query: 180	GTATATCGAGTTTTCGCGGGTTGTAGCTGGCTCATAC	GGGGCATGTGCAGCGCTGGCTCATCACTTCAACCTCTGTGCACATTAT						
Seq1: 200	GTATATCGAGTTTTCGCGGGTTGTAGCTGGCTCATAC	GGGGCATGTGCAGCGCTGGCTCATCACTTCAACCTCTGTGCACATTAT						
Query: 240	ATCGATGAAGAACGACGGAATGCGATAAGTAATGTGAATGCAGAAT	TCAGTGAATCATCGAATCTTTGAACGACCTTGCCTCCCTGATTCG						
Seq1: 260	ATCGATGAAGAACGACGGAATGCGATAAGTAATGTGAATGCAGAAT	TCAGTGAATCATCGAATCTTTGAACGACCTTGCCTCCCTGATTCG						
Query: 300	TGGAATCTTGAACGACCTTGCCTCCCTGATTCG	GGGGCATGTGCAGCGCTGGCTCATCACTTCAACCTCTGTGCACATTAT						
Seq1: 320	TGGAATCTTGAACGACCTTGCCTCCCTGATTCG	GGGGCATGTGCAGCGCTGGCTCATCACTTCAACCTCTGTGCACATTAT						
Query: 360	TGATGAGTCTGAGCTTGAATGATTTTATGAGGCTTGAATGAGTCTG							
Seq1: 380	TGATGAGTCTGAGCTTGAATGATTTTATGAGGCTTGAATGAGTCTG							
Query: 420	GTGAGTCTGAGCTTGAATGATTTTATGAGGCTTGAATGAGTCTG							
Seq1: 440	GTGAGTCTGAGCTTGAATGATTTTATGAGGCTTGAATGAGTCTG							
Query: 480	TGATGAGTCTGAGCTTGAATGATTTTATGAGGCTTGAATGAGTCTG							
Seq1: 500	TGATGAGTCTGAGCTTGAATGATTTTATGAGGCTTGAATGAGTCTG							
Query: 540	ATGCTCTTCAAGGGCAATTAACCTGACTTTTGGACTCAATCAG	GTAGGACTACCGCTGAACCTTAAGCATCAATAGCGGAGGATCATAG						
Seq1: 560	ATGCTCTTCAAGGGCAATTAACCTGACTTTTGGACTCAATCAG	GTAGGACTACCGCTGAACCTTAAGCATCAATAGCGGAGGATCATAG						
Query: 580	CGCTGAATCTAAGCATATCAATAAGCGGAGGATCATAG							
Seq1: 600	CGCTGAATCTAAGCATATCAATAAGCGGAGGATCATAG							
Query: 620	CGCTGAATCTAAGCATATCAATAAGCGGAGGATCATAG							
Seq1: 640	CGCTGAATCTAAGCATATCAATAAGCGGAGGATCATAG							

↑ LOCUS MN856290 662 bp DNA linear PLN 25-DEC-2019

Commented [CT70]: Same results-analysis-annotation as the one before (Purple Majesty-1 Phlebiopsis flavidolba MN856290)... Does the strain or any other detail need to be altered, adjusted, edited, etc? Or anything else overlooked?

Commented [CT71R70]: Assuming such is just displaying of the diversity in differing host EndoPhyteRange that this same EndoPathogen is present in, (albeit the same genus-species-cultivar,) just different accessions / etc. of harboring plant samples, etc. ...

Commented [CT72]: The current closest identity match sequence in the NLM-NCBI is a longer sequence length (662 > 638) and has a species determination beyond just the Genera alone, please see previous comment for greater detail.

Commented [CT73R72]: flavidolba strain WZ-144, as species-strain ?

4/28/2024

VERSION
KEYWORDS
SOURCE *Fusarium avenaceum*
ORGANISM [Fusarium avenaceum](#)
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae;
Fusarium; *Fusarium tricinum* species complex.

FEATURES	Location/Qualifiers
----------	---------------------

```
/country="USA:Maryland"  
/lat_lon="39.026,-76.925"  
/collection_date="2021"  
/primers_fwd1_name=Ef_fwd1_seq: GAYTTTCATCAAGAACATGAT, rev1_name=Er_rev1_seq: GACGTTGAADCCCRCTGTGT"  
/fwd2_name=Ef13_fwd1_seq: gtaaaacggcgagGAYTTTCATCAAG, rev1_name=Er13_rev2_seq: caggaaacagcatgacGAGTTGAADCCRC
```

```
<1..>1011
/gene="tef1"
/codon_start=3
/product="translation elongation factor 1-alpha"
```

[illegible]

Commented [CT78]: Should this script be included? Is it necessarily necessary to include like information incorporated into the other samples-accessions-submissions? Please let me know when you get the chance; thanks ...

Commented [CT79R78]: As per past comments-questions, for different samples-accessions, with like scripts, this seems more applicable when a larger part of the chromosome is sequenced, or the whole thing....

4/28/2024

TCTACCTGAGGTTCACGGCTCATACCTTTCTGGAAATCAT
 CTACATCTGTTCTGTCGGGGATAGGCGTCCCTTCAAGAAAGACGCTCC
 TCAAGTACGACGGAGAACCTCCGCGGGACGCGGGCGCTCCGCGGAG
 TAACCAACTCTATTGAACCAAGTCTTCTGATGCAATGAACCAAG
 CAGTCAAAATTAACCAAGTACCTTGGTTCGGCATGACGAAGAC
 GAACGAAATGCAATGAATGAATCTTGACGAATACGTGAATACATG
 AATCTTTGAAGACCAATTCAGCTCCGACAGCATTCGGCGGGACCTGCT
 TGAGCGTCAATCTTCAACCTCAAGCTCTTGTTGTTGGGGCTACGG
 CTGACGTAGGCCCTCAAGGATGTGGCGGACCTCCCGAGCTCTTTG
 CTGATGAACATCTGCTCGCATCGTACGCTGGAGGAGCATCTTGCAG
 TAACCCCAATTTCAAAAGGTTGACTCGGGATGACGAGGAATACCCG
 TGACTTAAGCATATCAATGACGGGACAGGATCATAGCTGTTCTCGAAN

Range 1: 30 to 596 [GetBook](#) [Graphics](#) [FieldMatch](#) [PreviousMatch](#)

Query	1038	bits	gap	identities	gaps	positives	Plus/Minus
	1038	bits	gap	100%	100%	100%	
Query 2	1038	1038	0	100%	100%	100%	01
Query 3	1038	1038	0	100%	100%	100%	01
Query 4	1038	1038	0	100%	100%	100%	01
Query 5	1038	1038	0	100%	100%	100%	01
Query 6	1038	1038	0	100%	100%	100%	01
Query 7	1038	1038	0	100%	100%	100%	01
Query 8	1038	1038	0	100%	100%	100%	01
Query 9	1038	1038	0	100%	100%	100%	01
Query 10	1038	1038	0	100%	100%	100%	01
Query 11	1038	1038	0	100%	100%	100%	01
Query 12	1038	1038	0	100%	100%	100%	01
Query 13	1038	1038	0	100%	100%	100%	01
Query 14	1038	1038	0	100%	100%	100%	01
Query 15	1038	1038	0	100%	100%	100%	01
Query 16	1038	1038	0	100%	100%	100%	01
Query 17	1038	1038	0	100%	100%	100%	01
Query 18	1038	1038	0	100%	100%	100%	01
Query 19	1038	1038	0	100%	100%	100%	01
Query 20	1038	1038	0	100%	100%	100%	01
Query 21	1038	1038	0	100%	100%	100%	01
Query 22	1038	1038	0	100%	100%	100%	01
Query 23	1038	1038	0	100%	100%	100%	01
Query 24	1038	1038	0	100%	100%	100%	01
Query 25	1038	1038	0	100%	100%	100%	01
Query 26	1038	1038	0	100%	100%	100%	01
Query 27	1038	1038	0	100%	100%	100%	01
Query 28	1038	1038	0	100%	100%	100%	01
Query 29	1038	1038	0	100%	100%	100%	01
Query 30	1038	1038	0	100%	100%	100%	01
Query 31	1038	1038	0	100%	100%	100%	01
Query 32	1038	1038	0	100%	100%	100%	01
Query 33	1038	1038	0	100%	100%	100%	01
Query 34	1038	1038	0	100%	100%	100%	01
Query 35	1038	1038	0	100%	100%	100%	01
Query 36	1038	1038	0	100%	100%	100%	01
Query 37	1038	1038	0	100%	100%	100%	01
Query 38	1038	1038	0	100%	100%	100%	01
Query 39	1038	1038	0	100%	100%	100%	01
Query 40	1038	1038	0	100%	100%	100%	01
Query 41	1038	1038	0	100%	100%	100%	01
Query 42	1038	1038	0	100%	100%	100%	01
Query 43	1038	1038	0	100%	100%	100%	01
Query 44	1038	1038	0	100%	100%	100%	01
Query 45	1038	1038	0	100%	100%	100%	01
Query 46	1038	1038	0	100%	100%	100%	01
Query 47	1038	1038	0	100%	100%	100%	01
Query 48	1038	1038	0	100%	100%	100%	01
Query 49	1038	1038	0	100%	100%	100%	01
Query 50	1038	1038	0	100%	100%	100%	01
Query 51	1038	1038	0	100%	100%	100%	01
Query 52	1038	1038	0	100%	100%	100%	01
Query 53	1038	1038	0	100%	100%	100%	01
Query 54	1038	1038	0	100%	100%	100%	01
Query 55	1038	1038	0	100%	100%	100%	01
Query 56	1038	1038	0	100%	100%	100%	01
Query 57	1038	1038	0	100%	100%	100%	01
Query 58	1038	1038	0	100%	1		

↑ LOCUS MN856254 596 bp DNA linear PLN 25-DEC-2019

4/28/2024

ACCESSION
VERSION

KEYWORDS -
SOURCE Colletotrichum boninense
ORGANISM [Colletotrichum boninense](#)
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Hypocreomycetidae; Glomerellales; Glomerellaceae;
Colletotrichum; Colletotrichum boninense species complex.

REFERENCE 1 (bases 1 to 591)
AUTHORS Unpublished

AUTHORS Unpublished
TITLE Unpublished

JOURNAL Unpublished

FEATURES	Location
1. 2000	2000

source 1.591
/organism="Colletotrichu

```
/mol_type="genomic DNA"  
/strain="WZ-97"  
/isolation_source="stems"  
/host="Solanum tuberosum 'Purple Majesty'"  
/db_xref="taxon:200359"  
/country="USA:Maryland"  
/lat_lon="39.026,-76.925"  
/collection_date="2021"
```

```
/PCR_primers="fwd_name: ITS5, fwd_seq:
ggaagtaaaagtcgtaacaagg, rev_name: ITS4, rev_seq:
tcctcccttattgatatc"
```

Gene [1.591](#)
/gene="" contains small subunit ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"

mRNA <1..>591
/gene="" contains small subunit ribosomal RNA, internal
transcribed spacer 1, 5.8S ribosomal RNA, internal
transcribed spacer 2, and large subunit ribosomal RNA"

CDS
/product="Colletotrichum boninense strain WZ-97"
<1..591
/gene=""" contains small subunit ribosomal RNA, internal
transcribed spacer 1, 5.8S ribosomal RNA, internal
transcribed spacer 2, and large subunit ribosomal RNA"
/product="Colletotrichum boninense strain WZ-97"

ORIGIN

1 TTATCTAGAGGTTACCGCTCTATAACCTTTGTGAACATCTACAACGTTGCTGCGG

61 GGATGACAGCGCTCCCTGGAAGAGACGCTCTCGGCGCGCGACGCGACGCGCGGCGGCG

111 TTTGATGAGGCTGCGCGAGATACCAACATATTATGAGGATCTCTTTTGTAGTGGG

161 ATGATACCAAAATTAACAACTTTTCAACGAGATCTCTGGTCTGCGATCGAAGAA

211 CGCGCGAAGATCGATAGATTAATGTGAATTCGACAAATCATGCAATTCATGATTC

261 ACGCATCAATGCGCGCGACGATCTTGGCGGGATCTGCTGAGGCTGATCTCAATCC

311 TCAAGTCTGCTGTGGTGTGGGGCTCATGCGCATGAGCGATGGCCCTCAAAAGTAGTGGCG

361 CCACTCCGAGCATGCTGCTAGTAAATCAATTTGCTCGCGAGTGGCGGAGGAG

411 CTGCTGATCAAAACCCCAATTTTCAAAGGTCATCGGATCGGATCGATGAGTAATCCG

541 CTTGCACTAAGCATCTACAATGCGGAGGCTCATGCTGCTTCTGTAAC

Commented [CT80]: When you get the chance, may you please provide primers for this sample? No associated primers, ITS or TEF were associated with this fungi, when looking at Table 1 'Endophyte isolation...' ... thanks

Commented [CT81R80]: ITS

4/28/2024

Purple Majesty-5 *Colletotrichum gloeosporioides* MW774951

CATCTACGTTAAGCTGTACCAACCTCTGTGTGAGAA
 CATTACATTAAGTGTCTCTGGCGGGTAGGATGCTCCGGACATCCCTCGG
 CTCTCGCGGCCCGGGCGGGCTGGCGCGCGCGGAGATGAACAACATCTG
 TTAAATGACGAGCTTCTCTGAGTGTCAGCAAGAAATAAATCAAACTTTA
 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 TAAGTAAATGATGATGCAAAATCATGAATCAATCTAATTCTGTGAACGA
 CATTCTGGCGCGCAGCATCTTGGCGGGAGTCTTCTGAGAGCTCATTTAC
 AAGCTACGAGCTCTGCTTGGTTGTGTGGGGCATCTGGCGAGTGTAGGGCC
 CAAGGATGTGCGGCAAGCTCCGGAGAGCTCTCTCTGTGATAATTAATCTAC
 TGTGCGCATCGGTCGCGGAGGAGGATCTGTGCTGTAAACCCCAATTT
 CCAAGGATCTGGGATGAGTACAGTAGGATAACCGTCGATATTAAGTATA
 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 GATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 GTGGTCTGTAACCCCGCCATCTCCGCTCTCTCGGAAGAGGAGGAGGAG
 GATTATTAATCAATCGAGCTGAGTACGTGTAGGAGACATCCGCGTCAAT
 TATGACATACATGAACGGGAGAGATGACAGTCTGTTTTCCTCNGAA

Colletotrichum gloeosporioides isolate QSY1005-52.1 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: [MW774952.1](#) Length: 599 Number of Matches: 2

Range 1: 50 to 599 [GetLink](#) [Graphics](#) [▼ Next Match](#) & [Previous Match](#)[illegible]

Range Z: 340 to 399 [Get Data](#) [Graphics](#) [▼ Last Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Identical	Gaps	Strand
76.8 bits(41)	9e-09	50/54(93%)	1/54(1%)	Plus/Plus
Query	789	CCTCAGAT-TGGTACGATACCCCGTGAACCTTAAGCATATCAATAAGCGGAGGA		761
Subject	546	CCTCGGATCAGGTGAAGATAACCCCGTGAACCTTAAGCATATCAATAAGCGGAGGA		509

↑ LOCUS MW774952 599 bp DNA linear PLN 24-MAR-2021

Commented [CT82]: When BLASTing @ NCBI, this also matched (higher) in similarity to OQ253548.1 / Colletotrichum gloeosporioides isolate WH2-4, which is 2 years more current, than the given GenBank #; should the strain be Q5Y1005-52.1 to correspond to MW774952.1, or WH2-4 to correspond to OQ253548.1?

Commented [CT83R82]: Leaning towards the latter
OQ253548.1 / WH2-4

LOCUS 835 bp DNA linear PLN 24-APR-2024
DEFINITION Colletotrichum ignotum strain E183 translation elongation factor 1
alpha gene, partial cds.

ACCESSION
VERSION
KEYWORDS
SOURCE Colletotrichum fructicola
ORGANISM Colletotrichum fructicola
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Sordariomycetes; Hypocreomycetidae; Glomerellales; Glomerellaceae;
Colletotrichum; Colletotrichum gloeosporioides species complex.

REFERENCE 1 (bases 1 to 835)
AUTHORS Unpublished
TITLE Unpublished
JOURNAL Unpublished

FEATURES Location/Qualifiers
source 1..835
/organism="Colletotrichum fructicola"
/mol_type="genomic DNA"
/host="Solanum tuberosum 'Purple Majesty'"
/db_xref="taxon:990756"
/country="USA:Maryland"
/lat_lon="39.026, -76.925"
/collection_date="2021"
/primers="fwd1_name: Ef, fwd1_seq: GAYTTCATCAAGAACATGAT, rev1_name: Er, rev1_seq: GACGTTGAADCCACRTTGTG"
"fwd2_name: EF13, fwd2_seq: gtaaaagccgacgAYTTCATCAAG, rev1_name: E1r13, rev2_seq: caggaaacagctatgacgacgTTGAADCCAC"
mRNA <1..983
/product="translation elongation factor 1 alpha"
CDS <1..983
/codon_start=2
/product="translation elongation factor 1 alpha"
/protein_id="ADG55441.1"

ORIGIN
1 NNCCTCTGTTGAGCTGCTCGTGGTCATCTCCAGCGACTGGACTCGGTGGTGAACCTTGG
63 CAGGAGCGAAGGTGACCACTGCGGGGTGAGGATACCGGTCTGATAGCGCCGACGCG
121 GCACCTTGCCTGACCACTGCTTGATGACATCTGGAGGGAAGGACGAGTGGGCTGTG
181 CGGTGGGAGCGCTCGGGGGGCTCATGGAGTCTGATGGCTCCAGGAGGGTCTTCCGGGTGA
241 CCTTGCCACCTTGCCCTCTCTCTCCCCCTTGGACCTCTAAGCGTGGTGGTGGGGG
301 CAACCTTGTCTCCCGAGGAAGCGGAGATGGGGACGACGAGCGACGCTTGGGTTGT
361 AGCCGACCTTCTTGATGAAGTGGAGGTCTCTTGATGATCTCGTGATACGGTCTCGAG
421 ACCACTGGTGGTGTCCATCTGTTGATGGGACNATCACTGCTTGACACCTCGGTGT
481 ATGCAMGCAATCGTCTCGGGTCTGGCCATCTTGGAGATACCACTCGAACCACTCAE
541 CANNACCGGGCGGCGATNATGAGATATGACAGTCTGCTGGGAATGACCAATGATCATGT
601 GCTGNNANTCTGNNNNNTTTNNANAGCAAGCTGACCACTCGGGGCTGTAATGGC
661 ATNACCTTGTGACGAAGACNACNATACGCTGGACCACTGACGGGCGAGACGAA
721 GTGTCACGGGCTCGGGGACATCGACCGTCAGAGGCGGCGACGACGANNTTGGACCGCTCC
781 ATGTTGGCTGACCACTGATCATCTCTTGAGGAATNNNGCCCTTTTAAAAA
//

Commented [CT87]: Some iterations-entries in NLM-NCBI are marked as /pcr_primers, others as /primers, without the pcr ... which script is correct to use, format wise? Just let me know whenever possible...

Main Synopsis Analysis-Questions/Comments: (Please see individual comments pertaining to each associated given sample, in web) of NLM-NCBI EndoPhyteFungi Submissions

- As far as [REDACTED]
 - Coniochaeta sp. / KF367565, in 'Pontiac-8'
 - Should the species for this genus of fungi be velutina or deborreae? The former is what I induced-inferred from BLASTing-etc. @ NCBI ...
 - Fungal endophyte / J1448999, in Solanum tuberosum 'Kennebec-7' (Pg.40-41) ... determination of Genera-species?
 - Possible: ON121591.1 / Chaetopyrena penicillata isolate 3MAB-1
 - Fungal endophyte sp. / KT922239, in Solanum tuberosum 'Pontiac-7' (Pg.76-77) ... determination of Genera-species?
 - Possible: Alternaria angustiovoidea / MK9100601
 - Phlebiopsis spp(7) / MN856290, in Solanum tuberosum 'Purple Majesty 2' (Pg.86-87) ...
 - Possible: flavidoolba strain WZ-144 ?
 - This EndoPhyteFungi also has a slightly longer identical matching sequence most recently submitted-reported to NLM-NCBI (Please see below)
 - Fusarium endophyte sp. 1022 / J0809614, in 'Purple Majesty-3' (Pg.88-89) ...
 - Should the species for this Fusarium be annotated as avenaceum? That is the closer inferred-induced match-similarity in alignment, when BLASTing at NCBI, or is F. oxysporum the more accurate determination? Leaning towards the former ...
- While BLASTing @ NCBI, [REDACTED]
 - [REDACTED] what should be done in these scenarios-cases? These are marked throughout the document with individual comments.
 - Cladosporium cladosporioides / MT466517, in Solanum microdontum-2 (Pg.16-17) ... accuracy of strain?
 - CN8842 ?
 - Paraboeremia sp / MN764237, in Kennebec-6 (pg.38-39) ... accuracy of Genera?
 - Phoma as the Genera, and not Paraboeremia?
 - Cladosporium cladosporioides / MT466517, in Kennebec-2 (Pg.22-23) ... accuracy of species-strain?
 - cladosporioides or pseudocladosporioides, as the species?
 - Colletotrichum siamense / OQ625290, in Solanum tuberosum 'Kennebec' (Pg.32-33) ... accuracy of species?
 - gloeosporioides, not siamense ?
 - Pestalotiopsis fci / M1407813152, in Solanum tuberosum 'Pontiac' (Pg.50-51) ... accuracy of Genera-species?
 - Neopestalotiopsis hypericin, not Pestalotiopsis fci ?
 - Cladosporium cladosporioides / OX697235, in Solanum tuberosum 'Pontiac' (Pg.54-55) ... accuracy of species?
 - cladosporioides or oxysporum ?
 - Cladosporium tenuissimum / MT218371, in Solanum tuberosum 'Pontiac' (Pg.56-57) ... accuracy of strain?
 - TSP1, VUJ-5, MITC, etc. ?
 - Moesziomyces rugulosus / KP323133, in Solanum tuberosum 'Pontiac' (Pg.62-63) ... accuracy of strain?
 - antarcticus, not rugulosus?
 - Ceratobasidium sp. / OR490369, in Solanum tuberosum 'Pontiac' (Pg. 70-71) ... accuracy of species?
 - Rhizoctonia solani, not Ceratobasidium spp(s). ?
 - Coniochaeta sp. KF367565, in Solanum tuberosum 'Pontiac' (Pg.78-79) ... accuracy of Genera and / or Genera-species?
 - Aureobasidium, not Coniochaeta ?
 - velutina, not deborreae ?
 - Colletotrichum gloeosporioides / MN774951, in Solanum tuberosum 'Purple Majesty 5' (Pg. 94-95) ... accuracy of the strain?
 - WIG-4, not QD10205-52.1 ?
 - Colletotrichum ignotum / GU394501, in Solanum tuberosum 'Purple Majesty 5' (Pg. 96-98) ... accuracy of species?
 - siamense, not ignotum ?
- While using BLAST in the NCBI of the NLM, with some of these samples-accessions, the whole chromosome [REDACTED] for some.
 - [REDACTED] is being used as a placeholder / [REDACTED] have closest non-whole chromosome identity match marked instead, what should be done here for the annotations/submissions?
 - Parastagonospora avenae OQ677885 (Pg. 4-5)
 - Exserohilum rostratum OQ857405 (Pg. 20-21)
 - Fusarium oxysporum MN329692 (Pg.36-37)
 - Moesziomyces rugulosus KP323133, in Solanum tuberosum 'Pontiac' (Pg.62-63)
 - Diversity of EndoPhyteRange for this Fungi, as well (Please see below)
 - Ceratobasidium sp. / OR490369, in (Pg. 70-71)
 - Also has an accuracy-clarity possible problem with Genera-species determination (Rhizoctonia solani, not Ceratobasidium spp 7) [REDACTED]
- Some of these EndoPathogens of Plants / Crops Seemed to appear in multiple hosts (differing cultivars, locations, times, etc.); just wanted to make sure this was the accurate determination for biological quality assurance, and not a differing error for whatever reasons.
 - Moesziomyces rugulosus KP323133, in Solanum tuberosum 'Kennebec' (Pg.20-29)
 - & Moesziomyces rugulosus KP323133, in Solanum tuberosum 'Pontiac' (Pg.62-63)
 - The latter (Moesziomyces rugulosus KP323133) also has possible issues with strain accuracy and the whole genome is sequenced for [REDACTED] [REDACTED]
 - Colletotrichum siamense KY421040, in Solanum tuberosum 'Kennebec' (Pg.30-31)
 - & Colletotrichum siamense OQ625290, in Solanum tuberosum 'Kennebec' (Pg.32-33)
 - The latter [Colletotrichum siamense OQ625290, in Solanum tuberosum 'Kennebec' (Pg.32-33)], also seems to maybe have an accuracy of species issue; [REDACTED] (gloeosporioides, not siamense) ?
- A few of these samples / accessions of EndoPhyteFungi have the same Genera-species-strain classification in the NCBI of the NLM, however the provided EndoFungi Sequence slightly shorter in sequence length, than the most recent update-submission there ...
 - Didymella bellidis / MN274963, in Solanum tuberosum 'Pontiac' (Pg.64-65)
 - Coniochaeta deborreae / MN800106, in Solanum tuberosum 'Pontiac' (Pg.80-81)
 - Phlebiopsis / MN856290, Solanum tuberosum 'Purple Majesty - 2' (Pg. 86-87)
 - Possible species determination for this EndoFungi of plants: flavidoolba strain WZ-144 ? [REDACTED]

