

GAAGGCAGGCTGGCACCTCCGGGTGCCAGCCTGCTGAATTATTCCACCCGTGCTTTCGCTACTCTGTTCCCTGGTGGCTGCCACCACAAGGACCAACCCATA
 AACCTTTGCAATGGCAATCAGCGTCAGTAACAATGTAATAATTACAACITICAACAACGGATCTCTGGTCTGGCATCGATGAAGAACGCAGCGAAATCGATAAGTA
 GTGTGAATTGAGAATTCACTGAAATCGAACATTGCGCACATTGCCCTTGGTATTCAAAGGGCATGCCGAGCGTCAAGCTTGTACCCCAAGCT
 TGTIGGGCGTCTTGTCTCCCTGCGGAGACTCGCCTAAAGTCATTGCGAGCCGCTACTGGTTCGGAGGCCAGCACAAGTCGCGCTCTCCAGCCCCAAGCT
 AGCATCCACCAAGCCTTTTCAACTTGTACCTCGATCAGTAGGGATACCGCTGAACCTAACATATCAATAAGCGGAGGAAAGAAACCAACAGGGATTGCC
 GTAACGGCGAGTGAAGCGCAACAGCTCAAATTGAAATCTGGCTCTTAGAGTCCGAGTTGTACTTGAGAGGGCGTTGGCTTGGCAGCGTCCAAGTCCTGG
 CAGGACGTCACAGAGGGTGAGAATCCGTACGTGGTCGCTGGCTATTGCCGTGTAAGGCCCTCGACGAGTCGAGTTGTTGGGAAATGCAGCTCAA
 ATGGGAGGTACATTCTCTAAAGCTAAATATTGCCAGAGACCGATAGCCACAAGTAGAGTATCGAAAGATGAAAAGCACTTGGAAAGAGACTCAA
 AACAGCACGTAAAGTCTGAGGCTTGCAGCCAGACTGCTCATCCGGCTTTGCCCGTGACTCTCTGTAGGCAGGCCAGCATCAGTTGGCGTAGGATA
 CGTACCTCCCTTGGGGAGGCCTATAGGGGAGGCGACATACTACCAGCCTGACTGAGGTCCCGCATCTGCTAGGATGCTGGCGTAATGGCTGTA
 AACACGGACCAAGGAGTCTAACATCTATGCGACTGTTGGGTGCAAGCCCAGCGCGTAATGAAAGTGAACGGAGGTGGAAACCGCAAGGTC
 ACCATCGACCGATCTGAGGATTGAGTAAGAGCATGGCTGTTGGGACCCGAAAGATGGTAACTATGCTGAATAGGGTAAGCCAGAGGAAACT
 CTGGTGAGGCTCGCAGTCAAATTGGCATAGGGCGAAAGACTAATCGAACTATCTAGTAGCTGGT

Figure S1. Nucleotide sequence of the amplified DNA fragment from the determined using the ITS5–LR5 primer system and covering the intergenic region and genes encoding 5.8S RNA and (partially) 28S RNA.

Table S1. Results of the BLAST analysis of the DNA fragment obtained from the *Alternaria solani* isolate.

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Alternaria solani</i> isolate NL03003 chromosome 2, complete sequence	2623	31458	100%	0.0	99.93%	CP022025.1
<i>Alternaria solani</i> isolate altNL03003/CBS 143772 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	2584	2584	98%	0.0	99.93%	OL865410.1
<i>Alternaria alternata</i> strain SRC1lrK2f 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	2385	2385	100%	0.0	97.05%	OM337556.1
<i>Alternaria alternata</i> strain Z7 chromosome 7, complete sequence	2385	28483	100%	0.0	97.05%	CP061881.1
<i>Alternaria malorum</i> var. <i>polymorpha</i> strain STE-U 4570 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	2359	2359	98%	0.0	97.21%	AY251080.2
<i>Cladosporium malorum</i> strain STE-U 4571 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	2355	2355	98%	0.0	97.21%	AY251081.2
<i>Alternaria thalictrigena</i> strain CPC 13410 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	2340	2340	98%	0.0	96.81%	EU040211.1

<i>Cladosporium malorum</i> strain STE-U 4572 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	2333	2333	98%	0.0	96.92%	AY251079.2
<i>Alternaria tenuissima</i> voucher culture Y311A internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	2324	2324	97%	0.0	96.98%	MW791881.1
<i>Alternaria tenuissima</i> strain CZ041 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	2324	2324	97%	0.0	97.05%	FJ755190.1
<i>Alternaria tenuissima</i> strain CZ305B internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	2318	2318	97%	0.0	96.97%	FJ755192.1