1) 20-A7-1.M19 ---------- BIM F-795 G (Belarusian collection of non-pathogenic microorganisms)

2) 20-A7-1.M29 ---------- BIM F-796 G (Belarusian collection of non-pathogenic microorganisms)

As the object of study served isolated from the foci of mold lesions fungal strains of genus *Phoma* that arose under extreme conditions of East Antarctica on samples of anthropogenic materials delivered from the construction site of the Belarusian Antarctic Station collected during 7th Belarusian Antarctic Expedition (2014-2015), in the places where scientific expedition team worked (Russia: East Antarctica, Enderby Land, oasis Mount Vechernyaya).

DNA- Sequences

20-A7-1.M19 internal transcribed spacer 1

GAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTA
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TTCCTCGGTGGGTTCGCCCGCCGATTGGACAATTTAAACCCTTTGCAGTTGCAATCA
GCGTCTGAAAAACATAATAGTTACAACTTTCAACAACGGATCTCTTGGTTCTGGCAT
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CATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCATGGGGCATGCCTGTTC
GAGCGTCATTTGTACCTTCAAGCATTGCTTGGTGTTGGGTGTTTGTCTCGCCTTTGCG
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20-A7-1.M29 internal transcribed spacer 1

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TCTCGCCTTTGCGTGTAGACTCGCCTTAAAACAATTGGCAGCCGGCGTATTGATTTC
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TAACACTCTGACCTCGGATCAGGTAGGGATACCCA

20-A7-1.M19 tef translation elongation factor 1-alpha (tef1) gene, partial cds

TCATCGAGAAGTTCGAGAAGGTACGTAACATTTTTTTTTTCCCTCTGAGCCAACACC
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TACCACCGCCTACAAATATTCTGACAACGTCACAGGGAGCCGCCGAACTCGGAAAG
GGTCCCTTCAAGAA

20-A7-1.M29 tef translation elongation factor 1-alpha (tef1) gene, partial cds

TCATCGAGAAGTTCGAGAAGGTACGTAACATTTTTTTTTTCCCTCTGAGCCAACACC
ACACGCTTTTGCAGTCTTTGAACGAGTCGCCTCTTTCTGGGCTTATCGTTCATTGAGG
GGCATTTTTGGTGGGGTTGTGCGAGCTTTTCGCGCGCGCACGCTAGTGCGTTTGGGG
CGCTCGCCAACTTCAACACCATGCCCCACATTACTTTTTGCATCGCGAGCTTTTGGCC

TTTTTGGTCGATGGCTACAACATCTTTCGCCATATCATCTTCAGTTTCATAATACTGA
TACCACCGCCTACAAATATTCTGACAACGTCACAGGAAGCCGCCGAACTCGGCAAG
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20-A7-1.M19 beta-tubulin (tub2) gene, partial cds

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CCGGCGAGCATGGCCTCGACGGCTCCGGTGTCTACAATGGCACCTCGGATCTCCAGC
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CGGACTGCGAGTGCTGACCTTTTGTAGGCTTCCGGCAACAAGTTCGTTCCCCGTGCC
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CATGTCGTCT

20-A7-1.M29 beta-tubulin (tub2) gene, partial cds

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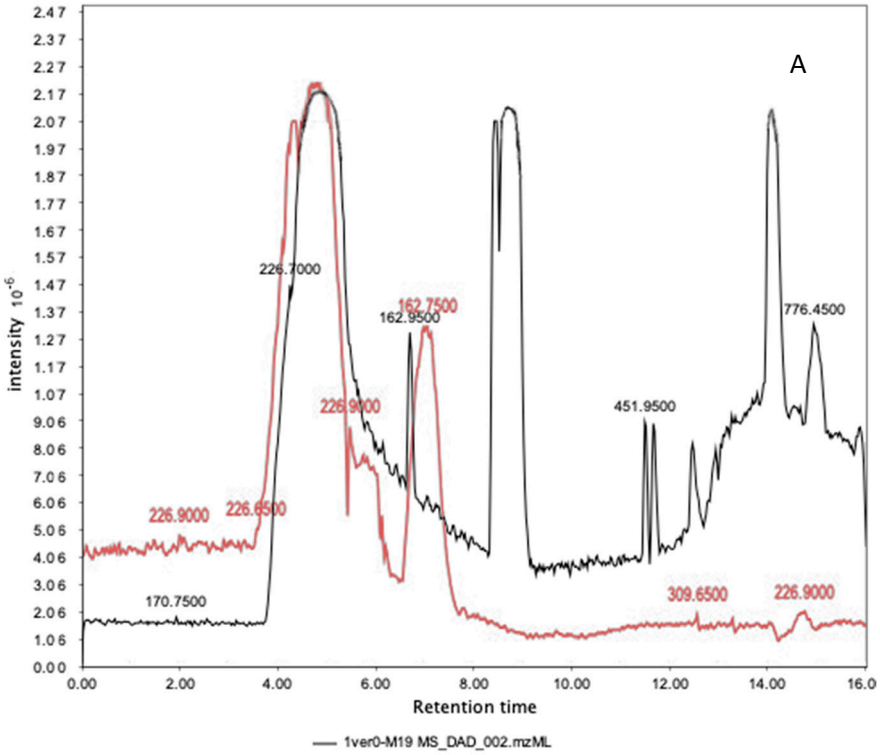
CCGGTGTCTACAATGGCACCTCGGATCTCCAGCTTGAGCGCATGAACGTCTACTTCA
ACGAGGTACGAGAAATGGCACACTCTACTTCGACGGACTGCGAGTGCTGACCTTTTG
TAGGCTTCCGGCAACAAGTTCGTTCCCCGTGCCGTCCTCGTCGATTTGGAGCCTGGT
ACAATGGACGCTGTCCGCGCTGGC

Table S1. Reference Sequences

Strain/isolate	Locus		
	internal transcribed spacer	translational elongation factor 1	beta-tubulin
Paraphoma fimeti UTHSC:DI16-296	LT796872.1	LT797112.1	LT796952.1
Phoma herbarum CBS 615.75	KF251212.1	KF253168.1	KF252703.1
Phoma exigua strain CBS 101211	GU237722.1	KY484711.1	GU237507.1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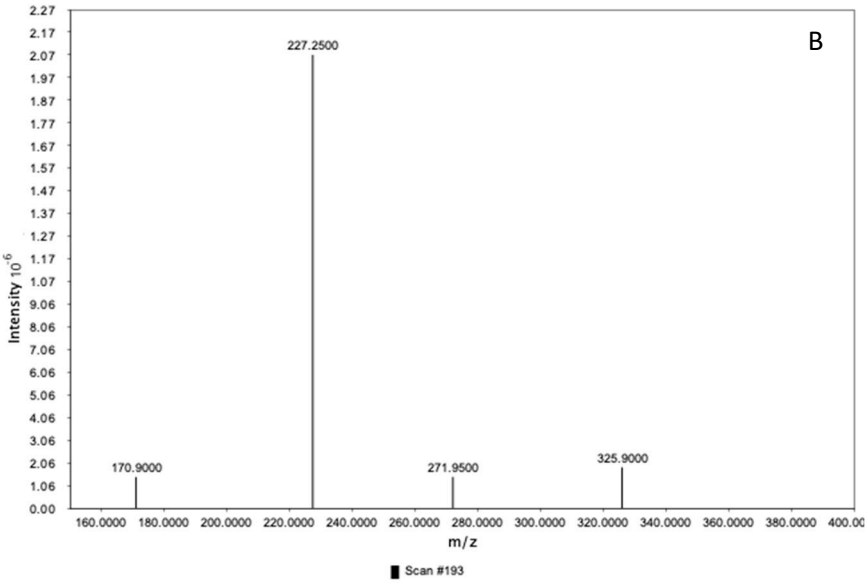
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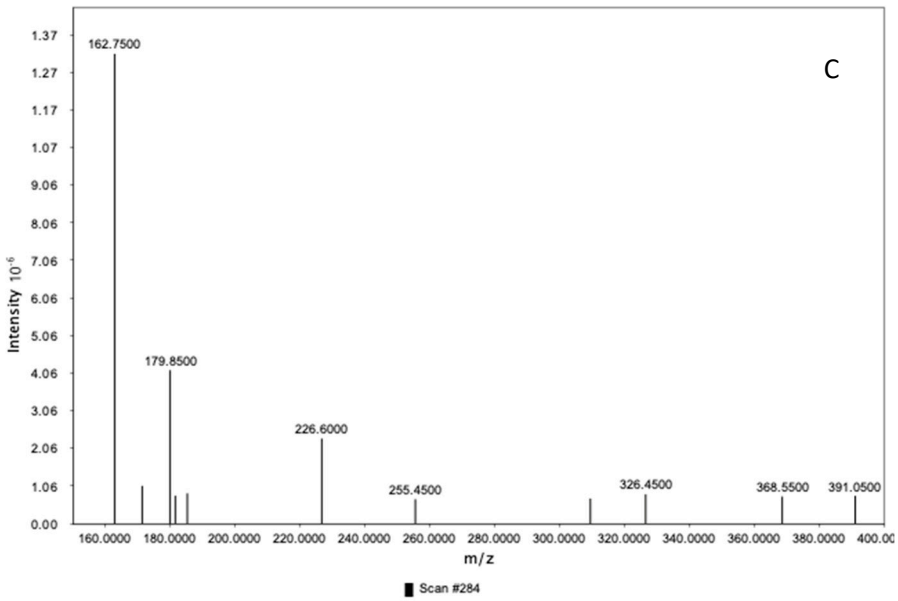
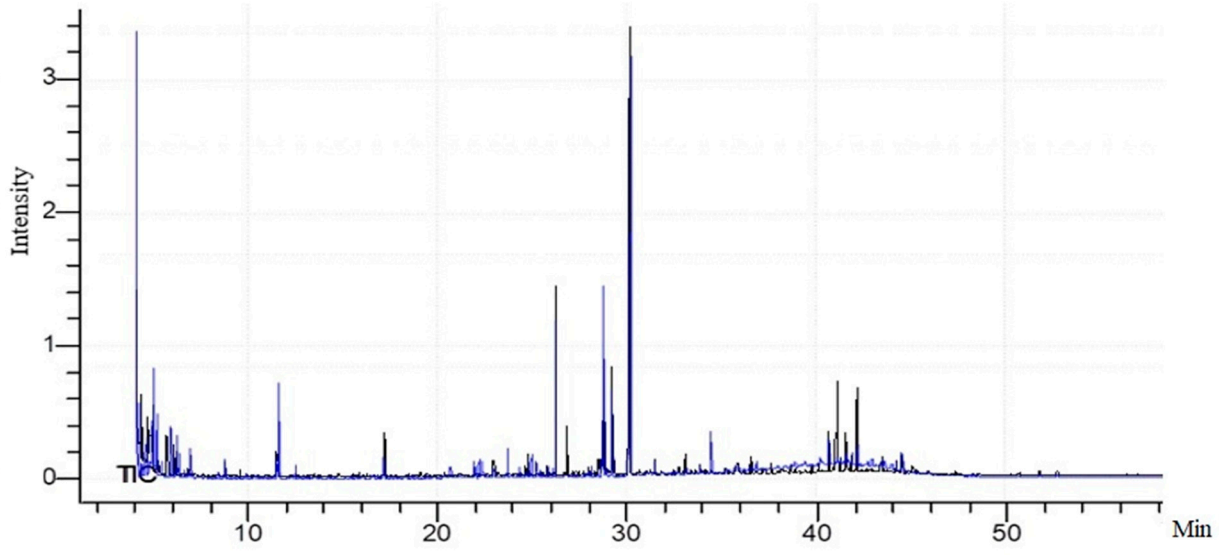
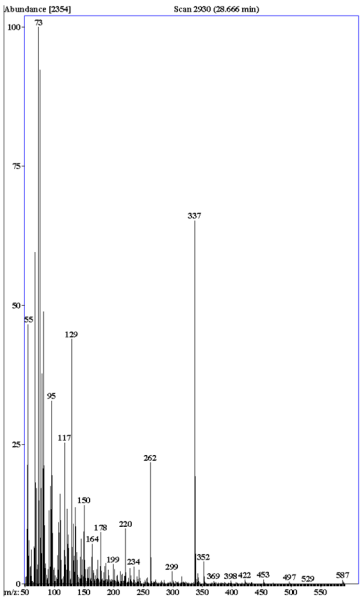


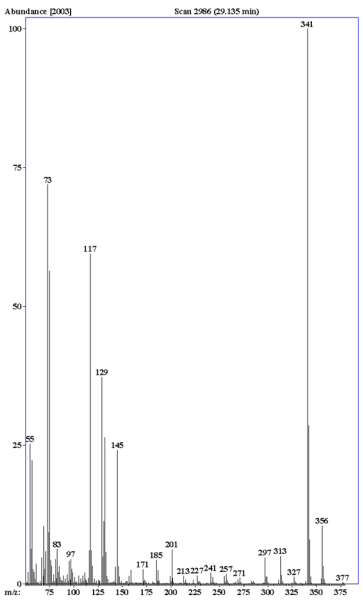
Figure S1. High performance liquid chromatography–mass spectrometry analysis of *Phoma herbarum.* (A) Chromatogram of crude mycelium extract (CME) of the strains M19 (black) and M29 (brown); (B) MS spectrum RT=4.93; (C) MS spectrum RT=7.07. HPLC analysis was performed on C18 5 µm column (4.6 × 250 mm) using a mobile phase of gradient acidified water (0.1% trifluoroacetic acid) mixture of acetonitrile and with a flow rate of 0.6 mL/min. The gradient started with 100% acidified water for 3 min, and then increased linearly to 100% acetonitrile with 0.1% (v:v) trifluoroacetic acid at a flow rate of 1 ml/min and absorbance was monitored at 227 nm. The injection volume of each extract or standard solution was 5 µL.



(A)



(B)



(C)

Figure S2. Gas chromatography–mass spectrometry (GC-MS) analysis of *Phoma herbarum*. (A) Gas chromatogram of crude mycelium extract (CME) of the M19 (B) and M29 (C) strains. (B) MS spectrum RT=…; (C) MS spectrum RT=….