

Supplementary Information

1 Media Formulations

1.1 Composition of the CYS80 medium (1 L volume)

Sucrose	80.0g
Corn meal	50.0g
Yeast extract	1.0g
MgSO ₄ · 7H ₂ O	0.5g
Agar	20.0g
Nanopure water	to 1.0L

1.2 Composition of the DRYES medium (1 L volume)

Sucrose	150.0g
Yeast extract	20.0g
MgSO ₄ · 7H ₂ O	0.5g
Dichloran (0.2% in EtOH)	1.0mL
Rose bengal (5%, w/v)	0.5mL
Agar	20.0g
Nanopure water	to 1.0L

1.3 Composition of the MMK2 medium (1 L volume)

Mannitol	40.0g
Yeast extract	5.0g
Murashige and Skoog Salts	4.3g
Agar	20.0g
Nanopure water	to 1.0L

1.4 Composition of the ZM2 medium (1L volume)

Molasses	5.0g
Oatmeal	5.0g
Sucrose	4.0g
D-glucose	1.5g
CaCO ₃	1.5mg
Edamin	0.5g
(NH ₄) ₂ SO ₄	0.5g
Agar	20.0g
Nanopure water	to 1.0L

1.5 Composition of the PDA medium (1 L volume)

Metabolomics Profiling of *Alternaria* spp.

Potato extract	4.0g
Dextrose	20.0g
Agar	15.0g
Nanopure water	to 1.0L

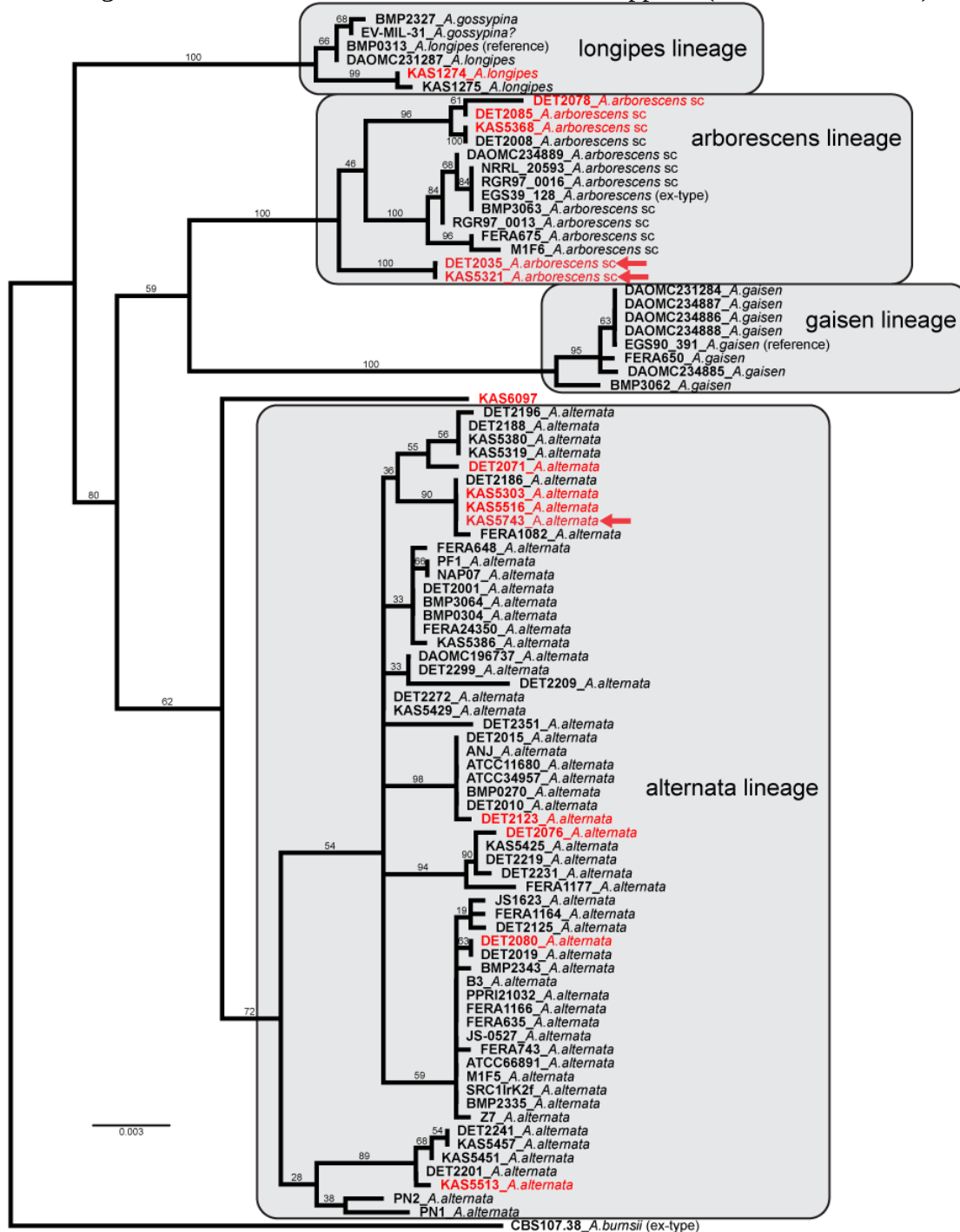
2 Chemical and Solvent List

Chemical	Manufacturer
Ethanol (EtOH)	Thermo-Fisher Scientific
Ethyl acetate (HPLC-grade)	EMD Millipore
Methanol (LCMS-grade)	VWR Chemicals
Acetonitrile (Optima, LCMS-grade)	Thermo-Fisher Scientific
Water (Optima, LCMS-grade)	Thermo-Fisher Scientific
Nanopure water	Thermo-Fisher Scientific, Barnstead Nanopure
Sucrose	Anachemia
Corn meal	Unico
Yeast extract	Oxoid
MgSO ₄ × 7H ₂ O	BDH
Agar	VWR
Dichloran	Sigma-Aldrich
Rose bengal	Sigma-Aldrich
Mannitol	Sigma-Aldrich
Murashige and Skoog Salts	Phytotechnology Laboratories
Molasses	Grandma's®, B&G Foods Inc.
Oatmeal	Quaker Oats Company
D-glucose	Sigma-Aldrich
CaCO ₃	Thermo-Fisher Scientific
Edamin	Sigma-Aldrich
(NH ₄) ₂ SO ₄	Thermo-Fisher Scientific
Formic acid	Sigma-Aldrich

3 Phylogenetic placement of *Alternaria* strains used for metabolomics profiling.

Maximum likelihood tree constructed from combined sequence analysis from three loci: *ASA-10*, *ASA-19*, and *rpb2* (RNA polymerase II second largest subunit). The fifteen taxa highlighted in red are examples of taxa included in the metabolomics profiling. Red arrows indicate the placement of dehydrocurvularin-producing strains. Bootstrap support (percentages) are displayed on major branches. Substitution model selection and tree construction were performed with IQ-TREE (2.0). The MODELFINDER module was used to choose the best-fit substitution model and the optimal

partitioning scheme for the three datasets combined was applied (-m MFP+MERGE).



4 Dehydrocurvularin production and structure elucidation

4.1 Scaled up cultivation of DET2035

Alternaria arborescens strain DET2035 was 3-point inoculated onto 300 Petri plates of CYS80 agar and incubated at 25 °C with a light/dark cycle of 8/16 hrs for 14 days. Plates were subsequently

harvested by cutting the culture into squares (1 cm x 1 cm) using a scalpel into a 5 x 2 L Erlenmeyer flasks to a volume of 600 mL in each flask, to which 1300 mL of ethyl acetate (EtOAc) was then added and covered with aluminum foil. In a chemical fume hood, extractions were performed on a rotary shaker at 160 RPM for 4 hours. The resulting solvent extracts were vacuum filtered through filter paper (Whatman 5230-110, Grade 230, diam 100 mm) concentrated in vacuo using a rotary evaporator (IKA RV10).

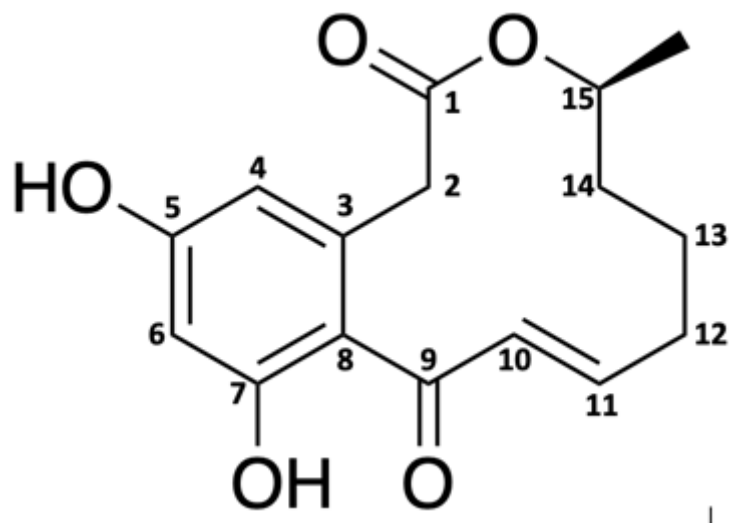
4.2 Extraction and purification of dehydrocurvularin

A de-fatting step was performed by re-suspending the extract in methanol and carrying out a liquid:liquid partition with an equal volume of hexanes in a 2 L separatory funnel. The methanol fraction was retained and concentrated in vacuo. The dried bulk extract was re-suspended in MeOH and filtered through a 0.45 μ m PTFE Acrodisc (Pall Corporation, MI, USA) syringe filter prior to fractionation by preparative HPLC (1260 Infinite Series, Agilent Technologies, CA, USA coupled to Fraction collector) on a Phenomenex Kinetex C18 100Å LC column (100 x 30.0 mm, 5 μ m). Fractionation of the extract was carried out iteratively using various ACN (+0.05% formic acid) : H₂O (+0.05% formic acid) gradients to obtain DHC in a semi-purified state. Each fraction was evaporated in vacuo to dryness using a GeneVac EZ-Elite 2 (SP Scientific, Ipswich, UK). An aliquot of each fraction was retained for analytical UPLC-HRMS/DAD/CAD analysis. Final purification of DHC was performed by thin layer chromatography using silica gel plates (GF₂₅₄, Merck, 20 x 20 cm with 0.25 mm thickness) and 5% MeOH in chloroform as the mobile phase.

4.3 NMR conditions

¹H-NMR, ¹³C-NMR, and HSQC data were obtained using a Bruker Avance HD 600 of the NMR Facility of the University of Ottawa. The ¹H-NMR data was obtained at 600 MHz and ¹³C-NMR data was obtained at 150 MHz. To allow for direct comparison to literature, DHC was re-suspended in CD₃OD for NMR analyses.

4.4 Dehydrocurvularin molecular structure and Carbon numbering



4.5 Dehydrocurvularin structure elucidation

To confirm the molecular structure of unknown 1 as dehydrocurvularin, ^1H -NMR, ^{13}C -NMR, and HSQC analysis were performed. The ^1H -NMR analysis of the spectra revealed two aromatic protons (δ_{H} of 6.30 ppm and δ_{H} of 6.30 ppm) as well as two alkene protons (δ_{H} of 6.51 ppm and δ_{H} of 6.59 ppm). The alkene protons show a large coupling constant ($J=15.4$ Hz), suggesting a *trans* olefin. Two olefinic protons form the AB portion. Protons at δ_{H} 3.74 ppm and 3.45 ppm each have identical coupling constants ($J=16.6$ Hz), consistent with geminal coupling. The three protons at δ_{H} of 1.20 ppm are a doublet with $J=6.4$ Hz, consistent with a methyl group coupled to a single adjacent hydrogen.

Inspection of the ^{13}C -NMR revealed 6 aromatic carbons (C3-C8). δ_{C} of 162.02 and 162.30 ppm are consistent with aromatic carbons experiencing the added de-shielding of being bound to an OH group. The resonance of 173.04 ppm (C1) is consistent with a carbonyl carbon that is experiencing de-shielding from at least one neighboring heteroatom (an ester group). Furthermore, the resonance at 72.4 (C15) is consistent with a saturated carbon bound to the oxygen. Combined, these two signals suggest an ester. The observed resonance at 200.08 ppm (C9) suggests there is a ketone in the structure. The resonances observed at 133.4 ppm and 154.4 ppm (C10 and C11, respectively) are consistent with an olefin connected to an electron withdrawing group. With the ketone, this suggests an α,β -unsaturated ketone is present. The remaining resonances of 34.2 (C12), 25.5 (C13), 35.2 (C14), and 20.4 (CH3) are all consistent with alkane chain carbons.

Analysis of the HSQC confirms that the carbons at δ_{C} of 200 ppm, 173 ppm, 137.3 ppm, 162.02, 162.30, and 117.88 ppm have no attached hydrogens. The carbons at 112.20 ppm and 102.8 ppm are attached to the aromatic protons at δ_{H} of 6.30 and 6.26 respectively. The alkene protons at δ_{H} of 6.50 ppm and 6.59 ppm are connected to the carbons at 133.4 and 154.4, respectively. Lastly, the carbon δ_{C} 74.3 ppm is indicative of a carbon with a single bond to an electronegative heteroatom and is connected to the proton at δ_{H} 4.82 ppm.

Four alkane carbons are clearly identifiable. The carbon at δ_{C} 42.4 ppm couples to the protons at δ_{H} 3.74 ppm and 3.46 ppm. The carbon at δ_{C} 35.2 ppm couples to the protons at δ_{H} 1.91 – 1.81 ppm and

1.64 – 1.55 ppm. The carbon at δ_C 34.2 ppm couples to the protons at δ_H 2.41 ppm and 2.36 – 2.26 ppm. Finally, the methyl carbon at δ_C 20.4 ppm couples to three protons at δ_H 1.20 ppm.

These data are consistent with the functional groups found in dehydrocurvularin, a tetrasubstituted electron, a rich aromatic, an α,β - unsaturated ketone, an ester, four aliphatic groups and a single methyl group. The assignment is further supported by comparison of NMR data to literature NMR data (Hassan, 2007; Aly et al., 2010).

4.6 ^1H -NMR data table for dehydrocurvularin obtained in MeOD

H number*	δ_H (ppm) - (multiplicity, coupling (Hz), integral)	δ_H (ppm) - (multiplicity, coupling (Hz), integral)
		(reported in Hassan, 2007)
1		
2A	3.74 (d, J = 16.6Hz, 1H)	3.72 (d, J = 16.6Hz, 1H)
2B	3.46 (d, J = 16.6Hz, 1H)	3.44 (d, J = 16.6Hz, 1H)
3		
4	6.30 (d, J = 2.3Hz, 1H)	6.28 (d, J = 2.0Hz, 1H)
5		
6	6.26 (d, J = 2.3Hz, 1H)	6.24 (d, J = 2.0Hz, 1H)
7		
8		
9		
10	6.51 (dt, J = 15.6, 1.1Hz, 1H)	6.49 (d, J = 15.4Hz, 1H)
11	6.59 (ddd, J = 15.5, 8.4, 5.7Hz, 1H)	6.57 (ddd, J = 15.4, 8.2, 5.6Hz, 1H)
12A	2.41 (dddd, J = 14.7, 7.4, 5.8, 2.7, 1.4 Hz, 1H)	2.38 (m, 1H)
12B	2.36-2.26 (m, 1H)	2.29 (m, 1H)
13A	2.01-1.93 (m, 1H)	1.96 (m, 1H)
13B	1.64-1.55 (m, 2H)**	1.56 (m, 1H)
14A	1.91-1.81 (m, 1H)	1.85 (m, 1H)
14B	1.64-1.55 (m, 2H)**	1.58 (m, 1H)
15	4.82 (tdd, J = 12.8, 6.2, 4.2Hz, 1H)	4.82 (m, 1H)
CH ₃	1.20 (d, J=6.4Hz, 3H)	1.18 (d, J=6.6Hz, 3H)

* = Numbering of atoms is in accordance with literature (Hassan, 2007) and SI-1.3.4.

** = two peaks are indistinguishable from one another so are integrated together.

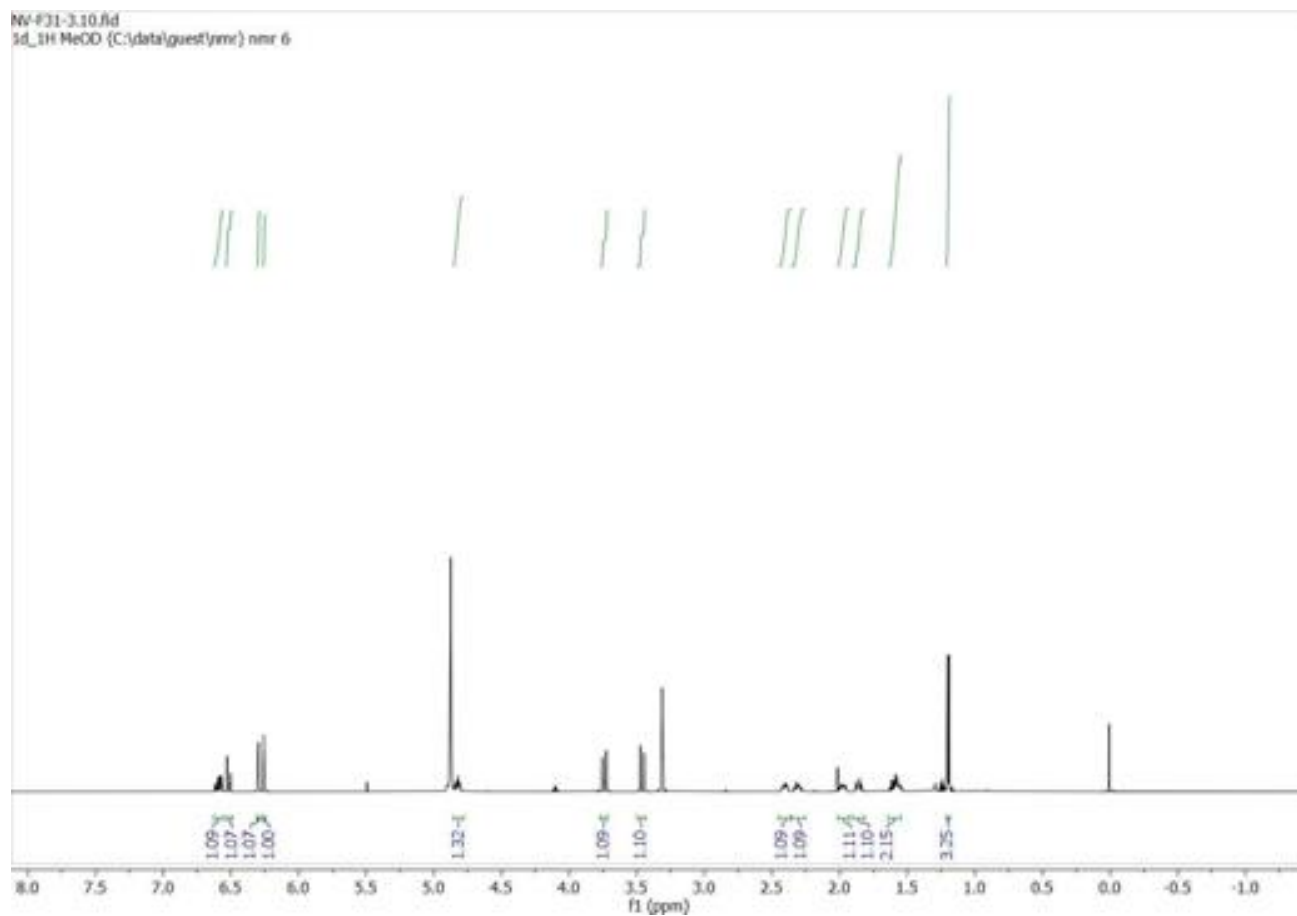
1H belongs to 13B (closed to 1.55) and the other 1H belongs to 14B (closer to 1.64).

4.7 ^{13}C -NMR data table for dehydrocurvularin obtained in MeOD

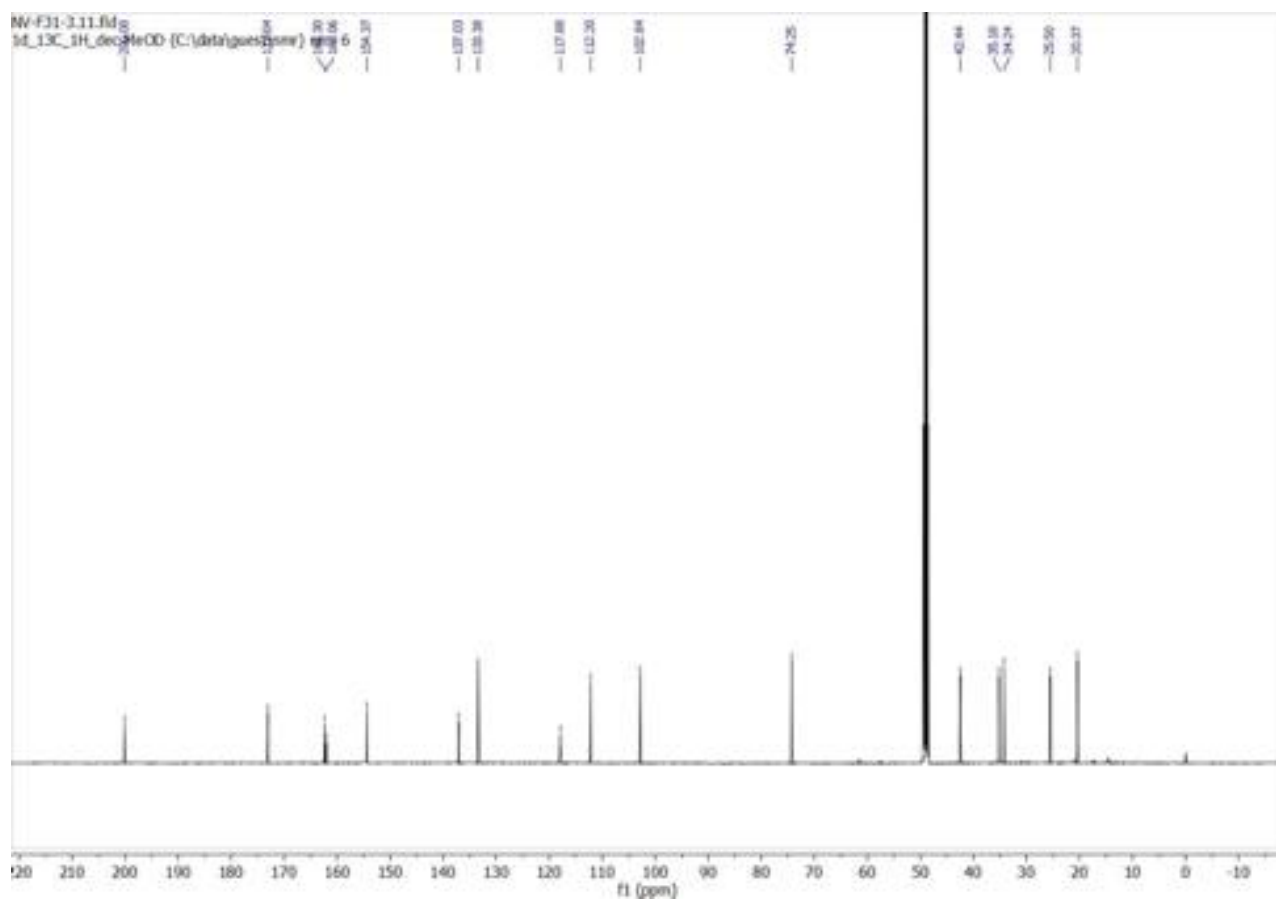
C number*	δc (ppm)	δc (ppm)
		(reported in Hassan, 2007)
1	173	173
2	42.4	42.4
3	137	137
4	112.2	112.2
5	162	162
6	102.8	102.8
7	162.3	162.2
8	117.9	117.8
9	200.1	200
10	133.4	133.3
11	154.4	154.3
12	34.2	34.2
13	25.5	25.4
14	35.2	35.1
15	74.3	74.2
CH_3	20.4	20.3

* = Numbering of atoms is in accordance with literature (Hassan, 2007) and SI-1.3.4.

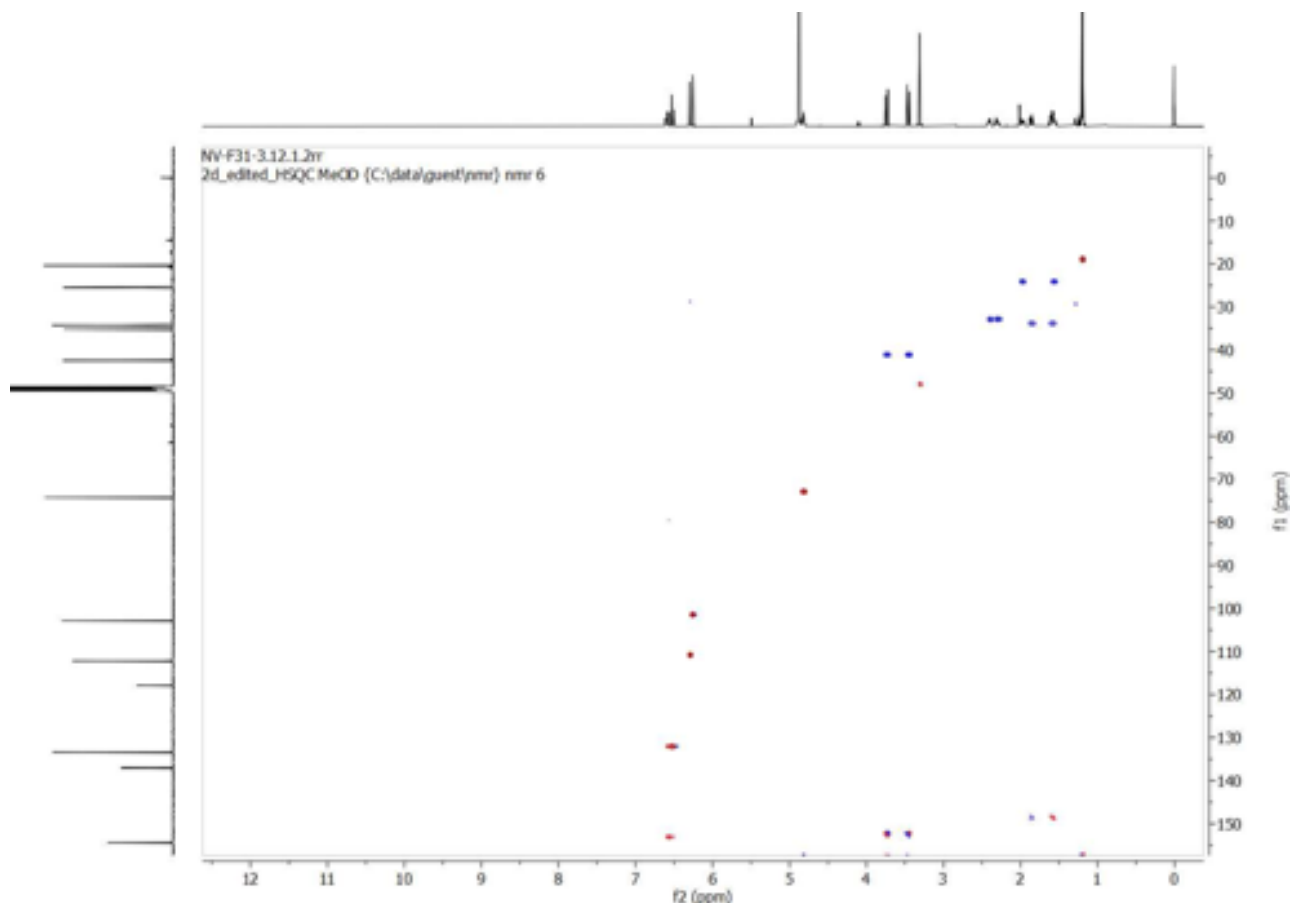
4.8 ^1H -NMR spectrum of dehydrocurvularin in MeOD (Bruker Avance HD 600, at 600 MHz)structure elucidation



4.9 ^{13}C -NMR spectrum of dehydrocurvularin in MeOD (Bruker Avance HD 600, at 600 MHz) structure elucidation



4.10 HSQC spectrum of dehydrocurvularin in MeOD (Bruker Avance HD 600) – ^1H -NMR displayed on the x-axis and ^{13}C -NMR on the y-axis.



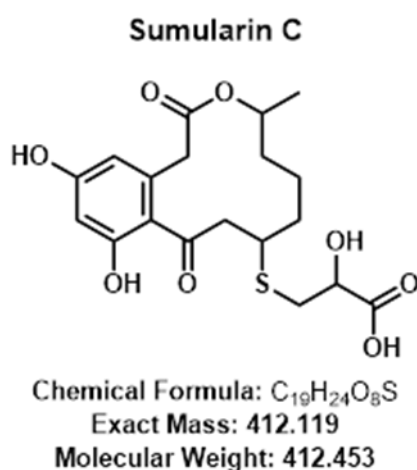
5 Rational for MSⁿ structural characterization of sumalarin C

The mass feature with a m/z of 413.1254 was identified to show similar characteristics as dehydrocurvularin after metabolomics processing with MZmine 2. After iterative attempts to purify m/z 413.1254 from large scale cultures using preparative thin layer chromatography and semi-preparative HPLC, this compound could not be completely isolated from dehydrocurvularin and other degradation products in a sufficient quantity for NMR characterization. UPLC-HRMS/MS scans were compared to freely available libraries of experimentally derived MS² data via the GNPS online interface (version 28.2) and m/z 413.1254 could tentatively be assigned as sumalarin C based on a molecular formula of $\text{C}_{19}\text{H}_{25}\text{O}_8\text{S}$. To further increase the confidence in the assignment of sumalarin C annotation, tandem MS (MSⁿ) spectra were acquired. Dehydrocurvularin and sumalarin C are structurally similar, with sumalarin C containing an additional 2-hydroxy-3-mercaptopropanoic acid appended at C11 of the curvularin macrocycle (SI-4.1).

Comparison of MS² spectra of dehydrocurvularin and sumalarin C contained similar fragment ions (SI-5.2 and SI-5.4) that indicates a high degree of structural similarity between the two compounds. Table SI-5.4 gives proposed fragment ions structures found in tandem MS data where each were

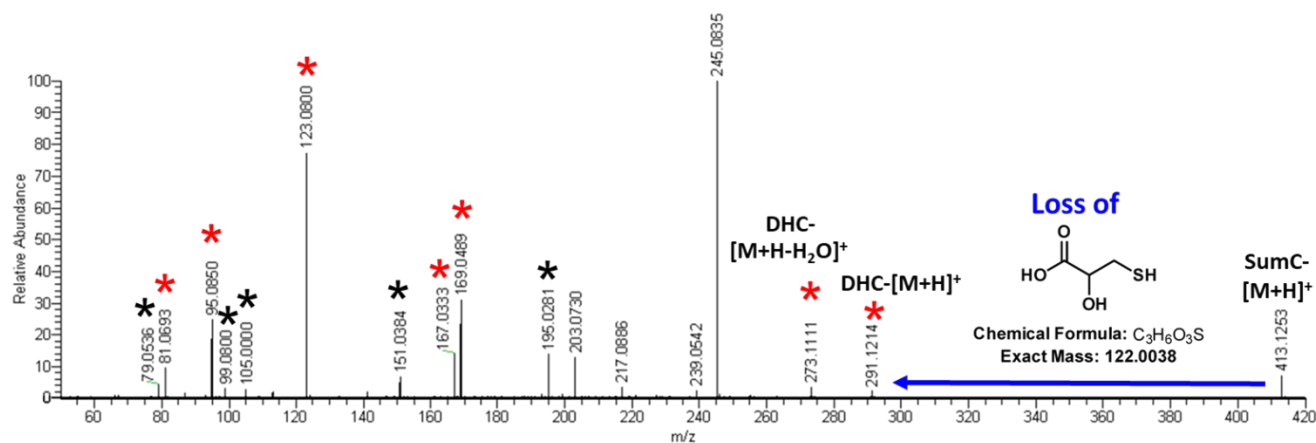
observed below 10 ppm error. Key fragment ions, m/z 291.12 and 273.11, 169.05, 167.03, 123.08, 95.09 and 81.07 are observed in the MS^2 spectra of both sumalarin C and dehydrocurvularin suggesting similar structural features. Critically, the fragment ion m/z 291.12 is produced by the loss of 2-hydroxy-3-mercaptopropanoic acid to regenerate dehydrocurvularin (see SI-5.2: $DHC-[M+H]^+$ and $DHC-[M+H-H_2O]^+$). Furthermore, a fragment ion with a m/z of 245.08 was uniquely observed in the MS^2 spectrum of sumalarin C, and further activation ($MS^2 \rightarrow MS^3$) of this fragment ion produced a characteristic loss of 2-hydroxy-3-mercaptopropanoic acid (m/z 245 $\rightarrow$ m/z 123) as well as hydrocarbon fragments $C_8H_{11}O^+$, $C_7H_{11}^+$, and $C_6H_9^+$ that can be found in both MS^2 spectra of sumalarin C and dehydrocurvularin (SI-5.2 and SI-5.3). From these data, we are confident in the annotation of the m/z 413.13 mass feature to be sumalarin C.

5.1 Molecular structure of sumalarin C.



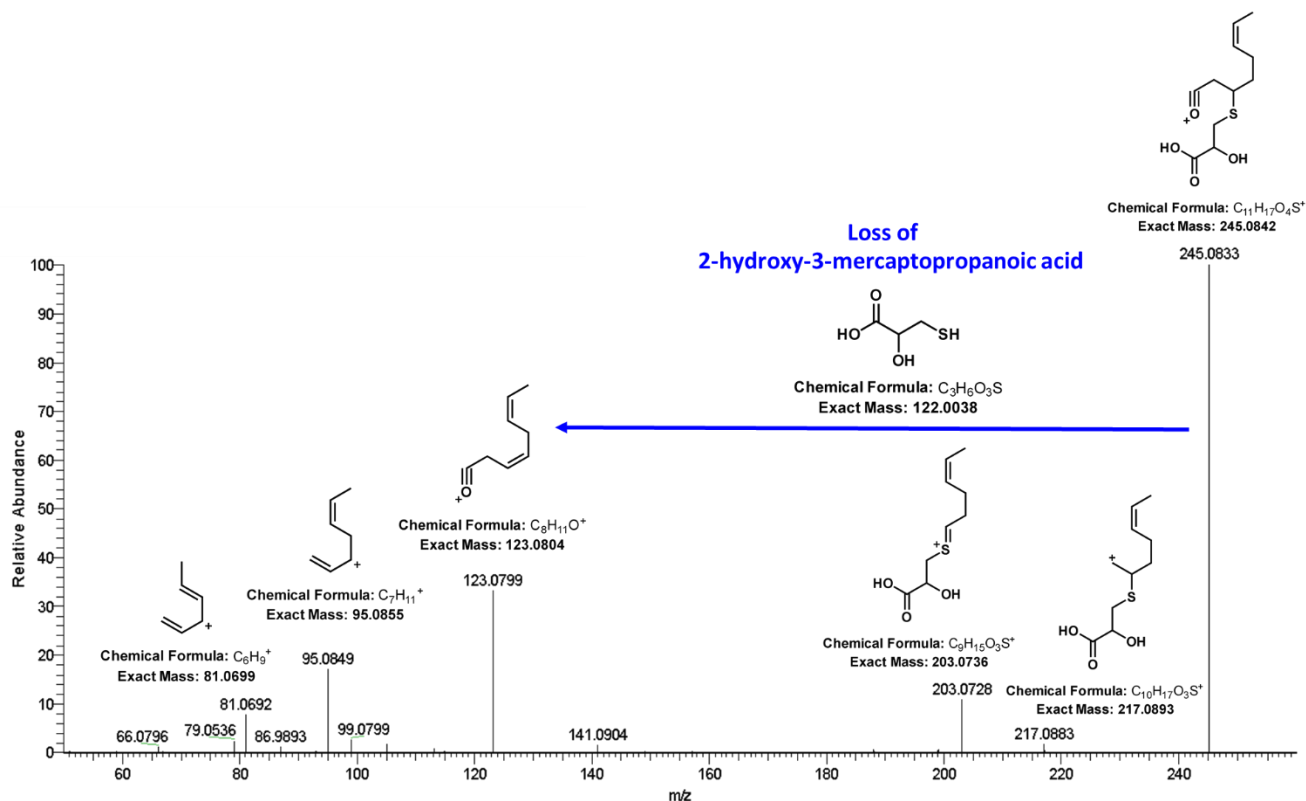
5.2 MS^2 spectrum of sumalarin C (SumC) $[M+H]^+$ ion (m/z 413.1254).

Asterisks indicate fragment ions also found in MS^2 spectra of dehydrocurvularin (DHC) $[M+H]^+$ ion (m/z 291.1216), Red asterisks denote fragment ions presented in SI-5.4.

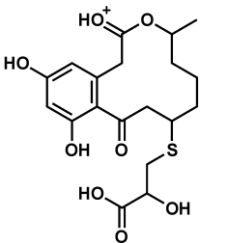
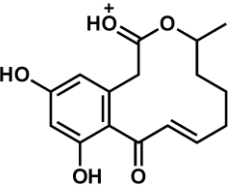
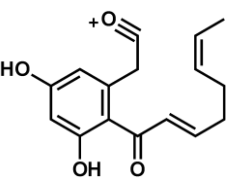
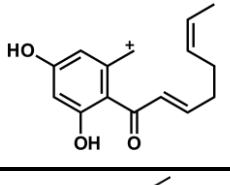
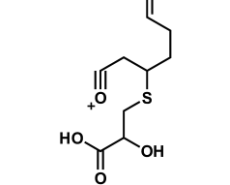
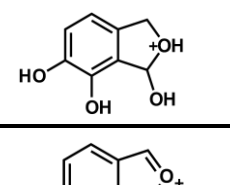
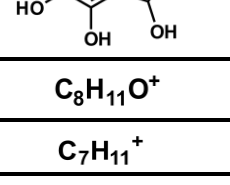


5.3 MS³ spectrum of sumalarin C MS² [M+H]⁺ critical fragment ion (*m/z* 245.0833).

Neutral loss confirms the presence of 2-hydroxy-3-mercaptopropanoic acid. Low mass range fragment ions are consistent with those observed from MS² spectra of dehydrocurvularin and sumalarin C (presented in SI-5.2 and SI-5.4).



5.4 Table of proposed fragment structures observed from sumalarin C (SumC) and dehydrocurvularin (DHC).

Proposed Fragment Structure	Calculated m/z	Experimental m/z	Experimental m/z
		(DHC)	(SumC)
	413.1265	n/a	413.1253 (-2.9 ppm)
	291.1227	291.1217 (-3.4 ppm)	291.1217 (-3.4 ppm)
	273.1121	273.1113 (-2.9 ppm)	273.1113 (-2.9 ppm)
	245.1172	245.1163 (-3.7 ppm)	n/a
	245.0842	n/a	245.0836 (-2.4 ppm)
	169.0495	169.0489 (-3.5 ppm)	169.0490 (-3.0 ppm)
	167.0339	167.0333 (-3.6 ppm)	167.0334 (-3.0 ppm)
C₈H₁₁O⁺	123.0804	123.0799 (-4.1 ppm)	123.0800 (-3.2 ppm)
C₇H₁₁⁺	95.0855	95.0850 (-5.3 ppm)	95.0850 (-5.3 ppm)
C₆H₉⁺	81.0699	81.0693 (-7.4 ppm)	81.0693 (-7.4 ppm)

6 Annotation of UPLC-HRMS mass features based on tandem MS data

6.1 Table of secondary metabolite mass feature MS² annotations based on GNPS and Massbank spectral library matches (cosine scores) and SIRIUS/CSI-FingerID *in silico* fragmentation analysis rankings (% score).

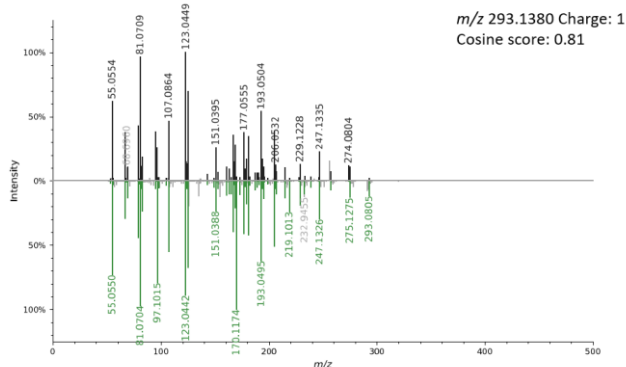
Secondary Metabolite	GNPS library match (cosine score)	CSI FINGER-ID rank (% score)
11-hydroxycurvularin	-	1 (97.80)
11-methoxycurvularin	-	1 (96.45)
3-aipta	-	1 (51.15)
altenuene	Yes (0.94)	1 (88.52)
altenusin	-	1 (77.73)
alternariol	-	1 (96.92)
alternariol monomethyl ether	-	1 (90.74)
altersetin	-	1 (92.83)
curvularin	Yes (0.81)	1 (98.13)
cyclosulfoxycurvularin	-	1 (80.43)
cyclothiocurvularin	-	1 (68.09)
dehydrocurvularin (DHC)	Yes (0.74)	1 (85.36)
dihydrotentoxin	-	1 (80.00)
sulfoxycurvularin	-	not in structural databases
sumalarin A	-	1 (66.23)
sumalarin C	Yes (0.86)	1 (97.55)
tentoxin	-	1 (62.79)
tenuazonic acid	Yes (0.78)	1 (93.90)
tricycloalternarene 2b	Yes (0.73)	2 (73.06)

6.2 Mirror plots comparing top database spectral matches to MS² spectra from mass features annotated in this study.

Comparisons performed as part of GNPS FBMN workflow. Top spectra (black) are from the present study, bottom spectra (green) are from online databases.

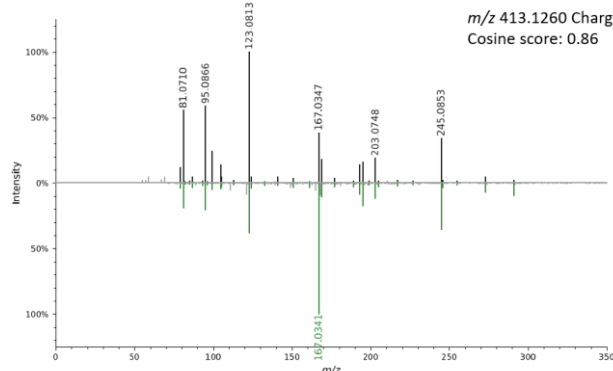
A) Curvularin

Bottom: mzspect:GNPS:GNPS:GNPS-LIBRARY:accession:CCMSLIB00004692096



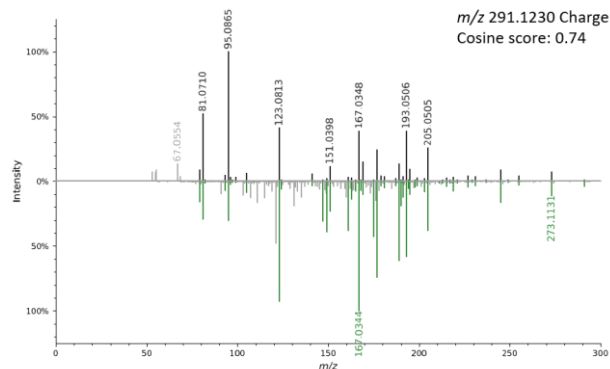
B) Sumalarin C

Bottom: mzspect:GNPS:GNPS:GNPS-LIBRARY:accession:CCMSLIB00000849306



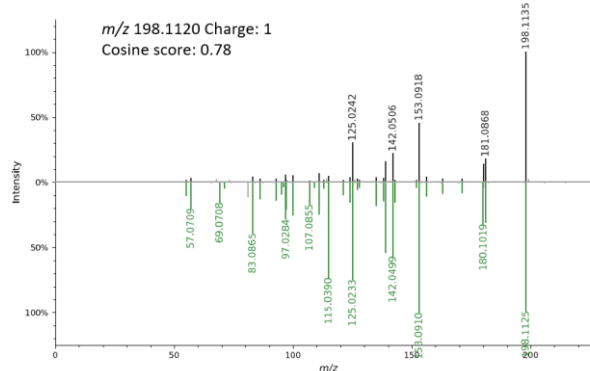
C) Dehydrocurvularin

Bottom: mzspect:GNPS:GNPS:GNPS-LIBRARY:accession:CCMSLIB00000852998



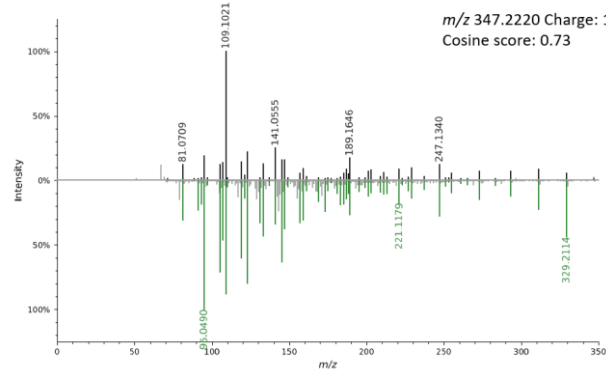
D) Tenuazonic acid

Bottom: mzspect:GNPS:GNPS:GNPS-LIBRARY:accession:CCMSLIB00005727818



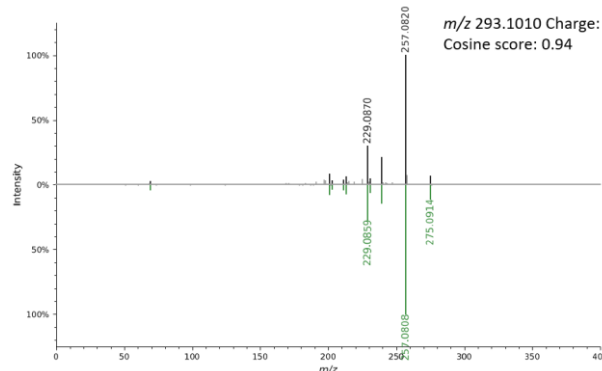
E) Tricycloalternarene 2b

Bottom: mzspect:GNPS:GNPS:GNPS-LIBRARY:accession:CCMSLIB00000853881



F) Altenuene

Bottom: mzspect:GNPS:GNPS:GNPS-LIBRARY:accession:CCMSLIB00005727230



7 Summary statistics for whole-genome assemblies from Illumina short-read sequences for dehydrocurvularin producing *Alternaria* strains.

Isolate name	DET2035	KAS5321	KAS5743
Species	<i>A. arborescens</i>	<i>A. arborescens</i>	<i>A. alternata</i>
Fold sequence coverage	135.4	115.8	124.2
Contig number (>500 bp)	163	125	211
N50 (kb)	671.5	667.2	1354.8
L50 (contigs)	17	14	10
Length (Mb)	33.10	33.00	34.11
GC%	51.1	51.1	51.1
Complete BUSCO genes (%)	99.3	99.3	99.1
Missing BUSCO genes (%)	0.7	0.7	0.8
NCBI accession	JAERP1000000000	JAERNY0000000000	JAERND0000000000

8 Results returned with greater than 80% sequence similarity from BLASTn search of the full NCBI nt database using each of the four core *A. arborescens* DET2035 *dhc* gene sequences as queries.

Taxon	Strain	Query locus	Hit locus	Query Cover	% Identity	Accession
<i>Alternaria atra</i>	CS162	<i>dhc2</i>	LOCUS59, mRNA	93%	98.8	XM_043307652.1
		<i>dhc3</i>	LOCUS61, mRNA	83%	97.0	XM_043307654.1
		<i>dhc4</i>	LOCUS62, mRNA	93%	98.2	XM_043307655.1
		<i>dhc5</i>	LOCUS63, mRNA	98%	98.5	XM_043307656.1
<i>Alternaria solani</i>	NL03003	<i>dhc2</i>	chromosome 8, complete sequence	100%	94.9	CP022031.1
		<i>dhc3</i>	chromosome 8, complete sequence	100%	95.2	CP022031.1
		<i>dhc4</i>	chromosome 8, complete sequence	100%	95.4	CP022031.1
		<i>dhc5</i>	chromosome 8, complete sequence	99%	95.0	CP022031.1
<i>Pyrenophora tritici-repentis</i>	Pt-1C-BFP	<i>dhc2</i>	MFS gliotoxin efflux transporter GliA, mRNA	92%	90.5	XM_001934686.1
		<i>dhc3</i>	phenolphthiocerol synthesis polyketide synthase ppsB, mRNA	96%	86.3	XM_001934685.1
		<i>dhc4</i>	C6 zinc finger domain containing protein, mRNA	96%	88.0	XM_001934684.1
		<i>dhc5</i>	conidial yellow pigment biosynthesis polyketide synthase, mRNA	93%	88.2	XM_001934683.1

*see Manuscript Table 3 for *A. cinerariae* genes

9 List of whole-genome assemblies of 281 Pleosporalean fungi from various public sources.

Species	Strain	Source	Accession	Family
<i>Aaosphaeria arxii</i>	CBS 175.79	NCBI	GCF_010015735.1	Dacampiaceae (?)
<i>Aaosphaeria arxii</i>	FJI-L9-BK-P1	NCBI	GCA_020086995.1	Dacampiaceae (?)
<i>Alternaria alstroemeriae</i>	CBS 118809	NCBI	GCA_020284155.1	Pleosporaceae
<i>Alternaria alternata</i>	ATCC11680	JGI	mycocosm.jgi.doe.gov; Alalt1	Pleosporaceae
<i>Alternaria alternata</i>	ATCC34957	NCBI	GCA_001443195.2	Pleosporaceae
<i>Alternaria alternata</i>	ATCC66891	JGI	mycocosm.jgi.doe.gov; Alalte1	Pleosporaceae
<i>Alternaria alternata</i>	B2a	NCBI	GCA_001696825.1	Pleosporaceae
<i>Alternaria alternata</i>	B3	NCBI	GCA_014154925.1	Pleosporaceae
<i>Alternaria alternata</i>	BMP0270	JGI	mycocosm.jgi.doe.gov; Aalte1	Pleosporaceae
<i>Alternaria alternata</i>	DET2001	NCBI	GCA_020736775.1	Pleosporaceae
<i>Alternaria alternata</i>	DET2010	NCBI	GCA_020736745.1	Pleosporaceae
<i>Alternaria alternata</i>	DET2019	NCBI	GCA_020736755.1	Pleosporaceae
<i>Alternaria alternata</i>	EV-MIL-31	NCBI	GCA_016097525.1	Pleosporaceae
<i>Alternaria alternata</i>	FERA1177	NCBI	GCA_004154755.1	Pleosporaceae
<i>Alternaria alternata</i>	hznu325	NCBI	GCA_020449105.1	Pleosporaceae
<i>Alternaria alternata</i>	JS-0527	NCBI	GCA_011420255.1	Pleosporaceae
<i>Alternaria alternata</i>	JS-1623	NCBI	GCA_009650635.1	Pleosporaceae
<i>Alternaria alternata</i>	KAS5516	NCBI	GCA_020736765.1	Pleosporaceae
<i>Alternaria alternata</i>	MOD1-FUNGI5	NCBI	GCA_004634295.1	Pleosporaceae
<i>Alternaria alternata</i>	MPI-PUGE-AT-0064	JGI	mycocosm.jgi.doe.gov; Altalt1	Pleosporaceae
<i>Alternaria alternata</i>	NAP07	NCBI	GCA_009932595.1	Pleosporaceae
<i>Alternaria alternata</i>	PF1	NCBI	GCA_018104255.1	Pleosporaceae
<i>Alternaria alternata</i>	PN1	NCBI	GCA_011420445.1	Pleosporaceae
<i>Alternaria alternata</i>	PN2	NCBI	GCA_011420565.1	Pleosporaceae
<i>Alternaria alternata</i>	SRC1lrK2f	NCBI	GCA_001642055.1	Pleosporaceae
<i>Alternaria alternata</i>	Y784-BC03	NCBI	GCA_020085065.1	Pleosporaceae
<i>Alternaria alternata</i>	Z7	NCBI	GCA_014751505.1	Pleosporaceae
<i>Alternaria alternata</i> (A. citriarbasti)	BMP2343	JGI	mycocosm.jgi.doe.gov; Altci1	Pleosporaceae
<i>Alternaria alternata</i> (A. limoniasperae)	BMP2335	JGI	mycocosm.jgi.doe.gov; Altli1	Pleosporaceae
<i>Alternaria alternata</i> (A. mali)	BMP3064	JGI	mycocosm.jgi.doe.gov; Amal3064	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	ANJ	NCBI	GCA_017589455.1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	BMP0304	JGI	mycocosm.jgi.doe.gov; Altte1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	FERA1082	NCBI	GCA_004154745.1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	FERA1164	NCBI	GCA_004156015.1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	FERA1166	NCBI	GCA_004156035.1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	FERA24350	NCBI	GCA_004154735.1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	FERA635	NCBI	GCA_004168565.1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	FERA648	NCBI	GCA_004154765.1	Pleosporaceae
<i>Alternaria alternata</i> (A. tenuissima)	FERA743	NCBI	GCA_004154845.1	Pleosporaceae
<i>Alternaria arborescens</i>	BMP0308	JGI	mycocosm.jgi.doe.gov; Altar1	Pleosporaceae
<i>Alternaria arborescens</i>	DET2008	NCBI	GCA_020736785.1	Pleosporaceae
<i>Alternaria arborescens</i>	EGS39-128	NCBI	GCA_000256225.1	Pleosporaceae
<i>Alternaria arborescens</i>	FERA675	NCBI	GCA_004154835.1	Pleosporaceae
<i>Alternaria arborescens</i>	MOD1-FUNGI6	NCBI	GCA_004634205.1	Pleosporaceae
<i>Alternaria arborescens</i>	NRRL20593	NCBI	GCA_013282825.1	Pleosporaceae
<i>Alternaria arborescens</i>	RGR97.0013	NCBI	GCA_004155955.1	Pleosporaceae
<i>Alternaria arborescens</i>	RGR97.0016	NCBI	GCA_004154815.1	Pleosporaceae

Metabolomics Profiling of *Alternaria* spp.

Species	Strain	Source	Accession	Family
<i>Alternaria arborescens</i> (A. mali)	BMP3063	JGI	mycocosm.jgi.doe.gov; Amal3063	Pleosporaceae
<i>Alternaria atra</i>	CS162	NCBI	GCA_907166805.1	Pleosporaceae
<i>Alternaria atra</i>	MOD1-FUNGI7	NCBI	GCA_004634305.1	Pleosporaceae
<i>Alternaria brassicae</i>	J3	NCBI	GCA_004936725.1	Pleosporaceae
<i>Alternaria brassicicola</i>	Abra43	NCBI	GCA_002796735.1	Pleosporaceae
<i>Alternaria brassicicola</i>	Altbr1	JGI	mycocosm.jgi.doe.gov; Altbr1	Pleosporaceae
<i>Alternaria brassicicola</i>	ATCC96836	NCBI	GCA_000174375.1	Pleosporaceae
<i>Alternaria burnsii</i>	CBS107.38	NCBI	GCA_013036055.1	Pleosporaceae
<i>Alternaria capsici</i>	BMP0180	JGI	mycocosm.jgi.doe.gov; Altca1	Pleosporaceae
<i>Alternaria carthami</i>	BMP1963	JGI	mycocosm.jgi.doe.gov; Altcar1	Pleosporaceae
<i>Alternaria consortialis</i>	JCM1940	NCBI	GCA_001950455.1	Pleosporaceae
<i>Alternaria crassa</i>	BMP0172	JGI	mycocosm.jgi.doe.gov; Altcr1	Pleosporaceae
<i>Alternaria dauci</i>	BMP0167	JGI	mycocosm.jgi.doe.gov; Altda1	Pleosporaceae
<i>Alternaria gaisen</i>	BMP2338	JGI	mycocosm.jgi.doe.gov; Altga1	Pleosporaceae
<i>Alternaria gaisen</i>	FERA650	NCBI	GCA_004156025.2	Pleosporaceae
<i>Alternaria gaisen</i> (A. fragaria)	BMP3062	JGI	mycocosm.jgi.doe.gov; Altfr1	Pleosporaceae
<i>Alternaria gansuensis</i>	LYZ1412	NCBI	GCA_009289805.1	Pleosporaceae
<i>Alternaria longipes</i>	BMP0313	JGI	mycocosm.jgi.doe.gov; Altlo1	Pleosporaceae
<i>Alternaria longipes</i>	CBS540.94	NCBI	GCA_019059555.1	Pleosporaceae
<i>Alternaria macrospora</i>	BMP1949	JGI	mycocosm.jgi.doe.gov; Altma1	Pleosporaceae
<i>Alternaria panax</i>	BNCC115425	NCBI	GCA_019702505.1	Pleosporaceae
<i>Alternaria porri</i>	BMP0178	JGI	mycocosm.jgi.doe.gov; Altpo1	Pleosporaceae
<i>Alternaria rosae</i>	MPI-PUGE-AT-0040	JGI	mycocosm.jgi.doe.gov; Altro1	Pleosporaceae
<i>Alternaria solani</i>	BMP0185	JGI	mycocosm.jgi.doe.gov; Altso1	Pleosporaceae
<i>Alternaria solani</i>	HWC-168-2012p	NCBI	GCA_002837235.1	Pleosporaceae
<i>Alternaria solani</i>	NL03003	NCBI	GCA_002952155.1	Pleosporaceae
<i>Alternaria</i> sp.	MG1	NCBI	GCA_003574525.1	Pleosporaceae
<i>Alternaria tangelonis</i>	BMP2327	JGI	mycocosm.jgi.doe.gov; Altta1	Pleosporaceae
<i>Alternaria tomatophila</i>	BMP2032	JGI	mycocosm.jgi.doe.gov; Alttom1	Pleosporaceae
<i>Amniculicola lignicola</i>	CBS 123094	NCBI	GCA_010015725.1	Amniculicolaceae
<i>Ampelomyces quisqualis</i>	BRIP 72107	NCBI	GCA_018398575.1	Leptosphaeriaceae (Phaeosphaeriaceae?)
<i>Ampelomyces quisqualis</i>	HMLAC05119	NCBI	GCA_010094095.1	Leptosphaeriaceae (Phaeosphaeriaceae?)
<i>Ascochyta fabae</i>	247/15	NCBI	GCA_004335285.1	Didymellaceae
<i>Ascochyta koolunga</i>	CND-11-149	NCBI	GCA_004151575.1	Didymellaceae
<i>Ascochyta koolunga</i>	GRP-15-464	NCBI	GCA_004151145.1	Didymellaceae
<i>Ascochyta koolunga</i>	PIN-15-415	NCBI	GCA_004151165.1	Didymellaceae
<i>Ascochyta lentis</i>	Al4	NCBI	GCA_004011705.1	Didymellaceae
<i>Ascochyta lentis</i>	F16132	NCBI	GCA_004335125.1	Didymellaceae
<i>Ascochyta lentis</i>	F16293-3	NCBI	GCA_004335145.1	Didymellaceae
<i>Ascochyta lentis</i>	FT16116	NCBI	GCA_004335135.1	Didymellaceae
<i>Ascochyta lentis</i>	JD202.22	NCBI	GCA_016097305.1	Didymellaceae
<i>Ascochyta lentis</i>	JD202.9	NCBI	GCA_016097315.1	Didymellaceae
<i>Ascochyta lentis</i>	JD202.ect	NCBI	GCA_016097295.1	Didymellaceae
<i>Ascochyta lentis</i>	Kewell	NCBI	GCA_016097375.1	Didymellaceae

Metabolomics Profiling of *Alternaria* spp.

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<i>Ascochyta rabiei</i>	ArDII	NCBI	GCA_001630375.1	Didymellaceae
<i>Ascochyta rabiei</i>	Me14	NCBI	GCF_004011695.1	Didymellaceae
<i>Ascochyta viciae</i>	FOR-16-616	NCBI	GCA_004335155.1	Didymellaceae
<i>Ascochyta viciae-villosae</i>	ONG-16-641	NCBI	GCA_004335205.1	Didymellaceae
<i>Beverwykella pulmonaria</i>	JCM 9230	NCBI	GCA_001599595.1	Melanommataceae (?)
<i>Bimuria novae-zelandiae</i>	CBS 107.79	NCBI	GCA_010015655.1	Didymosphaeriaceae
<i>Bipolaris cookei</i>	LSLP18.3	NCBI	GCA_002286855.1	Pleosporaceae
<i>Bipolaris maydis</i>	ATCC48331	NCBI	GCA_000354255.1	Pleosporaceae
<i>Bipolaris maydis</i>	BM1	NCBI	GCA_019454015.1	Pleosporaceae
<i>Bipolaris maydis</i>	C5	NCBI	GCA_000338975.1	Pleosporaceae
<i>Bipolaris maydis (Cochliobolus heterostrophus)</i>	C4-1	JGI	mycocosm.jgi.doe.gov; CocheC4-1	Pleosporaceae
<i>Bipolaris maydis (Cochliobolus heterostrophus)</i>	Hm540-1	JGI	mycocosm.jgi.doe.gov; ChetHm540-1	Pleosporaceae
<i>Bipolaris oryzae</i>	ATCC44560	NCBI	GCA_000523455.1	Pleosporaceae
<i>Bipolaris oryzae</i>	TG12bL2	NCBI	GCA_001675385.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	BRIP10943a	NCBI	GCA_008452735.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	BRIP27492a	NCBI	GCA_008452725.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	BS112	NCBI	GCA_004329375.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	Gansu	NCBI	GCA_013416765.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	ND90Pr	NCBI	GCA_000338995.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	Shoemaker	NCBI	GCA_013416765.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	WAI2406	NCBI	GCA_008452705.1	Pleosporaceae
<i>Bipolaris sorokiniana</i>	WAI2411	NCBI	GCA_008452715.1	Pleosporaceae
<i>Bipolaris victoriae</i>	FI3	NCBI	GCA_000527765.2	Pleosporaceae
<i>Bipolaris zeicola</i>	26-R-13	NCBI	GCA_000523435.1	Pleosporaceae
<i>Bipolaris zeicola</i>	GZL1	NCBI	GCA_016906865.1	Pleosporaceae
<i>Boeremia exigua</i>	MPI-SDFR-AT-0100	NCBI	GCA_020726555.1	Didymellaceae
<i>Byssothecium circinans</i>	CBS 675.92	NCBI	GCA_010015675.1	Massarinaceae (Dacampiaceae?)
<i>Clathrospora elyngae</i>	CBS 161.51	NCBI	GCA_010015635.1	Diademaceae
<i>Clavariopsis aquatica</i>	WD(A)-00-1	NCBI	GCA_013620735.1	?
<i>Clohesyomyces aquaticus</i>	CBS 115471	NCBI	GCA_002105025.1	Lindgomycetaceae
<i>Corynespora cassicola</i>	C7	NCBI	GCA_900169545.1	Corynesporascaceae
<i>Corynespora cassicola</i>	CAL-4	NCBI	GCA_006523515.1	Corynesporascaceae
<i>Corynespora cassicola</i>	CBS129.25	NCBI	GCA_002976015.1	Corynesporascaceae
<i>Corynespora cassicola</i>	CC_29	NCBI	GCA_019202905.1	Corynesporascaceae
<i>Corynespora cassicola</i>	CC01	NCBI	GCA_016906425.1	Corynesporascaceae
<i>Corynespora cassicola</i>	CSR11	NCBI	GCA_002975815.1	Corynesporascaceae
<i>Corynespora cassicola</i>	LPO7	NCBI	GCA_002975495.1	Corynesporascaceae
<i>Corynespora cassicola</i>	Philippines	NCBI	GCA_003016335.1	Corynesporascaceae
<i>Corynespora cassicola</i>	TCI3	NCBI	GCA_006519745.1	Corynesporascaceae
<i>Corynespora cassicola</i>	UM 591	NCBI	GCA_000603925.1	Corynesporascaceae
<i>Corynespora olivacea</i>	CBS 114450	NCBI	GCA_019202945.1	Corynesporascaceae
<i>Cucurbitaria berberidis</i>	CBS 394.84	NCBI	GCF_010015615.1	Cucurbitariaceae
<i>Curvularia eragrostidis</i>	C52	NCBI	GCA_020744315.1	Pleosporaceae
<i>Curvularia geniculata</i>	P1	NCBI	GCA_016162275.1	Pleosporaceae
<i>Curvularia geniculata</i>	W3	NCBI	GCA_002982235.1	Pleosporaceae
<i>Curvularia lunata</i>	CX-3	NCBI	GCA_000743335.1	Pleosporaceae
<i>Curvularia lunata</i>	W3	NCBI	GCA_005212705.1	Pleosporaceae
<i>Curvularia lunata (Cochliobolus lunatus)</i>	m118	JGI	Coclu2	Pleosporaceae
<i>Curvularia papendorfii</i>	UM_226	NCBI	GCA_000817285.1	Pleosporaceae
<i>Curvularia sp</i>	IFB-Z10	NCBI	GCA_002161795.1	Pleosporaceae
<i>Decorospora gaudefroyi</i>	Decga1	JGI	Decga1	Pleosporaceae
<i>Decorospora gaudefroyi</i>	P77	NCBI	GCA_010015605.1	Pleosporaceae
<i>Delitschia confertasporea</i>	ATCC 74209	NCBI	GCA_010093945.1	Delitschiaceae
<i>Dendryphion nanum</i>	MPI-CAGE-CH-0243	NCBI	GCA_020744415.1	Torulaceae
<i>Didymella arachidicola</i>	YY187	NCBI	GCA_016630955.1	Didymellaceae
<i>Didymella exigua</i>	CBS 183.55	NCBI	GCF_010094145.1	Didymellaceae
<i>Didymella heteroderae</i>	28M1	NCBI	GCA_011058895.1	Didymellaceae

Metabolomics Profiling of *Alternaria* spp.

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<i>Didymella keratinophila</i>	9M1	NCBI	GCA_011058865.1	Didymellaceae
<i>Didymella lethalis</i>	FOR-16-620	NCBI	GCA_004335255.1	Didymellaceae
<i>Didymella lethalis</i>	GRM-16-623	NCBI	GCA_004335245.1	Didymellaceae
<i>Didymella pinodes</i>	BAL-11-01	NCBI	GCA_004151185.1	Didymellaceae
<i>Didymella pinodes</i>	GRP-11-30	NCBI	GCA_004151295.1	Didymellaceae
<i>Didymella pinodes</i>	RIV-11-185	NCBI	GCA_004151305.1	Didymellaceae
<i>Didymella pinodes</i>	WTN-11-157	NCBI	GCA_004151525.1	Didymellaceae
<i>Didymella pinodes</i>	YEL-11-87	NCBI	GCA_004151515.1	Didymellaceae
<i>Didymella segeticola</i>	GZSQ-4	NCBI	GCA_004522025.1	Didymellaceae
<i>Didymosphaeria enalia</i>	CBS 304.66	NCBI	GCA_010094045.1	Didymosphaeriaceae
<i>Dothidotthia symphoricarpi</i>	CBS 119687	NCBI	GCF_010015815.1	Dothidotthiaceae
<i>Epicoccum latusicollum</i>	T41	NCBI	GCA_015266435.1	Didymellaceae
<i>Epicoccum nigrum</i>	cf0051	NCBI	GCA_019721275.1	Didymellaceae
<i>Epicoccum nigrum</i>	ICMP 19927	NCBI	GCA_002116315.1	Didymellaceae
<i>Epicoccum nigrum</i>	P16	NCBI	GCA_009761125.1	Didymellaceae
<i>Epicoccum sorghinum</i>	BS2-1	NCBI	GCA_020272525.1	Didymellaceae
<i>Epicoccum sorghinum</i>	USPMTOX48	NCBI	GCA_001879705.1	Didymellaceae
<i>Exserohilum rostratum</i>	ER1	NCBI	GCA_019453395.1	Pleosporaceae
<i>Exserohilum turcicum</i> (<i>Exserohilum turcica</i>)	Et28A	NCBI	GCF_000359705.1	Pleosporaceae
<i>Exserohilum turcicum</i> (<i>Setosphaeria turcica</i>)	NY001	JGI	Settur3	Pleosporaceae
<i>Helminthosporium solani</i>	B-AC-16A	NCBI	GCA_000498615.1	Massarinaceae
<i>Karstenula rhodostoma</i>	CBS 690.94	NCBI	GCA_010093485.1	Didymosphaeriaceae
<i>Laburnicola</i> sp.	JP-R-44	NCBI	GCA_009805535.1	Didymosphaeriaceae
<i>Laburnicola</i> sp.	R22_1	NCBI	GCA_014281115.1	Didymosphaeriaceae
<i>Lentithecium fluviale</i>	CBS 122367	NCBI	GCA_010405425.1	Lentitheciaceae
<i>Leptosphaeria biglobosa</i>	G12-14	NCBI	GCA_900465125.1	Leptosphaeriaceae
<i>Leptosphaeria maculans</i>	JN3	NCBI	GCF_000230375.1	Leptosphaeriaceae
<i>Leptosphaeria maculans</i>	NZT4	NCBI	GCA_900465115.1	Leptosphaeriaceae
<i>Lindgomyces ingoldianus</i>	ATCC 200398	NCBI	GCF_010093535.1	Lindgomycetaceae
<i>Lophiostoma macrostomum</i>	CBS 122681	NCBI	GCA_010405375.1	Lophiostomataceae
<i>Lophiotrema nucula</i>	CBS 627.86	NCBI	GCA_010015825.1	Lophiotremataceae
<i>Macroventuria anomochaeta</i>	CBS 525.71	NCBI	GCF_010093625.1	Didymellaceae
<i>Massarina eburnea</i>	CBS 473.64	NCBI	GCA_010093635.1	Massarinaceae
<i>Massariosphaeria phaeospora</i>	CBS 611.86	NCBI	GCA_011032825.1	Cyclothyriellaceae (?), Thyridariaceae (?)
<i>Melanomma pulvis-pyrius</i>	CBS 109.77	NCBI	GCA_010093585.1	Melanommataceae
<i>Neoscochyta</i> sp.	HWLR27	NCBI	GCA_019775935.1	Didymellaceae
<i>Neocamarosporium betae</i>	Pb1	NCBI	GCA_016612005.1	Pleosporaceae
<i>Nigrograna mackinnonii</i>	E5202H	NCBI	GCA_001007845.1	Nigrogranaeae
<i>Ophiobolus disseminans</i>	CBS 113818	NCBI	GCA_010093685.1	Leptosphaeriaceae (Phaeosphaeriaceae?)
<i>Paracamarosporium</i> sp.	OC-R06-R3	NCBI	GCA_019828545.1	Didymosphaeriaceae
<i>Paradendryphiella salina</i>	PS1_23737	NCBI	GCA_900634815.1	Pleosporaceae
<i>Paraphaeosphaeria minitans</i>	IMI134523	NCBI	GCA_015832175.1	Didymosphaeriaceae
<i>Paraphaeosphaeria minitans</i>	ZS-1	NCBI	GCA_009707825.1	Didymosphaeriaceae
<i>Paraphaeosphaeria sporulosa</i>	AP3s5-JAC2a	NCBI	GCF_001642045.1	Didymosphaeriaceae
<i>Paraphoma chrysanthemicola</i>	MPI-GEGE-AT-0034	NCBI	GCA_020744225.1	Phaeosphaeriaceae
<i>Paraphoma chrysanthemicola</i>	MPI-SDFR-AT-0120	NCBI	GCA_020744215.1	Phaeosphaeriaceae
<i>Paraphoma</i> sp.	B47-9	NCBI	GCA_001748405.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>avenae</i>	Mt. Baker	NCBI	GCA_003501955.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>avenae</i>	s258	NCBI	GCA_003501935.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>tritici</i>	82-4841	NCBI	GCA_003503125.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>tritici</i>	83-6011-2	NCBI	GCA_003502015.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>tritici</i>	Hartney99	NCBI	GCA_003503195.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>tritici</i>	IR10_5.2b	NCBI	GCA_003503205.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>tritici</i>	Jansen 4_55	NCBI	GCA_003503165.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>tritici</i>	SN11IR_2_1.1	NCBI	GCA_003502495.1	Phaeosphaeriaceae
<i>Parastagonospora avenae</i> f. sp. <i>tritici</i>	SN11IR_6_1.1	NCBI	GCA_003503115.1	Phaeosphaeriaceae

Metabolomics Profiling of *Alternaria* spp.

Species	Strain	Source	Accession	Family
<i>Parastagonospora avenae</i> f. <i>sp. tritici</i>	SN11IR_7_2.3	NCBI	GCA_003501975.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	14FG141	NCBI	GCA_020581275.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	15FG109	NCBI	GCA_020580655.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	16FG166	NCBI	GCA_020577905.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	FIN-2	NCBI	GCA_003497975.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	LDN03-Sn4	NCBI	GCA_002267005.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	Meck3	NCBI	GCA_020573915.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	SN15	NCBI	GCF_000146915.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	Sn2000	NCBI	GCA_002267045.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	Sn79-1087	NCBI	GCA_002267025.1	Phaeosphaeriaceae
<i>Parastagonospora nodorum</i>	SWE-3	NCBI	GCA_003497965.1	Phaeosphaeriaceae
<i>Periconia macrospinosa</i>	DSE2036	NCBI	GCA_003073855.1	Periconiaceae
<i>Phaeosphaeria</i> sp.	A1 3.1a	NCBI	GCA_003501895.1	Phaeosphaeriaceae
<i>Phaeosphaeria</i> sp.	H6.2b	NCBI	GCA_003503105.1	Phaeosphaeriaceae
<i>Phaeosphaeria</i> sp.	MPI-PUGE-AT-0046c	NCBI	GCA_020747045.1	Phaeosphaeriaceae
<i>Phoma herbarum</i>	JCM 15942	NCBI	GCA_001599375.1	Didymellaceae
<i>Phoma</i> sp.	RAV-16-625	NCBI	GCA_004335185.1	Didymellaceae
<i>Phoma</i> sp.	XZ068	NCBI	GCA_004835665.1	Didymellaceae
<i>Plenodomus tracheiphilus</i>	IPT5	NCBI	GCA_010093695.1	Leptosphaeriaceae
<i>Pleomassaria siparia</i>	CBS 279.74	NCBI	GCA_010093715.1	Pleomassariaceae
<i>Pleosporales</i> sp.	UM 1110	NCBI	GCA_000263175.2	?
<i>Polyplosphaeria fusca</i>	CBS 125425	NCBI	GCA_010093805.1	Tetraplosphaeriaceae
<i>Preussia</i> sp.	BSL10	NCBI	GCA_001553865.1	Sporormiaceae
<i>Pseudomonodictys</i> sp.	A73	NCBI	GCA_019022785.1	Macrodiplodipsidaceae
<i>Pseudopyrenochaeta lycopersici</i>	CRA-PAV_ER 1211	NCBI	GCA_000601435.1	Pseudopyrenochaetaceae
<i>Pseudopyrenochaeta lycopersici</i>	CRA-PAV_ER 1518	NCBI	GCA_003313425.1	Pseudopyrenochaetaceae
<i>Pyrenochaeta</i> sp.	DS3sAY3a	NCBI	GCA_001644535.1	Cucurbitariaceae
<i>Pyrenochaeta</i> sp.	MPI-SDFR-AT-0127	NCBI	GCA_020747015.1	Cucurbitariaceae
<i>Pyrenochaeta</i> sp.	UM 256	NCBI	GCA_000359685.2	Cucurbitariaceae
<i>Pyrenophora graminea</i>	CBS336.29	NCBI	GCA_012365135.1	Pleosporaceae
<i>Pyrenophora seminiperda</i>	CCB06	NCBI	GCA_000465215.2	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>maculata</i>	DEN2.6	NCBI	GCA_014334755.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>maculata</i>	FGOB10Ptm-1	NCBI	GCA_014334795.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>maculata</i>	NZKF2	NCBI	GCA_014334775.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>maculata</i>	P-A14	NCBI	GCA_014334815.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>maculata</i>	SG1	NCBI	GCA_900231935.2	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>maculata</i> (?)	LQA	NCBI	GCA_020027095.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	O-1	NCBI	GCA_006112615.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	15A	NCBI	GCA_008086755.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	6A	NCBI	GCA_008086725.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	BB25	NCBI	GCA_008086785.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	FGOH04Ptt-21	NCBI	GCA_008086845.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	HRS9122	NCBI	GCA_009728645.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	HRS9139	NCBI	GCA_009728635.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	NB29	NCBI	GCA_009728665.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	NB73	NCBI	GCA_009728655.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	NB85	NCBI	GCA_009728675.1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	Pyrtt1	JGI	Pyrtt1	Pleosporaceae
<i>Pyrenophora teres</i> f. <i>teres</i>	W1-1	NCBI	GCA_900232045.2	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	134	NCBI	GCA_003231325.1	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	239	NCBI	GCA_003231365.1	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	5213	NCBI	GCA_003231345.1	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	11137	NCBI	GCA_003231355.1	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	86-124	NCBI	GCA_003231425.2	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	ARCrossB10	NCBI	GCA_018492725.1	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	DW5	NCBI	GCA_003231415.2	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	M4	NCBI	GCA_003171515.2	Pleosporaceae

Metabolomics Profiling of *Alternaria* spp.

Species	Strain	Source	Accession	Family
<i>Pyrenophora tritici-repentis</i>	Pt-1C-BFP	NCBI	GCA_000149985.1	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	Pyrtr1	JGI	Pyrtr1	Pleosporaceae
<i>Pyrenophora tritici-repentis</i>	V0001	NCBI	GCA_008692205.1	Pleosporaceae
<i>Sclerotiophoma versabilis</i>	KC1	NCBI	GCA_012274445.1	Didymellaceae
<i>Setomelanomma holmii</i>	CBS 110217	NCBI	GCA_010015745.1	Phaeosphaeriaceae
<i>Shiraia</i> sp.	Sif14	NCBI	GCA_000498155.1	Shiraiaceae
<i>Sporormia fimetaria</i>	CBS 119925	NCBI	GCA_010093795.1	Sporormiaceae
<i>Stagonospora</i> sp.	SRC1sM3a	NCBI	GCA_001644525.1	Massariaceae (Phaeosphaeriaceae?)
<i>Stagonosporopsis cucurbitacearum</i>	DBTL4	NCBI	GCA_016920805.1	Didymellaceae
<i>Stagonosporopsis</i> sp.	XDPOP-RS-16W	NCBI	GCA_016767195.1	Didymellaceae
<i>Stagonosporopsis tanacetii</i>	four strains pooled	NCBI	GCA_000812845.1	Didymellaceae
<i>Stemphylium lycopersici</i>	CIDEFI212	NCBI	GCA_003268315.1	Pleosporaceae
<i>Stemphylium lycopersici</i>	CIDEFI213	NCBI	GCA_003268335.1	Pleosporaceae
<i>Stemphylium lycopersici</i>	CIDEFI-216	JGI	Stely1	Pleosporaceae
<i>Stemphylium vesicarium</i>	173-1a-13FI1M3	NCBI	GCA_004380135.1	Pleosporaceae
<i>Stemphylium vesicarium</i>	On16-391	NCBI	GCA_008271585.1	Pleosporaceae
<i>Stemphylium vesicarium</i>	On16-63	NCBI	GCA_008271615.1	Pleosporaceae
<i>Trematosphaeria pertusa</i>	CBS 122368	NCBI	GCF_010094035.1	Trematosphaeriaceae
<i>Westerdykella ornata</i>	CBS 379.55	NCBI	GCF_010094085.1	Sporormiaceae
<i>Westerdykella</i> sp.	P71	NCBI	GCA_019022765.1	Sporormiaceae

10 List of fungal species for which the dehydrocurvularin biosynthetic genes were found from the whole-genome sequence database (281 Pleosporalean fungi).

Species	Strain	Percent identity with DET 2035 gene			
		<i>dhc2</i>	<i>dhc3</i>	<i>dhc4</i>	<i>dhc5</i>
<i>Alternaria alternata</i>	KAS5743	98.45	97.95	97.66	98.12
<i>Alternaria arborescens</i>	DET2035	100.00	100.00	100.00	100.00
<i>Alternaria arborescens</i>	KAS5321	99.95	99.91	99.96	99.83
<i>Alternaria atra</i>	CS162	98.66	98.46 (i)	98.22	98.46
<i>Alternaria atra</i>	MOD1-FUNGI7	98.56	98.51 (i)	98.17	98.47 (s)
<i>Alternaria carthami</i>	BMP1963	94.91	95.57	95.28	95.04
<i>Alternaria consortialis</i>	JCM1940	98.45	98.29	98.17	98.27
<i>Alternaria macrospora</i>	BMP1949	95.02	95.51	94.60	94.81
<i>Alternaria porri</i>	BMP0178	94.19 (*)	95.41	95.37	94.99
<i>Alternaria solani</i>	BMP0185	94.91	95.28	95.41	94.99
<i>Alternaria solani</i>	HWC-168-2012p	94.86	95.25	95.41	94.98
<i>Alternaria solani</i>	NL03003	94.91	95.25	95.41	94.99
<i>Alternaria tomatophila</i>	BMP2032	95.02 (*)	95.35 (s)	95.20	94.68 (s)
<i>Pyrenophora tritici-repentis</i>	134	89.76	87.52	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	239	89.76	87.52	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	5213	89.76	87.52	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	11137	89.76	87.52	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	86-124	89.76	87.52	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	ARCrossB10	89.76	87.52	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	DW5	89.76	87.52	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	M4	89.76	87.55	87.34	88.23
<i>Pyrenophora tritici-repentis</i>	Pt-1C-BFP	89.76	87.52	87.34	88.20
<i>Pyrenophora tritici-repentis</i>	Pyrtr1	89.76	87.52	87.34	88.20
<i>Pyrenophora tritici-repentis</i>	V0001	89.76	87.52	87.34	88.22
<i>Stemphylium vesicarium</i>	173-1a-13FI1M3	98.23	97.92	97.62	98.19

(i) indicates an insertion occurs within the gene; (s) indicates the gene is split across multiple contigs; (*) indicates the entire gene is on a different contig than the other genes.