

SUPPLEMENTARY FILE S3*(Sayari et al - Ceratocystidaceae Polyketide biosynthesis gene clusters)*

The tables below show the sizes and positions of genes in the respective PKS clusters within the relevant contigs (GenBank Accession numbers are indicated in brackets), together with the blast scores for the top database hits (i.e, E value, % Coverage, % identity and the Accession number of the top hit).

A-1) *Ceratocystis eucalypticola* contig 320 (LJOA01000320), NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ-1	2451	22676-25127	<i>Coniochaeta ligniaria</i>	0	99	67	OIW28934
Helicase	1752	26132-27884	<i>Scedosporium apiospermum</i>	0	92	77	XP_016640511
NR-PKS-I	6824	49955-43131	<i>Scedosporium apiospermum</i>	0	99	64	XP_016640516
Transcription factor	1361	52636-54000	<i>Madurella mycetomatis</i>	0	99	34	KXX74404
Tetrahydroxy naphthalene reductase	839	54405-55244	<i>Scedosporium boydii</i>	0	100	76	AIC82365
Transcription factor	3340	56963-60303	<i>Colletotrichum incanum</i>	0	99	47	KZ171510

A-2) *Ceratocystis eucalypticola* contig 350 (LJOA01000350), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5489	92103-97592	<i>Sordaria macrospora</i>	0	53	43	XP_003348394
Major facilitator protein	2213	88670-90883	<i>Fusarium oxysporum</i>	0	87	51	ENH62002
R-PKS-I	7707	71853-79561	<i>Neonectria ditissima</i>	0	98	36	KPM39192
ATPase	7547	60663-69414	<i>Colletotrichum orchidophilum</i>	0	95	43	OHE96608
Hypothetical	685	58691-59376	<i>Verticillium dahliae</i>	0	72	53	XP_009656188
Hypothetical	914	56367-57281	<i>Neonectria ditissima</i>	0	100	39	KPM39715
Hydrolase	1977	50920-52897	<i>Purpureocillium lilacinum</i>	0	76	44	OAQ86162

A-3) *Ceratocystis eucalypticola* contig 157 (LJOA01000157), PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ribonuclease	6132	48585-54717	<i>Hirsutella minnesotensis</i>	0	96	61	KJZ76270
Mitochondrial carrier	917	55265-56182	<i>Phaeoacremonium minimum</i>	0	94	80	XP_007913083

Methyl transferase	935	62986-63921	<i>Scedosporium apiospermum</i>	0	69	49	XP_016638640
Ankyrin repeat	4859	64442-69301	<i>Purpureocillium lilacinum</i>	0	88	43	OAQ78721
Mitochondrial carrier	1492	70743-72233	<i>Scedosporium apiospermum</i>	0	98	81	XP_016638648
Bud 22	1572	72492-74068	<i>Nectria haematococca</i>	0	99	42	XP_003052505
PKS-III	1427	74361-75788	<i>Stachybotrys chlorohalonata</i>	0	100	58	KFA65321
Bfr-2	1877	77744-78124	<i>Phaeoacremonium minimum</i>	0	99	51	XP_007913055
Transcription factor	3869	78320-80230	<i>Colletotrichum salicis</i>	0	63	36	KXH54388

B-1) *Ceratocystis adiposa* contig 305 (LJOA01000305), NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ-1	2451	22676-25127	<i>Coniochaeta ligniaria</i>	0	99	67	OIW28934
Helicase	1752	26132-27884	<i>Scedosporium apiospermum</i>	0	92	77	XP_016640511
NR-PKS-I	6824	49955-43131	<i>Scedosporium apiospermum</i>	0	99	64	XP_016640516
Transcription factor	1361	52636-54000	<i>Madurella mycetomatis</i>	0	99	34	KXX74404
Tetrahydroxy naphthalene reductase	839	54405-55244	<i>Scedosporium boydii</i>	0	100	76	AIC82365
Transcription factor	3340	56963-60303	<i>Colletotrichum incanum</i>	0	99	47	KZ171510

B-2) *Ceratocystis adiposa* contig 355 (LJOA01000355), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5489	105161-110650	<i>Sordaria macrospora</i>	0	53	44	XP_003348394
Major facilitator protein	2213	101475-103950	<i>Fusarium oxysporum</i>	0	88	51	ENH62002
R-PKS-I	7707	84444-92151	<i>Neonectria ditissima</i>	0	98	36	KPM39192
ATPase	7547	74459-82006	<i>Colletotrichum orchidophilum</i>	0	95	41	OHE96608
Hypothetical	685	71295-71980	<i>Verticillium dahliae</i>	0	73	52	XP_009656188
Hypothetical	914	68973-69887	<i>Neonectria ditissima</i>	0	99	40	KPM39715
Hydrolase	1977	63568-65545	<i>Purpureocillium lilacinum</i>	0	76	45	OAQ86162

B-3) *Ceratocystis adiposa* contig 5 (LXGU01000005), PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
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Ribonuclease	6132	48585-54717	<i>Hirsutella minnesotensis</i>	0	96	61	KJZ76270
Mitochondrial carrier	917	55265-56182	<i>Phaeoacremonium minimum</i>	0	94	80	XP_007913083
Methyl transferase	935	62986-63921	<i>Scedosporium apiospermum</i>	0	69	49	XP_016638640
Ankyrin repeat	4859	64442-69301	<i>Purpureocillium lilacinum</i>	0	88	43	OAQ78721
Mitochondrial carrier	1492	70743-72233	<i>Scedosporium apiospermum</i>	0	98	81	XP_016638648
Bud 22	1572	72492-74068	<i>Nectria haematococca</i>	0	99	42	XP_003052505
PKS-III	1427	74361-75788	<i>Stachybotrys chlorohalonata</i>	0	100	58	KFA65321
Bfr-2	1877	77744-78124	<i>Phaeoacremonium minimum</i>	0	99	51	XP_007913055
Transcription factor	3869	78320-80230	<i>Colletotrichum salicis</i>	0	63	36	KXH54388

C-1) *Ceratocystis smalleyi* contig 511, NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ-1	2451	4550-7026	<i>Coniochaeta ligniaria</i>	0	99	67	OIW28934
Helicase	1751	8061-9812	<i>Scedosporium apiospermum</i>	0	92	77	XP_016640511
NR-PKS-I	6824	11290-18114	<i>Scedosporium apiospermum</i>	0	99	64	XP_016640516
Transcription factor	1361	22587-23948	<i>Madurella mycetomatis</i>	0	100	33	KXX74404
Tetrahydroxy naphthalene reductase	842	24600-25442	<i>Scedosporium boydii</i>	0	100	78	AIC82365
Transcription factor	3345	27784-31129	<i>Colletotrichum incanum</i>	0	98	48	KZ171510

C-2) *Ceratocystis smalleyi* contig 541, R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5489	4019-9523	<i>Sordaria macrospora</i>	0	53	45	XP_003348394
Major facilitator protein	2213	607-2820	<i>Fusarium oxysporum</i>	0	87	51	ENH62002
R-PKS-I	7700	3500-11200	<i>Neonectria ditissima</i>	0	98	37	KPM39192
ATPase	7540	12400-19940	<i>Colletotrichum orchidophilum</i>	0	95	43	OHE96608
Hypothetical	685	21200-21885	<i>Verticillium dahliae</i>	0	72	52	XP_009656188
Hypothetical	914	23689-24603	<i>Neonectria ditissima</i>	0	99	41	KPM39715
Hydrolase	1975	27600-29575	<i>Purpureocillium lilacinum</i>	0	78	44	OAQ86162

C-3) *Ceratocystis smalleyi* contig 600, PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Methyl transferase	935	14680-15615	<i>Scedosporium apiospermum</i>	0	69	49	XP_016638640
Ankyrin repeat	4892	8204-13096	<i>Purpureocillium lilacinum</i>	0	88	43	OAQ78721
Mitochondrial carrier	1494	5222-6716	<i>Scedosporium apiospermum</i>	0	98	81	XP_016638648
Bud 22	1572	3367-4948	<i>Nectria haematococca</i>	0	99	42	XP_003052505
PKS-III	1427	1599-3026	<i>Stachybotrys chlorohalonata</i>	0	100	58	KFA65321

D-1) *Ceratocystis albifundus* contig 1283 (JSSU010001283), NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ-1	2467	23261-25728	<i>Coniochaeta ligniaria</i>	0	99	67	OIW28934
Helicase	1760	26782-28542	<i>Scedosporium apiospermum</i>	0	92	76	XP_016640511
NR-PKS-I	6819	44805-51624	<i>Scedosporium apiospermum</i>	0	99	64	XP_016640516
Transcription factor	1376	54486-55862	<i>Madurella mycetomatis</i>	0	99	34	KXX74404
Tetrahydroxy naphthalene reductase	839	56314-57153	<i>Scedosporium boydii</i>	0	100	76	AIC82365
Transcription factor	3365	58929-62294	<i>Colletotrichum incanum</i>	0	99	44	KZ171510

D-2) *Ceratocystis albifundus* contig 1010 (JSSU010001010), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5490	22145-27635	<i>Sordaria macrospora</i>	0	53	43	XP_003348394
Major facilitator protein	1662	18842-21086	<i>Fusarium oxysporum</i>		85	46	ENH62002
R-PKS-I	7707	1538-9277	<i>Fusarium poae</i>	0	98	34	ALQ32896

D-3) *Ceratocystis albifundus* contig 1235 (JSSU010001235), PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ribonuclease	6157	18997-25154	<i>Colletotrichum incanum</i>	0	96	62	OHW96028
Mitochondrial carrier	918	25853-26770	<i>Phaeoacremonium minimum</i>	0	97	78	XP_007913083

Methyl transferase	1585	33255-34840	<i>Scedosporium apiospermum</i>	0	74	48	XP_016638640
Ankyrin repeat	4859	35386-40245	<i>Acremonium chrysogenum</i>	0	73	45	OAQ78721
Mitochondrial carrier	1494	41674-43168	<i>Scedosporium apiospermum</i>	0	97	77	XP_016638648
Bud 22	1589	43420-45009	<i>Metarhizium quizhouense</i>	4e-71	99	39	KID92810
PKS-III	1430	45327-46757	<i>Stachybotrys chlorohalonata</i>	0	98	57	KFA65321

E-1) *Ceratocystis fimbriata* contig 327 (APWK02000327), PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Methyl transferase	935	6189-7124	<i>Scedosporium apiospermum</i>	2e-42	69	46	XP_016638640
Ankyrin repeat	4859	7650-12509	<i>Purpureocillium lilacinum</i>	0	88	43	OAQ78721
Mitochondrial carrier	1492	13956-15452	<i>Scedosporium apiospermum</i>	0	98	81	XP_016638648
Bud 22	1572	15691-17267	<i>Nectria haematococca</i>	5e-92	99	42	XP_003052505
PKS-III	1427	17560-18987	<i>Stachybotrys chlorohalonata</i>	0	100	58	KFA65321

E-2) *Ceratocystis fimbriata* contig 188 (APWK02000188), R-PKS-I, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	4428	1-4428	<i>Sordaria macrospora</i>	0	65	43	XP_003348394
Major facilitator protein	2212	5638-7850	<i>Fusarium oxysporum</i>	7e-67	83	62	ENH62002
R-PKS-I	7704	16896-24600	<i>Neonectria ditissima</i>	0	98	36	KPM39192

E-1) *Ceratocystis harringtonii* contig 25 (MKGM01000025), NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NR-PKS-I	6847	8841-15688	<i>Colletotrichum incanum</i>	0	99	65	OHW97102
Transcription factor	1370	18423-19793	<i>Hypoxyton</i> Sp.	6e-51	98	32	OTA70491
Tetrahydroxy naphthalene reductase	840	20213-21052	<i>Scedosporium boydii</i>	0	100	75	AIC82365
Transcription factor	3068	22765-25833	<i>Colletotrichum lagenaria</i>	0	99	48	BAA75888

E-2) *Ceratocystis harringtonii* contig 465 (MKGM01000465), PKS-III cluster

Gene name	Size	Location on	Species	E value	% Coverage	% identity	Accession number
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	the contig			of top blast hit			
Ankyrin repeat	4880	518-5398	<i>Purpureocillium lilacinum</i>	0	76	50	OAQ78721
Mitochondrial carrier	1486	6835-8321	<i>Scedosporium apiospermum</i>	0	98	80	XP_016638648
Bud 22	1569	8588-10157	<i>Nectria haematococca</i>	0	99	43	XP_003052505
PKS-III	1427	10452-11879	<i>Colletotrichum sublineola</i>	0	99	59	KDN65911

E-3) *Ceratocystis harringtonii* contig 204 (MKGM01000204), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5483	21086-26569	<i>Sordaria macrospora</i>	0	52	42	XP_003348394
Major facilitator protein	2211	17625-19836	<i>Fusarium oxysporum</i>	0	87	50	ENH62002
R-PKS-I	8106	734-8440	<i>Neonectria ditissima</i>	0	98	35	KPM39192

F-1) *Ceratocystis manginecans* contig 364 (JJRZ01000364), NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NR-PKS-I	6824	10586-17410	<i>Scedosporium boydii</i>	0	99	65	AHA15770
Transcription factor	1361	6508-7869	<i>Hypoxylon</i> Sp.	0	98	31	OTA70491
Tetrahydroxy naphthalene reductase	839	5264-6103	<i>Scedosporium boydii</i>	0	100	76	AIC82365
Transcription factor	3545	1-3545	<i>Colletotrichum incanum</i>	0	99	47	KZ171510

F-2) *Ceratocystis manginecans* contig 60 (JJRZ01000060), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5489	105161-110650	<i>Sordaria macrospora</i>	0	53	43	XP_003348394
Major facilitator protein	2275	101475-103950	<i>Nectria haematococca</i>	0	87	51	XP_003052564
R-PKS-I	7707	84444-92151	<i>Neonectria ditissima</i>	0	98	36	KPM39192
ATPase	7547	74459-82006	<i>Colletotrichum orchidophilum</i>	0	96	43	OHE96608
Hypothetical	685	71295-71980	<i>Verticillium dahliae</i>	1e-20	63	51	XP_009656188
Hypothetical	914	68973-69887	<i>Fusarium graminearum</i>	1e-21	100	36	XP_011319935
Hydrolase	1977	63568-65545	<i>Purpureocillium lilacinum</i>	3e-106	76	43	OAQ86162

F-3) *Ceratocystis manginecans* contig 109 (JJRZ01000109), PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ribonuclease	6134	40411-46545	<i>Hirsutella minnesotensis</i>	0	66	61	KJZ76270
Mitochondrial carrier	917	38946-39863	<i>Phaeoacremonium minimum</i>	0	94	80	XP_007913083
Methyl transferase	935	31186-32121	<i>Scedosporium apiospermum</i>	2e-42	69	46	XP_016638640
Ankyrin repeat	4859	25807-30666	<i>Purpureocillium lilacinum</i>	0	88	43	OAQ78721
Mitochondrial carrier	1492	22873-24365	<i>Scedosporium apiospermum</i>	0	98	81	XP_016638648
Bud 22	1572	21066-22638	<i>Nectria haematococca</i>	4e-92	99	42	XP_003052505
PKS-III	1427	19346-20773	<i>Stachybotrys chlorohalonata</i>	0	100	58	KFA65321
Bfr-2	1913	14893-16809	<i>Phaeoacremonium minimum</i>	4e-149	99	51	XP_007913055
Transcription factor	3869	10759-14628	<i>Colletotrichum gloeosporioides</i>	0	70	34	XP_007286061

G-1) *Ceratocystis platani* contig 13 (LBBL01000013), NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ-1	2451	92143-94594	<i>Coniochaeta ligniaria</i>	0	99	67	OIW28934
Helicase	1753	95605-97358	<i>Scedosporium apiospermum</i>	0	92	77	XP_016640511
NR-PKS-I	6824	112717-119541	<i>Scedosporium boydii</i>	0	99	65	AHA15770
Transcription factor	1361	122222-123583	<i>Hypoxylon</i> Sp.	5e-50	98	31	OTA70491
Tetrahydroxy naphthalene reductase	839	123988-124827	<i>Scedosporium boydii</i>	0	100	76	AIC82365
Transcription factor	3340	126544-129659	<i>Colletotrichum incanum</i>	0	94	46	KZ171510

G-2) *Ceratocystis platani* contig 247 (LBBL01000247), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5540	14486-20026	<i>Sordaria macrospora</i>	0	52	43	XP_003348394
Major facilitator protein	2437	21234-23671	<i>Fusarium oxysporum</i>	3e-174	87	47	ENH62002
R-PKS-I	7708	32733-40441	<i>Neonectria ditissima</i>	0	98	35	KPM39192

G-3) *Ceratocystis platani* contig 21 (LBBL01000021), PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
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Mitochondrial carrier	1115	238828-239943	<i>Scedosporium apiospermum</i>	0	99	80	XP_016638648
Bud 22	1932	237021-238593	<i>Nectria haematococca</i>	6e-92	99	43	XP_003052505
PKS-III	1427	235300-236727	<i>Stachybotrys chlorohalonata</i>	0	100	58	KFA65321
Bfr-2	1913	230695-232608	<i>Phaeoacremonium minimum</i>	0	99	51	XP_007913055
Transcription factor	3874	226554-230428	<i>Colletotrichum gloeosporioides</i>	0	70	35	XP_007286061

H-1) *Bretziella fagacearum* contig 123 (MKGJ01000123), PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Mitochondrial carrier	1115	16138-17992	<i>Scedosporium apiospermum</i>	2e-180	98	75	XP_016638648
Bud 22	1932	14292-15825	<i>Nectria haematococca</i>	6e-92	99	43	XP_003052505
PKS-III	1427	10675-13782	<i>Stachybotrys chlorohalonata</i>	0	99	59	KFA65321
Bfr-2	1913	5787-7770	<i>Tolypocladium capitatum</i>	5e-172	99	44	PNY29487

H-3) *Bretziella fagacearum* contig 618 (MKGJ010000618), R-PKS-I, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Fatty acid desaturase	1471	25870- 27342	<i>Nectria haematococca</i>	0	98	58	XP_003040918
RSP	1936	27474-29410	<i>Metarhizium acridum</i>	0	99	73	XP_007814706
Transporter	1107	30249-31356	<i>Phaeoacremonium minimum</i>	0	99	69	XP_007916435
MPV-17	679	31685-32364	<i>Colletotrichum sublineola</i>	0	99	41	KDN72413
MFS	2431	33476-35907	<i>Fusarium mangiferae</i>	0	82	45	CVK91120
R-PKS-I	7315	43721-51036	<i>Trichoderma parareesei</i>	0	98	34	OTA01431
RNA polymerase	5461	64165-69629	<i>Scedosporium apiospermum</i>	0	83	42	XP_016641158
Pantothenate kinase	1508	70685-72193	<i>Neonectria ditissima</i>	0	96	74	KPM45051
ATP synthase	758	73023-73781	<i>Sordaria macrospora</i>	0	100	82	XP_003352487
NAC	758	78479-79264	<i>Oidiodendron malus</i>	0	89	71	KIN01556
60S ribosomal	688	79751-80439	<i>Trichoderma atroviride</i>	0	100	76	XP_013945638

H-4) *Bretziella fagacearum* contig 257 (MKGJ010000257), NR-PKS-I

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number
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							of top blast hit
BZZ-1	2479	578-3057	<i>Colletotrichum higginsianum</i>	0	99	66	XP_018155929
Helicase	1560	3989-5549	<i>Scedosporium apiospermum</i>	0	96	75	XP_016640511
NR-PKS-I	6863	18210-25073	<i>Colletotrichum chlorophyti</i>	0	99	66	OLN85997
Transcription factor	954	29576-30530	<i>Hypoxylon</i> Sp.	5e-50	98	31	OTA70491
Tetrahydroxy naphthalene reductase	903	31392-32295	<i>Scedosporium boydii</i>	0	100	74	AIC82365

I-1) *Huntiella savannae* contig 25 (LCZG01000025) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ1	2415	18479-20894	<i>Coniochaeta ligniaria</i>	0	99	64	OIW28934
Helicase	1681	21819-23500	<i>Scedosporium opiospermum</i>	0	86	76	XP_016640511
NR-PKS-I	6590	39678-46268	<i>Colletotrichum higginsianum</i>	0	99	58	CCF45141
THN reductase	875	48065-48940	<i>Scedosporium boydii</i>	0	100	77	ALC82365
Transcription factor	1469	49914-51383	<i>Valsa mali</i>	0	91	37	KUI58511
Transcription factor	3400	52000-55400	<i>Colletotrichum incanum</i>	0	99	47	KZ171510

I-2) *Huntiella savannae* contig 42 (LCZG01000042) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Fatty acid desaturase	1471	25870- 27342	<i>Nectria haematococca</i>	0	98	58	XP_003040918
RSP	1936	27474-29410	<i>Metarhizium acridum</i>	0	99	73	XP_007814706
Transporter	1107	30249-31356	<i>Phaeoacremonium minimum</i>	0	99	69	XP_007916435
MPV-17	679	31685-32364	<i>Colletotrichum sublineola</i>	0	99	41	KDN72413
MFS	2431	33476-35907	<i>Fusarium mangiferae</i>	0	82	45	CVK91120
R-PKS-I	7315	43721-51036	<i>Trichoderma parareesei</i>	0	98	34	OTA01431
RNA polymerase	5461	64165-69629	<i>Scedosporium apiospermum</i>	0	83	42	XP_016641158
Pantothenate kinase	1508	70685-72193	<i>Neonectria ditissima</i>	0	96	74	KPM45051
ATP synthase	758	73023-73781	<i>Sordaria macrospora</i>	0	100	82	XP_003352487
NAC	758	78479-79264	<i>Oidiodendron malus</i>	0	89	71	KIN01556
60S ribosomal	688	79751-80439	<i>Trichoderma atroviride</i>	0	100	76	XP_013945638

I-3) *Huntiella savannae* contig 45 (LCZG01000045) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ubiquitin enzyme	669	139281-139950	<i>Trichoderma gamsii</i>	0	96	78	XP_0186606678
Protein kinase	1657	136720-138377	<i>Verticillium longisporum</i>	0	99	60	CRK12389
Outer membrane protein	893	132799-133692	<i>Metarhizium anisopliae</i>	0	62	34	KFG86394
ABC transporter	4740	127895-132635	<i>Daldinia sp</i>	0	84	37	OTB17789
NIP SNAP family	1126	123602-124728	<i>Madurella mycetomatis</i>	0	99	67	KXX80314
Hydrolase	949	120457-121406	<i>Colletotrichum orchidophilum</i>	0	79	48	OHE99475
26S proteosome	1637	118686-120323	<i>Podospora anserina</i>	0	99	76	XP_001907151
Dehydrogenase	3713	114366-118079	<i>Diplodia corticola</i>	0	98	70	XP_020132279
Hydrolase	713	111185-111898	<i>Neonectria ditissima</i>	0	98	46	KPM39647
PKS	7561	102180-109741	<i>Scedosporium apiospermum</i>	0	97	33	XP_016645426
Cytochrome P-450	2178	98731-100909	<i>Phialocephala scopiformis</i>	0	51	22	XP_018071792

I-4) *Huntiella savannae* contig 97 (LCZG01000097) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Mitochondrial carrier	914	1-914	<i>Diaporthe ampelina</i>	0	98	79	KKY35686
Hypothetical	1572	1000-2572	<i>Colletotrichum orbiculare</i>	0	93	36	ENH_80387
Methyl transferase	1058	3168-2110	<i>Scedosporium apiospermum</i>	0	100	39	XP_016638640
Ankyrin repeat	4850	3449-8299	<i>Purpureocillium lilacinum</i>	0	88	39	OAQ78721
Mitochondrial carrier	1458	10167-11625	<i>Scedosporium apiospermum</i>	0	99	82	XP_016638648
Bud 22	1555	11909-13464	<i>Claviceps purpurea</i>	0	99	39	CCE30160
Oxidoreductase	1269	15332-16601	<i>Colletotrichum simmondsii</i>	0	98	51	KXH46771
PKS-III	1419	16865-18284	<i>Colletotrichum sublineola</i>	0	91	57	KDN65911
Transcription factor	575	20968-22828	<i>Colletotrichum orchidophilum</i>	0	97	59	OHE93445

J-1) *Huntiella decipiens* contig 155 (NETU00000155) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ1	2415	14985-17400	<i>Coniochaeta ligniaria</i>	0	99	64	OIW28934

Helicase	1681	18295-19976	<i>Scedosporium opiospermum</i>	0	86	76	XP_016640511
NR-PKS-I	6590	33774-40364	<i>Colletotrichum higginsianum</i>	0	99	58	CCF45141
THN reductase	876	42117-42993	<i>Scedosporium boydii</i>	0	100	77	ALC82365
Transcription factor	1034	51388-52422	<i>Valsa mali</i>	0	91	37	KUI58511
Transcription factor	2990	43961-46951	<i>Colletotrichum incanum</i>	0	99	47	KZ171510

J-2) *Huntia decipiens* contig 360 (NETU00000360) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Fatty acid desaturase	1471	25870- 27342	<i>Nectria haematococca</i>	0	98	58	XP_003040918
RSP	1936	27474-29410	<i>Metarhizium acridum</i>	0	99	73	XP_007814706
Transporter	1107	30249-31356	<i>Phaeoacremonium minimum</i>	0	99	69	XP_007916435
MPV-17	679	31685-32364	<i>Colletotrichum sublineola</i>	0	99	41	KDN72413
MFS	2431	33476-35907	<i>Fusarium mangiferae</i>	0	82	45	CVK91120
R-PKS-I	7315	43721-51036	<i>Trichoderma parareesei</i>	0	98	34	OTA01431
RNA polymerase	5461	64165-69629	<i>Scedosporium apiospermum</i>	0	83	42	XP_016641158
Pantothenate kinase	1508	70685-72193	<i>Neonectria ditissima</i>	0	96	74	KPM45051
ATP synthase	758	73023-73781	<i>Sordaria macrospora</i>	0	100	82	XP_003352487
NAC	758	78479-79264	<i>Oidiodendron malus</i>	0	89	71	KIN01556
60S ribosomal	688	79751-80439	<i>Trichoderma atroviride</i>	0	100	76	XP_013945638

J-3) *Huntia decipiens* contig 64 (NETU00000064) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ubiquitin enzyme	696	37383-38079	<i>Trichoderma gamsii</i>	0	96	78	XP_0186606678
Protein kinase	1657	34820-36477	<i>Verticillium longisporum</i>	0	99	60	CRK12389
Outer membrane protein	902	30950-31852	<i>Metarhizium anisopliae</i>	0	62	34	KFG86394
ABC transporter	4740	26058-30798	<i>Daldinia sp</i>	0	84	37	OTB17789
NIP SNAP family	1126	21745-22871	<i>Madurella mycetomatis</i>	0	99	67	KXX80314
Hydrolase	949	18586-19535	<i>Colletotrichum orchidophilum</i>	0	79	48	OHE99475
26S proteasome	1637	16815-18452	<i>Podospora anserina</i>	0	99	76	XP_001907151
Dehydrogenase	3713	12495-16208	<i>Diplodia corticola</i>	0	98	70	XP_020132279
Hydrolase	710	9323-10033	<i>Neonectria ditissima</i>	0	98	46	KPM39647
PKS	7877	1-7877	<i>Scedosporium apiospermum</i>	0	97	33	XP_016645426

J-4) *Huntiella decipiens* contig 360 (NETU00000360) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ankyrin repeat	4962	124741-129703	<i>Purpureocillium lilacinum</i>	0	90	39	OAQ78721
Mitochondrial carrier	1040	139781-140821	<i>Scedosporium apiospermum</i>	0	99	80	XP_016638648
Bud 22	1525	153090-154615	<i>Claviceps purpurea</i>	0	99	39	CCE30160
Oxidoreductase	1853	157067-158920	<i>Colletotrichum simmondsii</i>	0	99	53	KXH46771
PKS-III	2904	161652-164556	<i>Colletotrichum sublineola</i>	0	90	57	KDN65911
Transcription factor	575	20968-22828	<i>Colletotrichum orchidophilum</i>	0	97	59	OHE93445

K-1) *Huntiella bhutanensis* contig 56 (MJMS01000056) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ1	2415	19020-21435	<i>Valsa mali</i>	0	99	63	KUI72644
Helicase	1681	22336-24017	<i>Scedosporium opiospermum</i>	0	87	75	XP_016640511
NR-PKS-I	6590	39510-46100	<i>Colletotrichum higginsianum</i>	0	99	59	CCF45141
THN reductase	875	47857-48732	<i>Scedosporium boydii</i>	0	100	77	ALC82365
Transcription factor	2990	49712-52702	<i>Colletotrichum gloeosporioides</i>	3e-126	87	48	XP_007283600
Transcription factor	1034	57150-58184	<i>Colletotrichum incanum</i>	0	99	47	KZ171510

K-2) *Huntiella bhutanensis* contig 74 (MJMS01000074) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Fatty acid desaturase	1485	22334-23819	<i>Nectria haematococca</i>	0	98	58	XP_003040918
RSP	1936	23951-25887	<i>Fusarium graminearum</i>	0	100	66	XP_007814706
Transporter	1107	26732-27839	<i>Phaeoacremonium minimum</i>	2e-125	99	60	XP_007916435
MPV-17	679	28172-28851	<i>Colletotrichum sublineola</i>	0	99	41	KDN72413
MFS	2428	29833-32261	<i>Fusarium mangiferae</i>	5e-164	83	50	CVK91120
R-PKS-I	7315	39922-47237	<i>Fusarium euwallaceae</i>	0	98	34	ALQ32840
RNA polymerase	5450	55737-61187	<i>Scedosporium apiospermum</i>	0	73	42	XP_016641158
Pantothenate kinase	1498	62198-63696	<i>Neonectria ditissima</i>	0	96	75	KPM45051

ATP synthase	775	70020-70795	<i>Sordaria macrospora</i>	0	100	82	XP_003352487
NAC	693	71270-71963	<i>Oidiodendron malus</i>	0	89	71	KIN01556
60S ribosomal	777	73057-73852	<i>Trichoderma atroviride</i>	3e-72	100	75	XP_013945638

K-3) *Huntiella bhutanensis* contig 45 (MJMS01000045) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ubiquitin enzyme	669	37726-38395	<i>Hypoxylon</i> Sp.	0	96	79	OTA68503
Protein kinase	1657	35160-36817	<i>Verticillium longisporum</i>	0	99	59	CRK12389
ABC transporter	4740	26218-30958	<i>Daldinia</i> sp	0	83	37	OTB17789
NIP SNAP family	1126	21925-23051	<i>Acremonium chrysogenum</i>	1e-163	99	64	KFH42184
Hydrolase	803	18796-19599	<i>Colletotrichum orchidophilum</i>	0	79	48	OHE99475
26S proteosome	1637	17025-18662	<i>Podospora anserina</i>	0	97	76	XP_001907151
Dehydrogenase	3713	12705-16418	<i>Diplodia corticola</i>	0	98	70	XP_020132279
Hydrolase	710	9535-10245	<i>Neonectria ditissima</i>	0	98	46	KPM39647
PKS	7532	571-8103	<i>Neonectria ditissima</i>	0	97	45	KPM39648

K-4) *Huntiella bhutanensis* contig 25 (MJMS01000025) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Mitochondrial carrier	911	193271-194182	<i>Diaporthe ampelina</i>	0	98	79	KKY35686
Hypothetical	1552	189190-190742	<i>Colletotrichum orbiculare</i>	0	93	36	ENH_80387
Methyl transferase	1058	184564-185622	<i>Scedosporium apiospermum</i>	0	100	39	XP_016638640
Ankyrin repeat	4850	179434-184284	<i>Trichoderma atroviride</i>	0	87	39	XP_013942342
Mitochondrial carrier	1460	176117-177577	<i>Scedosporium apiospermum</i>	0	99	82	XP_016638648
Bud 22	1549	174290-175839	<i>Metarhizium brunneum</i>	9e-77	99	39	XP_014547323
Oxidoreductase	971	171831-172802	<i>Colletotrichum simmondsii</i>	0	98	51	KXH46771
PKS-III	2965	168816-171781	<i>Neonectria ditissima</i>	2e-162	51	62	KPM42895
Bfr2	1826	164133-165959	<i>Phaeoacremonium minimum</i>	2e-142	99	49	XP_007913055
Transcription factor	584	163279-163863	<i>Hypoxylon</i> Sp.	3e-70	97	55	OTA56277

L-1) *Huntiella moniliformis* contig 67 (JMSH01000067) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number
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							of top blast hit
Fatty acid desaturase	1481	115908-117389	<i>Nectria haematococca</i>	0	98	58	XP_003040918
RSP	1937	113854-115791	<i>Metarhizium acridum</i>	0	100	65	XP_007814706
Transporter	1116	111899-113015	<i>Phaeoacremonium minimum</i>	5e-157	99	69	XP_007916435
MPV-17	679	110798-111477	<i>Colletotrichum sublineola</i>	0	99	41	KDN72413
MFS	2426	107415-109841	<i>Fusarium mangiferae</i>	3e-139	82	45	CVK91120
R-PKS-I	7318	92100-99418	<i>Fusarium poae</i>	0	99	33	ALQ32896
RNA polymerase	4348	86993-91341	<i>Scedosporium apiospermum</i>	0	89	42	XP_016641158
Pantothenate kinase	1495	83396-84891	<i>Neonectria ditissima</i>	0	96	74	KPM45051
ATP synthase	928	76144-77072	<i>Sordaria macrospora</i>	0	100	82	XP_003352487
NAC	702	74931-75633	<i>Oidiodendron malus</i>	7e-67	89	71	KIN01556
60S ribosomal	793	73026-73819	<i>Trichoderma atroviride</i>	2e-73	100	76	XP_013945638

L-2) *Huntiella moniliformis* contig 157 (JMSH01000157) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
ABC transporter	4741	25707-30448	<i>Daldinia sp</i>	0	84	37	OTB17789
NIP SNAP family	1126	21431-22557	<i>Madurella mycetomatis</i>	1e-166	99	67	KXX80314
Hydrolase	947	18292-19239	<i>Colletotrichum orchidophilum</i>	0	79	48	OHE99475
26Sproteosome	1631	16515-18146	<i>Podospora anserina</i>	0	99	76	XP_001907151
Dehydrogenase	3713	12194-15907	<i>Diplodia corticola</i>	0	98	70	XP_020132279
Hydrolase	715	9028-9743	<i>Neonectria ditissima</i>	0	98	46	KPM39647
PKS	6903	1-6903	<i>Neonectria ditissima</i>	0	97	33	KPM39648

L-3) *Huntiella moniliformis* contig 3 (JMSH01000003) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Mitochondrial carrier	914	118207-119121	<i>Diaporthe ampelina</i>	5e-173	98	79	KKY35686
Hypothetical	1572	114089-115661	<i>Colletotrichum orbiculare</i>	0	93	36	ENH_80387
Methyl transferase	1062	109409-110471	<i>Scedosporium apiospermum</i>	1e-83	100	39	XP_016638640
Ankyrin repeat	4814	104328-109142	<i>Purpureocillium lilacinum</i>	0	88	39	OAQ78721
Mitochondrial carrier	1364	101003-102467	<i>Scedosporium apiospermum</i>	0	99	75	XP_016638648

Bud 22	1547	99182-100729	<i>Claviceps purpurea</i>	8e-184	99	39	CCE30160
Oxidoreductase	1286	96871-98157	<i>Colletotrichum simmondsii</i>	2e-132	98	51	KXH46771
PKS-III	1745	94841-96586	<i>Colletotrichum sublineola</i>	0	99	57	KDN65911
Transcription factor	1839	90393-92232	<i>Gaeumannomyces tritici</i>	5e-144	98	48	XP_009217207

M-1) *Huntia omanensis* contig 6319 (JSUI01006319) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
BZZ1	2415	10758-13173	<i>Verticillium longisporum</i>	0	99	66	CRK20861
Helicase	1681	14084-15765	<i>Scedosporium opiospermum</i>	0	87	75	XP_016640511
NR-PKS-I	6590	31011-37601	<i>Colletotrichum higginsianum</i>	0	99	59	CCF45141
THN reductase	875	37900-38775	<i>Scedosporium boydii</i>	0	100	77	ALC82365
Transcription factor	1469	39025-40494	<i>Valsa mali</i>	0	91	37	KUI58511
Transcription factor	3400	41562-44962	<i>Colletotrichum incanum</i>	0	99	47	KZ171510

M-2) *Huntia omanensis* contig 6417 (JSUI01006417) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Fatty acid desaturase	1471	1013-2493	<i>Nectria haematococca</i>	0	98	59	XP_003040918
RSP	1936	2625-4561	<i>Fusarium graminearum</i>	0	100	65	EYB28542
Transporter	1107	5405-6512	<i>Phaeoacremonium minimum</i>	8e-157	99	68	XP_007916435
MPV-17	679	6843-7522	<i>Colletotrichum sublineola</i>	2e-53	99	41	KDN72413
MFS	2431	8577-10076	<i>Fusarium mangiferae</i>	0	82	45	CVK91120
R-PKS-I	7315	22323-29640	<i>Purpureocillium lilacinum</i>	0	99	33	XP_018182849
RNA polymerase	5461	34245-38533	<i>Verticillium dahliae</i>	0	85	38	XP_009651476
Pantothenate kinase	1508	40803-42289	<i>Neonectria ditissima</i>	0	96	71	KPM45051
ATP synthase	758	48697-49504	<i>Sordaria macrospora</i>	0	100	83	XP_003352487
NAC	758	49966-50655	<i>Oidiodendron malus</i>	0	89	71	KIN01556
60S ribosomal	688	51760-52551	<i>Trichoderma atroviride</i>	0	100	76	XP_013945638

M-3) *Huntia omanensis* contig 6287 (JSUI01006287) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Outer membrane protein	851	1352-2203	<i>Scedosporium apiospermum</i>	4e-12	39	34	KFG86394

ABC transporter	4740	3240-7980	<i>Colletotrichum incanum</i>	0	84	34	OTB17789
NIP SNAP family	1126	11165-12291	<i>Colletotrichum orbiculare</i>	6e-165	99	64	ENH85583
Hydrolase	964	14497-15461	<i>Colletotrichum orchidophilum</i>	7e-73	82	44	OHE99475
26S proteosome	1842	15591-17433	<i>Podospora anserina</i>	0	97	70	XP_001907151
Dehydrogenase	3713	18040-21753	<i>Diplodia corticola</i>	0	98	70	XP_020132279
Hydrolase	710	24880-25590	<i>Neonectria ditissima</i>	0	98	46	KPM39647
PKS	7324	27036-34360	<i>Scedosporium apiospermum</i>	0	97	33	XP_016645426

M-4) *Huntia omanensis* contig 6053 (JSUI01006053) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Methyl transferase	701	17031-17732	<i>Scedosporium apiospermum</i>	1e-39	100	33	XP_016638640
Ankyrin repeat	4847	11904-16751	<i>Purpureocillium lilacinum</i>	0	87	39	OAQ78721
Mitochondrial carrier	1458	8210-9668	<i>Scedosporium apiospermum</i>	0	99	82	XP_016638648
Bud 22	1540	6383-7923	<i>Claviceps purpurea</i>	2e-78	99	38	CCE30160
Oxidoreductase	971	4548-5519	<i>Colletotrichum sublineola</i>	2e-96	100	50	KDN65921
PKS-III	1784	1598-3382	<i>Neonectria ditissima</i>	0	85	64	KPM42895

N-1) *Endoconidiophora polonica* contig 105 (LXKZ01000105) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number
Transcription factor	3054	67079-70282	<i>Colletotrichum salicis</i>	0	57	36	KXH54388
SET dom	588	71093-71680	<i>Hypoxyton</i>	0	97	55	OTA56277
Bfr-Z	1740	72286-74173	<i>Phaeoacremonium minimum</i>	0	99	49	XP_007913055
Hypo	522	74303-74824	<i>Colletotrichum orbiculare</i>	0	93	36	ENH_80387
PKS III	1281	76583-77995	<i>Sporothrix schenkii</i>	0	94	61	XP_016585873
Oxidoreductase	684	78437-79120	<i>Diaporthe helianthi</i>	0	92	61	OCW34331
Budzz	1515	79819-81402	<i>Nectria haematococca</i>	0	99	42	XP_003052505
Mitochondrial carrier	915	81875-83383	<i>Scedosporium apiospermum</i>	0	99	82	XP_016638648
Ankjrjn repeat	4839	84758-89596	<i>Stachybotrys chlorohalonata</i>	0	87	36	KFA68228

N-2) *Endoconidiophora polonica* contig 94 (LXKZ0100094) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
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Hydrolase	1013	80135-81148	<i>Scedosporium apiospermum</i>	0	75	53	XP_016639200
PCI domain containing protein	1662	78272-79934	<i>Stachybotrys chartarum</i>	0	97	79	KEY68004
Dehydrogenase	3804	73653-77457	<i>Diplodia corticola</i>	0	98	70	XP_020132279
Ribosomal protein	527	72697-73224	<i>Metarhizium album</i>	0	100	84	KHN99845
Hypothetical	554	71840-72394	<i>Numida meleagris</i>	0	53	22	XP_021239164
Hydrolase	773	68355-69128	<i>Madurella mycetomatis</i>	0	98	53	KXX79713
R-PKS-I	8064	57861-65925	<i>Ophiocordyceps sinensis</i>	0	99	35	EQL00980
Acetylglutamate kinase	2888	50574-53462	<i>Colletotrichum orbiculare</i>	0	98	68	ENH86021
Hypothetical	2927	46698-49625	<i>Fusarium langsethiae</i>	0	90	38	KPA42181
Dehydrogenase	1142	40180-41322	<i>Hypoxylon sp.</i>	0	97	57	OTA95510
Hydrolase	1788	36258-38046	<i>Verticillium longisporum</i>	0	98	53	CRK01929

N-3) *Endoconidiophora polonica* contig 94 (LXKZ0100094) R-PKS-I cluster, Clade D

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
R-PKS-I	8164	139349-147495	<i>Hirsutella minnesotensis</i>	0	99	45	KJZ77319
NUP54	1139	131863-132996	<i>Scedosporium apiospermum</i>	0	84	72	XP_016639210
Oxidoreductase	1023	129732-130755	<i>Neonectria ditissima</i>	0	97	69	KPM41977
Dehydrogenase	1771	123770-125542	<i>Fusarium proliferatum</i>	0	92	61	CVK91789
Co-A transferase	2447	119794-122242	<i>Neonectria ditissima</i>	0	97	61	KMP35363
Dehydrogenase	1223	115685-116927	<i>Nectria haematococca</i>	0	87	60	XP_003040638

N-4) *Endoconidiophora polonica* contig 174 (LXKZ0100174), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5482	95160-100643	<i>Sordaria macrospora</i>	0	53	43	XP_003348394
Major facilitator protein	2275	91475-93950	<i>Nectria haematococca</i>	0	87	51	XP_003052564
R-PKS-I	7706	74444-82151	<i>Neonectria ditissima</i>	0	98	36	KPM39192
ATPase	7548	64459-72014	<i>Colletotrichum orchidophilum</i>	0	96	43	OHE96608
Hypothetical	684	61296-61980	<i>Verticillium dahliae</i>	2e-175	63	50	XP_009656188
Hypothetical	914	58973-59887	<i>Fusarium graminearum</i>	1e-21	100	36	XP_011319935
Hydrolase	1972	52566-54545	<i>Purpureocillium lilacinum</i>	3e-106	76	43	OAQ86162

N-5) *Endoconidiophora polonica* contig 149 (LXKZ01000149) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
PKS	6648	122938-129622	<i>Scedosporium apiospermum</i>	0	99	68	XP_016640516
Helicase	1564	97258-98822	<i>Scedosporium apiospermum</i>	0	96	76	XP_016640511
BZZ-1	2451	93900-96351	<i>Colletotrichum gloeosporioides</i>	0	100	67	EQB45423

O-1) *Endoconidiophora laricicola* contig 29 (LXGT01000029) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number
Transcription factor	3370	51175-54545	<i>Colletotrichum gloeosporioides</i>	1e-82	57	36	XP_007286061
SET dom	587	49967-50554	<i>Hypoxylon</i>	6e-72	97	54	OTA56277
Bfr-2	1886	47448-49334	<i>Phaeoacremonium minimum</i>	0	99	49	XP_007913055
Hypo	533	46785-47318	<i>Colletotrichum orbiculare</i>	0	93	36	ENH_80387
PKS III	1412	43656-45068	<i>Sporothrix schenkii</i>	0	94	61	XP_016585873
Oxidoreductase	683	42531-43214	<i>Diaporthe helianthi</i>	0	92	61	OCW34331
Bud22	1583	40255-41838	<i>Colletotrichum salicis</i>	9e-89	99	38	KXH59727
Mitochondrial carrier	1510	38271-39781	<i>Scedosporium apiospermum</i>	0	99	78	XP_016638648
Ankyrin repeat	4553	32066-36919	<i>Stachybotrys chlorohalonata</i>	0	86	36	KFA68228

O-2) *Endoconidiophora laricicola* contig 85 (LXGT01000085) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydrolase	1022	16338-17360	<i>Scedosporium apiospermum</i>	0	75	53	XP_016639200
PCI domain containing protein	1662	17561-19223	<i>Colletotrichum salicis</i>	0	99	72	KXH50315
Dehydrogenase	3804	20027-23831	<i>Diplodia corticola</i>	0	98	70	XP_020132279
Ribosomal protein	533	24262-24795	<i>Metarhizium album</i>	0	100	84	KHN99845
Hypothetical	554	25103-25657	<i>Numida meleagris</i>	6e-132	53	22	XP_021239164
Hydrolase	1191	27983-29174	<i>Madurella mycetomatis</i>	6e-67	98	53	KXX79713
R-PKS-I	8076	31583-39659	<i>Ophiocordyceps sinensis</i>	0	99	35	EQL00980
Acetylglutamate kinase	2888	44066-46954	<i>Colletotrichum orbiculare</i>	0	98	68	ENH86021

Hypothetical	2927	47904-50831	<i>Fusarium langsethiae</i>	0	90	38	KPA42181
Dehydrogenase	1142	56217-57359	<i>Hypoxyton sp.</i>	0	97	57	OTA95510
Hydrolase	1889	59540-61429	<i>Verticillium longisporum</i>	0	98	53	CRK01929

O-3) *Endoconidiophora laricicola* contig 269 (LXGT01000269), R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5489	104160-109649	<i>Sordaria macrospora</i>	0	53	43	XP_003348394
Major facilitator protein	2275	101375-102950	<i>Nectria haematococca</i>	0	87	51	XP_003052564
R-PKS-I	7706	85443-93150	<i>Neonectria ditissima</i>	0	98	36	KPM39192
ATPase	7547	74459-82006	<i>Colletotrichum orchidophilum</i>	0	96	43	OHE96608
Hypothetical	685	71285-71970	<i>Verticillium dahliae</i>	1e-20	63	51	XP_009656188
Hypothetical	914	68973-69887	<i>Fusarium graminearum</i>	1e-21	100	36	XP_011319935
Hydrolase	1977	62547-64524	<i>Purpureocillium lilacinum</i>	3e-106	76	43	OAQ86162

O-4) *Endoconidiophora laricicola* contig 11 (LXGT01000011) R-PKS-I cluster, Clade D

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
R-PKS-I	8164	156966-165130	<i>Hirsutella minnesotensis</i>	0	99	45	KJZ77319
NUP54	1139	171476-172615	<i>Scedosporium apiospermum</i>	0	84	72	XP_016639210
Oxidoreductase	1023	173724-174747	<i>Neonectria ditissima</i>	0	97	69	KPM41977
Dehydrogenase	1771	178890-180661	<i>Fusarium proliferatum</i>	0	92	61	CVK91789
Co-A transferase	2447	182126-184573	<i>Neonectria ditissima</i>	0	97	61	KMP35363
Dehydrogenase	1223	184802-186025	<i>Nectria haematococca</i>	0	87	60	XP_003040638

O-5) *Endoconidiophora laricicola* contig 40 (LXGT01000040) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
PKS	6648	551-7254	<i>Scedosporium apiospermum</i>	0	99	68	XP_016640516

Helicase	1564	31618-33183	<i>Scedosporium apiospermum</i>	0	96	76	XP_016640511
BZZ-1	2451	34098-36549	<i>Colletotrichum gloeosporioides</i>	0	100	67	EQB45423

P-1) *Davidsoniella virescens* contig 178 (LJZU010000178) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydrolase	1017	19067-20084	<i>Scedosporium apiospermum</i>	0	95	47	XP_016639200
Dehydrogenase	3806	22758-26564	<i>Diplodia corticola</i>	0	98	70	XP_020132279
PKS	8050	38540-46590	<i>Neonectria ditissima</i>	0	99	38	KPM39648
Cytochrome P-450	1390	47496-48886	<i>Sporothrix brasiliensis</i>	0	40	38	KIH89700

P-2) *D. virescens* contig 150 (LJZU010000150) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transcription factor	3202	88741-90976	<i>Pochinia chlamydosporia</i>	0	56	31	XP_018149805
Methyl transferase	515	88093-88608	<i>Scedosporium apiospermum</i>	0	80	45	XP_016638640
PKS-III	1425	84736-86161	<i>Stachybotrys chlorohalonata</i>	0	97	62	KFA65321
Bud22	1576	8178783363	<i>Nectria haematococca</i>	0	99	42	XP_003052505
Mitochondrial carrier	1450	79856-81306	<i>Scedosporium apiospermum</i>	0	98	78	XP_016638648
Ankyrin repeat protein	4910	73207-78117	<i>Stachybotrys chlorohalonata</i>	0	88	33	KFA68228

P-3) *D. virescens* contig 126 (LJZU010000126) R-PKS-I cluster, Clade C

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Mitochondrial carrier	1260	100279-101539	<i>Aschersonia aleyrodis</i>	0	97	69	KZZ96742
Transcription factor	3183	103264-106447	<i>Metarhizium rileyi</i>	0	92	56	OAA47735
Hydroxylase	803	119543-120346	<i>Metarhizium anisopliae</i>	0	100	85	KJK80232
PKS	1972	122702-124674	<i>Hirsutella minnesotensis</i>	0	99	42	KJZ77319
GTP binding protein	8029	128631-136660	<i>Colletotrichum orbiculare</i>	0	99	77	ENH80466
Dehydrogenase	2144	142955-145099	<i>Nectria haematococca</i>	0	94	61	XP_003045936
Protein kinase	1206	145989-147195	<i>Colletotrichum chlorophyti</i>	0	89	54	OLN88104

P-4) *D. virescens* contig 35 (LJZU010000035) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Histidine kinase	5476	92106-97582	<i>Sordaria macrospora</i>	0	53	43	XP_003348394
Major facilitator protein	2211	88600-90880	<i>Fusarium oxysporum</i>	0	87	51	ENH62002
R-PKS-I	7702	71853-79559	<i>Neonectria ditissima</i>	0	98	36	KPM39192
ATPase	7547	60663-69414	<i>Colletotrichum orchidophilum</i>	0	95	43	OHE96608
Hypothetical	685	58691-59376	<i>Verticillium dahliae</i>	0	72	53	XP_009656188
Hypothetical	914	56367-57281	<i>Neonectria ditissima</i>	0	100	39	KPM39715
Hydrolase	1977	49920-50897	<i>Purpureocillium lilacinum</i>	0	76	44	OAQ86162

P-5) *D. virescens* contig 44 (LJZU010000044) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transcription factor	3554	107544-111098	<i>Colletotrichum incanum</i>	0	99	53	KZL71510
Hypothetical	1121	111719-112840	<i>Colletotrichum gloeosporioides</i>	0	63	55	EQB49816
Tetra hydroxy naphthalene reductase	833	122067-122900	<i>Scedosporium boydii</i>	0	97	76	ALC82365
Transcription factor	1323	123447-124770	<i>Colletotrichum gloeosporioides</i>	0	83	29	EQB49815
PKS	6691	130554-137245	<i>Scedosporium apiospermum</i>	0	99	68	XP_016640516
Helicase	1935	160315-162250	<i>Scedosporium apiospermum</i>	0	96	76	XP_016640511
BZZ-1	2054	166814-168868	<i>Colletotrichum higginsianum</i>	0	100	65	XP_018155929

Q-1) *Thielaviopsis punctulata* contig 214 (LAEV01000214) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydrolase	1109	110366-111475	<i>Colletotrichum incanum</i>	0	94	49	KZL86035
ATPase	870	118637-119507	<i>Colletotrichum higginsianum</i>	0	78	85	XP_018154267
Oxidoreductase	539	128065-128604	<i>Gaeumannomyces tritici</i>	0	98	74	XP_009227616
Mitochondrial carrier	931	129572-130503	<i>Nectria haematococca</i>	0	98	60	XP_003053161
PKS	7380	133076-140457	<i>Fusarium commune</i>	0	99	35	ALQ32804
Major facilitator protein	2086	152696-154782	<i>Trichoderma virens</i>	0	96	48	XP_013951147
Histidine kinase	4751	156458-161209	<i>Sordaria macrospora</i>	0	60	44	XP_003348394

Q-2) *Thielaviopsis punctulata* contig 1486 (LAEV01001486) R-PKS-I cluster, Clade B

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NAC	778	120126-120886	<i>Hypoxyton</i> Sp.	6e-76	100	69	OTA75457
60S ribosomal	636	122056-122690	<i>Trichoderma virens</i>	1e-71	100	73	XP_013951194
ATPase	4038	124846-127676	<i>Colletotrichum higginsianum</i>	0	78	85	XP_018154267
Oxidoreductase	518	128065-128604	<i>Gaeumannomyces tritici</i>	2e-42	98	73	XP_009227616
Mitochondrial carrier	1014	129572-130503	<i>Nectria haematococca</i>	2e-61	97	61	XP_003053161
PKS	7396	133076-140457	<i>Hirsutella minnesotensis</i>	0	99	35	KJZ75926
Major facilitator protein	2084	152696-154782	<i>Fusarium proliferatum</i>	0	97	48	CZR42444
Histidine kinase	4832	156458-161209	<i>Sordaria macrospora</i>	0	62	43	XP_003348394
MPV-17	798	173033-173831	<i>Daldinia</i> Sp.	1e-58	100	43	OTB10979
Transporter	2441	174339-175472	<i>Verticillium longisporum</i>	0	99	61	CRK27104
RSP	2032	176614-178628	<i>Metarhizium acridum</i>	0	100	71	XP_007814706
Fatty acid desaturase	1754	178748-180281	<i>Acremonium chrysogenum</i>	0	99	61	KFH40550

Q-3) *T. punctulata* contig 1437 (LAEV01001437) R-PKS-I cluster, Clade D

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Co-A transferase	1887	4611-6498	<i>Neonectria ditissima</i>	0	100	60	KMP35363
Dehydrogenase	1829	6629-8458	<i>Fusarium proliferatum</i>	0	86	58	CZR42660
Oxidoreductase	821	10785-11606	<i>Cordyceps brongniartii</i>	0	97	69	KPM41977
NUP54	1179	12391-13570	<i>Scedosporium apiospermum</i>	0	75	73	XP_016639210
R-PKS-I	8029	17150-25179	<i>Hirsutella minnesotensis</i>	0	99	45	KJZ77319
Acetyl transferase	1694	25655-27349	<i>Grosmannia clavigera</i>	0	89	36	XP_014174978
Dehydrogenase	3245	32035-35280	<i>Scedosporium apiospermum</i>	0	99	67	XP_016639211

Q-4) *T. punctulata* contig 372 (LAEV01000372) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transcription factor	581	3633-4214	<i>Colletotrichum graminicola</i>	0	99	60	XP_008099484

Bfr-2	1925	4489-6414	<i>Madurella mycetomatis</i>	0	100	50	KXX75334
PKS-III	1434	8190-9624	<i>Stachybotrys chlorohalonata</i>	0	99	58	KFA65321
Oxidoreductase	1290	10045-11329	<i>Colletotrichum simmondsii</i>	0	98	55	KXH46771
Bud22	1542	11381-12369	<i>Colletotrichum salicis</i>	0	99	40	KXH59727
Mitochondrial carrier	1412	12396-14150	<i>Scedosporium apiospermum</i>	0	99	82	XP_016638648
Ankyrin repeat protein	5045	14415-15826	<i>Stachybotrys chlorohalonata</i>	0	84	49	KFA68228
Methyl transferase	1488	18915-23903	<i>Scedosporium apiospermum</i>	0	80	46	XP_016638640
Mitochondrial carrier	1017	24364-25371	<i>Hirsutella minnesotensis</i>	0	94	83	KJZ71631
Ribonuclease	3922	25874-26775	<i>Hirsutella minnesotensis</i>	0	63	60	KJZ76270

Q-5) *T. punctulata* contig 301 (LAEV01000301) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transcription factor	3300	53100-56400	<i>Colletotrichum lagenaria</i>	0	99	51	BAA75888
THN reductase	875	52123-52998	<i>Scedosporium boydii</i>	0	100	77	ALC82365
Transcription factor	1469	49913-51382	<i>Magnaporthe oryzae</i>	0	85	32	XP_003715433
NR-PKS-I	6650	37063-43713	<i>Scedosporium boydii</i>	0	99	67	AHA15770
Helicase	1543	21779-23322	<i>Scedosporium apiospermum</i>	0	96	75	XP_016640511
BZZ-1	2442	18018-20460	<i>Thielavia terrestris</i>	0	100	63	XP_003648771

R-1) *Thielaviopsis musarum* contig 214 (LKBB01000214) R-PKS-I cluster, Clade A

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NAC	778	143477-144255	<i>Hypoxyylon Sp.</i>	6e-76	100	69	OTA75457
60S ribosomal	636	141680-142316	<i>Trichoderma virens</i>	1e-71	100	73	XP_013951194
ATPase	4038	136463-140501	<i>Colletotrichum higginsianum</i>	0	78	85	XP_018154267
Oxidoreductase	518	135682-136200	<i>Gaeumannomyces tritici</i>	2e-42	98	73	XP_009227616
Mitochondrial carrier	1014	133749-134763	<i>Nectria haematococca</i>	2e-61	97	61	XP_003053161
PKS	7396	124701-132097	<i>Hirsutella minnesotensis</i>	0	99	35	KJZ75926
Major facilitator protein	2084	110408-112492	<i>Fusarium proliferatum</i>	0	97	48	CZR42444
Histidine kinase	4832	103948-108780	<i>Sordaria macrospora</i>	0	62	43	XP_003348394
Transporter	2441	90762-93203	<i>Verticillium longisporum</i>	0	99	61	CRK27104
RSP	2032	87554-89586	<i>Metarhizium acridum</i>	0	100	71	XP_007814706
Fatty acid desaturase	1754	85263-87017	<i>Acremonium chrysogenum</i>	0	99	61	KFH40550

R-2) *T. musarum* contig 112 (LKBB01000112) R-PKS-I cluster, Clade D

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Co-A transferase	1887	71658-73545	<i>Neonectria ditissima</i>	0	100	60	KMP35363
Dehydrogenase	1829	69698-71527	<i>Fusarium proliferatum</i>	0	86	58	CZR42660
Oxidoreductase	821	66627-67448	<i>Cordyceps brongniartii</i>	0	97	69	KPM41977
NUP54	1179	64663-65842	<i>Scedosporium apiospermum</i>	0	75	73	XP_016639210
R-PKS-I	8014	53054-61083	<i>Hirsutella minnesotensis</i>	0	99	45	KJZ77319
Acetyl transferase	1694	50884-52578	<i>Grosmannia clavigera</i>	0	89	36	XP_014174978
Dehydrogenase	3245	43430-46675	<i>Scedosporium apiospermum</i>	0	99	67	XP_016639211

R-3) *T. musarum* contig 144 (LKBB01000144) PKS-III cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transcription factor	578	18641-19219	<i>Colletotrichum graminicola</i>	0	99	60	XP_008099484
Bfr-2	1930	19635-21565	<i>Gaeumannomyces tritici</i>	0	99	48	XP_009217207
PKS-III	1436	23837-25273	<i>Stachybotrys chlorohalonata</i>	0	99	58	KFA65321
Oxidoreductase	1290	25875-27165	<i>Colletotrichum simmondsii</i>	0	98	55	KXH46771
Bud22	1542	27713-29255	<i>Colletotrichum salicis</i>	0	99	40	KXH59727
Mitochondrial carrier	1412	29552-30964	<i>Scedosporium apiospermum</i>	0	99	82	XP_016638648
Ankyrin repeat protein	5045	33475-38520	<i>Stachybotrys chlorohalonata</i>	0	84	49	KFA68228
Methyl transferase	1488	39060-40548	<i>Scedosporium apiospermum</i>	0	80	46	XP_016638640
Mitochondrial carrier	1017	48235-49252	<i>Hirsutella minnesotensis</i>	0	94	83	KJZ71631
Ribonuclease	3922	49739-53661	<i>Hirsutella minnesotensis</i>	0	63	60	KJZ76270

R-4) *T. musarum* contig 5 (LKBB01000005) NR-PKS-I cluster

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transcription factor	3135	131850-134985	<i>Colletotrichum lagenaria</i>	0	99	51	BAA75888
THN reductase	901	137596-138497	<i>Scedosporium boydii</i>	0	100	77	ALC82365
Transcription factor	1386	138845-140231	<i>Magnaporthe oryzae</i>	0	85	32	XP_003715433
NR-PKS-I	6643	143489-150132	<i>Scedosporium boydii</i>	0	99	67	AHA15770
Helicase	1574	165223-166797	<i>Scedosporium apiospermum</i>	0	96	75	XP_016640511

BZZ-1	2497	167963-170460	<i>Thielavia terrestris</i>	0	100	64	XP_003648771
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