

Supplementary materials for

# Whole-genome sequence analysis of an endophytic fungus *Alternaria* sp. SPS-2 and its biosynthetic potential of bioactive secondary metabolites

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Table S1. Genome assembly integrity assessment for strain SPS-2.

Property	Number	Percentage (%)
Complete BUSCO	276	95.2
Missing genes	10	3.4
Total BUSCO group searched	290	100

Table S2. CAZyme profiles of strain SPS-2 and other twelve *Alternaria* strains deposited in CAZyme database.

Strain	CAZy family					PL	Total
	GH	CBM	CE	AA	GT		
<i>Alternaria solani</i>	249	46	36	80	107	20	538
<i>A. longipes</i>	273	45	37	85	111	25	576
<i>A. fragariae</i>	265	48	37	86	109	23	568
<i>A. destruens</i>	316	48	36	84	125	26	635
<i>A. dauci</i>	252	40	37	97	111	22	559
<i>A. cassiae</i>	240	42	34	83	104	22	525
<i>A. carthami</i>	255	39	40	83	110	22	549
<i>A. brassicicola</i> abra43	231	38	32	60	103	20	484
<i>A. brassicae</i> J3	241	38	33	71	104	21	508
<i>A. alternata</i> PN1	260	41	35	80	103	23	542
<i>A. alternata</i> PN1	261	48	36	77	107	21	550
<i>A. alternata</i> ATCC34957	264	53	37	87	109	21	622
SPS-2	257	15	118	146	83	25	644

Table S3. The number and type of secondary metabolite BGCs in strain SPS-2 and other selective *Alternaria* strains deposited in NCBI database.

BGC Type	Strain									
	MG1	BMP0032	M3908	M3903	S3601	BMP2799	Ai002NY15	BMP2768	BMP2772	SPS-2
PKS	7	11	8	8	8	11	11	8	10	7
NRPS/NRPS-like	11	8	10	11	10	8	8	9	8	10
Fungal-RiPP	-	1	1	1	-	-	1	1	1	1
NRPS, PKS	1	1	3	2	3	2	2	-	2	0
Terpene	4	3	5	4	3	3	3	3	4	4

Table S4. Secondary metabolite BGCs of strain SPS-2 by antiSMASH analysis.

Gene cluster	Type	Gene cluster position	predicted product (similarity)
Region 1.1	NRPS	3405290-3461377	Unknown
Region 2.1	Terpene	1004114-1024548	Unknown
Region 3.1	T3PKS	985697-1026775	Unknown
Region 4.1	Terpene	388980-408695	Squalestatin S1 (40%)
Region 4.2	Terpene	2345955-2367289	Unknown
Region 5.1	T1PKS	1087051-1131054	Oxazolepoxidomycin A (13%)
Region 5.2	T1PKS	2115332-2162885	Abscisic acid (50%)
Region 6.1	T1PKS	252626-300167	Equisetin (18%)
Region 7.1	Fungal-RiPP	280898-318613	Unknown
Region 7.2	NRPS	1415890-1477928	Cyclic hydrophobic tetrapeptide (100%)
Region 8.1	T1PKS	160848-205614	Melanin (100%)
Region 8.2	T1PKS	918158-961487	1,3,6,8-tetrahydroxynaphthalene (100%)
Region 8.3	NRPS	1667861-1723346	Unknown
Region 9.1	NRPS, indole	74519-134677	Unknown
Region 9.2	Terpene	1083778-1105346	Unknown
Region 9.3	NRPS-like	1628313-1671303	Unknown
Region 11.1	NRPS	383909-428735	Equisetin (45%)
Region 12.1	NRPS-like	821562-865410	Unknown
Region 17.1	NRPS-like	305087-348950	Unknown
Region 19.1	NRPS	260997-319962	Dimethylcoprogen (100%)
Region 21.1	NRPS-like	36305-79148	Unknown
Region 21.2	T1PKS	174713-214266	Betaenone (62%)

Table S5. BGC component for equisetin in strain SPS-2.

Gene location	Description	MIBiG cluster	Identity	Coverage
ctg11_494	equisetin synthetase	BGC0001255	55%	100.4%
ctg11_495	equisetin synthetase	BGC0001255	76%	93.6%
ctg11_496	equisetin synthetase	BGC0001255	56%	101.0%
ctg11_497	equisetin synthetase	BGC0001255	65%	100.5%
ctg11_498	equisetin synthetase	BGC0001255	65%	100.0%
ctg11_500	equisetin synthetase	BGC0001255	89%	99.1%
ctg11_501	equisetin synthetase	BGC0001255	78%	98.6%
ctg11_502	hypothetical protein	BGC0001255	55%	69.9%
ctg11_505	equisetin enoylreductase	BGC0001255	70%	100.0%
ctg11_508	C6_transcription_factor	BGC0001738	21%	109.6%
ctg11_512	putative fungal transcription factor	BGC0001255	60%	99.7%
ctg11_513	putative fungal transcription factor	BGC0001255	47%	39.5%
ctg11_515	putative MFS transporter	BGC0001255	81%	81.7%

Table S6. BGC component for betaenones in strain SPS-2.

Gene location	Description	MIBiG cluster	Identity	Coverage
ctg21_238	putative FAD binding domain protein	BGC0001280	78%	97.8%
ctg21_239	putative FAD binding domain protein	BGC0001280	76%	62.8%
ctg21_242	short-chain dehydrogenase	BGC0001280	85%	87.1%
ctg21_243	P450_monooxygenase	BGC0000818	36%	99.0%
ctg21_244	zinc-binding dehydrogenase family protein	BGC0001280	87%	100.0%
ctg21_246	cytochrome_P450	BGC0001280	90%	79.6%
ctg21_248	polyketide synthase	BGC0001280	88%	81.1%
ctg21_249	polyketide synthase	BGC0001280	81%	98.7%
ctg21_250	polyketide synthase	BGC0001280	85%	99.7%
ctg21_251	MFS transporter, putative	BGC0001280	52%	79.5%

Table S7. BGC component for alternariol in strain SPS-2.

Gene location	Description	MIBiG cluster	Identity	Coverage
ctg8_1212	PtaR3	BGC0000121	26%	73.3%
ctg8_1214	monooxygenase, FAD binding domain cpaO	BGC0001563	36%	85.4%
ctg8_1218	o-methyltransferase B	BGC0000004	40%	73.5%
ctg8_1221	polyketide synthase	BGC0001284	85%	100.0%
ctg8_1222	polyketide synthase	BGC0001284	68%	90.4%
ctg8_1223	polyketide synthase	BGC0001284	85%	98.9%
ctg8_1224	polyketide synthase	BGC0001284	84%	96.3%



Table S8. BGC component for dimethylcoprogen in strain SPS-2.

Gene location	Description	MIBiG cluster	Identity	Coverage
ctg19_345	Bcaba1	BGC00001893	41%	88.3%
ctg19_355	nonribosomal_peptide_synthetase_6	BGC0001249	98%	99.8%
ctg19_363	SirA	BGC0001044	36%	96.4%
ctg19_364	multidrug resistance protein	BGC0000337	26%	85.8%
ctg19_365	lysine N(6)-hydroxylase/L-ornithine-N(5)-oxygenase family protein	BGC0002001	29%	73.8%

Table S9. BGC component for melanin in strain SPS-2.

Gene location	Description	MIBiG cluster	Identity	Coverage
ctg8_253	polyketide synthase	BGC00001265	88%	99.5%