

**Table S1. Summary of original sequencing data of *C. sojina* from Illumina and Pacbio**

Sequencing technology	Insert size (bp)	Reads length (bp)	Raw data		Trimmed data	
			Read counts	Total bases (Gb)	Read counts	Total bases (Gb)
Illumina	270	150	12,637,470	3.18	11,871,845	2.99
Pacbio	10,000	8,279	450,876	5.14	593,849	4.92

**Table S2. Major features of assembled *C. sojina* genome**

Type	Count	Min length (bp)	Max length (bp)	Mean length (bp)
<b>N25</b>	2	3,695,260	6,706,376	5,200,818
<b>N50</b>	6	1,594,415	6,706,376	3,440,875
<b>N75</b>	15	933,043	6,706,376	2,093,804
<b>N90</b>	23	451,093	6,706,376	1,600,775
<b>All</b>	62	17,575	6,706,376	658,651

**Table S3. Statistic analysis of specific motif for transmethylase**

Motif	Position	Type of modification	Fraction	nDetected	nGenome	meanScore
ATATRGCAD	1	m6A	0.17588	299	1700	38.24415
GCRVNNNG	1	Modified base	0.12090	79267	655644	36.67279
RAGGYASYW	2	m6A	0.11483	1379	12009	40.31110
GNNNNNNH	1	Modified base	0.10059	1595026	15857335	37.32386
HGWGADTBG	2	Modified base	0.05528	1090	19718	36.11193
DCSVNDBH	2	m4C	0.04430	27524	621346	39.74034
CNNNNVNH	1	m4C	0.03446	420851	12212118	39.50249
GGNNDTBGV	1	Modified base	0.02562	4831	188560	35.85096
CNNNTB	1	m4C	0.01214	54010	4449757	39.88760
RTVVADNNG	2	Modified base	0.01049	3196	304530	35.50532
TNNNDNNH	1	Modified base	0.00837	85541	10225018	36.40618
TNNNCVVH	1	Modified base	0.00439	9674	2205772	34.62022

Note: **m6A**, 6-methyl-adenosine; **m4C**, 4-methyl-cytosine; **Fraction**, the percentage of base modification in genome; **nDetected**, the number of modified motif; **nGenome**, the number of motif in *Cercospora sojina* genome; **meanScore**, mean score of the motif.

**Table S4. Characteristic of the annotated *C. soja* genes**

<b>Database</b>	<b>Number</b>	100<=Protein length<300	Protein length>=300
GO_Annotation	4195	836	3308
KEGG_Annotation	3172	695	2421
KOG_Annotation	5417	1032	4335
Pfam_Annotation	7388	1545	5767
Swissprot_Annotation	6240	1229	4940
TrEMBL_Annotation	9493	2235	7117
nr_Annotation	9487	2237	7109
<b>All Annotated</b>	9506	2239	7125

**Table S5. Expression of putative effector-coding genes in *C. sojae* during starvation treatment**

<b>Response at both 24 and 48 hpt</b>	<b>Fold Change (24 h.p.t.)</b>	<b>Fold Change (48 h.p.t.)</b>	<b>Pfam Domain</b>
CS_10225	4.462860175	6.451122157	
CS_10796	1.093041246	1.058943252	
CS_11263	1.678911042	1.24540773	PF01083.20;PF08237.9;PF02230.14;PF03583.12
CS_11868	1.317582711	1.134881439	
CS_12453	1.550828123	1.78915476	PF01822.17;PF03105.17
CS_12982	2.422350654	2.477382393	
CS_13698	1.203629935	1.470235322	
CS_13826	1.632887725	2.3850588	
CS_14180	1.776664748	1.805394421	PF01975.15;PF08194.10
CS_1450	2.639810041	3.0850408	
CS_2192	1.598962605	1.537557821	PF05572.11
CS_2462	1.357751802	2.01494863	
CS_2849	3.765488288	3.030392536	PF01083.20
CS_3627	4.32425922	4.693243029	PF01299.15
CS_4305	1.650706185	2.189434012	
CS_5126	1.597164044	1.329395773	
CS_5549	2.64639633	1.522746502	PF04616.12
CS_5993	1.645775359	2.095618051	PF02102.13
CS_6375	2.443678064	3.808943577	
CS_6507	1.186628649	1.771001614	
CS_6519	1.522234394	1.13988111	
CS_7013	1.347134813	2.689969162	PF01464.18
CS_7825	1.399848688	2.128585474	PF06766.9
CS_8980	1.14890451	2.128585474	PF13855.4
<b>24 hpt specific response</b>			
CS_5950	1.143471121	0	
CS_14378	1.123675009	0	
CS_6648	1.630961042	0	PF16541.3
CS_6343	1.105598855	0	PF14295.4
CS_7181	1.074128655	0	PF01764.23;PF12146.6;PF11187.6;PF12695.5
CS_3041	1.605806429	0	PF10428.7
CS_5895	1.619667526	0	PF00722.19
CS_4322	1.089572782	0	
CS_10049	1.481232563	0	
<b>48 hpt specific response</b>			
CS_6351	0	1.073464646	
CS_6880	0	1.067245421	
CS_7842	0	1.942956812	
CS_10678	0	1.104120746	PF06362.9
CS_10793	0	1.154404406	PF08277.10;PF08088.10
CS_5724	0	2.313772305	
CS_4711	0	1.726524857	PF00188.24
CS_2102	0	1.35045466	
CS_13996	0	2.447081338	PF06101.9
CS_14211	0	1.425949938	PF09543.8
CS_10092	0	1.19315987	
CS_5669	0	2.344956818	PF08278.9;PF02601.13
CS_13308	0	1.446219519	PF06766.9;PF04107.11
CS_7636	0	1.514760614	PF11937.6
CS_1033	0	1.440295757	PF07510.9;PF13395.4
CS_9858	0	1.112990029	PF06766.9;PF07172.9;PF03153.11
CS_10515	0	1.284793937	PF14787.4;PF09055.9;PF11371.6;PF00322.15

**Table S6. Fold changes of the back bone genes involved in secondary metabolisms after starvation treatment**

<b>ID</b>	<b>Fold change (24 h.p.t.)</b>	<b>Fold change (48 h.p.t.)</b>	
CS_7943	-2.53959	-4.245443	NRPS
CS_10271	-2.11139	-3.158072	NRPS
CS_8069	0	-2.003614	NRPS
CS_7792	0	-1.880083	NRPS-Like
CS_13554	-1.67396	-1.701354	NRPS-Like
CS_12309	1.857102	0	NRPS
CS_1378	1.509871	0	NRPS
CS_3644	1.468157	0	NRPS
CS_4803	1.875562	0	PKS
CS_4808	1.223659	0	NRPS
CS_4966	1.12403	0	NRPS
CS_6274	1.258769	0	NRPS-Like
CS_8012	1.002131	0	NRPS-Like
CS_9051	1.486261	0	NRPS
CS_9632	1.335495	0	NRPS
CS_9769	4.260817	0	NRPS-Like
CS_1751	1.735149	1.0550677	NRPS
CS_8530	2.051354	1.2652224	PKS
CS_3310	1.729707	1.503723	PKS
CS_3706	1.810788	1.5680306	PKS
CS_4538	1.097265	1.6445481	NRPS-Like
CS_8162	1.783491	1.7085898	NRPS-Like
CS_3555	2.03392	1.8009415	NRPS-Like
CS_8963	1.516497	2.3610022	PKS
CS_14194	3.095503	2.7913783	NRPS
CS_8968	3.697095	3.1196359	NRPS-Like

**Table S7. Annotation of putative back-bone genes of secondary metabolisms.**

Gene ID	UniProt entry	Protein name	Organism	E value
CS_10271	<a href="#">Q31826</a>	Putative acyl-CoA synthetase YngI (EC 6.2.1.-)	Bacillus subtilis	7.00E-50
CS_10382	<a href="#">Q4WLW5</a>	Nonribosomal peptide synthetase 12 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	4.00E-97
CS_10530	<a href="#">Q12397</a>	Putative sterigmatocystin biosynthesis polyketide synthase	Emericella nidulans(Aspergillus nidulans)	0
CS_12309	<a href="#">Q4WVN4</a>	Nonribosomal peptide synthetase 8 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_12869	<a href="#">Q9Y7D5</a>	Lovastatin diketide synthase LovF (LDKS) (EC 2.3.1.244)	Aspergillus terreus	0
CS_13554	<a href="#">Q70LM4</a>	Linear gramicidin synthase subunit D [Includes: ATP-dependent D-leucine adenylase (D-LeuA) (D-leucine activase); Leucine racemase [ATP-hydrolyzing] (EC 5.1.1.-); ATP-dependent tryptophan adenylase (TrpA) (Tryptophan activase); ATP-dependent glycine adenylase (GlyA) (Glycine activase); Linear gramicidin--PCP reductase (EC 1.-.-.-)]	Brevibacillus parabrevis	4.00E-119
CS_1378	<a href="#">Q00869</a>	Enniatin synthase [Includes: N-methylcyclopeptide synthetase (EC 6.3.2.-); S-adenosyl-L-methionine-dependent N-methyltransferase (EC 2.1.1.-)]	Fusarium equiseti (Fusarium scirpi)	0
CS_1392	<a href="#">Q00869</a>	Enniatin synthase [Includes: N-methylcyclopeptide synthetase (EC 6.3.2.-); S-adenosyl-L-methionine-dependent N-methyltransferase (EC 2.1.1.-)]	Fusarium equiseti (Fusarium scirpi)	0
CS_14194	<a href="#">Q30409</a>	Tyrocidine synthase 3 (Tyrocidine synthase III) [Includes: ATP-dependent asparagine adenylase (AsnA) (Asparagine activase); ATP-dependent glutamine adenylase (GlnA) (Glutamine activase); ATP-dependent tyrosine adenylase (TyrA) (Tyrosine activase); ATP-dependent valine adenylase (ValA) (Valine activase); ATP-dependent ornithine adenylase (OrnA) (Ornithine activase); ATP-dependent leucine adenylase (LeuA) (Leucine activase)]	Brevibacillus parabrevis	0
CS_14650	<a href="#">Q9Y7D5</a>	Lovastatin diketide synthase LovF (LDKS) (EC 2.3.1.244)	Aspergillus terreus	0
CS_14653	<a href="#">Q12053</a>	Noranthrone synthase (EC 2.3.1.221) (Aflatoxin biosynthesis polyketide synthase) (PKS) (Aflatoxin biosynthesis protein C) (Polyketide synthase A)	Aspergillus parasiticus	0
CS_1751	<a href="#">Q4WZ44</a>	Nonribosomal peptide synthetase 7 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_2372	<a href="#">Q9Y7D5</a>	Lovastatin diketide synthase LovF (LDKS) (EC 2.3.1.244)	Aspergillus terreus	0
CS_2572	<a href="#">Q03149</a>	Conidial yellow pigment biosynthesis polyketide synthase(PKS) (EC 2.3.1.-)	Emericella nidulans (Aspergillus nidulans)	0
CS_3028	<a href="#">Q12397</a>	Putative sterigmatocystin biosynthesis polyketide synthase	Emericella nidulans(Aspergillus nidulans)	0
CS_3310	<a href="#">A1CLY8</a>	Polyketide synthase-nonribosomal peptide synthetase (PKS-NRPS) (EC 2.3.1.-) (EC 6.3.2.-) (Cytochalasin biosynthesis protein A)	Aspergillus clavatus	0
CS_3555	<a href="#">P0C064</a>	Gramicidin S synthase 2	Brevibacillus brevis (Bacillus brevis)	6.00E-65
CS_3644	<a href="#">Q4WLW5</a>	Nonribosomal peptide synthetase 12 (EC 6.3.2.-)	Neosartorya fumigata (Aspergillus fumigatus)	0
CS_3702	<a href="#">Q9Y7D5</a>	Lovastatin diketide synthase LovF (LDKS) (EC 2.3.1.244)	Aspergillus terreus	4.00E-147
CS_3706	<a href="#">Q03149</a>	Conidial yellow pigment biosynthesis polyketide synthase(PKS) (EC 2.3.1.-)	Emericella nidulans (Aspergillus nidulans)	2.00E-166
CS_4538	<a href="#">Q31826</a>	Putative acyl-CoA synthetase YngI (EC 6.2.1.-)	Bacillus subtilis	7.00E-38
CS_4551	<a href="#">Q12397</a>	Putative sterigmatocystin biosynthesis polyketide synthase	Emericella nidulans(Aspergillus nidulans)	0
CS_4672	<a href="#">A1DA59</a>	Nonribosomal peptide synthetase 13 (EC 6.3.3.-) (Brevianamide F synthase) (Fumitremorgin biosynthesis protein A)	Neosartorya fischeri (strain ATCC 1020 / DSM 3700 / CBS 544.65 / FGSC A1164 / JCM 1740 / NRRL 181 / WB 181) (Aspergillus fischerianus)	0
CS_4803	<a href="#">Q9Y7D5</a>	Lovastatin diketide synthase LovF (LDKS) (EC 2.3.1.244)	Aspergillus terreus	3.00E-172
CS_4808	<a href="#">Q4WLW5</a>	Nonribosomal peptide synthetase 12 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_4966	<a href="#">Q01886</a>	HC-toxin synthetase (HTS) (EC 6.3.2.-)	Cochliobolus carbonum (Maize leaf spot fungus) (Bipolaris zeicola)	0
CS_5102	<a href="#">Q03149</a>	Conidial yellow pigment biosynthesis polyketide synthase(PKS) (EC 2.3.1.-)	Emericella nidulans (Aspergillus nidulans)	6.00E-130

CS_5256	<a href="#">Q4WLW5</a>	Nonribosomal peptide synthetase 12 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_5769	<a href="#">Q03149</a>	Conidial yellow pigment biosynthesis polyketide synthase(PKS) (EC 2.3.1.-)	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	0
CS_6205	<a href="#">Q4WVN4</a>	Nonribosomal peptide synthetase 8 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	2.00E-94
CS_6274	<a href="#">Q4WAW3</a>	Nonribosomal peptide synthetase 13 (EC 6.3.3.-) (Brevianamide F synthase) (Fumitremogin biosynthesis protein A)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	1.00E-145
CS_6745	<a href="#">O94297</a>	Putative 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase) (mtKAS)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	5.00E-159
CS_7145	<a href="#">Q4WF61</a>	Nonribosomal peptide synthetase 3 (EC 6.3.2.-) (Siderophore peptide synthase E)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_7580	<a href="#">Q4WAZ9</a>	PKS-NRPS hybrid synthetase <i>psaA</i> (EC 2.3.1.-) (EC 6.3.2.-) (Nonribosomal peptide synthetase 14) (NRPS14) (Pseurotin biosynthesis protein A)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_7792	<a href="#">P37693</a>	Polyketide synthase HetM	Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576)	4.00E-21
CS_7943	<a href="#">Q4WVN4</a>	Nonribosomal peptide synthetase 8 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_8012	<a href="#">Q70LM4</a>	Linear gramicidin synthase subunit D [Includes: ATP-dependent D-leucine adenylyase (D-LeuA) (D-leucine activase); Leucine racemase [ATP-hydrolyzing] (EC 5.1.1.-); ATP-dependent tryptophan adenylyase (TrpA) (Tryptophan activase); ATP-dependent glycine adenylyase (GlyA) (Glycine activase); Linear gramicidin--PCP reductase (EC 1.-.-.-)]	Brevibacillus parabrevis	3.00E-21
CS_8069	<a href="#">Q4WF53</a>	Nonribosomal peptide synthetase 4 (EC 6.3.2.-) (Siderophore peptide synthase D)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_8162	<a href="#">Q4WLW5</a>	Nonribosomal peptide synthetase 12 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	9.00E-104
CS_8530	<a href="#">Q9Y7D5</a>	Lovastatin diketide synthase LovF (LDKS) (EC 2.3.1.244)	Aspergillus terreus	0
CS_8963	<a href="#">Q03149</a>	Conidial yellow pigment biosynthesis polyketide synthase(PKS) (EC 2.3.1.-)	Emericella nidulans (Aspergillus nidulans)	0
CS_9051	<a href="#">Q4WR82</a>	Nonribosomal peptide synthetase 2 (EC 6.3.2.-) (Siderophore peptide synthase C)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_9052	<a href="#">Q4WR82</a>	Nonribosomal peptide synthetase 2 (EC 6.3.2.-) (Siderophore peptide synthase C)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	0
CS_9162	<a href="#">Q4WLW5</a>	Nonribosomal peptide synthetase 12 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	8.00E-92
CS_9448	<a href="#">Q4WLW5</a>	Nonribosomal peptide synthetase 12 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	4.00E-110
CS_949	<a href="#">A1CLY8</a>	Polyketide synthase-nonribosomal peptide synthetase (PKS-NRPS) (EC 2.3.1.-) (EC 6.3.2.-) (Cytochalasin biosynthesis protein A)	Aspergillus clavatus	0
CS_9632	<a href="#">Q9P7T1</a>	Hydroxamate-type ferrichrome siderophore peptide synthetase (EC 6.-.-.-)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	0
CS_9769	<a href="#">Q4WT66</a>	Nonribosomal peptide synthetase 1 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	6.00E-110
CS_9876	<a href="#">Q4WVN4</a>	Nonribosomal peptide synthetase 8 (EC 6.3.2.-)	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	1.00E-94
CS_9957	<a href="#">Q12397</a>	Putative sterigmatocystin biosynthesis polyketide synthase (PKS)	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	0
CS_7958	<a href="#">W7N2C1.1</a>	Non-canonical non-ribosomal peptide synthetase FUB8 (EC 2.3.1.-) (Fusaric acid biosynthesis protein 8)	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	1.00E-122
CS_8968	<a href="#">S0DXJ2</a>	Non-canonical non-ribosomal peptide synthetase FUB8 (EC 2.3.1.-) (Fusaric acid biosynthesis protein 8)	Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	3.00E-88

**Table S8. Annotation of putative NRPS and PKS by functional domains**

Gene type	Gene ID	Domain SBSPKS	Domain antiSMASH
NRPS	CS_3555	AT	AP
	CS_3644	CATCCATC	CAPECAPC
	CS_1378	ATC	APCA
	CS_1392	ATC	APCAPCAPCAPCAPCAPCAPCAPCA
	CS_10271	A	AC
	CS_10382	TC	PC
	CS_9769	A	A
	CS_9876	A	A-NAD
	CS_5256	CATCAT	CAPCAP
	CS_8968	A	AP-NAD
	CS_9051	ATCCTC	APCCC
	CS_9052	A	AC
	CS_9162	ATC	APC
	CS_4538	A	AC
	CS_4672	ATATC	APCAPC
	CS_4808	CATCCATCATC	CAPCCAPCAPE
	CS_12309	ATC	CAPCAPCPECAPECAPECPECAPCAPC
	CS_4966	CATECATCAT	CAPECAPCAP
	CS_13554	AT	AP-KR
	CS_14194	CATCATCATCATCATCATCATC	CAPCAPCAPCAPCAPCAPCAPC
	CS_8069	ATCT	APCPC
	CS_8162	AT	APC
	CS_9448	A	APC
	CS_9632	ACATCTCACTC	ACAPCPCACPCC
	CS_6205	CA	CA
	CS_6274	AT	AP
	CS_7145	ATCATC	APCAPC
	CS_7792	ATC	A
	CS_7943	ATCATCATCATCATC	APCAPCAPCAPCAPC
	CS_7958	ATC	A-NAD
	CS_8012	ATC	A
	CS_1751	ATCAT	APCAPC
	PKS	CS_949	KS
CS_2572		-	KS-AT
CS_3028		-	KS-AT-TE
CS_3310		KS	KS-AT-DH-ER-KR
CS_3702		KS	KS-AT-DH-ER-KR
CS_3706		-	KS-AT-TE
CS_5102		-	KS-AT
CS_9957		ACP	KS-AT-TE
CS_5769		-	KS-AT-TE
CS_8963		-	KS-AT-DH-TE
CS_4551		-	KS-AT
CS_14650		KS	KS-AD-DH-KR
CS_14653		-	KS-AT-DH-TE
CS_4803		KS	KS-AT-DH-ER-KR
CS_12869		-	KS-AT-DH-ER-KR
CS_6745		KS	KS
CS_7580		KS	KS-AT-DH-KR-C-A
CS_2372		KS	KS-AT-DH-ER-KR
CS_10530		-	KS-AT-DH-TE
CS_8530		KS	KS-AT-DH-ER-KR

**Table S9. Comparison of Carbohydrate-active enzymes (CAZymes) between *C. soja* and several other ascomycetes**

Protein family	Cs	Mo	Nc	An	Fg	Bc	Ss
cutinase	3	18	3	4	12	11	8
Auxiliary activity family	73	104	64	85	104	83	72
Carbohydrate-binding module family	34	55	40	86	51	40	41
CBM1 family	1	9	14	7	7	8	6
Carbohydrate esterase	108	122	68	103	122	100	90
Glycoside hydrolase	252	244	176	277	243	226	210
Glycosyltransferase	122	100	90	89	101	100	88
Polysaccharide lyase	7	5	4	21	20	12	5
CAZymes	596	630	442	661	641	561	506

Note: Cs, *Cercospora soja*; Mo, *Magnaporthe oryzae*; Nc, *Neurospora crassa*; An, *Aspergillus nidulans*; Fg, *Fusarium graminearum*; Bc, *Botrytis cinerea*; Ss, *Sclerotinia sclerotiorum*.

**Table S10. Annotated GH109 family members in *C. soja*, *M. oryzae*, *B. cinerea*, and *N. crassa***

Species	Predicted GH109 family members
<i>C. soja</i>	CS_10112, CS_11283, CS_12100, CS_12444, CS_12722, CS_13299, CS_13397, CS_13604, CS_14356, CS_2770, CS_2984, CS_3368, CS_7753, CS_8689
<i>M. oryzae</i>	MGG_02902T0, MGG_05346T0, MGG_07463T0, MGG_08115T0, MGG_08569T0, MGG_08695T0, MGG_10499T0, MGG_11542T0
<i>B. cinerea</i>	BC1T_01052, BC1T_02503, BC1T_04110, BC1T_07162, BC1T_14802
<i>N. crassa</i>	NCU01704T0, NCU08882T0, NCU09533T0, NCU09794T0

**Table S11 Putative effectors can be annotated by PHI database**

Gene	E value	Annotation
CS_5557	0	Ktr4 PHI:3096 J5K093 176275 Beauveria_bassiana reduced_virulence_
CS_11276	2.00E-108	pnl1 PHI:3226 T2C7K6 36651 Penicillium_digitatum reduced_virulence_
CS_5966	1.00E-101	PHI:811 MGG_10510 EDK06580 318829 Magnaporthe_oryzae Reduced_virulence
CS_9887	3.00E-93	PHI:2209 endo-1,4-beta-xylanase_[GH10_family] MGG_07868 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
CS_12662	3.00E-78	PHI:2897 BEC1019 KJ571201.1 62688 Blumeria_graminis_f._sp._hordei Effector_(plant_avirulence_determinant)
CS_3288	7.00E-76	PHI:479 MEP1 AAQ07436 199306 Coccidioides_posadasii Reduced_virulence
CS_5928	8.00E-73	PHI:2208 endo-1,4-beta-xylanase_[GH10_family] MGG_05464 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
CS_14682	1.00E-64	PHI:61 BGL2 AAA21151 5476 Candida_albicans Reduced_virulence
CS_6365	1.00E-62	PHI:2896 BEC1005 CCU82697 62688 Blumeria_graminis_f._sp._hordei Effector_(plant_avirulence_determinant)
CS_10321	8.00E-62	PHI:479 MEP1 AAQ07436 199306 Coccidioides_posadasii Reduced_virulence
CS_14119	3.00E-60	PHI:179 PELA AAA33338 140110 Nectria_haematococca_(related:_Fusarium_solani) Reduced_virulence
CS_2192	2.00E-52	PHI:479 MEP1 AAQ07436 199306 Coccidioides_posadasii Reduced_virulence
CS_4985	2.00E-54	PHI:71 ECP2 CAA78401 5499 Cladosporium_fulvum Effector_(plant_avirulence_determinant)
CS_1128	1.00E-34	PHI:816 MGG_04582 EDJ95999 318829 Magnaporthe_oryzae Reduced_virulence
CS_7154	4.00E-38	PHI:2118 MgSM1 MGG_05344 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Effector_(plant_avirulence_determinant)
CS_4417	4.00E-21	PHI:2404 SLP_1 G4N906 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
CS_6397	3.00E-20	PHI:653 GIP2 AAL11721 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
CS_9858	1.00E-18	PHI:487 MHP1 Q94196 148305 Magnaporthe_grisea Reduced_virulence
CS_13636	9.00E-17	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
CS_2543	3.00E-16	PHI:2644 thioredoxin_1 P0AA28 90371 Salmonella_enterica_serovar_Typhimurium Reduced_virulence
CS_5993	1.00E-14	PHI:201 AVR-Pita_(related:_AVR2-YAMO) AAK00131 318829 Magnaporthe_oryzae Effector_(plant_avirulence_determinant)
CS_1457	3.00E-13	PHI:184 RBT4 AAG09789 5476 Candida_albicans Reduced_virulence
CS_10055	1.00E-12	PHI:201 AVR-Pita_(related:_AVR2-YAMO) AAK00131 318829 Magnaporthe_oryzae Effector_(plant_avirulence_determinant)
CS_2945	2.00E-11	PHI:184 RBT4 AAG09789 5476 Candida_albicans Reduced_virulence
CS_4711	2.00E-10	PHI:184 RBT4 AAG09789 5476 Candida_albicans Reduced_virulence
CS_7825	2.00E-11	PHI:487 MHP1 Q94196 148305 Magnaporthe_grisea Reduced_virulence
CS_1450	3.00E-09	PHI:2901 BEC1040 CCU82707 62688 Blumeria_graminis_f._sp._hordei Effector_(plant_avirulence_determinant)
CS_4239	1.00E-58	PHI:2925 lip2 J9MBA2 59765 Fusarium_oxysporum_f._sp._Lycopersici Unaffected_pathogenicity
CS_6874	7.00E-53	PHI:2849 cutA Q99174 70790 Fusarium_solani_f._sp._cucurbitae Unaffected_pathogenicity
CS_14017	2.00E-18	PHI:2978 MoCel12A G4N5V2 148305 Magnaporthe_oryzae Unaffected_pathogenicity
CS_13308	1.00E-09	PHI:291 CPPH1 CAD10781 5111 Claviceps_purpurea Unaffected_pathogenicity
CS_7363	6.00E-162	PHI:3 PGN1 AAA79885 5017 Cochliobolus_carbonum Unaffected_pathogenicity
CS_7914	1.00E-152	PHI:115 PGX1 AAC26146 5017 Cochliobolus_carbonum Unaffected_pathogenicity
CS_4002	4.00E-07	PHI:2807 Ss-Si2 A7EKS0 5180 Sclerotinia_sclerotiorum Unaffected_pathogenicity
CS_13926	1.00E-07	PHI:747 um00445 Not_available 5270 Ustilago_maydis Unaffected_pathogenicity
CS_4096	4.00E-07	PHI:1856 GzZC171 11S377 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
CS_6725	1.00E-33	PHI:2807 Ss-Si2 A7EKS0 5180 Sclerotinia_sclerotiorum Unaffected_pathogenicity
CS_4686	7.00E-32	PHI:552 BcLCC2 AAK77953 40559 Botrytis_cinerea Unaffected_pathogenicity
CS_7181	4.00E-21	PHI:2924 lip1 J9MXG1 59765 Fusarium_oxysporum_f._sp._Lycopersici Unaffected_pathogenicity
CS_1544	1.00E-19	PHI:541 LIP1 AAU87359 332648 Botrytis_cinerea Unaffected_pathogenicity

**Table S12. Comparison of *C. sojina* race 1 genome sequence with sequenced *C. sojina* isolate (Genome ID:2506520004)**

<b>C. sojina isolates</b>	<b>Mapped(%)</b>	<b>Average depth</b>	<b>Cov_ratio_1X(%)</b>	<b>Cov_ratio_5X(%)</b>	<b>Cov_ratio_10X(%)</b>
<i>C. sojina</i> race 1 (Sequencing by SMRT in this study)	98.9	127 ×	99.36	99.23	99.10
<i>C. sojina</i> isolate (Download from JGI database, IMG genome id: 2506520004)	72.88	125 ×	99.86	99.85	99.94

JGI database, Joint genome institute database (<http://jgi.doe.gov/>); IMG, integrated microbial genomes & microbiome samples. Cov\_ratio, coverage ratio.

The data of *C. sojina* strain FLS21 (SAR number, SRR5152073) were retrieved from National Center for Biotechnology Information Search database (NCBI, <https://www.ncbi.nlm.nih.gov/>) and used for mapping to the genome of *C. sojina* race 1 and sequenced *C. sojina* isolate (Genome ID:2506520004). In total, the data contains 56,140,492 reads.