

Supplemental Figures

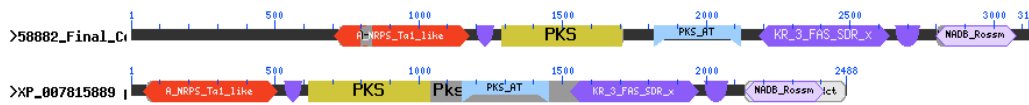


Figure S1. Domain order of PKS-NRPS5882 and polyketide synthase of *Metarhizium acridum* XP_07815889. A=adenylation, PKS = ketoacyl synthase, AT= acyl transferase, KR = ketoreductase, NADB Rossm = NAD binding Rossman folding.

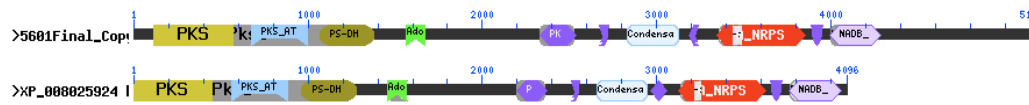


Figure S2. Domain order of PKS-NRPS5601 and hypothetical protein of *Setosphaeria turcica* XP_008025924. PKS = ketoacyl synthase, AT= acyl transferase, DH = dehydratase, Ado = methyltransferase, Condensa = condensation, A = adenylation, NADB = NAD binding.

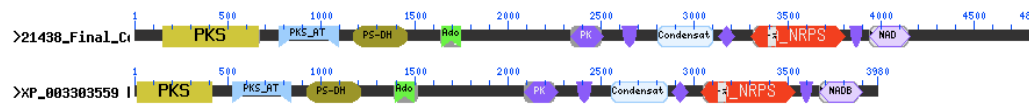


Figure S3. Domain order of PKS-NRPS21438 and hypothetical protein of *Pyrenophora teres* XP_003303559.

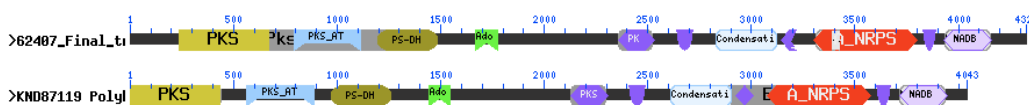


Figure S4. Domain order of PKS-NRPS62407 and hypothetical protein of *Tolypocladium ophioglossoides* KND87119.

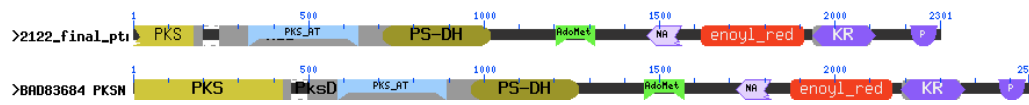


Figure S5. Domain order of PKS2122 and ALT5 of *Alternaria solani* BAD83684. PKS = ketoacyl synthase, AT= acyl transferase, DH = dehydratase, AdoMet = methyltransferase, NA = neuraminidase, enoyl red = enoyl reductase, KR = ketoreductase, P = acyl carrier protein.

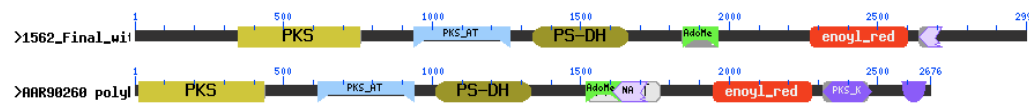


Figure S6. Domain order of PKS1562 and PKS5 of *Bipolaris maydis* AAR90268.



Figure S7. Domain order of PKS59499 and hypothetical protein of *Aspergillus nomius* KNG90368. PKS = ketoacyl synthase, AT= acyl transferase, DH = dehydratase, AdoMet = methyltransferase, MDR superfamily = medium chain dehydrogenases/reductases, KR = ketoreductase, P = acyl carrier protein?

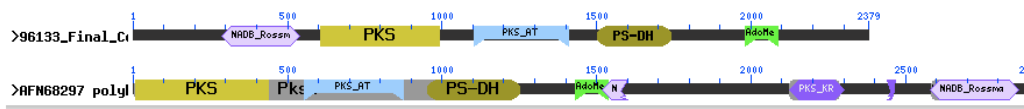


Figure S8. Domain order of PKS96133 and PKSF of *Alternaria alternata* AFN68297. NADB Rossm = NAD binding Rossman folding.

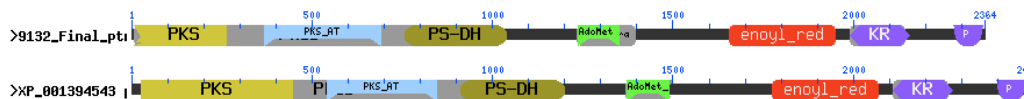


Figure S9. Domain order of PKS9132 and PKSD of *Aspergillus niger* XP_001394543. enoyl red = enoyl reductase, KR = ketoreductase, P = acyl carrier protein.

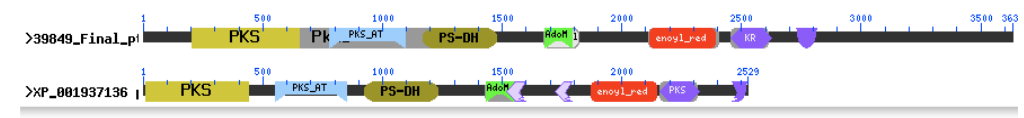


Figure S10. Domain order of PKS39849 and PPSA of *Pyrenophora tritici-repentis* XP_001937136. PKS = keTable 11. Domain order of PKS17612 and PPSB of *Pyrenophora tritici-repentis* XP_001934720.

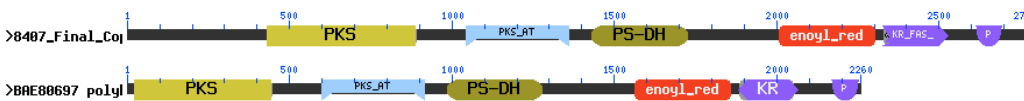


Figure S11. Domain order of PKS8407 and *Alternaria solani* PKSF BAE80697. PKS = ketoacyl synthase, AT= acyl transferase, DH = dehydratase, AdoMet = methyltransferase, enoyl red = enoyl reductase, KR = ketoreductase.

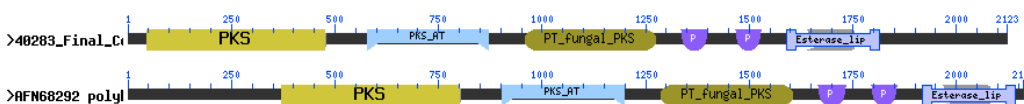


Figure S12. Domain order of PKS40283 and PKSA of *Alternaria alternata* AFN68292. PKS = ketoacyl synthase, AT= acyl Table 14. Domain order of PKS3398 and polyketide synthase of *Metarhizium brunneum* KID62944.

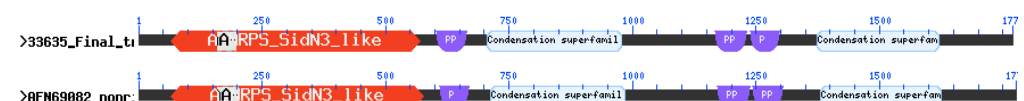


Figure S13. Domain order of NRPS33635 and NPS6 of *Alternaria alternata* AFN69082. A=adenylation, Condensation superfamil = condensation, PP = peptidyl carrier protein?

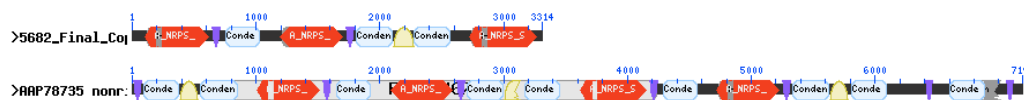


Figure S14. Domain order of PKS5682 and *Alternaria brassicae* nrps1 AAP78735.

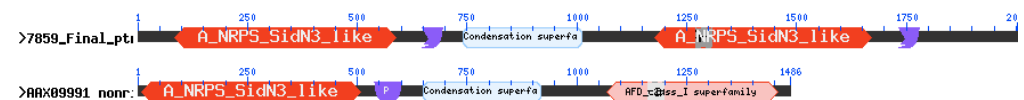


Figure S15. Domain order of NRPS7859 and NPS9 of *Cochliobolus heterostrophus* AAX09991. A=adenylation, Condensation superfamil = condensation, P = peptidyl carrier protein?

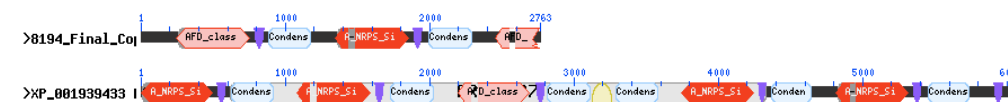


Figure S16. Domain order of NRPS8194 and HC-toxin synthetase of *Pyrenophora tritici-repentis*.

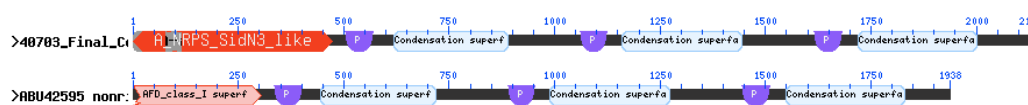


Figure S17. Domain order of NRPS40703 and NPS2 of *Alternaria brassicicola*.

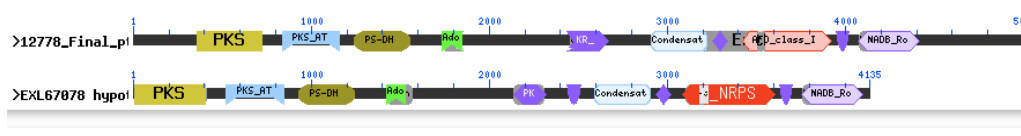


Figure S18. Domain order of PKS12778 and hypothetical protein from *Fusarium oxysporum* f. sp. *conglutinans* EXL67078. PKS = ketoacyl synthase, AT= acyl transferase, DH = dehydratase, AdoMet = methyltransferase, KR = ketoreductase, Condensat = condensation, A NRPS = adenylation, NADB Ro = NAD binding Rossman folding.

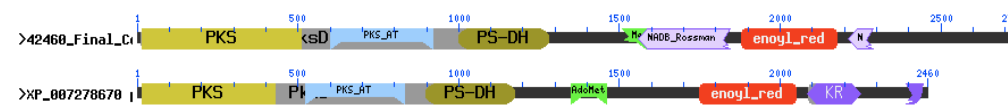


Figure S19. Domain order of PKS42460 and hypothetical polyketide synthase of *Colletotrichum gloeosporioides* XP_007270670. Enoyl red = enoyl reductase .

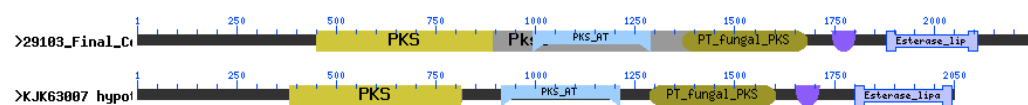


Figure S20. Domain order of PKS29103 and hypothetical protein of *Aspergillus parasiticus* KJK63007.

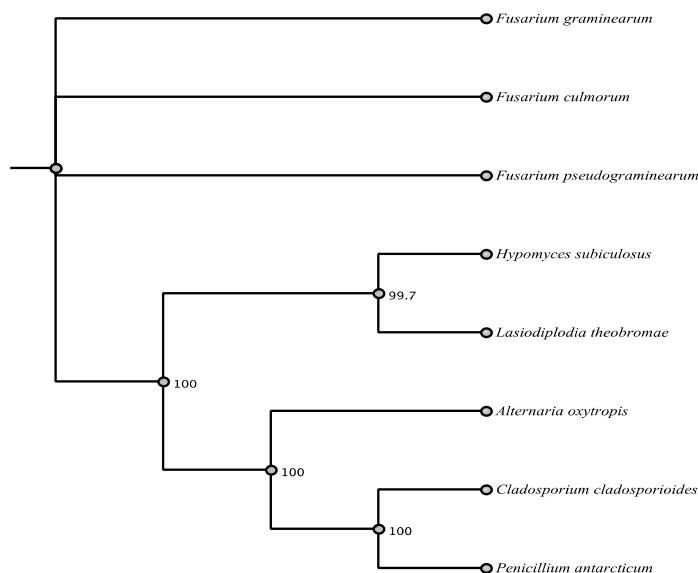


Figure S21. Maximum parsimony tree (MUSCLE alignment and 1000 replicates). *Lasiodiplodia theobromae* was used as the outgroup. Fungi in tree are pblast results of 17612 sequence.

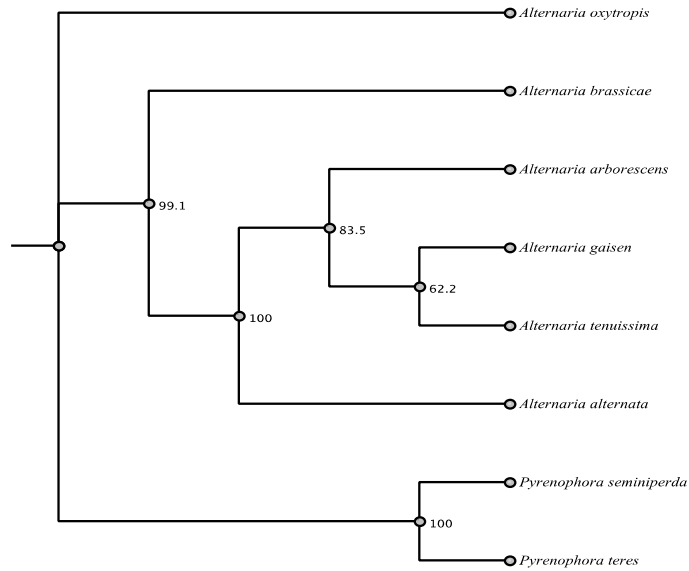


Figure S22. Maximum parsimony tree (MUSCLE alignment and 1000 replicates). *Pyrenophora teres* was used as the outgroup. Fungi in tree are pblast results of 5682 sequence.

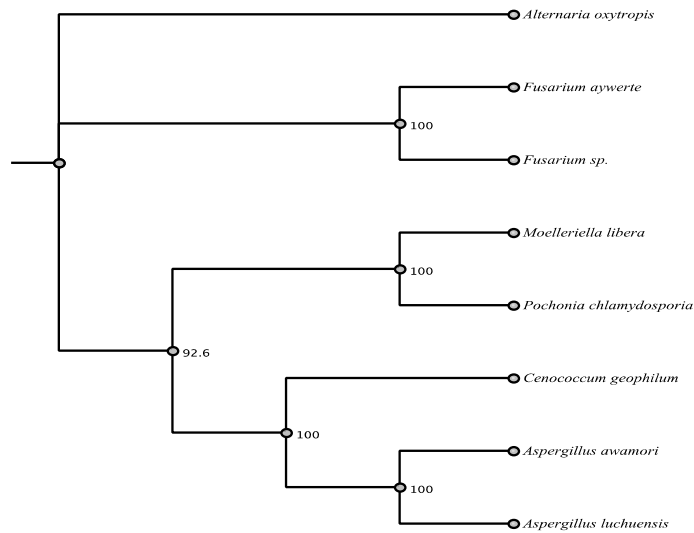


Figure S23. Maximum parsimony tree (MUSCLE alignment and 1000 replicates). *Aspergillus luchuensis* was used as the outgroup. Fungi in tree are pblast results of 9132 sequence.

Table S1. GenBank accession numbers and amino acid percent identity of blast results of 2122 sequence. .

Organism	Accession	Amino Acid Percent Identity
<i>Alternaria alternantherae</i>	AOO87092.1	89.59%
<i>Alternaria tenuissima</i>	RYN35181.1	88.97%
<i>Alternaria solani</i>	BAD83684.1	90.13%
<i>Pyrenophora teres</i>	EFQ86427.1	89.01%
<i>Alternaria alternata</i>	XP_018381235.1	89.08%
<i>Alternaria arborescens</i>	RYN41486.1	89.13%
<i>Alternaria gaisen</i>	RYO51295.1	89.09%

Table S2. Genbank accession numbers and amino acid percent identity of blast results of 17612 sequence. .

Organism	Accession	Amino Acid Percent Identity
<i>Penicillium antarcticum</i>	OQD80247.1	64.45%

<i>Cladosporium cladosporioides</i>	A0A0Y0M151.1	62.81%
<i>Hypomyces subiculosus</i>	ACD39758.1	58.65%
<i>Fusarium pseudograminearum</i>	XP_009258258.1	58.00%
<i>Fusarium graminearum</i>	EYB31080.1	57.96%
<i>Lasiodiplodia theobromae</i>	AHV78245.1	56.92%
<i>Fusarium culmorum</i>	PTD11157.1	57.28%

Table S3. Genbank accession numbers and amino acid percent identity of blast results of 8407 sequence. .

Organism	Accession	Amino Acid Percent Identity
<i>Alternaria solani</i>	BAE80697.1	81.14%
<i>Alternaria arborescens</i>	RYO53185.1	80.47%
<i>Alternaria tenuissima</i>	RYN97731.1	80.46%
<i>Alternaria alternata</i>	OWY52567.1	80.50%
<i>Alternaria alternantherae</i>	AOO87095.1	79.93%
<i>Pyrenophora seminiperda</i>	RMZ66475.1	69.35%
<i>Pyrenophora teres</i>	EFQ92739.1	69.54%

Table S4. Genbank accession numbers and amino acid percent identity of blast results of 3398 sequence. .

Organism	Accession	Amino Acid Percent Identity
<i>Lepidopterella palustris</i>	OCK76486.1	74.49%
<i>Metarhizium brunneum</i>	XP_014539917.1	63.54%
<i>Metarhizium robertsii</i>	XP_007819463.1	64.25%
<i>Metarhizium guizhouense</i>	KID81569.1	63.31%
<i>Metarhizium anisopliae</i>	KJK77000.1	64.03%
<i>Aspergillus fischeri</i>	XP_001265535.1	62.66%
<i>Aspergillus terreus</i>	XP_001213896.1	63.00%

Table S5. GenBank accession numbers and amino acid percent identity of blast results of 40283 sequence. .

Organism	Accession	Amino Acid Percent Identity
<i>Alternaria tenuissima</i>	RYN42853.1	95.17%
<i>Alternaria alternata</i>	AFN68292.1	95.21%
<i>Alternaria arborescens</i>	RYO71336.1	95.26%
<i>Alternaria gaisen</i>	RYO46317.1	94.47%
<i>Alternaria alternantherae</i>	AOO87097.1	93.54%
<i>Stemphylium lycopersici</i>	KNG52671.1	90.05%
<i>Bipolaris sorokiniana</i>	XP_007696213.1	88.93%

Table S6. Genbank accession numbers and amino acid percent identity of blast results of 33635 sequence. .

Organism	Accession	Amino Acid Percent Identity
<i>Alternaria alternata</i>	AFN69082.1	91.40%
<i>Alternaria tenuissima</i>	RYN35257.1	91.46%
<i>Alternaria arborescens</i>	XP_028502413.1	91.63%
<i>Alternaria gaisen</i>	RYO50458.1	91.18%
<i>Stemphylium lycopersici</i>	KNG49863.1	85.82%
<i>Bipolaris oryzae</i>	XP_007684283.1	82.59%
<i>Exserohilum turcica</i>	XP_008020405.1	82.62%

Table S7. Genbank accession numbers and amino acid percent identity of blast results of 5682 sequence. .

Organism	Accession	Amino Acid Percent Identity
<i>Alternaria tenuissima</i>	RYN60358.1	90.75%

<i>Alternaria alternata</i>	XP_018382376.1	90.69%
<i>Alternaria arborescens</i>	RYN26111.1	90.51%
<i>Alternaria gaisen</i>	RYO35725.1	90.23%
<i>Alternaria brassicae</i>	AAP78735.1	89.47%
<i>Pyrenophora teres</i>	EFQ92073.1	80.96%
<i>Pyrenophora seminiperda</i>	RMZ69649.1	79.25%

Table S8. Genbank accession numbers and amino acid percent identity of blast results of 9132 sequence.

Organism	Accession	Amino Acid Percent Identity
<i>Fusarium</i> sp.	RBR08923.1	74.84%
<i>Fusarium aywerte</i>	ALQ32761.1	72.71%
<i>Moelleriella libera</i>	KZZ87545.1	69.00%
<i>Pochonia chlamydosporia</i>	XP_022284243.1	67.00%
<i>Cenococcum geophilum</i>	OCK93825.1	61.71%
<i>Aspergillus luchuensis</i>	OJZ90116.1	58.53%
<i>Aspergillus awamori</i>	GCB20567.1	58.30%