

Table 1 – Predicted *B. bassiana* NRPS and NRPS-like enzymes, domain structures, broad phylogenetic grouping and gene cluster conservation. Domain abbreviations: A: adenylation C: condensation; T: thiolation; MT: methyltransferase; KS: ketoacyl synthase; Py: pyoverdine/dityrosine biosynthesis; TE: thioesterase.

Accession	Domain Structure	AA#	Group <sup>1</sup>	Gene cluster conservation <sup>2</sup>	Comment
EJP70094.1	A T C	1,525	ferricrocin	<i>C. militaris</i> and <i>Aspergillus spp.</i>	
EJP68628.1	C A T C A M T T T C	3,147	enniatin and beauvericin	not conserved	BSLS
EJP66735.1	A T T E T E?	1,289	AAR-like	<i>Trichoderma spp.</i> and <i>Metarhizium spp.</i>	
EJP65768.1	A T C	1,417	ferricrocin	Ascomycota	
EJP62835.1	T C A T C C A T C A T C C	4,857	emicellamide	<i>C. militaris</i> and <i>Aspergillus spp.</i>	
EJP62709.1	A T C T C	1,903	peramine module 2	two <i>M. robertsii</i> NRPS gene clusters	
EJP62373.1	A	851	<i>B. bassiana</i> EJP63622.1	<i>Fusarium spp.</i>	within a trichothecen e-like gene cluster
EJP62375.1	TC	551	N/A	<i>Fusarium spp.</i>	within a trichothecen e-like gene cluster
EJP68775.1	A T C	1,254	ergot PS4	not conserved	
EJP67097.1	A T C C A T C A T T E	3,920	ergot, multiple modules	<i>C. posadasii</i>	
EJP64345.1	A T C A T C A T C A T C	4,530	<i>M. robertsii</i> EXU97071.1 and EXU95985.1	<i>C. militaris</i> , <i>M. robertsii</i>	
EJP63622.1	A T C? T C A T C	2,922	<i>B. bassiana</i> EJP62373.1	<i>C. militaris</i>	
EJP63413.1	A T C A T C	2,378	ferricrocin	not conserved	
EJP60951.1	A T C A T C	2,172	<i>C. heterostrophus</i> NPS8 module2	not conserved	
EJP67034.1	C A T K S	1,864	ferricrocin	<i>M. acridum</i> and <i>G. graminicola</i>	
EJP65355.1	A C	1,698	long chain fatty acid/acyl CoA ligases	<i>C. militaris</i> and <i>T. atroviride</i>	
EJP62859.1	A C	1,383	ferricrocin	<i>C. militaris</i>	
EJP66334.1	A T C A T C A T T E	3,326	ergot (module 1 and 2) and AM-toxin (module 3)	not conserved	
EJP66049.1	A C A T C T C A T C T C T C	4,814	ferricrocin	Ascomycota	sidC
EJP63992.1	A T C T C	1,843	coprogen	Ascomycota	sidD
EJP61332.1	C A T C A M T T T C	3,119	enniatin and bassianolide	<i>Gibberella spp.</i>	BEAS
EJP62735.1	A T T E	1,176	AAR	not conserved	LYS2
EJP63735.1	Py A T C	1,562	<i>M. robertsii</i> EXV04551.1	<i>M. robertsii</i> , <i>C. militaris</i> and other Clavicipitaceae	

<sup>1</sup>inferred from maximum likelihood phylogeny

<sup>2</sup> a gene cluster is considered conserved when at least 3 proteins are found in both query and subject (evaluate cutoff: 10<sup>-5</sup>) and the cumulative BLAST score > 2,000.

AAR = alpha-aminoadipate reductase

Table 2 – Predicted *M. robertsii* NRPS and NRPS-like enzymes, domain structures, broad phylogenetic grouping and gene cluster conservation. Domain abbreviations: A: adenylation C: condensation; T: thiolation; MT: methyltransferase; Py: pyoverdine/dityrosine biosynthesis; TE: thioesterase.

Accession	Domain Structure	AA#	Group <sup>1</sup>	Gene cluster conservation <sup>2</sup>	Comment
EXV05490.1	A T C A T C T C A T C T C T C	4,845	ferricrocin	conserved among Ascomycota	sidC
EXV04526.1	C C A T C	2,772	serynocyclin module 2	conserved in <i>Fusarium spp.</i> and <i>M. acridum</i>	
EXV04699.1	A T C T C	1,800	coprogen	conserved among Ascomycota	sidD
EXV03721.1	A T T E	1,173	AAR	not conserved	LYS2
EXV00331.1	A T C	871	gliotoxin/sirodesmin	ochratoxin cluster	the cluster includes the PKS EXV00332.1
EXV00333.1	A T C A	1,975	module 1: <i>M. robertsii</i> EXU97432.1 ; module2: ergot	ochratoxin cluster	the cluster includes the PKS EXV00332.
EXV00362.1	A C C	1,366	loosely associated with echinocandin clade	<i>T. equinum</i> and <i>A. fumigatus</i>	
EXU99143.1	A T C A T C	2,032	gliotoxin/sirodesmin	conserved in <i>Trichoderma spp.</i> and <i>L. maculans</i>	
EXU98277.1	A T C C A T C A T C A T C C	5,433	complex	conserved in <i>M. acridum</i>	pesA
EXU97504.1	A T C A T E	1,818	ergot	conserved in <i>M. acridum</i> , <i>Claviceps spp.</i> and <i>Epichloë</i>	ergot cluster
EXU97506.1	A T C	1,301	ergot	conserved in <i>M. acridum</i> , <i>Claviceps spp.</i> and <i>Epichloë</i>	ergot cluster
EXU97071.1	A T C A T C A T C C A T C A T C C A T C C A T C A T C T	10,310	<i>M. robertsii</i> EXU95985.1	conserved in <i>M. acridum</i> , <i>C. militaris</i> , <i>B. bassiana</i> , dermatophytes	
EXU96645.1	A T C A T C C A T	3,447	<i>C. heterostrophus</i> NPS8	conserved in <i>Trichophyton spp.</i>	
EXU96313.1	A T C A T C C A T C	3,552	module 1 and 3: peramine; module 2: <i>M. robertsii</i> EXU95985.1	conserved in <i>M. acridum</i>	
EXU96269.1	A T C C A T C A T C A T C C A T C C A T C C A T C	9,415	6 out of 7 modules are in the ergot clade	conserved in <i>M. acridum</i>	NPS1
EXU95985.1	A T C A T C A T C C A T C A T C C A T C A T C C A T C	10,188	<i>M. robertsii</i> EXU97071.1	conserved in <i>M. acridum</i> , <i>C. militaris</i> , <i>B. bassiana</i>	
EXU95951.1	A C A T C	2,139	gliotoxin/sirodesmin		similar to sirodesmin cluster
EXU95958.1	A T C A T C C A T C A T C A M T T C A M T T C	7,913	modules 1, 2, 3, 4: peramine, modules 5, 6: <i>C. heterostrophus</i> NPS3	not conserved	DXS
EXV04551.1	Py A T C	1,600	<i>B. bassiana</i> EJP63735 and ochratoxin clade	Conserved in <i>Clavicipitaceae</i> and	

EXU98659.1	A T TE	1,077	ochratoxin	<i>Trichophyton spp.</i>	not conserved	
EXU98130.1	A	370	no clade		not conserved	
EXU98131.1	A T	669	<i>C. heterostrophus</i> NPS9		not conserved	
EXV00390.1	A T TE	999	terrequinone-like		conserved in Dermatophites	
EXU99364.1	A T TE	918	terrequinone-like		conserved in Dermatophites	
orphan_07	C A C T	1,647	<i>B. bassiana</i> EJP60751.1		conserved in <i>M. acridum</i>	associated with NRPS orphan_07

<sup>1</sup>inferred from maximum likelihood phylogeny

<sup>2</sup> a gene cluster is considered conserved when at least 3 proteins are found in both query and subject (evalue cutoff:  $10^{-5}$ ) and the cumulative BLAST score > 2,000.

AAR = alpha-aminoadipate reductase

Table 3 – Predicted *B. bassiana* PKS and PKS/NRPS hybrid, domain structures, broad phylogenetic grouping and gene cluster conservation. Domain abbreviations:

A: adenylation C: condensation; T: thiolation; MT: methyltransferase; TE: thioesterase; KS: ketoacyl synthase; AT: acyl transferase; DH: dehydratase; ER: enoyl reductase; KR: ketoacyl reductase; P: acyl carrier protein; R: reductase.

Accession	Domain Structure	AA#	Group <sup>1</sup>	Cluster conservation <sup>2</sup>	Comment
EJP70098.1	KS AT DH KR P	2,397	<i>B. bassiana</i> EJP65765.1, equisetin	<i>C. militaris</i>	closely associated with NRPS EJP70094.1
EJP65765.1	KS AT DH KR C A T R	3,945	<i>B. bassiana</i> EJP70098.1, equisetin	<i>Aspergillus spp. C. militaris</i>	closely associated with NRPS EJP65768.1
EJP64619.1	KS AT DH? P P TE	2,145	<i>M. robertsii</i> EXU96629.1	<i>C. militaris</i>	melanin?
EJP62792.1	KS AT DH? P P TE	2,211	no specific clade	<i>Aspergillus spp</i>	oosporein? (laccase, MFS)
EJP62832.1	KS AT DH MT ER KR P	2,522	<i>A. nidulans</i> emericellamide easB	<i>C. militaris</i> and <i>A. nidulans</i> emericellamide cluster	emicellamid e-like product?
EJP60751.1	KS AT DH MT ER KR P	2,499	<i>M. robertsii</i> orphan_06	not conserved	
EJP68806.1	KS AT DH MT ER KR P	2,503	<i>M. robertsii</i> EXU96285.1	not conserved	
EJP67836.1	KS AT DH MT ER KR P	2,468	<i>M. robertsii</i> EXU97187.1	<i>Aspergillus spp.</i>	
EJP67236.1	KS AT DH ER KR P	2,413	<i>M. robertsii</i> EXV03186.1 and <i>A. fumigatus</i> fumagillin PKS	<i>C. militaris, A. fumigatus</i>	
EJP66434.1	KS AT DH MT ER KR P	2,524	no specific clade	not conserved	
EJP63694.1	KS AT DH MT KR C A T R	4,235	<i>A. fumigatus</i> aspyridone, <i>M. robertsii</i> EXU98291.1	Ascomycota	tens
EJP63776.1	KS AT DH KR P	2,102	<i>M. robertsii</i> EXU95771.1 and <i>A. solani</i> alternapyrone	not conserved	
EJP61308.1	KS AT DH ER KR P	2,393	<i>M. robertsii</i> EXV02084.1 and <i>G. zeae</i> zearalenone PKS4	Ascomycota	no zearalenone PKS13-like associated with the cluster
EJP61198.1	KS AT DH MT KR C A T R	4,016	EXU96139.1 <i>Aspergillus terreus</i> lovastatin nonaketide LovB	Ascomycota	
EJP70141.1	KS AT DH ER KR P	2,284	<i>C. heterostrophus</i> t-toxin PKS2	<i>Trichoderma spp., Verticillium spp.</i>	

<sup>1</sup>inferred from maximum likelihood phylogeny

<sup>2</sup>a gene cluster is considered conserved when at least 3 proteins are found in both query and subject (evaluate cutoff: 10<sup>-5</sup>) and the cumulative BLAST score > 2,000.

Table 4 – Predicted *M. robertsii* PKS and PKS/NRPS hybrid, domain structures, broad phylogenetic grouping and gene cluster conservation. Domain abbreviations:

A: adenylation C: condensation; T: thiolation; MT: methyltransferase; TE: thioesterase; KS: ketoacyl synthase; AT: acyl transferase; DH: dehydratase; ER: enoyl reductase; KR: ketoacyl reductase; P: acyl carrier protein; R: reductase; CH: carnitine O-palmitoyltransferase.

Accession	Domain Structure	AA#	Group <sup>1</sup>	Cluster conservation <sup>2</sup>	Comment
EXV04383.1	KS AT DH ER KR P C A T R	3,883	no specific clade	Ascomycota	
EXV03186.1	KS AT DH ER KR P	2,408	<i>B. bassiana</i> EJP67236.1 and <i>A. fumigatus</i> fumagillin PKS	<i>Aspergillus</i> spp.	
EXV02536.1	KS AT P P TE	2,151	<i>M. robertsii</i> EXU95796.1; <i>G. zeae</i> aurofusarin PKS12	<i>M. acridum</i>	pigment-like
EXV02084.1	KS AT DH ER? KR P	2,359	<i>B. bassiana</i> EJP61308.1 and <i>G. zeae</i> zearalenone PKS4	Ascomycota	no zearalenone PKS13-like associated with the cluster
EXV00332.1	KS AT DH MT ER KR P	2,581	ochratoxin	<i>A. niger</i>	associated with NRPS EXV00333.1 , which clusters with ochratox NRPSs ccc
EXV00352.1	KS AT P	1,795	<i>A. nidulans</i> monodictyphenone mdpG		
EXU99168.1	KS AT DH MT? ER KR P	2,515	<i>G. zeae</i> zearalenone PKS4	<i>T. virens</i>	
EXU99173.1	KS AT DH? P	1,706	<i>G. zeae</i> zearalenone PKS13, <i>A. nidulans</i> orsellinic acid orsA	<i>T. virens</i>	
EXU99208.1	KS AT DH MT KR P C A T R	3,935	<i>Gibberella</i> fusarins	Ascomycota	NGS1
EXU98965.1	KS AT P MT TE	2,627	<i>A. nidulans</i> aspernidine A pkfA	<i>M. acridum</i> and <i>C.</i> <i>posadasii</i>	
EXU98661.1	KS AT DH ER? KR P CH	2,971	<i>A. alternata</i> AF toxin	<i>Aspergillus</i> spp.	associated with NRPS- like EXU98659.1
EXU98425.1	KS AT DH MT KR P	2,492	no specific clade	not conserved	
EXU98505.1	KS AT DH MT? KR P C A T R	3,994	<i>A. fumigatus</i> pseurotin psoA	<i>A. fumigatus</i>	
EXU98524.1	KS AT DH? P TE	2,088	<i>B. bassiana</i> EJP64619.1.	Ascomycota	pigment-like
EXU98208.1	KS AT DH MT ER? KR P	2,669	<i>A. alternata</i> AF toxin, <i>A.</i> <i>nidulans</i> emericellamide	not conserved	NO NRPS in the cluster
EXU98291.1	KS AT DH MT? KR P C A T	3,627	<i>A. fumigatus</i> aspyridone, <i>B.</i> <i>bassiana</i> EJP63694.1	not conserved	
EXU97982.1	A T KS AT KR P TE	2,488	<i>C. heterostrophus</i> NPS7	<i>Trichophyton</i> spp.	
EXU97632.1	KS AT	1,187	loosely associated with <i>G.</i> <i>zeae</i> zearalenone PKS4 clade	not conserved	
EXU97553.1	KS AT DH MT KR P C	2,968	<i>A. clavatus</i> cytochalasin E CcsA	not conserved	structure similar to lovastatin

EXU97310.1	KS AT P P	1,789	<i>P. aethiopicum</i> viridicatumtoxin VrtA	<i>M. acridum</i> , <i>P. aethiopicum</i> , <i>Aspergillus</i> spp., <i>T. tonsurans</i>	nonaketide synthase
EXU97187.1	KS AT DH MT? ER KR P	2,529	<i>B. bassiana</i> EJP67836.1	<i>A. fumigatus</i> , <i>M. graminicola</i>	
EXU96629.1	KS AT DH P TE	2,186	<i>B. bassiana</i> EJP64619.1	not conserved	pigment-like
EXU96285.1	KS AT DH MT ER KR P	2,470	<i>B. bassiana</i> EJP68806.1	not conserved	
EXU96139.1	KS AT DH MT KR P	2,538	<i>EJP61198.1</i> <i>Aspergillus terreus</i> lovastatin nonaketide LovB	<i>Ascomycota</i>	
EXU95974.1	KS AT DH MT? ER KR P	2,574	<i>A. nidulans</i> pkhB	<i>G. clavigera</i> , <i>A. niger</i>	associated with PKS
EXU95978.1	KS AT P TE	2,333	<i>A. nidulans</i> pkha	<i>G. clavigera</i> , <i>A. niger</i>	EXU95978.1 associated with PKS
EXU95948.1	KS MT ER KR P	1,536	no specific clade	not conserved	EXU95974.1 associated with ergot like cluster
EXU95862.1	KS AT DH MT KR P C A T TD	3,928	<i>A. solani</i> aslanipyronone PKSF	several <i>Ascomycota</i>	
EXU95796.1	KS AT DH? P P TE	2,148	<i>M. robertsii</i> EXV02536.1; <i>G. zeae</i> aurofusarin PKS12	<i>Trichoderma</i> spp., <i>Trichophyton</i> spp.	
EXU95756.1	DH MT KR C	1,656	N/A	N/A	
EXU95771.1	KS AT DH ER	1,661	<i>B. bassiana</i> EJP63776.1 and <i>A. solani</i> alternapyronone	not conserved	truncated gene?
EXU95681.1	KS AT P MT	2,181	no specific clade	<i>M. acridum</i>	truncated gene?
orphan_06	KS AT DH MT ER KR P	2,508	<i>B. bassiana</i> EJP60751.1	<i>M. acridum</i>	associated with NRPS orphan_07

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