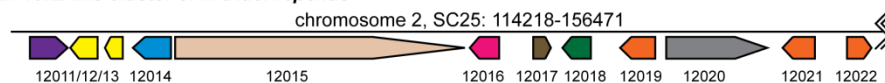


A. Putative Histone deacetylase inhibitor cluster in *P. tritici-repentis*



B. Tox2-like cluster of *P. tritici-repentis*



<i>P. tritici-repentis</i>		Best BlastP hit			
Locus	Proposed function	Accession Number	Organism	Annotation	e value
12011	FAD-linked oxidoreductase	ACZ66255.1	<i>F. incarnatum</i>	APS9	9e-160
		XP_001209092.1	<i>A. terreus</i>	conserved hypothetical	4e-104
12012	Short chain dehydrogenase	XP_965074.1	<i>N. crassa</i>	conserved hypothetical	8e-80
		XP_001239054.1	<i>C. immitis</i>	conserved hypothetical	1e-77
12013	Short chain dehydrogenase	XP_001820062.1	<i>A. oryzae</i>	hypothetical protein	3e-68
		XP_002374381.1	<i>A. flavus</i>	short chain type dehydrogenase, putative	9e-68
12014	MFS transporter	ACZ66257.1	<i>F. incarnatum</i>	APS11	1e-123
		sp:Q00357	<i>C. carbonum</i>	HC-toxin efflux carrier	2e-102
12015	NRPS	ACZ66258.1	<i>F. incarnatum</i>	APS1	0.0
		sp:Q01886.2	<i>C. carbonum</i>	HC-toxin synthetase	0.0
12016	Basic leucine zipper transcription factor	ACZ66248.1	<i>F. incarnatum</i>	APS2	2e-26
		sp:O74205	<i>C. carbonum</i>	Transcription factor ToxE	2e-16
12017	Thioesterase	XP_001799397.1	<i>S. nodorum</i>	hypothetical protein SNOG_09095	2e-24
		XP_002378766.1	<i>A. flavus</i>	hypothetical protein	1e-23
12018	Aminotransferase	sp:Q9Y885.1	<i>C. carbonum</i>	Aminotransferase ToxF	9e-123
		ACZ66250.1	<i>F. incarnatum</i>	APS4	6e-105
12019	cytochrome P450	XP_001555869.1	<i>B. fuckeliana</i>	hypothetical protein	4e-105
		XP_001795303	<i>S. nodorum</i>	hypothetical protein	1e-96
12020	Fatty acid synthase	ACZ66251.1	<i>F. incarnatum</i>	APS5	0.0
		XP_002146311.1	<i>P. marneffeii</i>	3-oxoacyl-[acyl-carrier-protein] synthase	0.0
12021	cytochrome P450	XP_001275091.1	<i>A. clavatus</i>	benzoate 4-monooxygenase, cytochrome P450	3e-134
		ACZ66253.1	<i>F. incarnatum</i>	APS7	8e-125
12022	cytochrome P450	ACZ66254.1	<i>F. incarnatum</i>	APS8	2e-109
		XP_002477830.1	<i>T. stipitatus</i>	cytochrome P450, putative	2e-76

Figure S6 Modular architecture and biosynthetic cluster of a putative histone deacetylase inhibitor biosynthetic cluster in *P. tritici-repentis*. (A) Modular architecture of PTRG_12015, APS1 (Apicidin synthetase) and HTS1 (HC-toxin synthetase). Domains (Adenylation, Thiolation, Condensation, and Epimerization) and spacing are to scale. (B) Putative biosynthetic cluster containing PTRG_12015. Putative open reading frames are designated as arrows. Proteins with similar function are coded with a similar color. Blastp search was performed against the NCBI nr database. Proposed function as determined by KOG or GO classification.