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Supplementary data file:

Novel Genetic Dysregulations and Oxidative Damage in *Fusarium graminearum* Induced by Plant Defense Eliciting Psychrophilic *Bacillus atrophaeus* TS1

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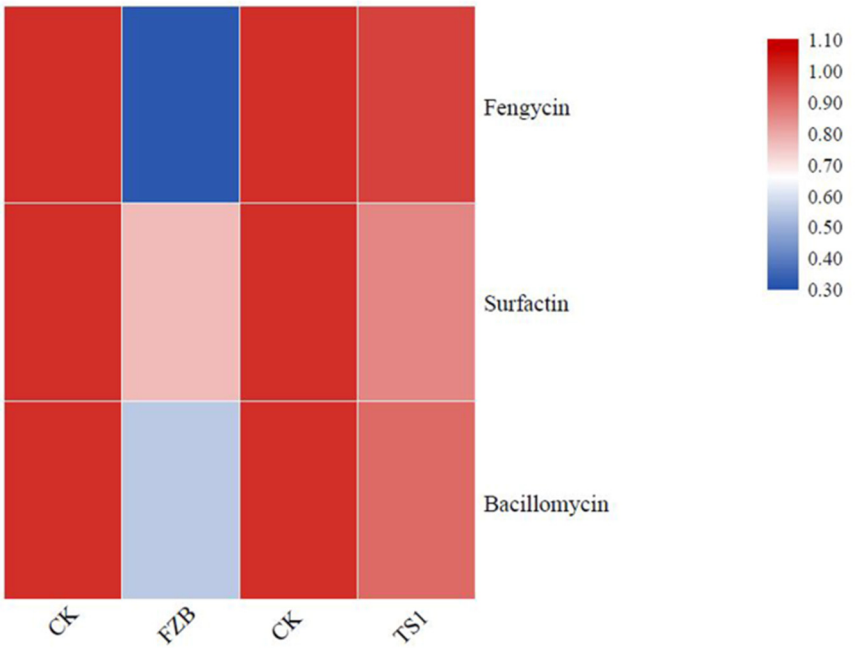


Figure S1. The heat map represents the expression profiling of LPs encoding genes in *Bacillus* spp. under cold temperature. The expression study was repeated thrice with similar results.

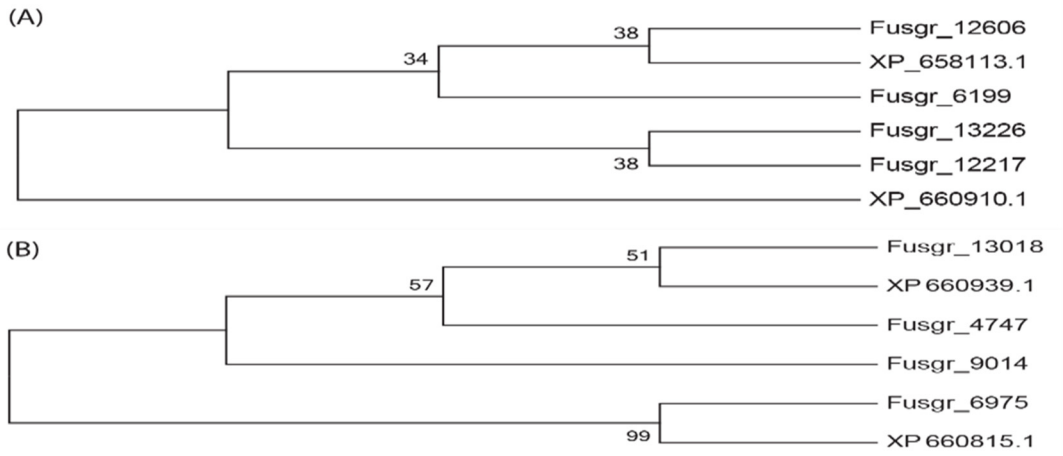


Figure S2. The phylogenetic relationship of (A) HCE gene family and (B) NPP1 gene family in *F. graminearum* genome.

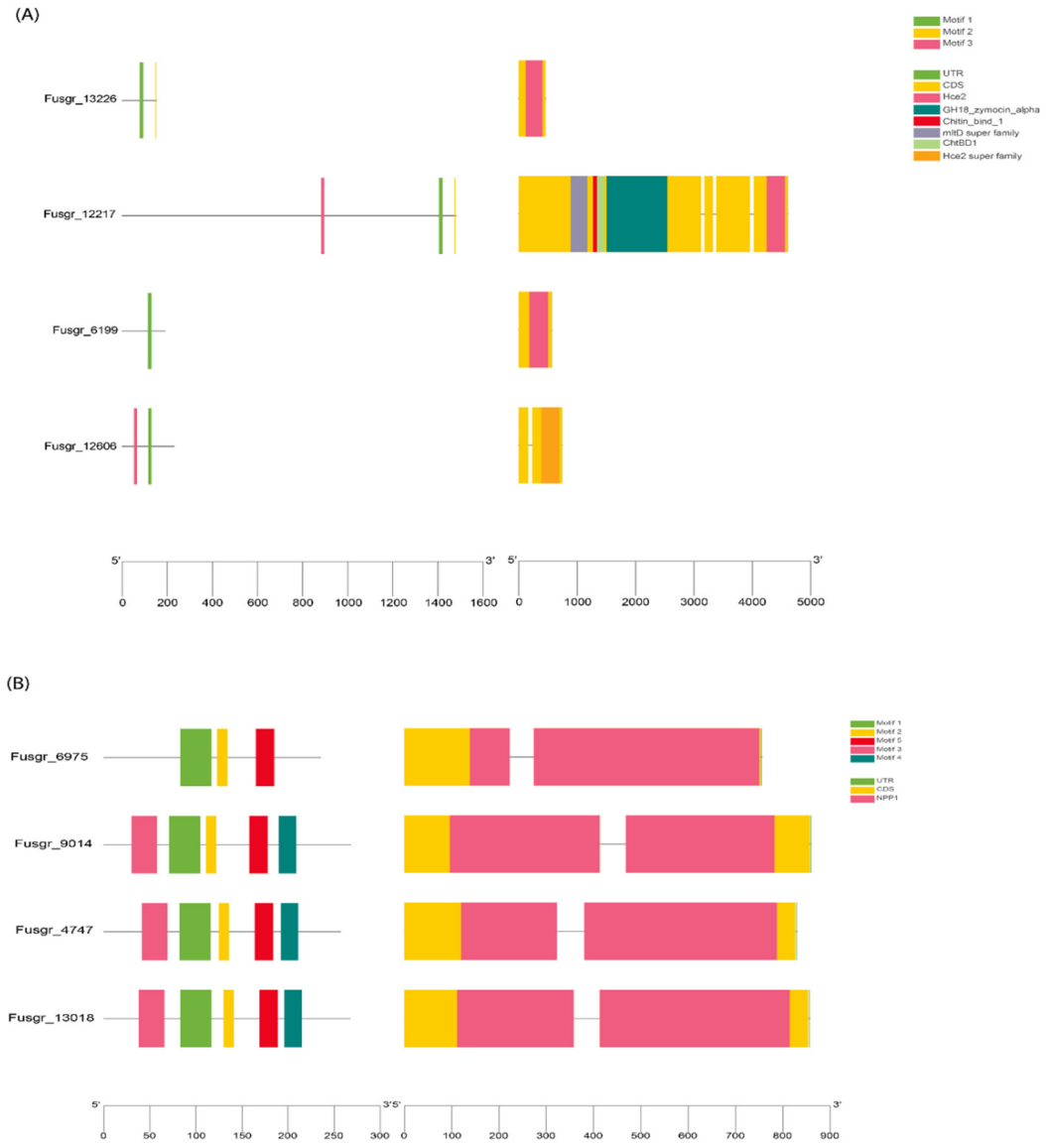


Figure S3. Structural and motif analysis of (A) HCE gene family and (B) NPP1 gene family in *F. graminearum*.

Table S1. The assigned m/z and peak intensities of detected homologues of LPs produced by *Bacillus* spp. FZB42 and TS1 at 15 °C and 25 °C.

Strains	Temperature	Mass (m/z) $[M+H]^+$	Compound	Peak Intensity
TS1	25 °C	1057.56	Bacillomycin	5.49e^6
		1071.58	Bacillomycin	1.33e^7
		1085.59	Bacillomycin	5.90e^5
		1008.65	Surfactin	1.68e^6
		1022.67	Surfactin	1.80e^5
		1435.76	Fengycin	1.29e^6
		1449.77	Fengycin	3.07e^6
		1463.78	Fengycin	7.95e^6
		1505.83	Fengycin	1.23e^6
	15 °C	1057.56	Bacillomycin	3.78e^6
		1071.58	Bacillomycin	9.86e^6
		1085.59	Bacillomycin	2.93e^4
		1008.65	Surfactin	9.65e^5
		1022.67	Surfactin	8.29e^3
		1435.76	Fengycin	7.23e^5
		1449.77	Fengycin	1.74e^6
		1463.78	Fengycin	5.93e^5
		1505.83	Fengycin	8.32e^5
FZB42	25 °C	1031.54	Bacillomycin	2.28e^6
		1045.55	Bacillomycin	1.54e^7
		1057.56	Bacillomycin	9.00e^5
		1059.57	Bacillomycin	6.42e^6
		1073.58	Bacillomycin	4.14e^6
		994.64	Surfactin	6.31e^6
		1008.66	Surfactin	1.42e^7
		1022.67	Surfactin	5.60e^6
		1036.67	Surfactin	3.18e^6
		1050.69	Surfactin	2.94e^6
		1435.76	Fengycin	6.07e^5
		1449.78	Fengycin	2.49e^6
		1463.78	Fengycin	3.65e^8
		1505.84	Fengycin	1.21e^6
	15 °C	1031.54	Bacillomycin	9.24e^3
		1045.55	Bacillomycin	2.74e^4
		1057.56	Bacillomycin	
		1059.57	Bacillomycin	4.47e^3
		1073.58	Bacillomycin	8.69e^2
		994.64	Surfactin	3.71e^4
		1008.66	Surfactin	4.83e^5
		1022.67	Surfactin	5.21e^4
		1036.67	Surfactin	8.37e^3
		1050.69	Surfactin	1.71e^4
		1435.76	Fengycin	2.31e^2
		1449.78	Fengycin	
		1463.78	Fengycin	7.90e^3
		1505.84	Fengycin	6.53e^2

Table S2: Primers used in this study for detection of genes and qPCR expression analysis.

Detection of genes in *Bacillus* strain TS1		
S.No	**Oligo Name**	**Sequence 5/ to 3/**
1	*eglS* (F)	ATGAAACGGTCAATCTCTATTTTTATTA
	eglS (R)	CTAATTTGGTTCTGTTCCCCAAATCAGT
2	*estA* (F)	ATGAAATTTGTAAAAAGAAGGATCATTG
	estA (R)	TTAATTCGTATTCTGGCCCCCG
3	*amyE* (F)	ATGTTTGCAAAACGATTCAAAACCTCTT
	amyE (R)	TCAATGGGGAAGAGAACCGCTTAA
4	*clpP* (F)	ATGAATTTAATACCTACAGTCATTGAACA
	clpP (R)	TTACTTTTTGTCTTCTGTGTGAGTCAAA
5	*sbp* (F)	GTGAACGCACAGTTATCGGCTAA
	sbp (R)	TCATACCCGTACACCTGCAGATTC
6	*Pvd* (F)	ATGAGACGGGAAGCGTTAAAGAATG
	Pvd (R)	TTAGTTATTCACATTTACGTCCTGTAACG
Lipopeptide biosynthesis genes in *Bacillus* spp. FZB42 and TS1		
1	*Bmy* (F)	CTGTCGGAGATGTCACAAGAA
	Bmy (R)	CGGCTTTCAGGCGTTTAATATC
2	*Fen* (F)	GTCGCAGAGCTTCAGAGAAA
	Fen (R)	GATGGACCGTCAGAAACAAGTA
3	*Sfb* (F)	GAACGCTATAAACGCGATGTG
	Sfb (R)	ATGATTGCTCCAGACGAGATAC
4	*rpsj* (F)	GAAACGGCAAAACGTTCTGG
	rpsj (R)	GTGTTGGGTTCACAATGTCG
***F. graminearum* pathogenicity-linked genes**		
1	*PAL* (F)	AGTCTATGGGCGGTAATGTTG
	PAL (R)	TTGTGCGAGTTGAGTAGCG
2	*SOD* (F)	ATTCCTCTGCCTAAATTCCCC
	SOD (R)	TCAGAAACTCGCTCAAACCAG

3	*CBH* (F)	GACGAGAACACCTACCAGATG
	CBH (R)	GGGCATCACAGTAACCAGTAC
4	*β-XSD* (F)	CGATGCTGGATTTGAGAATGATC
	β-XSD (R)	GTATTTGCCGTTCTTGTGGG
5	*TRI6* (F)	GCTACTCAGAATGCCCTCAG
	TRI6 (R)	TGATCTCGCATGTTATCCACC
6	*TRI10* (F)	TGGACCATGTTGACTATTCTCG
	TRI10 (R)	GTCTGTCGGTAGCCTTTGTAG
7	*PKS4* (F)	TGTGGGTTGGAAGTGTGAAG
	PKS4 (R)	AGGGTTTGGACTAGCGAAATG
8	*NPS1* (F)	CCATCGTCAACTGTGTCTACTG
	NPS1 (R)	CCAGTCTATCTCCAAAGCATCG
9	*NPS6* (F)	AAGCCAAGGATGAAGGAGATG
	NPS6 (R)	GACACGAGGTAGGGAATCTTG
10	*HCE1 (F)*	TTCCACCTTCGAGAACAAGTC
	HCE1 (R)	GCAGCGTTCATGTTTGATCC
11	*HCE2 (F)*	AAGATACACTCAGACGCCAAG
	HCE2 (R)	GCTCATATAAGACACCCATTCGG
12	*HCE3 (F)*	GATATCGTCAAGTCTGGTTCCTG
	HCE3 (R)	TTACACTTGACAGAACCACGAG
13	*HCE4 (F)*	CAGATGGCCTCTTACTTCCAG
	HCE4 (R)	AATTCACGAGCCCTATTCCG
14	*NPP1-1* (F	ACCTGAAGTACAAGCCTTTCG
	NPP1-1 (R)	GAGTACATGATGGCGTATCGG
15	*NPP1-2* (F)	CTGCCTTGAGTGGACATAGAC
	NPP1-2 (R)	CTTTGTGGTAGACTAGCTTGGG
16	*NPP1-3* (F)	ACAGCAACACCTATTCTCGC
	NPP1-3 (R)	TGAAGGAGCAACACGAAGG
17	*NPP1-4* (F)	CTATTGTAACTGTCCTCGCCG

	NPP1-4 (R)	TGTTACCGTCCTTGTCGATG
18	*Actin* (F)	TCTTCCAGCCTTCTGTCCTTG
	Actin (R)	AATGGAACCACCGATCCAGA
Defense-related genes in wheat plant		
1	*GNS* (F)	TTCCTACGAGTGTGCAATCC
	GNS (R)	GTTACCGATGTCGAGGATGAG
2	*HMGR* (F)	CGTTGTGGTTAGTTGGGTTG
	HMGR (R)	CAATCACGTCACCAACTTTCG
3	*PR-1* (F)	GGCTAATCTTTCCCAGGCG
	PR-1 (R)	TTGCAGTCGTTGATCCTCTG
4	*PAL* (F)	CTCACTTGGTCTGATCTCATCC
	PAL (R)	TGTTCATGCTCAGGGTCTTC
5	*SOD* (F)	TTGGGAATTGATGTCTGGGAG
	SOD (R)	ACAGCGGGAAACTCAAGAG
6	*LOX1* (F)	CCTTCATCCACACCATCACTAG
	LOX1 (R)	CTTGCTCTCGATCTCCACTAG
7	*MPK6* (F)	GACAAGATGGTACAGGGCAC
	MPK6 (R)	GTAGACGTAGCTGATGGACATG
8	*Actin* (F)	TGGATCGGTGGCTCTATTTTG
	Actin (R)	TTTGTAAGTCCCCTTCACCG