

Supplementary Table S1. Summary of reads available for genome assembly

Strain ID	Yield (bp) Illumina	Yield (bp) ONT	Mean length (bp) ONT	Coverage Illumina	Coverage ONT
S02	1,555,571,650	8,073,984,100	1,144	256.7×	1332.2×
S25	981,251,546	5,129,702,300	5,088	164.7×	860.8×

Supplementary Table S2. General genomic characteristics of *Paenibacillus* sp. strains S02 and S25

Strain ID	Genome size (bp)	GC content (%)	No. of tRNA	No. of tmRNA	No. of rRNA	No. of gene	No. of CDS
S02	6,060,529	45.60	92	1	33	5,436	5,310
S25	5,958,851	45.72	92	1	36	5,306	5,177

Supplementary Table S4. Plant growth-promoting genes in the genomes of *Paenibacillus* sp. strains S02 and S25, and *P. polymyxa* strain CR1

Trait	Gene Name	<i>Paenibacillus</i> sp. S02	<i>Paenibacillus</i> sp. S25	<i>P. polymyxa</i> CR1
Nitrogen fixation				
	<i>nifB</i>	KAI36_01039	KAI37_00991	YP_008910495
	<i>nifH</i>	KAI36_01040	KAI37_00992	YP_008910496
	<i>nifD</i>	KAI36_01041	KAI37_00993	YP_008910497
	<i>nifK</i>	KAI36_01042	KAI37_00994	YP_008910498
	<i>nifE</i>	KAI36_01043	KAI37_00995	YP_008910499
	<i>nifN</i>	KAI36_01044	KAI37_00996	YP_008910500
	<i>nifX</i>	KAI36_01045	KAI37_00997	YP_008910501
	<i>hesA/moeB</i>	KAI36_01046	KAI37_00998	YP_008910502
	<i>nifV</i>	KAI36_01047	KAI37_00999	YP_008910503
Phosphate solubilization				
	<i>gcd</i>	KAI36_02793	KAI37_02644	YP_008912273
	<i>gad</i>	–	–	–
Phosphonate cluster (<i>phn</i>)				
	<i>phnA</i>	KAI36_05309	KAI37_05177	YP_008914717
	<i>phnB</i>	KAI36_00880	KAI37_00854	YP_008910326
	<i>phnC</i>	KAI36_04607	KAI37_04494	YP_008913947
	<i>phnD</i>	KAI36_04606	KAI37_04493	YP_008913946
	<i>phnE</i>	KAI36_04608	KAI37_04495	YP_008913948
	<i>phnW</i>	KAI36_05275	KAI37_05152	YP_008914692
	<i>phnX</i>	KAI36_00485	KAI37_00496	YP_008909947
	<i>ppd</i>	KAI36_05276	KAI37_05153	YP_008914693
	<i>pepM</i>	KAI36_05277	KAI37_05154	YP_008914694
Phosphate transporter (<i>pst</i>)				
	<i>pstS</i>	KAI36_01689	KAI37_01595	YP_008911198
	<i>pstA</i>	KAI36_01691	KAI37_01597	YP_008911200
	<i>pstB</i>	KAI36_01692	KAI37_01598	YP_008911201
	<i>pstC</i>	KAI36_01690	KAI37_01596	YP_008911199
	<i>phoP</i>	KAI36_01703	KAI37_01609	YP_008911212
	<i>phoR</i>	KAI36_01702	KAI37_01608	YP_008911211
Indole-3-acetic acid production				
	<i>ipdC</i>	KAI36_01475	KAI37_01435	YP_008911027
	auxin efflux carriers	KAI36_02845	KAI37_02683	YP_008912813
		KAI36_03330	KAI37_03351	YP_008912323
		KAI36_05253	KAI37_05129	YP_008911849

Gene identifiers for *Paenibacillus* sp. strains S02 and S25 were from the annotated genomes described in section 2.2. Gene identifiers for *P. polymyxa* CR1 were from Eastman, et al.¹⁶

Supplementary Table S5. Percentage identity of plant growth-promoting genes in the genome of strains *Paenibacillus* sp. S02/S25 and *P. polymyxa* CR1

Trait	Gene Name	S02 VS S25	S02 VS CR1	S25 VS CR1
Nitrogen fixation				
	<i>nifB</i>	97.13	98.00	96.80
	<i>nifH</i>	95.39	98.15	94.69
	<i>nifD</i>	98.96	98.62	98.27
	<i>nifK</i>	98.24	97.45	97.39
	<i>nifE</i>	98.24	98.60	98.16
	<i>nifN</i>	97.25	97.55	97.63
	<i>nifX</i>	98.46	97.69	97.69
	<i>hesA/moeB</i>	96.47	98.04	96.34
	<i>nifV</i>	98.50	98.59	97.80
Phosphate solubilization				
	<i>gcd</i>	98.11	97.60	98.39
	<i>gad</i>	-	-	-
Phosphonate cluster (<i>phn</i>)				
	<i>phnA</i>	98.53	98.53	98.82
	<i>phnB</i>	98.21	98.43	99.78
	<i>phnC</i>	97.66	97.81	98.39
	<i>phnD</i>	98.14	99.07	97.63
	<i>phnE</i>	98.25	97.78	97.43
	<i>phnW</i>	98.74	98.47	98.20
	<i>phnX</i>	98.04	97.92	98.81
	<i>ppd</i>	98.97	98.62	98.79
	<i>pepM</i>	99.33	99.44	99.00
Phosphate transporter (<i>pst</i>)				
	<i>pstS</i>	98.92	98.48	99.13
	<i>pstA</i>	96.99	97.55	98.22
	<i>pstB</i>	98.81	98.70	98.22
	<i>pstC</i>	99.14	98.71	98.82
	<i>phoP</i>	98.09	97.81	97.94
	<i>phoR</i>	98.28	97.45	97.89
Indole-3-acetic acid production				
	<i>ipdC</i>	99.54	99.48	99.14
	auxin efflux carriers 1	99.13	98.15	98.37
	auxin efflux carriers 2	97.92	97.60	98.85
	auxin efflux carriers 3	98.58	98.96	99.05

Supplementary Table S6. Secondary metabolite gene clusters identified in *Paenibacillus* sp. strains S02 and S25

ID	Type	Location		Most similar known cluster (similarity)
		S02	S25	
C1	Nrps	62,712-130,949	62,863-131,149	fusaricidin B (100%)
C2	siderophore	1,060,830-1,078,231	1,021,525-1,038,926	–
C3	bacteriocin	1,226,685-1,236,921	1,163,825-1,174,061	–
C4	Nrps transAT-PKS	1,276,170-1,374,849	1,234,262-1,333,113	–
C5	lassopeptide	1,410,732-1,434,848	1,369,083-1,393,199	paeninodin (40%)
C6	Nrps	1,496,857-1,557,694	1,452,621-1,513,241	marthiapeptide A (33%)
C7	lanthipeptide	1,752,471-1,779,477	1,717,117-1,742,305	paenilan (100%)
C8	lanthipeptide	–	1,865,337-1,891,786	paenicidin B (71%)
C9	Nrps-like	2,147,919-2,191,265	2,068,326-2,110,857	–
C10	Nrps	2,564,994-2,657,512	2,538,234-2,631,151	tridecaptin (100%)
C11	Nrps transAT-PKS	2,800,573-2,881,430	2,762,852-2,843,624	paenilipoheptin (S02, 73%; S25, 76%)
C12	Nrps	–	2,847,977-2,929,143	–
C13	Nrps betalactone	–	3,004,139-3,056,727	–
C14	Nrps T3PKS transAT-PKS	3,755,116-3,856,856	3,756,437-3,858,120	aurantinin B/C/D (35%)
C15	Nrps	5,189,939-5,270,981	5,092,876-5,173,931	polymyxin (100%)
C16	phosphonate	5,879,383-5,920,282	5,775,191-5,816,090	–

Nrps: Nonribosomal peptide synthetase

transAT-PKS: transAT-polyketide synthase

T3PKS: Type III polyketide synthase

Clusters in bold: Known antimicrobial compounds

Supplementary Table S7. The average colony diameter (\pm standard error) of fungal pathogens when exposed to the two *Paenibacillus* sp. strains (S02 and S25) in a bioprotection assay (*in vitro*)

Pathogen ID	S02/cm	S25/cm	Blank/cm
<i>Colletotrichum graminicola</i>	1.03 \pm 0.02 ^b	3.77 \pm 0.04 ^a	4.10 \pm 0.20 ^a
<i>Fusarium verticillioides</i>	2.93 \pm 0.04 ^c	6.15 \pm 0.14 ^b	6.80 \pm 0.08 ^a
<i>Microdochium nivale</i>	5.12 \pm 0.11 ^a	5.18 \pm 0.12 ^a	5.27 \pm 0.04 ^a

^{a, b, c}: Different letters are statistically significantly ($P < 0.05$) different.

S02/S25: *Paenibacillus* sp. strains

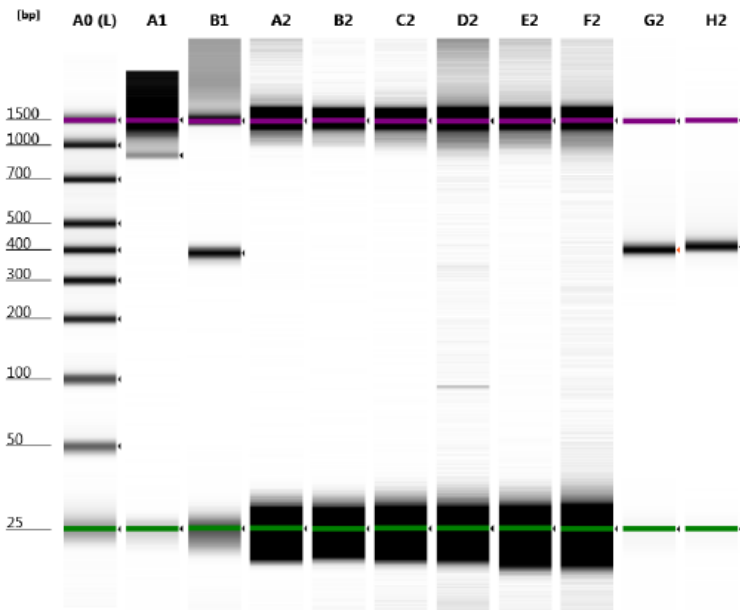
Supplementary Table S8. The percentage of mapped reads when quantifying transcript of each sample using the transcriptome sequences of *F. verticillioides* 7600 as the reference

Sample	No. of mapped reads	Mapping rate
S02_ctrl_1	4	too low
S02_ctrl_2	1	too low
S02_ctrl_3	2	too low
S02_treated_1	3	too low
S02_treated_2	1,492	0.0082%
S02_treated_3	1,366	0.0089%
S25_ctrl_1	1	too low
S02_ctrl_2	0	0%
S02_ctrl_3	0	0%
S25_treated_1	33,944	0.2817%
S25_treated_2	17,987	0.1407%
S25_treated_3	22,684	0.1395%

too low: 0–0.0001%; ctrl: Without *F. verticillioides*; treated: With *F. verticillioides*
 S02/S25: *Paenibacillus* sp. strains isolated in this study

Supplementary Table S9. Pathogens used in the *in vitro* bioprotection assay.

VPRI Acc. No.	Taxonomic Details	Host Taxonomic Details	State	Collection Date
32315	<i>Colletotrichum graminicola</i>	<i>Cynosurus echinatus</i> .	Vic.	27-Apr-05
42586a	<i>Fusarium verticillioides</i>	<i>Zea mays</i> L.	Vic.	27-Feb-15
43403	<i>Microdochium nivale</i>	<i>Lolium perenne</i>	Vic.	11-Nov-17



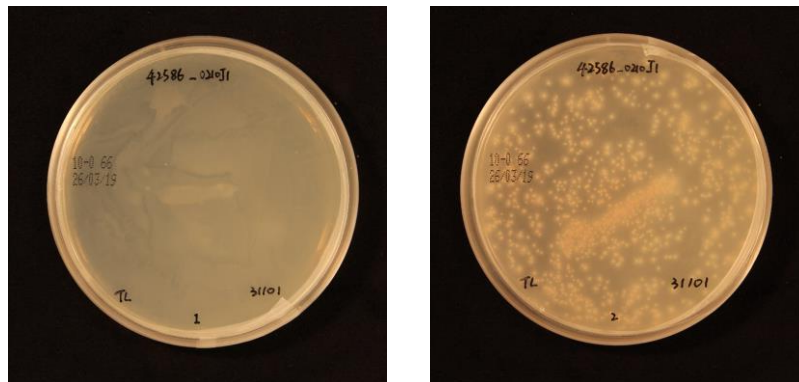
Supplementary Figure S1. Amplicons of the expected size (~ 400 bp) were produced using the DNA extracted from two (G2 and H2) of eight replicates of the 10^{-2} dilution (A2–H2). Results of the 10^{-3} dilutions were not shown since no amplicon was produced. A0: DNA ladder; A1: No template control; B1: Positive control, *Rhizobium leguminosarum* bv. *trifolii* WSM1325 DNA



Supplementary Figure S2. A single 110 Kb read containing the entire *P. polymyxa nif* operon (nine genes) of *P. polymyxa* YC0136 identified via BLAST analyses. The *nifH* gene was highlighted.



Supplementary Figure S3. Representative images of the in vitro bioprotection assay when challenging strain S02 (left) and S25 (middle) with *Fusarium verticillioides*. The control plate (pathogen-only) was shown on the right.



Supplementary Figure S4. Images of Potato Dextrose Agar plates containing samples of *Paenibacillus* sp. S02 co-incubated *F. verticillioides* (six hours). The first biological replicate (S02_treated_1, left) showed no visual growth of the pathogen, and only had three mapped fungal reads. The second biological replicate (S02_treated_2, right) had 1,492 mapped fungal reads.