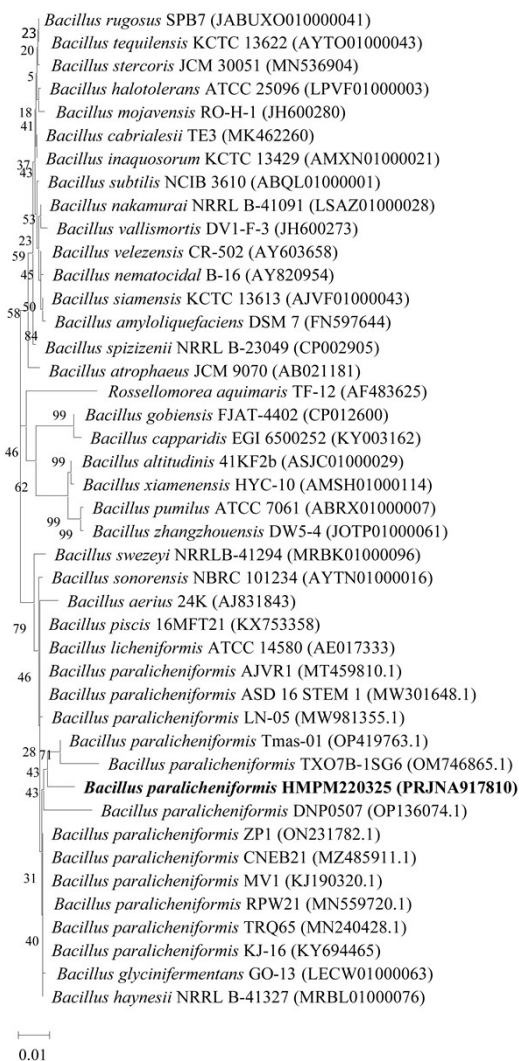
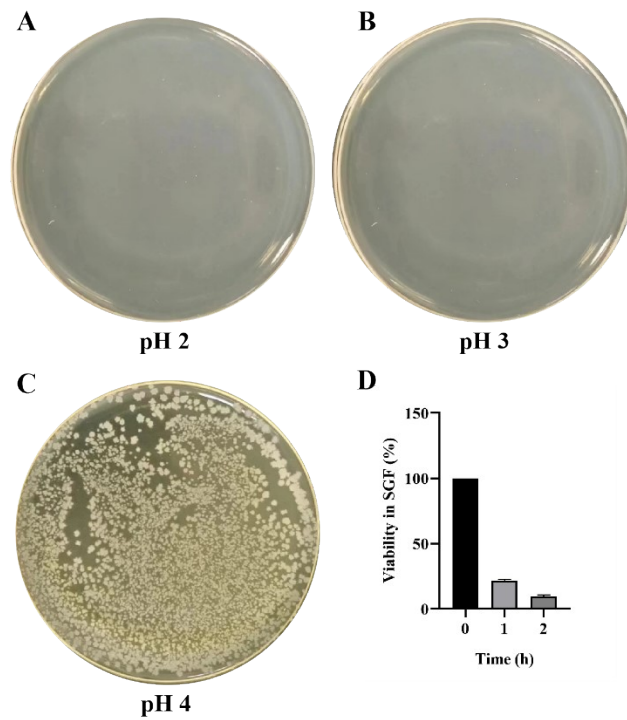


Supplementary Materials

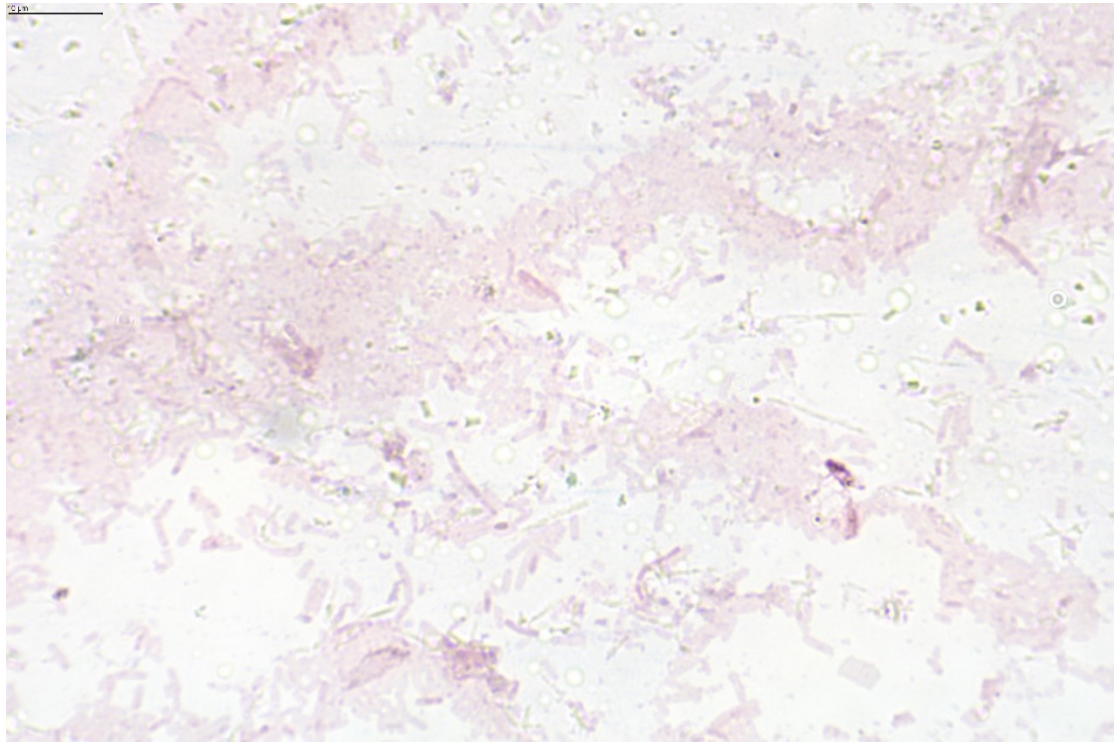
Supplemental Figures and Tables



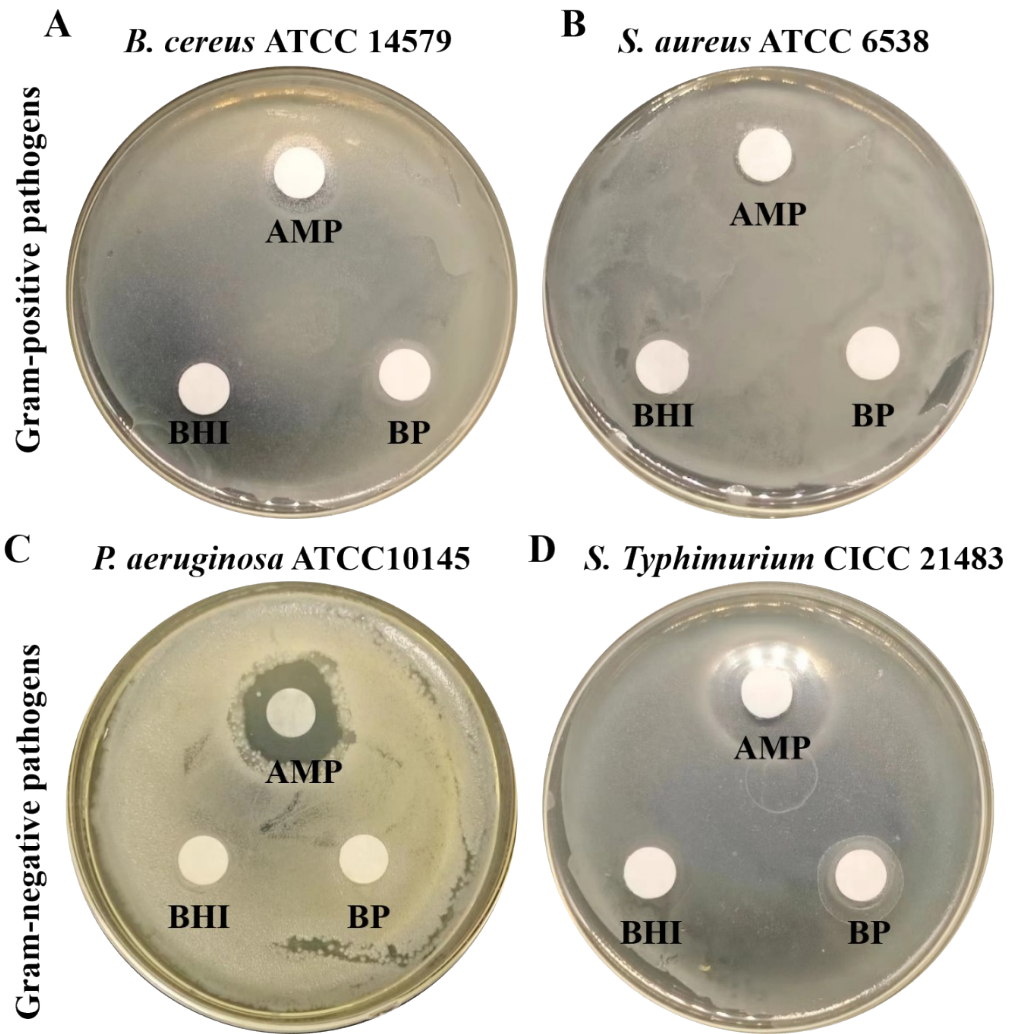
Supplementary Fig. 1 Phylogenetic analysis of *B. paralicheniformis* HMPM220325.



Supplementary Fig. 2 (A-C) Acid tolerance assay of *B. paralicheniformis* HMPM220325. (D) Viability of *B. paralicheniformis* HMPM220325 in simulated gastric fluid (SGF).



Supplementary Fig. 3 Schaeffer-Fulton staining of *B. paralicheniformis* HMPM220325.



Supplementary Fig. 4 Antimicrobial activity of *B. paralicheniformis* HMPM220325. (A) *B. cereus* ATCC 14579, (B) *S. aureus* ATCC 6538, (C) *P. aeruginosa* ATCC10145 and (D) *S. Typhimurium* CICC 21483. AMP, ampicillin; BHI, Brain Heart Infusion medium; BP, *B. paralicheniformis* HMPM220325's fermentation broth.

Supplementary Table 1 Examples of probiotic supplements containing *Bacillus* spp. available in global market.

Product	Strain (only <i>Bacillus</i> spp. are shown)	Country
Bactisubtil®	<i>B. cereus</i> IP 5832	France
BioKult®	<i>B. subtilis</i> PXN 21	United Kingdom
Biosporin®	<i>B. subtilis</i> 2335 and <i>B. licheniformis</i> 2336	Russia
Biovicerin®	<i>B. cereus</i> GM	Brazil
Sustenex®	<i>B. coagulans</i> GBI-30	United States
Nutrition essentials	<i>B. coagulans</i> 15B	United States
Probiotic		
LifeinU™	<i>B. subtilis</i> CU1	Europe
Just Thrive	<i>B. indicus</i> HU36™, <i>B. coagulans</i> SC-208, <i>B. clausii</i> SC-109, <i>B. subtilis</i> HU58™	United States
MegaSporeBiotic	<i>B. indicus</i> HU36™, <i>B. subtilis</i> HU58™, <i>B. coagulans</i> SC-208, <i>B. licheniformis</i> SL-307, <i>B. clausii</i> SC-109	United Kingdom
BioPlus 2B®	<i>B. subtilis</i> CH201/DSM5749 and <i>B. licheniformis</i> CH200/DSM5749	Denmark
GanedenBC ³⁰	<i>B. coagulans</i> GBI-30, 6086	United States
Bispan®	<i>B. polyfermenticus</i> SCD	South Korea

Supplementary Table 2 Assignment of proteins in the draft genome of *B. paralicheniformis* HMPM220325 to COG functional categories

COG Functional categories	No. of genes	% of total genes
Metabolism:		
Energy production and conversion (C)	184	42.31
Amino acid transport and metabolism (E)	356	
Nucleotide transport and metabolism (F)	100	
Carbohydrate transport and metabolism (G)	365	
Coenzyme transport and metabolism (H)	203	
Lipid transport and metabolism (I)	160	
Inorganic ion transport and metabolism (P)	215	
Secondary metabolites biosynthesis, transport and catabolism (Q)	84	
<i>Total</i>	1667	
Cellular Processes and Signalling:		
Cell cycle control, cell division, chromosome partitioning (D)	227	27.41
Cell wall/membrane/envelope biogenesis (M)	214	
Cell motility (N)	47	
Posttranslational modification, protein turnover, chaperones (O)	155	
Signal transduction mechanisms (T)	228	
Intracellular trafficking, secretion, and vesicular transport (U)	36	
Defense mechanisms (V)	128	
Extracellular structures (W)	5	
Cytoskeleton (Z)	6	
Mobilome: prophages, transposons (X)	34	
<i>Total</i>	1080	
Information Storage and Processing:		
Translation, ribosomal structure and biogenesis (J)	246	18.60
Transcription (K)	370	
Replication, recombination and repair (L)	117	
<i>Total</i>	733	
Poorly Characterized:		
General function prediction only (R)	292	11.68
Function unknown (S)	168	
<i>Total</i>	460	
Total number of genes	3940	

Supplementary Table 5 Putative virulence genes detected using Virulence Factor Database (VFDB) with role in classic physiological functions

Virulence gene	Protein	Description	COG category
<i>ClpC</i>	Endopeptidase Clp ATP-binding chain C	An ATPase promoting early escape from the phagosome of macrophages; ClpC is also required for adhesion and invasion, possibly by modulating the expression of InlA, InlB and ActA	O
<i>EF-Tu</i>	Elongation factor Tu	Surface-expressed elongation factor-Tu (EF-Tu) mediates attachment by interacting with host cell nucleolin	J
<i>Capsule</i>	NADP-dependent phosphogluconate dehydrogenase	Assisting in evading the host immune system by protecting bacteria from opsonophagocytosis and serum killing	G
<i>ClpP</i>	ATP-dependent Clp protease proteolytic subunit	Serine protease involved in proteolysis and is required for growth under stress conditions	O

Supplementary Table 6 Putative genes in *B. paralicheniformis* HMPM220325 involved in spore formation and germination

Function	Genes	Gene Len (bp)	Gene ID	
Spore germination	Ger(x)C family spore germination protein	1224	gene0470	
		1197	gene2264	
	Spore germination protein KA	1674	gene0469	
		1437	gene1241	
	Spore germination protein GerT	453	gene2365	
	Spore germination protein YndE	1101	gene2265	
	Spore germination protein YndD	1569	gene2267	
	Spore germination protein AA	1443	gene3596	
	Spore germination lipase LipC	639	gene0519	
Germination-specific N-acetylmuramoyl-L-alanine amidase CwID	714	gene0184		
Spore formation	Sporulation initiation phosphotransferase B	579	gene3048	
	Sporulation initiation phosphotransferase F	375	gene4024	
Pre-septation	Stage 0 sporulation protein YaaT	828	gene0046	
Post-septation	Stage II sporulation protein E	2490	gene0080	
		768	gene2586	
	Stage II sporulation protein M	657	gene2595	
		555	gene2771	
	Stage II sporulation protein P	1206	gene2843	
	Stage II sporulation protein D	981	gene3984	
	Stage II sporulation protein R	660	gene4005	
	Post-engulfment	Stage III sporulation protein AE	1206	gene2710
		Stage III sporulation protein AD	366	gene2711
		Stage III sporulation protein AC	207	gene2712
		Stage III sporulation protein AB	516	gene2713
Stage III sporulation protein AA		924	gene2714	
Stage IV sporulation protein A		1479	gene2515	
Stage IV sporulation protein B		1284	gene2694	
Stage V sporulation protein T		537	gene0070	
Stage V sporulation protein R		1410	gene1056	
Stage V sporulation protein D		1935	gene1771	
Stage V sporulation protein E	Stage V sporulation protein E	1026	gene1775	
		261	gene1953	
	Stage V sporulation protein SpoVS	261	gene1953	
	Stage V sporulation protein K	966	gene2059	
	Stage V sporulation protein AE	603	gene2580	
	351	gene2581		
	Stage V sporulation protein AD	1020	gene2582	
	Stage V sporulation protein AC	450	gene2583	
	Stage V sporulation protein AF	1473	gene2579	

		1455	gene2760
	Stage V sporulation protein AB	426	gene2584
	Stage V sporulation protein AA	621	gene2585
	Stage V sporulation protein B	1554	gene3017
	Stage VI sporulation protein F	258	gene1339
Spore coat formation and sporulation regulation	KinB signaling pathway activation protein	600	gene0187
	Stage 0 sporulation protein YaaT, Cell fate regulator YaaT, PSP1 superfamily (controls sporulation, competence, biofilm development)	828	gene0046
	Spore germination protein GerPA/GerPF (inner spore coat)	219	gene1216
		222	gene1221
		207	gene1258
		222	gene3468
	Spore germination protein GerPB, DUF2539 family (inner spore coat)	246	gene1220
	Spore germination protein GerPC (inner spore coat)	615	gene1219
	Spore germination protein GerPD (inner spore coat)	183	gene1218
	Spore germination protein GerPE (inner spore coat)	384	gene1217
	RNA polymerase sporulation specific sigma factor SigK	726	gene2870
		270	gene2881
	Sporulation inhibitor of replication protein SirA	438	gene2113
	RNA polymerase sporulation specific sigma factor SigF	768	gene2586
	Spore maturation protein A	588	gene2558
	Spore maturation protein B	537	gene2557
	Spore cortex-lytic enzyme CwlJ	429	gene0365
	Spore cortex-lytic enzyme SleB	966	gene2528
	Spore germination protein YpeB	1353	gene2527
Sporulation-specific extracellular nuclease NucB	429	gene2107	
3'-5' exonuclease KapD, inhibitor of KinA- controlled sporulation	618	gene3437	
Spore coat protein rfbE	1092	gene0850	
Spore coat protein CotF	648	gene1027	
Spore coat associated protein CotJA	234	gene1200	
Spore coat protein CotJB	264	gene1201	
Spore coat protein CotO	480	gene1330	
Spore coat protein CotZ	450	gene1331	

Spore coat protein CotY	483	gene1332
Spore coat protein CotV/CotX	513	gene1333
Spore coat protein W	405	gene1334
Spore coat protein CotV	387	gene1335
Spore coat protein YsxE	1023	gene3068
Spore coat protein GerQ	537	gene4062
Endospore coat-associated protein YutH	1005	gene3519
Endospore coat-associated protein YheD	1083	gene1112
Inner spore coat protein H	1086	gene1224
Sporulation protein cse60	183	gene3263
Gamma-type small acid-soluble spore protein	165	gene0938
Alpha/beta-type small acid-soluble spore protein	204	gene1106
	198	gene1584
	213	gene3209
Small acid-soluble spore protein Tlp	237	gene2125
Small acid-soluble spore protein H	180	gene3032
Small acid-soluble spore protein SspI	216	gene3127
Sporulation membrane protein YtaF	633	gene3167
Spore transcriptional regulator GerE	225	gene3101

Supplementary Table 7 Antineoplastic genes identified and their location in the *B. paralicheniformis* HMPM220325 genome

Resistance	Gene ID	KO ID	KO Name	KO Description
Antifolate resistance	gene0737	K00602	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]
	gene1254	K00297	metF, MTHFR	methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]
	gene2106	K00560	thyA, TYMS	thymidylate synthase [EC:2.1.1.45]
	gene2414	K00287	DHFR, folA	dihydrofolate reductase [EC:1.5.1.3]
	gene3998	K00600	glyA, SHMT	glycine hydroxymethyltransferase [EC:2.1.2.1]
Platinum drug resistance	gene3665	K17686	copA, ctpA, ATP7	P-type Cu ⁺ transporter [EC:7.2.2.8]