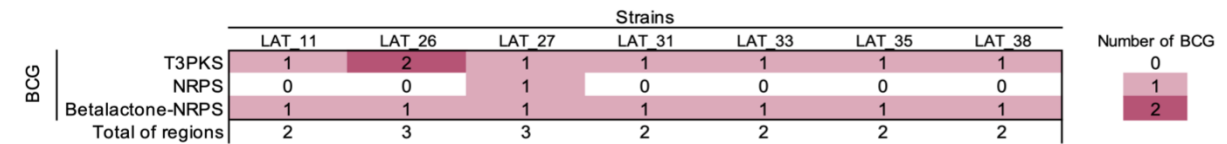


Supplementary Material

Supplementary Figures

a



b

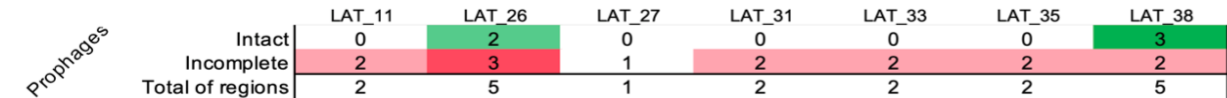


Figure S1. a) Biosynthetic gene clusters (BGCs) observed in *Anoxybacillus* strains using antiSMASH 5.0. Blank boxes indicate the absence of BGCs, light pink boxes indicate one BGC, and dark pink boxes indicate two related BGCs. b) Prophages identified in the strains using PHASTER. Green boxes indicate intact prophages, and pink boxes indicate questionable prophages.

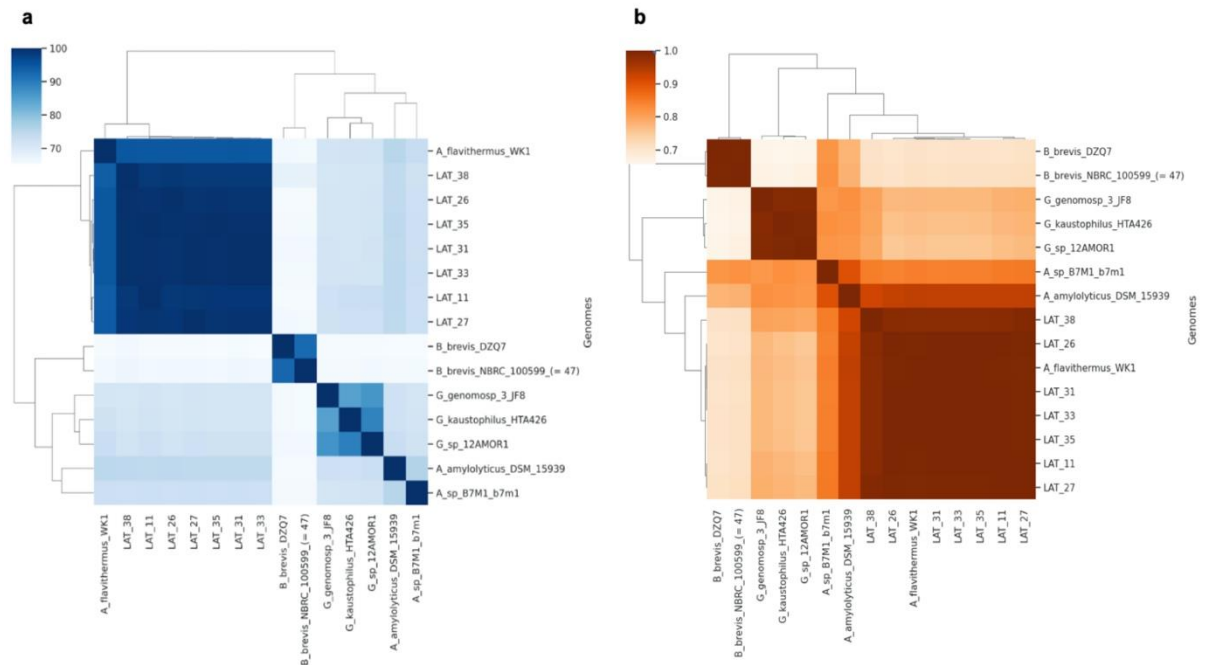


Figure S2. Genome comparison of different *Anoxybacillus* strains and Bacillaceae members based on ANI and TETRA values (%). Based on the ANI values, the strains were grouped into two clusters; the Antarctic strains clustered with *A. flavithermus* WK1 (a). The same pattern was observed using TETRA values (b).

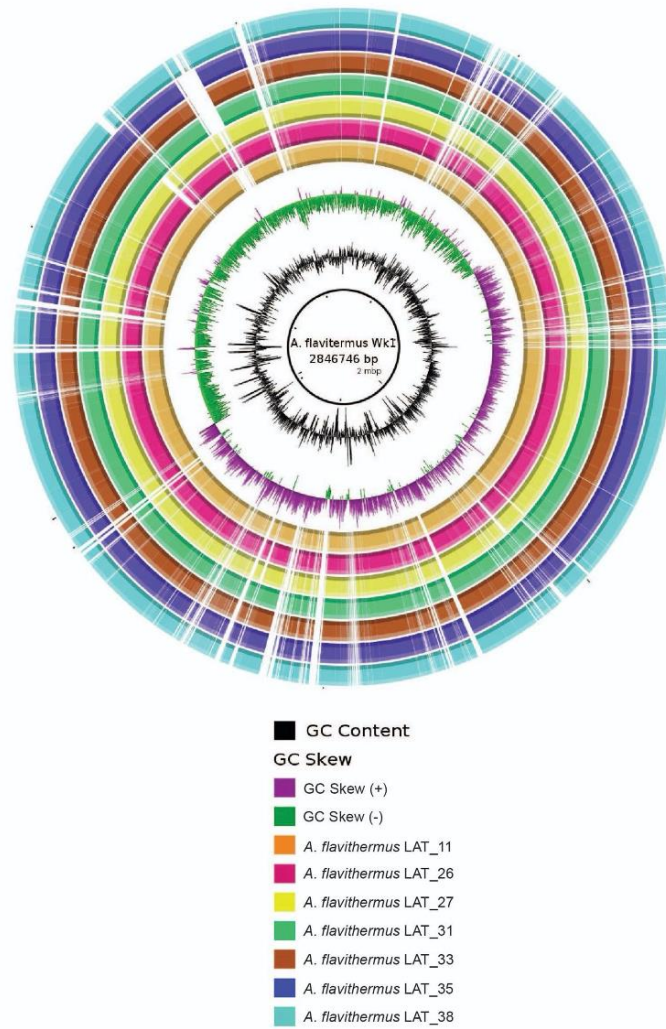


Figure S3. Circular visualization generated by BRIG for comparing the genomes of *Anoxybacillus* strains using *A. flavithermus* WK1 (complete genome) as the reference strain. The inner black circle contains the reference genome, and the intensity of each color indicates the similarity between the strains.

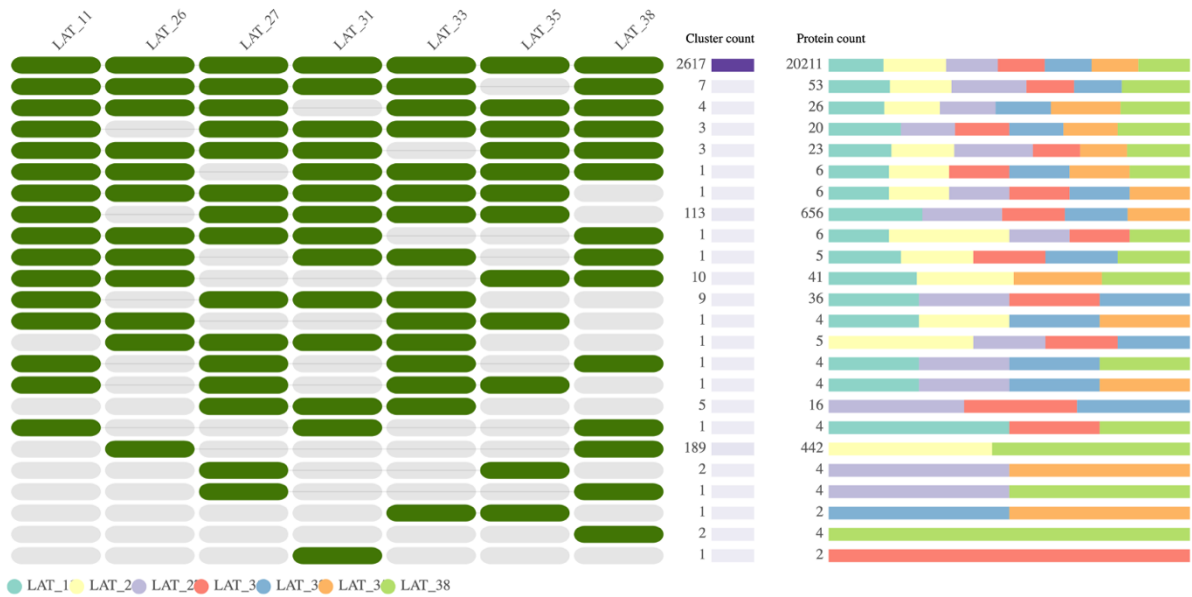


Figure S4. Orthologous groups belonging to the seven *Anoxybacillus* strains analyzed in the present study. From left to right: The orthologous groups present in the genomes; dark green color represents the presence of orthologous groups in each strain, while light gray color represents their absence. Number of protein orthologous groups shared in the genomes, marked with dark lilac in the preceding columns “Cluster count.” Total number of proteins (Protein count column) recorded in the shared orthologous groups; the colors represent the proportion of proteins belonging to each strain (light blue = LAT_11; yellow = LAT_26; lilac = LAT_27; red = LAT_31; blue = LAT_33; orange = LAT_35; and green = LAT_38).

2 Supplementary Tables

Table S1. Published data retrieved from databases used in the systematic review of the genus *Anoxybacillus*

Authors	Year	Reference	Link
Acer et al. [82]	2015	Acer Ö, Bekler FM, Pirinçcioğlu H, Güven RG, Güven K. Purification and Characterization of Thermostable and Detergent-Stable α -Amylase from <i>Anoxybacillus</i> sp. AH1. Food Technol Biotechnol. 2016 , 54, 70-77.	https://pubmed.ncbi.nlm.nih.gov/27904395/ . accessed on 30 June 2021.
Al-Kahem Al-Balawi Al-balawi et al. [83]	2017	Al-Kahem Al-Balawi TH, Wood AL, Solis A, Cooper T, Barabote RD. <i>Anoxybacillus</i> sp. Strain UARK-01, a New Thermophilic Soil Bacterium with Hyperthermostable Alkaline Laccase Activity. Curr Microbiol. 2017 , 74, 762-771.	https://pubmed.ncbi.nlm.nih.gov/28389772/ . accessed on 30 June 2021.
Atanassova et al. [84]	2008	Atanassova M, Derekova A, Mandeva R, Sjöholm C, Kambourova M. <i>Anoxybacillus bogrovensis</i> sp. nov., a novel thermophilic bacterium isolated from a hot spring in Dolni Bogrov, Bulgaria. Int J Syst Evol Microbiol. 2008 , 58, 2359-62.	https://pubmed.ncbi.nlm.nih.gov/18842856/ . accessed on 30 June 2021.
Belduz et al. [85]	2003	Belduz AO, Dulger S, Demirbag Z. <i>Anoxybacillus gonensis</i> sp. nov., a moderately thermophilic, xylose-utilizing, endospore-forming bacterium. Int J Syst Evol Microbiol. 2003 , 53, 1315-1320.	https://pubmed.ncbi.nlm.nih.gov/13130012/ . accessed on 30 June 2021.
Chai et al. [86]	2001	Chai YY, Kahar UM, Md Salleh M, Md Illias R, Goh KM. Isolation and characterization of pullulan-degrading <i>Anoxybacillus</i> species isolated from Malaysian hot springs. Environ Technol. 2012 , 33, 1231-8.	https://pubmed.ncbi.nlm.nih.gov/22856294/ . accessed on 30 June 2021.
Chan et al. [77]	2016	Chan CS, Sin LL, Chan KG, Shamsir MS, Manan FA, Sani RK, Goh KM. Characterization of a glucose-tolerant β -glucosidase from <i>Anoxybacillus</i> sp. DT3-1. Biotechnol Biofuels. 2016 , 9, 174.	https://pubmed.ncbi.nlm.nih.gov/27555880/ . accessed on 30 June 2021.
Chen et al. [87]	2004	Chen XG, Stabnikova O, Tay JH, Wang JY, Tay ST. Thermoactive extracellular proteases of <i>Geobacillus caldoproteolyticus</i> , sp. nov., from sewage sludge. Extremophiles. 2004 , 8, 489-98.	https://pubmed.ncbi.nlm.nih.gov/15322950/ . accessed on 30 June 2021.
Chen et al. [88]	2015	Chen J, Zheng J, Li Y, Hao HH, Chen JM. Characteristics of a novel thermophilic heterotrophic bacterium, <i>Anoxybacillus contaminans</i> HA, for nitrification-aerobic denitrification. Appl Microbiol Biotechnol. 2015 , 99, 10695-702.	https://pubmed.ncbi.nlm.nih.gov/26293335/ . accessed on 30 June 2021.
Cheng et al. [89]	2021	Cheng JH, Wang Y, Zhang XY, Sun ML, Zhang X, Song XY, Zhang YZ, Zhang Y, Chen XL. Characterization and Diversity Analysis of the Extracellular Proteases of Thermophilic <i>Anoxybacillus</i>	https://pubmed.ncbi.nlm.nih.gov/33796092/ . accessed on 30 June 2021.

		caldiproteolyticus 1A02591 From Deep-Sea Hydrothermal Vent Sediment. <i>Front Microbiol.</i> 2021 , <i>12</i> , 643508.	
Cihan et al. [90]	2011	Cihan AC, Ozcan B, Cokmus C. <i>Anoxybacillus salavatliensis</i> sp. nov., an α -glucosidase producing, thermophilic bacterium isolated from Salavatli, Turkey. <i>J Basic Microbiol.</i> 2011 Apr;51(2):136-46.	https://pubmed.ncbi.nlm.nih.gov/21077116/ . accessed on 30 June 2021.
Cihan et al. [91]	2014	Cihan AC, Cokmus C, Koc M, Ozcan B. <i>Anoxybacillus calidus</i> sp. nov., a thermophilic bacterium isolated from soil near a thermal power plant. <i>Int J Syst Evol Microbiol.</i> 2014 Jan;64(Pt 1):211-219. doi: 10.1099/ijs.0.056549-0. Epub 2013 Sep 19. Erratum in: <i>Int J Syst Evol Microbiol.</i> 2014 , <i>64</i> , 2926. Erratum in: <i>Int J Syst Evol Microbiol.</i> 2014 Jul;64(Pt 7):2508.	https://pubmed.ncbi.nlm.nih.gov/24052627/ . accessed on 30 June 2021.
Clerck et al. [92]	2004	Clerck E, Rodríguez-Díaz M, Vanhoutte T, Heyrman J, Logan NA, De Vos P. <i>Anoxybacillus contaminans</i> sp. nov. and <i>Bacillus gelatini</i> sp. nov., isolated from contaminated gelatin batches. <i>Int J Syst Evol Microbiol.</i> 2004 , <i>54</i> , 941-946.	https://pubmed.ncbi.nlm.nih.gov/15143046/ . accessed on 30 June 2021.
Coorevits et al. [93]	2012	Coorevits A, Dinsdale AE, Halket G, Lebbe L, De Vos P, Van Landschoot A, Logan NA. Taxonomic revision of the genus <i>Geobacillus</i> : emendation of <i>Geobacillus</i> , <i>G. stearothermophilus</i> , <i>G. jurassicus</i> , <i>G. toebii</i> , <i>G. thermodenitrificans</i> and <i>G. thermoglucosidans</i> (nom. corrig., formerly 'thermoglucosidasius'); transfer of <i>Bacillus thermantarcticus</i> to the genus as <i>G. thermantarcticus</i> comb. nov.; proposal of <i>Caldibacillus debilis</i> gen. nov., comb. nov.; transfer of <i>G. tepidamans</i> to <i>Anoxybacillus</i> as <i>A. tepidamans</i> comb. nov.; and proposal of <i>Anoxybacillus caldiproteolyticus</i> sp. nov. <i>Int J Syst Evol Microbiol.</i> 2012 , <i>62</i> , 1470-1485.	https://pubmed.ncbi.nlm.nih.gov/21856988/ . accessed on 30 June 2021.
Deep et al. [94]	2013	Deep K, Poddar A, Das SK. <i>Anoxybacillus suryakundensis</i> sp. nov, a moderately thermophilic, alkalitolerant bacterium isolated from hot spring at Jharkhand, India. <i>PLoS One.</i> 2013 , <i>8</i> , e85493. doi: 10.1371/journal.pone.0085493. PMID: 24376881; PMCID: PMC3869905.	https://pubmed.ncbi.nlm.nih.gov/24376881/ . accessed on 30 June 2021.
Derekova et al. [95]	2007	Derekova A, Sjøholm C, Mandeva R, Kambourova M. <i>Anoxybacillus rupiensis</i> sp. Nov., a novel thermophilic bacterium isolated from Rupi basin (Bulgaria). <i>Extremophiles.</i> 2007 , <i>11</i> , 577-83. doi: 10.1007/s00792-007-0071-4. Epub 2007 May 16. PMID: 17505776.	https://pubmed.ncbi.nlm.nih.gov/17505776/ . accessed on 30 June 2021.
Dulger et al. [96]	2004	Dulger S, Demirbag Z, Belduz AO. <i>Anoxybacillus ayderensis</i> sp. nov. and <i>Anoxybacillus kestanbolensis</i> sp. nov. <i>Int J Syst Evol Microbiol.</i> 2004 , <i>54</i> , 1499-1503. doi: 10.1099/ijs.0.02863-0. PMID: 15388701.	https://pubmed.ncbi.nlm.nih.gov/15388701/ . accessed on 30 June 2021.

Filippidou et al. [97]	2016	Filippidou S, Jaussi M, Junier T, Wunderlin T, Jeanneret N, Palmieri F, Palmieri I, Roussel-Delif L, Vieth-Hillebrand A, Vetter A, Chain PS, Regenspurg S, Junier P. <i>Anoxybacillus geothermalis</i> sp. nov., a facultatively anaerobic, endospore-forming bacterium isolated from mineral deposits in a geothermal station. <i>Int J Syst Evol Microbiol.</i> 2016 , 66, 2944-2951. doi: 10.1099/ijsem.0.001125. Epub 2016 Apr 28. PMID: 27126386.	https://pubmed.ncbi.nlm.nih.gov/27126386/ . accessed on 30 June 2021.
Gao et al. [98]	2010	Gao Y, Dai J, Peng H, Liu Y, Xu T. Isolation and characterization of a novel organic solvent-tolerant <i>Anoxybacillus</i> sp. PGDY12, a thermophilic Gram-positive bacterium. <i>J Appl Microbiol.</i> 2011 , 110, 472-8. doi: 10.1111/j.1365-2672.2010.04903.x. Epub 2010 Dec 13. PMID: 21155953.	https://pubmed.ncbi.nlm.nih.gov/21155953/ . accessed on 30 June 2021.
Gul-Guven et al. [99]	2008	Gul-Guven R, Guven K, Poli A, Nicolaus B. <i>Anoxybacillus kamchatkensis</i> subsp. <i>asaccharedens</i> subsp. nov., a thermophilic bacterium isolated from a hot spring in Batman. <i>J Gen Appl Microbiol.</i> 2008 , 54, 327-34. doi: 10.2323/jgam.54.327. PMID: 19164875.	https://pubmed.ncbi.nlm.nih.gov/19164875/ . accessed on 30 June 2021.
Heinen et al. [2]	1982	Heinen W, Lauwers AM, Mulders JW. <i>Bacillus flavothermus</i> , a newly isolated facultative thermophile. <i>Antonie Van Leeuwenhoek.</i> 1982 , 48, 265-72. doi: 10.1007/BF00400386. PMID: 7125637.	https://pubmed.ncbi.nlm.nih.gov/7125637/ . accessed on 30 June 2021.
Inan et al. [100]	2012	Inan K, Belduz AO, Canakci S. <i>Anoxybacillus kaynarzensis</i> sp. nov., a moderately thermophilic, xylanase producing bacterium. <i>J Basic Microbiol.</i> 2013 , 53, 410-9. doi: 10.1007/jobm.201100638. Epub 2012 Jun 26. PMID: 22736500.	https://pubmed.ncbi.nlm.nih.gov/22736500/ . accessed on 30 June 2021.
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Khan et al. [103]	2018	Khan IU, Habib N, Xiao M, Devi AM, Habib M, Hejazi MS, Salam N, Zhi XY, Li WJ. <i>Anoxybacillus sediminis</i> sp. nov., a novel moderately thermophilic bacterium isolated from a hot spring. <i>Antonie Van Leeuwenhoek.</i> 2018 , 111, 2275-2282. doi: 10.1007/s10482-018-1118-5. Epub 2018 Jun 21. PMID: 29931494.	https://pubmed.ncbi.nlm.nih.gov/29931494/ . accessed on 30 June 2021.

Khanna et al. [104]	2021	Khanna K, Mishra KP, Chanda S, Ganju L, Singh SB, Kumar B. Effect of Synbiotics on Amelioration of Intestinal Inflammation Under Hypobaric Hypoxia. <i>High Alt Med Biol.</i> 2021 , 22, 32-44.	https://www.liebertpub.com/doi/10.1089/ham.2020.0062?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%20%20pubmed . accessed on 30 June 2021.
Lee et al. [105]	2012	Lee, Sang-Jae & Lee, Yong-Jik & Ryu, Naeun & Park, Seulki & Jeong, Haeyoung & Lee, Sang Jun & Kim, Byoung-Chan & Lee, Dong-Woo & Lee, Han-Seung. Draft Genome Sequence of the Thermophilic Bacterium <i>Anoxybacillus kamchatkensis</i> G10. <i>Journal of bacteriology.</i> 2012 , 194, 6684-5. 10.1128/JB.01877-12.	https://www.researchgate.net/publication/233396557_Draft_Genome_Sequence_of_the_Thermophilic_Bacterium_Anoxybacillus_kamchatkensis_G10 . accessed on 30 June 2021.
Matpan-Bekler e Güven [106]	2014	Matpan-Bekler, Fatma & Guven, Kemal. (2014). Isolation and production of thermostable α -amylase from thermophilic <i>Anoxybacillus</i> sp. KP1 from Diyadin hot spring in Ağrı, Turkey. <i>Biologia.</i> 2014 , 69, 419-427.	https://www.researchgate.net/publication/260450268_Isolation_and_production_of_thermostable_alpha-amylase_from_thermophilic_Anoxybacillus_sp_KP1_from_Diyadin_hot_spring_in_Agri_Turkey . accessed on 30 June 2021.
Matpan-Bekler et al. [107]	2018	Matpan-Bekler, Fatma & Yalaz, Secil & Guven, Kemal. Molecular characterisation and numerical analysis of novel moderately thermophile <i>Anoxybacillus</i> sp. FMB1. <i>Romanian Biotechnological Letters.</i> 2018 , 23,13964-13975.	https://www.researchgate.net/publication/326416833_Molecular_characterisation_and_numerical_analysis_of_novel_moderately_thermophile_Anoxybacillus_sp_FMB1 . accessed on 30 June 2021.
Mittal at el. [108]	2017	Mittal, Parul & Saxena, Rituja & Sharma, Vineet. Draft Genome Sequence of <i>Anoxybacillus mongoliensis</i> Strain MB4, a Sulfur-Utilizing Aerobic Thermophile Isolated from a Hot Spring in Tattapani, Central India. <i>Genome Announcements.</i> 2017 , 5, e01709-16. 10.1128/genomeA.01709-16.	https://www.researchgate.net/publication/314190462_Draft_Genome_Sequence_of_Anoxybacillus_mongoliensis_Strain_MB4_a_Sulfur-Utilizing_Aerobic_Thermophile_Isolated_from_a_Hot_Spring_in_Tattapani_Central_India . accessed on 30 June 2021.
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Namsaraev et al. [110]	2010	Namsaraev ZB, Babasanova OB, Dunaevsky YE, Akimov VN, Barkhutova DD, Gorlenko VM, Namsaraev BB. <i>Anoxybacillus mongoliensis</i> sp. nov., a novel thermophilic proteinase producing bacterium isolated from alkaline hot spring, central Mongolia. <i>Mikrobiologiya.</i> 2010 , 79, 516-23. PMID: 21058505.	https://pubmed.ncbi.nlm.nih.gov/21058505/ . accessed on 30 June 2021.
Ottesen et al. [111]	2016	Ottesen A, Ramachandran P, Reed E, White JR, Hasan N, Subramanian P, Ryan G, Jarvis K, Grim C, Daquigan N, Hanes D, Allard M, Colwell R, Brown E, Chen Y. Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. <i>BMC Microbiol.</i> 2016 , 16, 275.	https://bmcmicrobiol.biomedcentral.com/articles/10.1186/s12866-016-0894-1 . accessed on 30 June 2021.

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Pikuta et al. [1]	2000	Pikuta E, Lysenko A, Chuvilskaya N, Mendrock U, Hippe H, Suzina N, Nikitin D, Osipov G, Laurinavichius K. Anoxybacillus pushchinensis gen. nov., sp. nov., a novel anaerobic, alkaliphilic, moderately thermophilic bacterium from manure, and description of Anoxybacillus flavitherms comb. nov. <i>Int J Syst Evol Microbiol.</i> 2000 , 50, 2109-2117.	https://pubmed.ncbi.nlm.nih.gov/11155986/ . accessed on 30 June 2021.
Poli et al. [10]	2006	Poli A, Esposito E, Lama L, Orlando P, Nicolaus G, de Appolonia F, Gambacorta A, Nicolaus B. Anoxybacillus amylolyticus sp. nov., a thermophilic amylase producing bacterium isolated from Mount Rittmann (Antarctica). <i>Syst Appl Microbiol.</i> 2006 , 29, 300-7.	https://pubmed.ncbi.nlm.nih.gov/16682297/ . accessed on 30 June 2021.
Poli et al. [60]	2009	Poli A, Romano I, Cordella P, Orlando P, Nicolaus B, Ceschi Berrini C. Anoxybacillus thermarum sp. nov., a novel thermophilic bacterium isolated from thermal mud in Euganean hot springs, Abano Terme, Italy. <i>Extremophiles.</i> 2009 , 13, 867-74.	https://pubmed.ncbi.nlm.nih.gov/19710998/ . accessed on 30 June 2021.
Reis et al. [113]	2020	Reis SVD, Beys-da-Silva WO, Tirloni L, Santi L, Seixas A, Termignoni C, Silva MVD, Macedo AJ. The extremophile Anoxybacillus sp. PC2 isolated from Brazilian semiarid region (Caatinga) produces a thermostable keratinase. <i>J Basic Microbiol.</i> 2020 , 60, 809-815.	https://pubmed.ncbi.nlm.nih.gov/32602226/ . accessed on 30 June 2021.
Sahm et al. [114]	2013	Sahm K, John P, Nacke H, Wemheuer B, Grote R, Daniel R, Antranikian G. High abundance of heterotrophic prokaryotes in hydrothermal springs of the Azores as revealed by a network of 16S rRNA gene-based methods. <i>Extremophiles.</i> 2013 , 17, 649-62.	https://link.springer.com/article/10.1007/s00792-013-0548-2 . accessed on 30 June 2021.
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Xia et al. [117]	2015	Xia, Wenjie and Dong, Hao and Zheng, Chenggang and Cui, Qingfeng and He, Panqing and Tang, Yongchun. Hydrocarbon degradation by a newly isolated thermophilic Anoxybacillus sp. with bioemulsifier production and new alkB genes. <i>RSC Adv.</i> 2015 , 5, 102367-102377. The Royal Society of Chemistry.	https://pubs.rsc.org/en/content/articlelanding/2015/ra/c5ra17137g#!divAbstract . accessed on 30 June 2021.

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Zhang et al. [120]	2011	Zhang CM, Huang XW, Pan WZ, Zhang J, Wei KB, Klenk HP, Tang SK, Li WJ, Zhang KQ. <i>Anoxybacillus tengchongensis</i> sp. nov. and <i>Anoxybacillus eryuanensis</i> sp. nov., facultatively anaerobic, alkalitolerant bacteria from hot springs. <i>Int J Syst Evol Microbiol.</i> 2011 , 61, 118-122.	https://pubmed.ncbi.nlm.nih.gov/20173008/ . accessed on 30 June 2021.
Zhang et al. [121]	2013	Zhang XQ, Zhang ZL, Wu N, Zhu XF, Wu M. <i>Anoxybacillus vitaminiphilus</i> sp. nov., a strictly aerobic and moderately thermophilic bacterium isolated from a hot spring. <i>Int J Syst Evol Microbiol.</i> 2013 , 63, 4064-4071.	https://pubmed.ncbi.nlm.nih.gov/23728374/ . accessed on 30 June 2021.
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Table S2. List of described species of the genus *Anoxybacillus* and their characteristics (identification, isolation, and growth)

Reference	Species	Location	Source	Substrate	Culture medium	Growth condition*	Temperature range	Optimal temperature	pH range	Optimal pH	Genome size	%GC	Accession number
Pikuta et al. [1]	<i>A. pushchinoensis</i> K1	Moscow, Russia	Fertilizer samples	Manure samples	Anaerobic basal medium with yeast extract and glucose as carbon source, added after sterilization	An/F. a	37–66°C	62°C	8.0–10.5	9.5–9.7	-	42.20%	NR_037100
Heinen et al. [2]	<i>A. flavithermus</i>	North Island, New Zealand	Hot spring	Rock surface grit	Bouillon agar with 5% casein	F. a	30–72°C	60–65°C	5.5–9.0	7.0	-	61%	-
Belduz et al. [85]	<i>A. gonensis</i> G2	Balikesir, Turkey	Hot spring	Mud and water	Nutrient broth for enrichment	F. an	40–70°C	55–60°C	6.0–10.0	7.5–8.0	-	57%	NR_025667
Dulger et al. [96]	<i>A. ayderensis</i> AB4	Rize, Turkey	Hot spring	Water	Nutrient broth for enrichment	F. an	40–70°C	50°C	6.0–11.0	7.5–8.5	-	54%	AF001963
Chen et al. [88]	<i>A. caldiproteolyticus</i> SF03	Seletar, Singapore	Sewage sludge samples	Sewage sludge	Nutrient broth agar, tryptic soy agar, and plate count agar	A	35–65°C	60°C	6.0–9.0	6.5	-	-	AY327448
Clerck et al. [92]	<i>A. contaminans</i> LMG21881	France	French production plant	Gelatin samples	Nutrient agar supplemented with 1–2% gelatin	F. an	50–60°C	50°C	4.0–10.0	7.0	-	44.40%	NR_029006.1
Dulger et al. [96]	<i>A. kestanbolensis</i> K4	Çanakkale, Turkey	Hot spring	Water	Nutrient broth for enrichment	F. an	40–70°C	50–55°C	6.0–10.5	7.5–8.5	-	50%	AY248711
Yumoto et al. [119]	<i>A. voinovskiensis</i> TH3	Kamchatka, Russia	Hot spring	Water	TH agar medium, containing 5 g peptone, 3 g yeast extract, 5 g NaCl, 15 g agar, 3.5 mg EDTA, 3 mg ZnSO ₄ ·7H ₂ O, 10 mg FeSO ₄ ·7H ₂ O, 2 mg MnSO ₄ ·nH ₂ O, 1 mg CuSO ₄ ·5H ₂ O, 2 mg Co(NO ₃) ₂ ·6H ₂ O and 1 mg H ₃ BO ₃ .	F. a	30–64°C	54°C	7.0–8.0	ND	-	43.90%	AB110008

Kevbrin et al. [102]	<i>A. kamchatkensis</i> JW/VK-KG4T	Kamchatka, Russia	Hot spring of the Valley of Geysers	Water sediment	Anaerobic mineral bicarbonate buffered medium	F. a	38–67°C	57–62°C	5.7–9.9	6.8–8.5	-	42.30%	AF510985
Poli et al. [10]	<i>A. amylolyticus</i> MR3C	Rittmann Mount, Antarctica	Geothermal soil	Geothermal soil	Enrichment media (A) containing Oxoid yeast extract (varying from 0.3% to 0.6%) and NaCl (0.3–0.6%) at pH 5.6 and pH 4.0	F. an	45–65°C	61°C	5.0–6.5	5.6	-	43.50%	AJ618979
Derekova et al. [95]	<i>A. rupienses</i> DSM 17127T	Rupi Basin, Bulgaria	Hot spring	Water and soil	PY medium (pH 7.0) containing peptone, 2 g l ⁻¹ and yeast extract, 1 g l ⁻¹	A	35–67°C	55°C	5.5–8.5	6.0–6.5	-	41.70%	AJ879076
Atanassova et al. [84]	<i>A. bogrovensis</i> BT-13	Sofia, Bulgaria	Hot spring	Mud	PY medium (pH 7.0) containing (g l ⁻¹): peptone, 2 and yeast extract, 1 Plated on PY agar (pH 7.0)	F. an	40–69°C	65°C	6.5–10.0	8.0	-	44.10%	AM409184.1
Gul-Guven et al. [99]	<i>A. kamchatkensis</i> subsp. <i>asaccharedens</i> KG8	Batman, Turkey	Hot spring	Mud	Medium (C) nutrient broth	A	35–65°C	55°C	5.5–9.5	7.5	-	-	AM999779
Kacagan et al. [101]	<i>A. pushchinoensis</i> A8	Turkey	Hot spring	Mud and water	Nutrient agar	F. an	50–60°C	55°C	6.5–11.0	6.5	-	-	AY248715
Poli et al. [60]	<i>A. thermarum</i> AF/04	Padova, Italy	Hot spring	Thermal mud	Enrichment media (A) containing (% values are in w/v): peptone, 0.8%; yeast extract, 0.4%; and NaCl 0.2%	A	55–67°C	65°C	6.0–7.5	7.2	-	53.50%	AM402982
Namsaraev et al. [110]	<i>A. mongoliensis</i> T4	Arkhangai Aimag, Central Mongolia	Hot spring	Water sediment	Aerobic medium containing (g l ⁻¹): KH ₂ PO ₄ , 0.5; NH ₄ Cl, 0.5; KCl, 0.5; NaCl, 0.5; Na ₂ SO ₄ , 0.5; MgSO ₄ ·7H ₂ O, 0.2; yeast extract, 1; peptone, 1; and glucose, 5; in addition	F. an	35–70°C	60°C	5.5–10.5	8.0	-	44%	EF654664

					to trace element solution, 1 ml								
Cihan et al. [90]	<i>A. salavatliensis</i> A343	Aydin, Turkey	Well pipeline sediment	Sediment	<i>Geobacillus thermoglucosidasius</i> medium (MI) containing 1% soluble starch (pH 7.0)	F. an	37–69°C	60°C	5.5–9.5	8.0–9.0	-	45.10%	EU326496
Gao et al. [98]	<i>Anoxybacillus</i> sp. PGDY12	Yunnan, China	Hot spring	Water sediment	LB medium supplemented with 0.05% toluene	A	65°C	55°C	5.0–10.0	7.0	-	-	FJ527829
Zhang et al. [120]	<i>A. eryuanensis</i> E-112	Yunnan, China	Hot spring	Water	LB medium	F. a	30–70°C	55°C	7.0–11.0	8.0	-	42.60%	GQ153549
Chai et al. [86]	<i>Anoxybacillus</i> sp. SK3-4	Sungai Klah, Malaysia	Hot spring	Water	Modified <i>Thermus</i> medium	A/An	30–65°C	55°C	6.0–10.0	7.0	-	42%	GQ184213
Zhang et al. [120]	<i>A. tengchongensis</i> T-11	Yunnan, China	Hot spring	Water	LB medium	F. a	30–75°C	50°C	7.0–11.0	8.5	-	41.10%	FJ438370
Coorevits et al. [95]	<i>A. caldiproteolyticus</i> R-35652	Singapore	Water reclamation plant	Sewage sludge	TSA	A	37–70°C	60°C	5.0–9.0	6.5–7.0	-	40.20%	NR_116989
Lee et al. [107]	<i>A. kamchatkensis</i> G10	Indonesia	Hot spring	-	-	F. an	-	-	-	-	2,962,568 bp	41.35%	ALJT01000000
Inan et al. [102]	<i>A. kaynarcensis</i> D1021	Izmir, Turkey	Hot spring	Water and mud	Nutrient broth for enrichment	A	35–70°C	60°C	6.0–10.0	7.0	-	42.90%	DSM 21706
Coorevits et al. [93]	<i>A. tepidamans</i> R-35643	Austria	Factory	Sugar beet extraction juice	TSA	F. an	40–65°C	55°C	6.0–9.0	5.0	-	43.20%	AY563003
Deep et al. [94]	<i>A. suryakundensis</i> JS1	Jharkhand, India	Hot spring	Sediment	TSA	F. an	40–60°C	55°C	5.5–11.5	7.5	-	42.10%	KC958552

Zhang et al. [120]	<i>A. vitaminiphilus</i> 3nP4	Sichuan, China	Hot spring	Water	Modified Brock medium, consisting of tryptone (3.0 g l ⁻¹), yeast extract (3.0 g l ⁻¹), and basic mineral medium	A	38–66°C	57–60°C	6.0–9.3	7.0–7.5	-	39.20%	FJ474084
Cihan et al. [91]	<i>A. calidus</i> C161ab	Denizli, Aegean Region, Turkey	Thermal power plant	Soil	<i>Geobacillus thermoglucosidasius</i> medium (MI) containing 1% soluble starch (pH 7.0)	F. an	35–70°C	55°C	6.5–9.0	8.0–8.5	-	37.80%	FJ430012
Matpan-Bekler and Guven [106]	<i>Anoxybacillus</i> sp. KP1	Ağrı, Turkey	Hot spring	Mud and water	Nutrient broth medium	A	40–65°C	60°C	6.5–9.5	8.0	-	-	KC525949
Chen et al. [87]	<i>A. contaminans</i> HA	China	BioDeNOx treatment system	-	Modified denitrification medium (MDM)	A	30–60°C	55°C	-	-	-	-	KF973318
Patel [112]	<i>Anoxybacillus</i> sp. BC01	Australia	Great Artesian Basin (GAB)	Microbial mat colonization	Medium D	F. an	-	50°C	-	7.5	2.8 Mb	41.70%	JRLC01000000
Xia et al. [117]	<i>Anoxybacillus</i> sp. WJ-4	Longhu Pao	Daqing Oil Field	Brine and oil	Minimal medium supplemented with crude oil	F. a	45–80°C	68–72°C	-	6.0–8.0	-	44.30%	KR153283
Filippidou et al. [97]	<i>A. geothermalis</i> GSsed3	North Germany	Soil in geothermal factory	Soil	D2216 modified marine broth (This medium was modified by using 5 g tryptone instead of peptone, omitting the addition of potassium bromide, and adjusting the pH to 5.2 with HCl)	F. an	40–65°C	60°C	5.0–9.5	7.0–8.0	7.2 Mb	46.80%	JYCG00000000
Mittal et al. [108]	<i>A. mongoliensis</i> MB4	Surguja, Chhattisgarh, India	Hot spring	Water	Nutrient agar medium	-	-	-	-	-	30,188.3 bp	58.3%	MRZM01000000
Acer et al. [82]	<i>Anoxybacillus</i> sp. AH1	Ağrı, Turkey	Hot spring	Water	Nutrient broth	A	40–70°C	55–60°C	6.0–11.0	9.0–10.0	-	-	KU997674

Chan et al. [77]	<i>Anoxybacillus</i> sp. DT3-1	Dusun Tua, Malaysia	Hot spring	Water	Modified <i>Thermus</i> medium	A/An	30–65°C	55°C	6.0–10.0	7.0	-	41.80%	GU129931
Al-Kahem Al-Balawi et al. [83]	<i>Anoxybacillus</i> sp. UARK-01	Arkansas, USA	Soil beneath grass	Soil	Media containing mineral salts and 0.5% (w/v) switchgrass as the sole carbon source	A	50–60°C	55°C	7.0–9.0	8.0	3,669,492 bp	42.60%	PRJNA379989
Yadav et al. [118]	<i>A. kamchatkensis</i> NASTPD13	Myagdi, Nepal	Hot spring	Water	Minimal salt medium (MSM)	F. an	37–75°C	-	5.0–11.0	-	-	-	KY373247
Khan et al. [103]	<i>A. sediminis</i> YIM 73012	Tibet, China	Qucai geothermal field	Sediment in geothermal site	R2A agar medium	A	37–65°C	45–50°C	6.0–8.5	7.0–7.5	-	43.60%	MG661737
Matpan-Bekler et al. [107]	<i>Anoxybacillus</i> sp. FMB1	Yozgat, Turkey	Hot spring	Water	Modified liquid <i>Thermus</i> medium	A	25–40°C	50°C	4.0–11.0	7.0	-	-	KP992869
Reis et al. [113]	<i>A. sp.</i> PC2	Caatinga, Brazil	Caatinga	Soil	Enrichment culture medium	F. an	50–60°C	50–60°C	5.0–10.0	7.0	-	-	MN937679
Cheng et al. [89]	<i>A. caldiproteolyticus</i> 1A02591	East of the Pacific Ocean	Deep sea hydrothermal vent	Sediment	2216E medium (0.5% Bacto peptone, 0.1% yeast extract, and artificial seawater; pH 7.5)	A	45–65°C	55°C	-	-	-	-	JAEILW0000000000

* **A = Aerobe; An = Anaerobe; F. a = Facultative aerobe; F. an = Facultative anaerobe**

Table S3. Metagenomic data on *Anoxybacillus*, retrieved from public databases

Reference	Species	Location	Source	Substrate
Khanna et al. [104]	<i>Anoxybacillus</i> sp.	-	Rat	Fecal samples
Najar et al. [109]	<i>A. gonensis</i> and <i>A. caldiproteolyticus</i>	Borong and Polok hot springs of South Sikkim, India	Hot springs	Water and soil
Ottesen et al. [111]	<i>Anoxybacillus</i> sp.	USA	Ice cream scoops	Ice cream

Sahm et al. [114]	<i>Anoxybacillus</i> sp.	Furnas Valley, Sao Miguel, Azores, Portugal	Hot spring	Sediment, biofilm, and water
Salam and Obayori [115]	<i>Anoxybacillus</i> sp.	Ilorin, Kwara State, Nigeria	Composite animal charcoal-polluted soil	Soil
Wu et al. [116]	<i>Anoxybacillus</i> sp.	Yangtze River, China	River and fish	Sediment, fish intestinal content, and fish mucosa
Zhao et al. [122]	<i>A. flavithermus</i>	Xiamen, China	Hot spring	Sediment

Table S4. Regions of phages in the Antarctic *Anoxybacillus flavithermus* strains isolated in the present study, as predicted using PHASTER

Genomes	Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most common phage	G + C content
LAT_11	1 - NODE_1_length_418483_cov_331812911	24.4 Kb	Incomplete	40	17	11894–36301	PHAGE_Bacill_phiNIT1_NC_021856(2)	39.69%
	2 - NODE_2_length_445795_cov_336731076	24.4 Kb	Incomplete	40	17	11894–36301	PHAGE_Staphy_SPbeta_like_NC_029119(2)	39.69%
LAT_26	1 - 04- edena/D136_FSP192285480-1a_HWNCGDSXX_L2__30	5.3 Kb	Incomplete	20	9	3–5358	PHAGE_Strept_Dp_1_NC_015274(2)	42.38%
	2 - NODE_18_length_49609_cov_303747719	33.6 Kb	Intact	140	50	15746–49378	PHAGE_Thermu_OH2_NC_021784(26)	41.44%

	3 - NODE_1_length_650285_cov_263 .707080	24.3 Kb	Incomplete	40	17	614060–638453	PHAGE_Bacill_phiNIT1_NC_021856(2)	39.68%
	4 - NODE_4_length_130475_cov_266 .489065	43.7 Kb	Intact	130	55	350–44128	PHAGE_Thermu_OH2_NC_021784(12)	41.32%
	5 - NODE_1_length_649997_cov_270 .183562	24.3 Kb	Incomplete	40	17	613772–638165	PHAGE_Bacill_phiNIT1_NC_021856(2)	39.68%
LAT_27	1 - NODE_1_length_456493_cov_294 .959721	24.4 Kb	Incomplete	40	17	11898–36305	PHAGE_Staphy_SPbeta_like_NC_029119(2)	39.69%
LAT_31	1 - NODE_1_length_457267_cov_52. 1925_component_0	24.3 Kb	Incomplete	40	17	420909–445302	PHAGE_Staphy_SPbeta_like_NC_029119(2)	39.68%
	2 - NODE_10_length_95172_cov_50. 4712_component_0	4.8 Kb	Incomplete	20	9	2–4805	PHAGE_Bacill_BCD7_NC_019515(2)	42.61%
LAT_33	1 - NODE_1_length_457267_cov_52. 1925_component_0	5.1 Kb	Incomplete	20	9	89034–94170	PHAGE_Bacill_BCD7_NC_019515(2)	42.52%
	2 - 04- edena/D144_FSP192285488- 1a_HWNCGDSXX_L3__12,size=1 20848,cov=496.29	24.4 Kb	Incomplete	40	17	12519–36926	PHAGE_Staphy_SPbeta_like_NC_029119(2)	39.69%
LAT_35	1 - 04- edena/D146_FSP192285490- 1a_HWNCGDSXX_L3__1,size=12 0698,cov=597.479	24.4 Kb	Incomplete	40	17	12369–36776	PHAGE_Bacill_phiNIT1_NC_021856(2)	39.69%
	2 - 04- edena/D146_FSP192285490- 1a_HWNCGDSXX_L3__37,size=1 8327,cov=588.787	5.1 Kb	Incomplete	20	9	3–5139	PHAGE_Bacill_BCD7_NC_019515(2)	42.52%

LAT_38	1 - 04- edena/D149_FDMS192285493- 1a_HWNCGDSXX_L3__1	5.6 Kb	Incomplete	20	9	1-5698	PHAGE_Strept_Dp_1_NC_015274(2)	42.01%
	2 - NODE_18_length_49621_cov_333 .261575	33.6 Kb	Intact	140	50	15752-49384	PHAGE_Thermu_OH2_NC_021784(26)	41.44%
	3 - NODE_1_length_501254_cov_426 .879991	24.4 Kb	Incomplete	40	17	11825-36232	PHAGE_Staphy_SPbeta_like_NC_029119(2)	39.69%
	4 - NODE_2_length_272886_cov_474 .757143	43.7 Kb	Intact	150	59	356-44134	PHAGE_Geobac_E2_NC_009552(13)	41.33%
	5 - NODE_17_length_49621_cov_333 .261575	33.6 Kb	Intact	140	50	15752-49384	PHAGE_Thermu_OH2_NC_021784(26)	41.44%

Table S5. Genes related to the lifestyle of *Anoxybacillus flavithermus* strains and their corresponding locus tag, annotated with GO FEAT

	Genes/Locus tag (when present)																						
Genomes	DnaK	DnaJ	GrpE	Hsp20	hcrA	ClpC	ClpP	yfjT	htpX	GroEL	GroES	CspB	CspD	Na+/H+ antiporter subunits A–G	nhaC	UvrA	UvrB	UVRc	MutS	MutL	LigA	RecR	RuV
LAT_11	N_01457	NFPJC LFB_01458	NFPJ CLFB_01456	NFPJC LFB_02018	-	NFPJ CLFB_00547	NFPJC LFB_00387 NFPJC LFB_02866	-	NFPJC LFB_00200	-	-	NFPJCL FB_00102	NFPJ CLFB_00325 NFPJ CLFB_01003	NFPJCLFB_01143 NFPJCLFB_01144	-	NFPJC LFB_02465 NFPJC LFB_02841 NFPJC LFB_02842 NFPJC LFB_03122	NFPJC LFB_02841	NFPJC LFB_02465 NFPJC LFB_03122	NFPJC LFB_00065 NFPJC LFB_02481 NFPJC LFB_02483 NFPJC LFB_03138 NFPJC LFB_03140	NFPJC LFB_00066	NFPJCL FB_00002 NFPJCL FB_00070 NFPJCL FB_00073 NFPJCL FB_00080 NFPJCL FB_00183 NFPJCL FB_00427 NFPJCL FB_00428 NFPJCL FB_00478 NFPJCL FB_00540 NFPJCL FB_00542*	NFPJC LFB_00998	NFPJC LFB_00017 NFPJC LFB_00018 NFPJC LFB_00113 NFPJC LFB_00758 NFPJC LFB_00783 NFPJC LFB_00996 NFPJC LFB_01048 NFPJC LFB_01121 NFPJC LFB_01150 NFPJC LFB_01151*

LAT_26	MKDE MENN_0204 7 MKDE MENN_0340 6	MKDE MENN_02046 MKDE MENN_03405	MKD EMEN N_02048 MKD EMEN N_03407	MKDE MENN_00384 MKDE MENN_01353	-	ILCL CDJK_00598	MKDE MENN_02382	-	MKDE MENN_01271	-	-	MKDE MENN_00017	MKD EME NN_0238 MKD EME NN_01105	MKDEME NN_00867 MKDEME NN_00868 MKDEME NN_03677 MKDEME NN_03678	-	MKDE MENN_00360 MKDE MENN_02101 MKDE MENN_02406 MKDE MENN_02407 MKDE MENN_03460	MKDE MENN_02407	MKDE MENN_02101 MKDE MENN_03460	MKDE MENN_00054 MKDE MENN_02083 MKDE MENN_02085 MKDE MENN_03442 MKDE MENN_03444	MKDE MENN_00053	MKDEM ENN_00039 MKDEM ENN_00046 MKDEM ENN_00049 MKDEM ENN_00116 MKDEM ENN_00408 MKDEM ENN_00409 MKDEM ENN_00459 MKDEM ENN_00521 MKDEM ENN_00523 MKDEM ENN_00576*	MKDE FPJCL FBME NN_01059	MKDE MENN_01059
LAT_27	AOKP IELD_02683	AOKP IELD_02682	AOKP IELD_02684	AOKPI ELD_00070 AOKPI ELD_00493 AOKPI ELD_02246	-	AOK PIEL D_02402	AOKP IELD_01161 AOKP IELD_02018	-	AOKP IELD_00838	-	-	AOKPI ELD_00017 AOKPI ELD_00630	AOKP IELD_000321 AOKP IELD_001299	AOKPIELD _00805 AOKPIELD _00806	-	AOKPI ELD_02042 AOKPI ELD_02043 AOKPI ELD_02926	AOKP IELD_02042 AOKP IELD_02043 AOKP IELD_02926	AOKP IELD_02926	AOKP IELD_00667 AOKP IELD_02942 AOKP IELD_02944	AOKP IELD_00666	AOKPIE LD_00039 AOKPIE LD_00046 AOKPIE LD_00049 AOKPIE LD_00079 AOKPIE LD_00082 AOKPIE LD_0010	AOKP IELD_00183	AOKP IELD_00006 AOKP IELD_00181 AOKP IELD_00270 AOKP IELD_00619 AOKP IELD_00714 AOKP IELD_

																					9 AOKPIE LD_0011 6 AOKPIE LD_0011 7 AOKPIE LD_0017 6 AOKPIE LD_0022 3*		00715 AOKP IELD_ 00730 AOKP IELD_ 00752 AOKP IELD_ 00753 AOKP IELD_ 00754*
LAT_31	INBD BCKJ_ 00691	INBDB CKJ_0 0690	INBD BCKJ_ _0069 2	INBDB CKJ_00 748 INBDB CKJ_01 997	-	INBD BCKJ_ _0212 2	INBD BCKJ_ 01132 INBD BCKJ_ 01424	-	INBD BCKJ_ 01772	-	INBDBC KJ_0271 6	INBDB CKJ_01 253	INBD BCKJ_ _0107 4 INBD BCKJ_ _0279 2	INBDBCKJ _01614 INBDBCKJ _01615	-	INBD BCKJ_ 00291 INBD BCKJ_ 01399 INBD BCKJ_ 01400	INBD BCKJ_ 01399	INBD BCKJ_ 00291	INBD BCKJ_ 00273 INBD BCKJ_ 00275 INBD BCKJ_ 01216	INBD BCKJ_ 01217	INBD BCKJ_ 02724	INBDBC KJ_0003 8 INBDBC KJ_0008 5 INBDBC KJ_0009 4 INBDBC KJ_0010 9 INBDBC KJ_0011 2 INBDBC KJ_0012 5 INBDBC KJ_0013 7 INBDBC KJ_0014 2 INBDBC KJ_0018 9 INBDBC KJ_0024 2 *	INBD BCKJ_ 00035 INBD BCKJ_ 00074 INBD BCKJ_ 00168 INBD BCKJ_ 00374 INBD BCKJ_ 00375 INBD BCKJ_ 00559 INBD BCKJ_ 00672 INBD BCKJ_ 00988 INBD BCKJ_ 01169 INBD BCKJ_ 01264*

LAT_33	ANMP AFOB_02765	ANMP AFOB_02766	ANM PAFO B_02764	ANMP AFOB_00546 ANMP AFOB_02225	-	ANM PAFO B_01441	ANMP AFOB_00745 ANMP AFOB_01713	-	ANMP AFOB_00083	-	ANMPA FOB_02633	ANMP AFOB_00209	ANM PAFO B_01771 ANM PAFO B_02683	ANMPAFO B_00165 ANMPAFO B_00166	-	ANMP AFOB_00769 ANMP AFOB_00770 ANMP AFOB_00875	ANMP AFOB_00770	ANMP AFOB_00875	ANMP AFOB_00875	ANMP AFOB_00245	ANMPA FOB_00066 ANMPA FOB_00189 ANMPA FOB_00238 ANMPA FOB_00241 ANMPA FOB_00301 ANMPA FOB_00526 ANMPA FOB_00528 ANMPA FOB_00535 ANMPA FOB_00826 ANMPA FOB_00827*	ANMP AFOB_02641	ANMP AFOB_00112 ANMP AFOB_00113 ANMP AFOB_00114 ANMP AFOB_00157 ANMP AFOB_00158 ANMP AFOB_00159 ANMP AFOB_00198 ANMP AFOB_00348 ANMP AFOB_00687 ANMP AFOB_00697*
LAT_35	LBOC MBFH_01052	LBOC MBFH_01051	LBOC MBFH_01053	LBOC MBFH_02160	-	LBOC MBF H_02066	LBOC MBFH_00213 LBOC MBFH_01797	-	LBOC MBFH_00778	-	LBOCM BFH_02607	LBOC MBFH_01380	LBOC MBF H_01281 LBOC MBF H_02513	LBOCMBF H_02326 LBOCMBF H_02327	-	LBOC MBFH_00237 LBOC MBFH_00238 LBOC MBFH_01637	LBOC MBFH_00238	LBOC MBFH_01637	LBOC MBFH_00297 LBOC MBFH_00299 LBOC MBFH_02092	LBOC MBFH_02091	LBOCM BFH_00076 LBOCM BFH_00089 LBOCM BFH_00090 LBOCM BFH_00295 LBOCM BFH_00311 LBOCM	LBOC MBFH_02494	LBOC MBFH_00107 LBOC MBFH_00108 LBOC MBFH_00155 LBOC MBFH_00165 LBOC MBFH_00394 LBOC

																				BFH_00 319 LBOCM BFH_00 320 LBOCM BFH_00 373 LBOCM BFH_00 420 LBOCM BFH_00 425*		MBFH_00908 LBOC MBFH_01033 LBOC MBFH_01364 LBOC MBFH_01369 LBOC MBFH_01536 *	
LAT_38	ILCLC DJK_0 1998	ILCLC DJK_0 1999	ILCL CDJK _0199 7	ILCLC DJK_00 501 ILCLC DJK_01 512	-	ILCL CDJK _0059 8	ILCLC DJK_0 2415	-	ILCLC DJK_0 0589	-	-	ILCLC DJK_00 219	ILCL CDJK _0035 5 ILCL CDJK _0128 3	ILCLCDJK _00027 ILCLCDJK _00028	-	ILCLC DJK_0 0477 ILCLC DJK_0 1944 ILCLC DJK_0 2439 ILCLC DJK_0 2440	ILCLC DJK_0 2440	ILCLC DJK_0 1944	ILCLC DJK_0 0256 ILCLC DJK_0 1960 ILCLC DJK_0 1962	ILCLC DJK_0 0255	ILCLCD JK_0000 4 ILCLCD JK_0012 9 ILCLCD JK_0013 5 ILCLCD JK_0014 0 ILCLCD JK_0014 2 ILCLCD JK_0016 3 ILCLCD JK_0018 3 ILCLCD JK_0024 1 ILCLCD JK_0024 8 ILCLCD JK_0025 1*	ILCLC DJK_0 1253	ILCLC DJK_0 0005 ILCLC DJK_0 0034 ILCLC DJK_0 0035 ILCLC DJK_0 0036 ILCLC DJK_0 0079 ILCLC DJK_0 0080 ILCLC DJK_0 0081 ILCLC DJK_0 0103 ILCLC DJK_0 0145 ILCLC DJK_0 0208*

*: More than 10 locus tags in the corresponding gene.

Table S6. Methodologies applied in previous related phylogenetic studies

Phylogeny/ Phylogenomics	Methodology	Gene	Reference
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Acer Ö, Bekler FM, Piriñcioğlu H, Güven RG, Güven K. Purification and characterization of thermostable and detergent-stable α -amylase from <i>Anoxybacillus</i> sp. AH1. Food Technol Biotechnol. 2016 , 54, 70-77. doi: 10.17133/ftb.54.01.16.4122. PMID: 27904395. PMCID: PMC5105632.
Phylogenetic analysis of 16S rRNA	Neighbor-joining and maximum likelihood methods	16S rRNA	Al-Kahem Al-Balawi TH, Wood AL, Solis A, Cooper T, Barabote RD. <i>Anoxybacillus</i> sp. strain UARK-01, a new thermophilic soil bacterium with hyperthermostable alkaline laccase activity. Curr Microbiol. 2017 , 74, 762-771. doi: 10.1007/s00284-017-1239-5. Epub 2017 Apr 8. PMID: 28389772.
Phylogenetic analysis of 16S rRNA	Maximum likelihood method	16S rRNA	Atanassova M, Derekova A, Mandeva R, Sjöholm C, Kambourova M. <i>Anoxybacillus bogrovensis</i> sp. nov., a novel thermophilic bacterium isolated from a hot spring in Dolni Bogrov, Bulgaria. Int J Syst Evol Microbiol. 2008 58, 2359-2362. doi: 10.1099/ij.s.0.65745-0. PMID: 18842856.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Matpan-Bekler F, Guven K. Isolation and production of thermostable α -amylase from thermophilic <i>Anoxybacillus</i> sp. KP1 from Diyadin hot spring in Ağrı, Turkey. Biologia. 2014 , 69, 419-427. doi: 10.2478/s11756-014-0343-2.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Matpan-Bekler F, Yalaz S, Guven K. Molecular characterisation and numerical analysis of novel moderately thermophile <i>Anoxybacillus</i> sp. FMB1. Rom Biotechnol Lett. 2018 , 23, 13964-13975. doi: 10.26327/RBL2018.150.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Chai YY, Kahar UM, Md Salleh M, Md Illias R, Goh KM. Isolation and characterization of pullulan-degrading <i>Anoxybacillus</i> species isolated from Malaysian hot springs. Environ Technol. 2012 , 33, 1231-1238. doi: 10.1080/09593330.2011.618935. PMID: 22856294.
Phylogenetic analysis of DT-Bgl and other β -glucosidases	Neighbor-joining method	DT-Bgl and other β -glucosidases	Chan CS, Sin LL, Chan KG, Shamsir MS, Manan FA, Sani RK, Goh KM. Characterization of a glucose-tolerant β -glucosidase from <i>Anoxybacillus</i> sp. DT3-1. Biotechnol Biofuels. 2016 , 9, 174. doi: 10.1186/s13068-016-0587-x. PMID: 27555880. PMCID: PMC4994278.
Phylogenetic analysis of 16S rRNA	Maximum likelihood method	16S rRNA	Chen XG, Stabnikova O, Tay JH, Wang JY, Tay ST. Thermoactive extracellular proteases of <i>Geobacillus caldoproteolyticus</i> sp. nov., from sewage sludge. Extremophiles. 2004 , 8, 489-498. doi: 10.1007/s00792-004-0412-5. Epub 2004 Aug 21. PMID: 15322950.

Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Chen J, Zheng J, Li Y, Hao HH, Chen JM. Characteristics of a novel thermophilic heterotrophic bacterium, <i>Anoxybacillus contaminans</i> HA, for nitrification-aerobic denitrification. Appl Microbiol Biotechnol. 2015 , 99, 10695-10702. doi: 10.1007/s00253-015-6870-0. Epub 2015 Aug 21. PMID: 26293335.
Phylogenetic analysis of 16S rRNA	Maximum likelihood method	16S rRNA	Cihan AC, Ozcan B, Cokmus C. <i>Anoxybacillus salavatliensis</i> sp. nov., an α -glucosidase producing, thermophilic bacterium isolated from Salavatli, Turkey. J Basic Microbiol. 2011 , 51, 136-146. doi: 10.1002/jobm.201000115. Epub 2010 Nov 12. PMID: 21077116.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Cihan AC, Cokmus C, Koc M, Ozcan B. <i>Anoxybacillus calidus</i> sp. nov., a thermophilic bacterium isolated from soil near a thermal power plant. Int J Syst Evol Microbiol. 2014 , 64, 211-219. doi: 10.1099/ij.s.0.056549-0. Epub 2013 Sep 19. Erratum in: Int J Syst Evol Microbiol. 2014 Aug;64(Pt 8):2926. Erratum in: Int J Syst Evol Microbiol. 2014 Jul;64(Pt 7):2508. PMID: 24052627.
Phylogenetic analysis of 16S rRNA	Maximum likelihood method	16S rRNA	Coorevits A, Dinsdale AE, Halket G, Lebbe L, De Vos P, Van Landschoot A, Logan NA. Taxonomic revision of the genus <i>Geobacillus</i> : emendation of <i>Geobacillus</i> , <i>G. stearothermophilus</i> , <i>G. jurassicus</i> , <i>G. toebii</i> , <i>G. thermodenitrificans</i> and <i>G. thermoglucosidans</i> (nom. corrig., formerly ' <i>thermoglucosidasius</i> '); transfer of <i>Bacillus thermantarcticus</i> to the genus as <i>G. thermantarcticus</i> comb. nov.; proposal of <i>Caldibacillus debilis</i> gen. nov., comb. nov.; transfer of <i>G. tepidamans</i> to <i>Anoxybacillus</i> as <i>A. tepidamans</i> comb. nov.; and proposal of <i>Anoxybacillus caldiproteolyticus</i> sp. nov. Int J Syst Evol Microbiol. 2012 , 62, 1470-1485. doi: 10.1099/ij.s.0.030346-0. Epub 2011 Aug 19. PMID: 21856988.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Deep K, Poddar A, Das SK. <i>Anoxybacillus suryakundensis</i> sp. nov, a moderately thermophilic, alkalitolerant bacterium isolated from hot spring at Jharkhand, India. PLoS One. 2013 20;8(12):e85493. doi: 10.1371/journal.pone.0085493. PMID: 24376881. PMCID: PMC3869905.
Phylogenetic analysis of 16S rRNA	Neighbor-joining and maximum likelihood methods	16S rRNA	Derekova A, Sjøholm C, Mandeva R, Kambourova M. <i>Anoxybacillus rupiensis</i> sp. Nov., a novel thermophilic bacterium isolated from Rupi basin (Bulgaria). Extremophiles. 2007 , 11, 577-583. doi: 10.1007/s00792-007-0071-4. Epub 2007 May 16. PMID: 17505776.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Dulger S, Demirbag Z, Belduz AO. <i>Anoxybacillus ayderensis</i> sp. nov. and <i>Anoxybacillus kestanbolensis</i> sp. nov. Int J Syst Evol Microbiol. 2004 , 54, 1499-1503. doi: 10.1099/ij.s.0.02863-0. PMID: 15388701.

Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Filippidou S, Jaussi M, Junier T, Wunderlin T, Jeanneret N, Palmieri F, Palmieri I, Roussel-Delif L, Vieth-Hillebrand A, Vetter A, Chain PS, Regenspurg S, Junier P. <i>Anoxybacillus geothermalis</i> sp. nov., a facultatively anaerobic, endospore-forming bacterium isolated from mineral deposits in a geothermal station. Int J Syst Evol Microbiol. 2016 , 66, 2944-2951. doi: 10.1099/ijsem.0.001125. Epub 2016 Apr 28. PMID: 27126386.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Gao Y, Dai J, Peng H, Liu Y, Xu T. Isolation and characterization of a novel organic solvent-tolerant <i>Anoxybacillus</i> sp. PGDY12, a thermophilic gram-positive bacterium. J Appl Microbiol. 2011 , 110, 472-478. doi: 10.1111/j.1365-2672.2010.04903.x. Epub 2010 Dec 13. PMID: 21155953.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Gul-Guven R, Guven K, Poli A, Nicolaus B. <i>Anoxybacillus kamchatkensis</i> subsp. <i>asaccharedens</i> subsp. nov., a thermophilic bacterium isolated from a hot spring in Batman. J Gen Appl Microbiol. 2008 , 54, 327-334. doi: 10.2323/jgam.54.327. PMID: 19164875.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Inan K, Belduz AO, Canakci S. <i>Anoxybacillus kaynarcensis</i> sp. nov., a moderately thermophilic, xylanase producing bacterium. J Basic Microbiol. 2013 , 53, 410-419. doi: 10.1002/jobm.201100638. Epub 2012 Jun 26. PMID: 22736500.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Kevbrin VV, Zengler K, Lysenko AM, Wiegel J. <i>Anoxybacillus kamchatkensis</i> sp. nov., a novel thermophilic facultative aerobic bacterium with a broad pH optimum from the Geyser valley, Kamchatka. Extremophiles. 2005 9, 391-398. doi: 10.1007/s00792-005-0479-7. Epub 2005 Sep 3. PMID: 16142505.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Khan IU, Habib N, Xiao M, Devi AM, Habib M, Hejazi MS, Salam N, Zhi XY, Li WJ. <i>Anoxybacillus sediminis</i> sp. nov., a novel moderately thermophilic bacterium isolated from a hot spring. Antonie Van Leeuwenhoek. 2018 , 111, 2275-2282. doi: 10.1007/s10482-018-1118-5. Epub 2018 Jun 21. PMID: 29931494.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Namsaraev ZB, Babasanova OB, Dunaevsky YE, Akimov VN, Barkhutova DD, Gorlenko VM, Namsaraev BB. <i>Anoxybacillus mongoliensis</i> sp. nov., a novel thermophilic proteinase producing bacterium isolated from alkaline hot spring, Central Mongolia. Mikrobiologiya. 2010 79, 516-523. PMID: 21058505.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Poli A, Esposito E, Lama L, Orlando P, Nicolaus G, de Appolonia F, Gambacorta A, Nicolaus B. <i>Anoxybacillus amylolyticus</i> sp. nov., a thermophilic amylase producing bacterium isolated from Mount Rittmann (Antarctica). Syst Appl Microbiol. 2006 , 29, 300-307. doi: 10.1016/j.syapm.2005.10.003. Epub 2005 Nov 3. PMID: 16682297.

Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Poli A, Romano I, Cordella P, Orlando P, Nicolaus B, Ceschi Berrini C. <i>Anoxybacillus thermarum</i> sp. nov., a novel thermophilic bacterium isolated from thermal mud in Euganean hot springs, Abano Terme, Italy. <i>Extremophiles</i> . 2009 , <i>13</i> , 867-874. doi: 10.1007/s00792-009-0274-y. Epub 2009 Aug 27. PMID: 19710998.
Phylogenetic analysis of 16S rRNA	Determined by the neighbor-joining algorithm and evaluated by maximum likelihood and maximum parsimony algorithms	16S rRNA	Xia W, Dong H, Zheng C, Cui Q, He P, Tang Y. Hydrocarbon degradation by a newly isolated thermophilic <i>Anoxybacillus</i> sp. with bioemulsifier production and new alkB genes. <i>RSC Adv</i> . 2015 , <i>5</i> , 102367-102377. doi: 10.1039/C5RA17137G.
Phylogenetic analysis of 16S rRNA	Maximum likelihood method	16S rRNA	Yadav P, Maharjan J, Korpole S, Prasad GS, Sahni G, Bhattarai T, Sreerama L. Production, purification, and characterization of thermostable alkaline xylanase from <i>Anoxybacillus kamchatkensis</i> NASTPD13. <i>Front Bioeng Biotechnol</i> . 2018 , <i>6</i> :65. doi: 10.3389/fbioe.2018.00065
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Yumoto I, Hirota K, Kawahara T, Nodasaka Y, Okuyama H, Matsuyama H, Yokota Y, Nakajima K, Hoshino T. <i>Anoxybacillus voinovskiensis</i> sp. nov., a moderately thermophilic bacterium from a hot spring in Kamchatka. <i>Int J Syst Evol Microbiol</i> . 2004 , <i>54</i> , 1239-1242. doi: 10.1099/ij.s.0.02889-0. PMID: 15280298.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Zhang CM, Huang XW, Pan WZ, Zhang J, Wei KB, Klenk HP, Tang SK, Li WJ, Zhang KQ. <i>Anoxybacillus tengchongensis</i> sp. nov. and <i>Anoxybacillus eryuanensis</i> sp. nov., facultatively anaerobic, alkalitolerant bacteria from hot springs. <i>Int J Syst Evol Microbiol</i> . 2011 , <i>61</i> , 118-122. doi: 10.1099/ij.s.0.020834-0. Epub 2010 Feb 19. PMID: 20173008.
Phylogenetic analysis of 16S rRNA	Neighbor-joining method	16S rRNA	Zhang XQ, Zhang ZL, Wu N, Zhu XF, Wu M. <i>Anoxybacillus vitaminiphilus</i> sp. nov., a strictly aerobic and moderately thermophilic bacterium isolated from a hot spring. <i>Int J Syst Evol Microbiol</i> . 2013 , <i>63</i> , 4064-4071. doi: 10.1099/ij.s.0.050096-0. Epub 2013 May 31. PMID: 23728374.

Table S7. Details of strains used in genomic analysis

Name	NCBI Ref Seq Assembly Accession	Status
<i>Geobacillus kaustophilus</i> strain HTA426	GCF_000009785.1	Complete genome
<i>Geobacillus genomo</i> sp. 3 JF8	GCF_000445995.2	Complete genome
<i>Geobacillus</i> sp. 12AMOR1	GCF_001028085.1	Complete genome
<i>Brevibacillus brevis</i> DZQ7	GCF_001039275.2	Complete genome
<i>Brevibacillus brevis</i> NBRC 100599	GCF_000010165.1	Complete genome
<i>Anoxybacillus amylolyticus</i> DSM 15939	GCF_001634285.1	Complete genome
<i>Anoxybacillus</i> sp. B7M1	GCF_001634305.1	Complete genome
<i>Anoxybacillus flavithermus</i> WK1	GCF_000019045.1	Complete genome