Paenibacillus lutrae sp. nov., a chitinolytic species isolated from a river otter in Castril Natural Park, Granada, Spain

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sis KCTC 3748^T (NR 025666) Paenibacillus koreensis YC300^T (NR 028747) Paenibecillus tianmuensis B27⁷ (FJ719490) Paenibecillus elgii SD17^T (NR 115140) Paenibacillus solanacearum T16R-228^T (NR 159229) nibacillus mucilaginosus VKPM B-7519⁷ (NR 116536) - Paenibacillus xylanisolvens X11-11 (AB495094) 88 — Paenibacillus validus JCM 9077¹ (NR 040892) – Paenibacillus soli DCY03¹ (NR 043708) Peenibacillus chinivensis WN9^T (NR 025024) nibacillus filicis S4⁺ (NR 117365) - Paenibecillus periandrae PM10[™] (NR 148839) - Paenibacillus esterisolvens CFH S0170⁺ (KP232 Paenibacillus yunnanensis YN2¹ (KJ914577)
 Paenibacillus vulneris CCUG 53270¹ (NR 117618) - Paenibacillus cavernae C4-5^T (NR 148613) Paenibacillus contaminans CKOBP-6^T (NR 044325) - Paenibacillus doosanensis CAU 1055⁷ (NR 133805) - Paenibacillus swuensis DY6⁺ (JQ958374) Paenibacillus gansuensis B518⁺ (NR 043219) 100 - Paenibacillus sp. N10^T (MG831947) nillus chitinolyticus NBRC 15660¹ (NR 113797) – Paenibacillus aestuani CJ25⁺ (NR 116365) Paenibacillus ginlingensis TEGT-2^T (NR 156153)
 Paenibacillus pocheonensis Gsoil 1138^T (NR 112585) Paenibacillus nebraskensis JJ-59^T (NR 159223) 86 Paenibacillus chondroitinus DSM 5051^T (NR 043415) – Paenibacillus ferrarius CY1⁺ (KF925453) Paenibacillus frigoriresistens YIM 016¹ (NR 109546) 99 – Paenibacillus alginolyticus DSM 5050¹ (NR 040893) — Xylanibacillus composti K13¹ (KX298897) Paenibacillus larvae DSM 7030^T (NR 042947) Paenibacillus castaneae Ch-32^T (NR 044403) Paenibacillus gorillae G1⁺ (NR 136879) Paenibacilius algorifonticola XJ259^T (NR 108602)
 Paenibacilius quercus 1-25^T (NR 134116) Paenibacillus agarexedens DSM 1327⁺ (NR 025489) cillus thailandensis S3-4A[⊤] (NR 041490) nibacillus agaridevorans DSM 1355⁷ (NR 025490) 79 Cobnella lubricantis KSS-154-50^T (KX581041) Cohnella rhizosphaerae CSE-5610^T (KF8407 ---- Cohnella thermotolerans CCUG 47242⁺ (AJ971483) - Cohneile hongkongensis HKU3^T (AF433165 - Paenibacillus beijingensis 7188⁺ (NR 132612) 99 Poenibacillus phyllospharae PALXILD41 (Art Savurus, Paenibacillus methanolicus BL24⁷ (NR 108263) Paenibacillus taihuensis THINBG22⁷ (NR 109595) Paenibacillus xylaniclasticus TW1⁺ (NR 116719)
 Paenibacillus curdianolyticus YK9⁺ (NR 040891) Paenibacillus cellulosilvticus PALXIL08⁺ (NR 043789) 78 Paenibacillus kobensis DSM 10249⁺ (NR 040894) - Paenibacillus susongensis M3271 (NR 134118) 100 Paenibacillus terrigena A35^T (NR 041398) -Paenibacillus guangzhouensis GSS02^T (NR 134114 - Paenibacillus sediminis GTH-37 (NR 108601) Paenibacillus aivei NBRC 3343[®] (NR 113577)
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Paenibacillus apiarius DSM 5581[®] (NR 040890)
D0[©] Paenibacillus profundus SI 79[®] (NR 132304) Fontibacillus solani A4STR04¹ (NR 136839) - Fontibacillus aquaticus GPTSA 19¹ (DQ02322) Fontibacillus phaseoli BAPVE7B^T (KF583881)
 Paenibacillus antibioticophila GD11^T (NR 144710) Paenibacillus macerans IAM 12467⁷ (NR 040886) mbacillus faecis CIP 101062^T (NR 145888) - Paenibacillus aceti L14^T (NR 151978) - Paenibacillus motobuensis MC10⁺ (NR 043153) 99 Paenibacilius macquariensis DSM 2^T (NR 112165) — Paenibacillus glacialis KFC91⁺ (NR 115080) – Paenibacillus pini JCM 16418[†] (NR 117366) Paenibacillus anaericanus MH21^T (NR 042089) 100 — Paenibacillus selenii strain W126^T (NR 134117) Paenibacillus zeae 6R2⁺ (KP965 — Paonibacillus uliginis N3/975⁺ (NR 117012) 71 Paenibacilius glucanolyticus DSM 5162¹ (NR 040883) Paenibacillus campinasensis 324^T (NR 024857) - Paenibacillus xylanilyticus XIL14^T (AY427832) Paenibacillus terreus D33⁺ (NR 147741)
 Paenibacillus medicaginis CC-Alfalfa-19⁺ (NR 145626) Paenibacillus lentus CMG1240^{*} (NR 118573) Paenibacillus bovis BD3526⁷ (NR 148789) 100 - Paonibacillus wulumuqionsis Y24⁺ (NR 136854) Paenibacillus peoriae NBRC 15541^T (NR 113769) 100 Paenibacillus polymyxa DSM 36^T (NR 114810) 91 Paenibacillus jamilae CECT 5266⁺ (NR 042009) Paenibacillus Initici RTAE36^T (NR 157638)
 Paenibacillus wynnii LMG 22176^T (NR 042244) 89 Paenibacillus borealis KK19[†] (NR 025299) — Paenibacillus sabinae T27[†] (NR 043729) – Paenibacillus sabinae T27[†] (NR 043729) – Paenibacillus yonginensis DCY84[†] (KF – Paenibacillus physcomitrellae XB[†] (NR 137363) insis DCY84T (KE915796) 99 98 Paenibacillus cookii LMG 18419^T (AJ250317) Paenibacillus relictisesami KB0549^T (NR 1338) Peenibacillus relictisesami KB0549^T (NR 133806) - Peenibacillus chibensis NBRC 15958^T (NR 113827) - Paenibacillus azoreducens CM1⁺ (NR 025391) Paenibacillus azoreducens Ch11 (NK U25391) Paenibacillus rhizosphaerae CECAP06⁺ (NR 043166) 100 - Paenibacillus favisporus GMP01⁺ (NR 029071) G3¹ Paenibacillus cineris LMG 18439^T (NR 042189) aenibacillus turicensis A1^T (AF378694)

Bacillus subtilis subsp. subtilis ATCC 6051T (NR 027552)

Figure S1: Phylogenetic position of strain N10^T based on the neighbor-joining algorithm of the 16S rRNA gene sequence and its relationship with other 100 related species. The GenBank/EMBL/DDBJ accession number of each sequence is shown in parenthesis. Bootstrap values are expressed as percentages of 1,000 replications, and those greater than 60% are shown at branch points. Bar shows sequence divergence. Bar, 0.01 substitutions per nucleotide position.



0.02

Figure S2: Molecular phylogenetic analysis of the 16S rRNA sequence according to the maximum likelihood method. Evolutionary history was inferred using the aforementioned method based on the Jukes-Cantor model. The tree with the highest log likelihood (-5308.40) is shown. Bootstrap values are expressed as percentages of 1,000 replications, and those over 60% are shown at branch points. The *Bacillus subtilis* subsp. *subtilis* ATCC 6051^T sequence was used as the outgroup.



Figure S3: Molecular phylogenetic analysis of the 16S rRNA sequence using the maximum parsimony method. The most parsimonious tree (length = 592) is shown. The consistency, retention and composite indices are 0.501114, 0.554672 and 0.344796 (0.277954), respectively, for all sites and parsimony-informative sites (in parentheses). Bootstrap values are expressed as percentages of 1,000 replications, and those over 60% are shown at branch points. The *Bacillus subtilis* subsp. *subtilis* ATCC 6051^T sequence was used as the outgroup.



Figure S4: Polar lipid profile of strain N10^T determined after two-dimensional TLC using molybdatophosphoric acid. AL: aminolipid; DPG: diphosphatidylglycerol; L: lipid; PE: phosphatidylethanolamine; PG: phosphatidylglycerol; PL: phospholipid; PNL: phosphoaminolipid.

Table S1: ANIb and ANIm (in brackets) values among the genomes of strain N10^T (1) and the most related species of *Paenibacillus* genus: *P. chitinolyticus* LMG18047^T (2), *P. polymyxa* CECT155^T (3), *P. elgii* SD17^T (4), *P. vulneris* CCUG 53270^T (5) and *P. qinlingensis* TEGT-2^T (6).

Strains	1	2	3	4	5	6

1		74.42	66.94	68.41	68.57	68.00
	-	[84.64]	[86.59]	[85.80]	[85.39]	[85.46]
2	74.43		66.93	69.22	68.48	67.91
	[84.64]	-	[86.68]	[85.76]	[84.88]	[87.86]
2	67.71	67.81		67.29	67.68	67.72
3	[86.61]	[86.66]	-	[86.34]	[85.81]	[86.66]
4	68.20	69.01	66.83		70.47	67.30
	[85.77]	[85.76]	[86.33]	-	[84.62]	[85.40]
5	68.16	68.19	66.88	70.34		67.86
	[85.39]	[84.88]	[85.69]	[84.59]	-	[83.75]
6	67.29	67.33	66.35	66.85	67.42	
	[85.44]	[87.86]	[85.94]	[85.40]	[84.69]	-

Table S2: Genome sequence similarity between N10^T strain and genome sequences of closely related type strains with available genomes.

Strains	OrthoANI (%)	dDDH (%)
P. chitinolyticus LMG18047 ^T	75.60	21.1
P. polymyxa CECT155 ⁺	68.40	31.4
P. elgii SD17 ^r	69.89	19.9
P. vulneris CCUG 53270 ^T	69.62	21.6
P. qinlingensis TEGT-2 ^T	69.19	19.3