

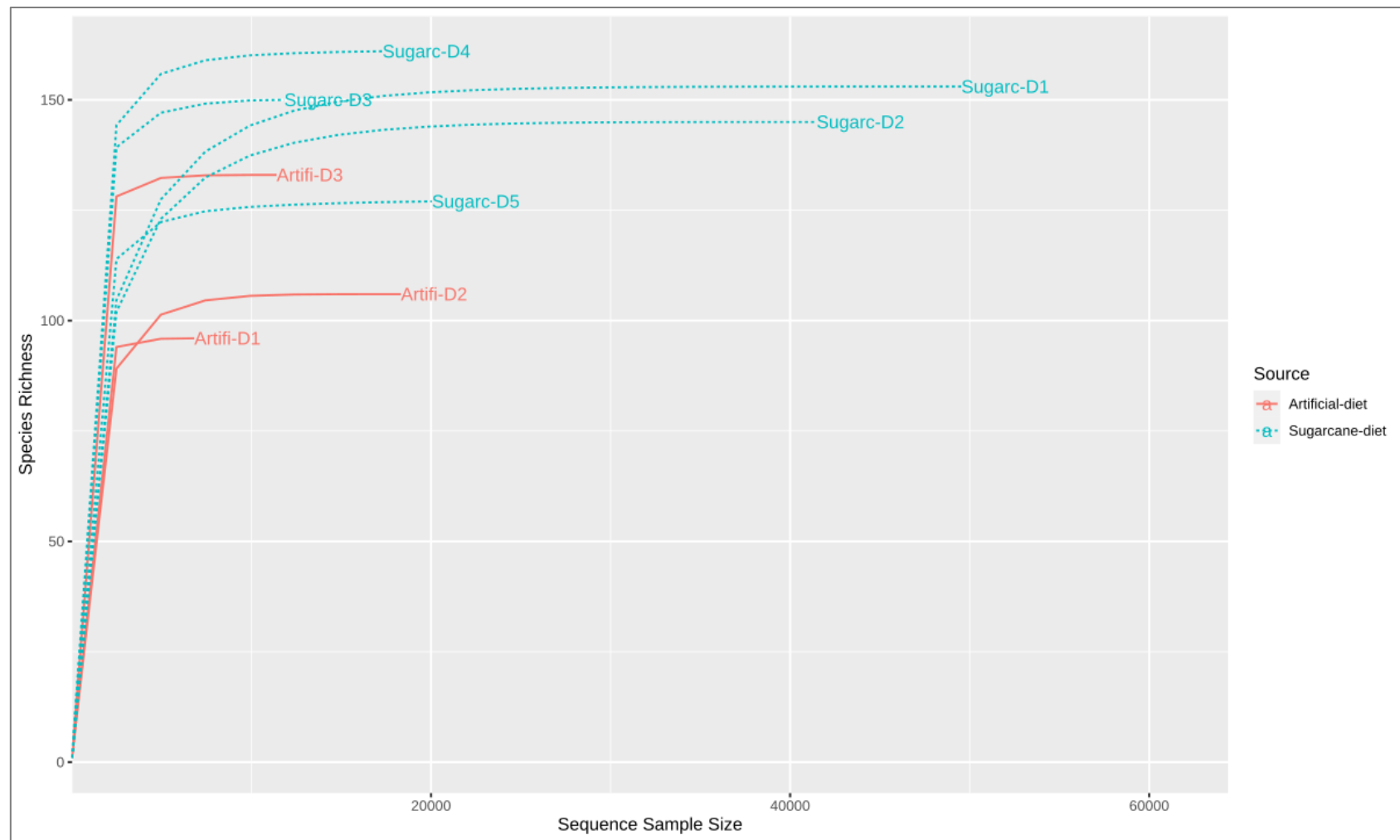


Figure S1. Rarefaction curves of the 16S rRNA gene amplicons obtained from the analyzed samples.

Table S1. Bacterial isolates with cellulolytic activity.

Strain	Morphology		Qualitative tests	
	Macroscopy	Microscopy	Sawdust	Congo red
GCEP-90	Circular, entire, flat, smooth, pale white, shiny	Gram negative cocci	+	+
GCEP-91	Circular, entire, flat, smooth, pale white, shiny	Gram negative cocci	+	+
GCEP-92	Circular, entire, flat, smooth, pale white, shiny	Gram negative cocci	+	++
GCEP-93	Irregular, wavy, flat, smooth, pale white, opaque	Gram positive bacilli	+	+
GCEP-94	Circular, entire, flat, smooth, pale white, shiny	Gram negative cocci	+	+
GCEP-95	Circular, entire, flat, smooth, pale white, shiny	Gram positive cocci	+	+
GCEP-96	Punctiform, entire, flat, smooth, pale white, translucent bright	Gram positive cocci	+	+
GCEP-97	Irregular, wavy, flat, smooth, pale white, opaque	Gram positive bacilli	+	+
GCEP-98	Circular, entire, flat, smooth, pale white, shiny	Gram negative cocci	+	+
GCEP-99	Circular, entire, flat, smooth, pale white, shiny	Gram positive cocci-bacilli	+	+
GCEP-100	Circular, entire, flat, smooth, pale white, shiny	Gram negative cocci	+	++
GCEP-101	Circular, entire, flat, smooth, pale white, shiny	Gram positive cocci	+	+++

Table S2. BLAST results of morphologically distinct cellulolytic isolates

Strain	Query Length (bp)	Closest BLAST hit	E value	Per. Ident	Query Cover
GCEP-92	1,362	<i>Klebsiella variicola</i>	0.0	99.63%	100%
GCEP-94	1,400	<i>Klebsiella variicola</i>	0.0	99.79%	100%
GCEP-95	1,414	<i>Pseudomonas nitroreducens</i>	0.0	99.79%	100%
GCEP-101	1,531	<i>Pseudomonas</i> sp. HS-18	0.0	99.67%	100%

Table S3. List of putative proteins associated to cellulose metabolism.

Enzyme	Symbol	KEGG Orthology	Associated pathway	EC number
Maltooligosyltrehalose trehalohydrolase	<i>treZ, glgZ</i>	K01236	map00500 Starch and sucrose metabolism	EC:3.2.1.141
Beta-glucosidase	<i>bglX</i>	K05349	map00500 Starch and sucrose metabolism	EC:3.2.1.21
Beta-N-acetylhexosaminidase	<i>nagZ</i>	K01207	map00531 Glycosaminoglycan degradation	EC:3.2.1.52
Hexosaminidase	HEXA_B	K12373	map00511 other glycan degradation	EC:3.2.1.52

			map00513 Various types of N-glycan biosynthesis	
			map00531 Glycosaminoglycan degradation	
Trehalose 6-phosphate synthase	<i>otsA</i>	K00697	map00500 Starch and sucrose metabolism	EC:2.4.1.15
Trehalose 6-phosphate phosphatase	<i>otsB</i>	K010087	map00500 Starch and sucrose metabolism map01100 Metabolic pathways	EC:3.1.3.12
4-alpha-glucanotransferase	<i>malQ</i>	K00705	map00500 Starch and sucrose metabolism	EC:2.4.1.25
Maltose alpha-D-glucosyltransferase / alpha-amylase	<i>treS</i>	K05343	map00500 Starch and sucrose metabolism	EC:5.4.99.16

Table S4. Average Nucleotide Identity (ANI) and digital DNA-DNA hybridization of isolate GCEP-101 with its closest relatives

Reference strain	Type strains	ANI (%)	Digital DNA:DNA hybridization values			
			d4	I.C. (%)	d6	I.C. (%)
<i>Pseudomonas</i> sp. GCEP-101	<i>Pseudomonas nicosulfuronedens</i> LAM1902T	90.27	41.5	39 - 44.1	64.9	61.5 - 68.1
	<i>Pseudomonas nitroreducens</i> NBRC 12694	90.12	40.9	38.4 - 43.4	68.2	64.8 - 71.5
	<i>Pseudomonas nitritireducens</i> WZBFD3-5A2	90.07	40.9	38.4 - 43.4	65.2	61.9 - 68.4
	<i>Pseudomonas multiresinivorans</i> populi	90.03	40.9	38.4 - 43.4	65.4	62.1 - 68.6
	<i>Pseudomonas</i> sp. HS-18	90.03	40.9	38.4 - 43.4	64.2	60.8 - 67.4
	<i>Pseudomonas nitroreducens</i> HBP1	89.94	40.8	38.3 - 43.3	56.8	53.7 - 60.0
	<i>Pseudomonas</i> sp. ATCC 13867	88.14	36.3	33.9 - 38.8	51.1	48.0 - 54.2
	<i>Pseudomonas</i> sp. SCB32	87.49	35.0	32.6 - 37.6	48.9	45.9-51.9
	<i>Pseudomonas humi</i> CCA1	83.64	28.5	26.1 - 31	37.3	34.4 - 40.4
	<i>Pseudomonas delhiensis</i> CCM 7361	83.52	28.3	25.9 - 30.8	39.1	36.1 - 42.1
	<i>Pseudomonas citronellolis</i> LMG 18378	83.48	28.2	25.8 - 30.7	37.6	34.7 - 40.7
	<i>Pseudomonas jinjuensis</i> JCM 21621	82.75	27.5	25.1 - 30	31.6	28.7 - 34.7

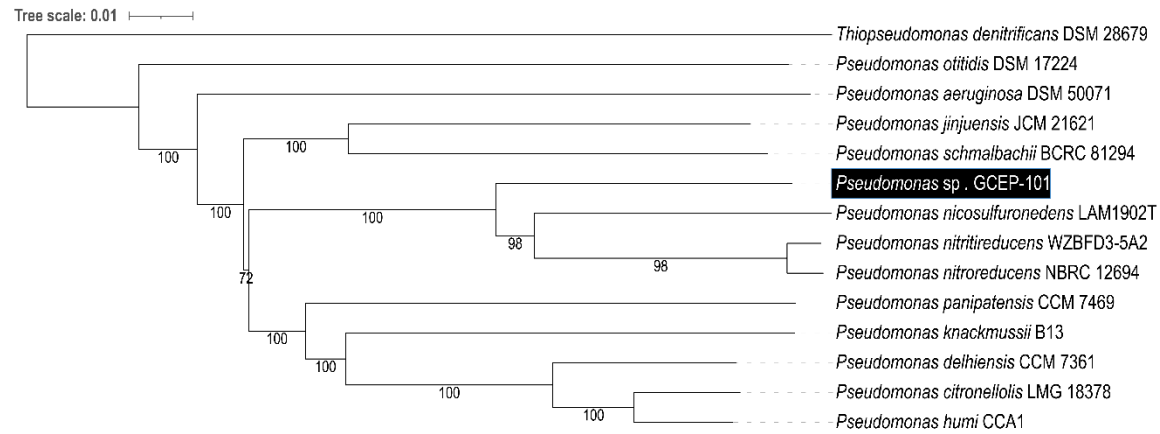


Figure S3. Tree inferred with FastME 2.1.6.1 from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d5. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 97.1 %.