

SUPPLEMENTARY INFORMATION

NCBI GenBank Accession numbers according to rDNA gene sequencing

Microbacterium sp.

The screenshot displays the NCBI GenBank record for *Microbacterium* sp. strain GISTAQ2 16S ribosomal RNA gene, partial sequence. The record includes the following details:

- LOCUS:** 928 bp DNA linear BCT 12-FEB-2022
- DEFINITION:** *Microbacterium* sp. strain GISTAQ2 16S ribosomal RNA gene, partial sequence.
- ACCESSION:** OMS48364
- VERSION:** OMS48364.1
- KEYWORDS:** Microbacterium sp.
- SOURCE:** *Microbacterium* sp.
- ORGANISM:** *Microbacterium* sp.; Bacteria; Bacillales; Actinomycetota; Actinomycetes; Micrococcales; Microbacteriaceae; Microbacterium.
- REFERENCE:** 1 (bases 1 to 928) Farias, A.R., Utges, F.M., Echeverria, M., Cuadra, P. and Fontana, G. Ferulic Biodegradation in Consortium through Bacillus licheniformis, *Microbacterium* sp. and *Brevundimonas* sp. Unpublished
- REFERENCE:** 2 (bases 1 to 928) Farias, A.R., Utges, F.M. and Hervot, F. Direct Submission
- JOURNAL:** Submitted (07-FEB-2022) GISTAQ, Universidad Tecnologica Nacional, French 424, Resistencia, Chaco 3580, Argentina
- COMMENT:** #Assembly-Data-START# Sequencing Technology :: Sanger didecoy sequencing #Assembly-Data-END#
- FEATURES:** Location/Qualifiers source 1..928 /organism="Microbacterium sp." /mol_type="genomic DNA" /strain="GISTAQ2" /isolation_source="soil sample" /db_xref="taxon:51671" c1..928 /product="16S ribosomal RNA"
- ORIGIN:** 1 agagctgctt agagctgttt gtgctgttt gtgtgaatn ccgggttca accctggan 61 nccgtggtt ccggcagag tagatgtgtt tgaattctt ggtgtgagc 121 tgaattgtt agtatctag agaacaccg atgagagag cagctctgtt agcgtatct 181 gctgttagc agcagagag tagagagag ccagctgtt atccctggtt agtccctcc 241 gtaagctgt gaaactggtt gtaggttca ttccagctgt tctgtgagc agctaacga 301 ttatgtctt cgtctagga gtaggtgtt aggtctaac cttaagagc ttgagagga 361 ccgctagag cagagagag ttgagttaa ttgagtagc agagagag cttaacagg 421 ctgtcatat agagagagc gctcaaatg gtcaacttt tgaactgtt taacagagt 481 gctgtggtt gctgtgctt cgtgtgtgtt gctgtgtgtt taagctgtt agagagga 541 accctgttt tctgtgttca gctgtgtt gtaggaact atgagctatc cctgagctt 601 atcagagga agtggaggtt gactcaatc catatgtc ctatgtttt aggtcttag 661 cctgtctaa tgcagcttc agagctgtt atctatctat gctgtgttc atcccaaaa 721 gctgtgttc gttgaggtt aggtcttca ctgactctt tgaagctga gctgtgata 781 atgctgctt agcagagag cagctgtgtt gttctgaggt ctgtcttca cctgtctt 841 agctatgaa gctgtctaa cctgagctt gttctgaggt cctgtgttc ggtgtgtc 901 aggtgtggt cgtgtgtt gactggt

Brevundimonas sp.

The screenshot displays the NCBI GenBank record for *Brevundimonas* sp. strain GISTAQ1 16S ribosomal RNA gene, partial sequence. The record includes the following details:

- LOCUS:** 899 bp DNA linear BCT 01-AUG-2021
- DEFINITION:** *Brevundimonas* sp. strain GISTAQ1 16S ribosomal RNA gene, partial sequence.
- ACCESSION:** MT787293
- VERSION:** MT787293.1
- KEYWORDS:** Brevundimonas sp.
- SOURCE:** *Brevundimonas* sp.
- ORGANISM:** *Brevundimonas* sp.; Bacteria; Pseudomonadati; Pseudomonadota; Alphaproteobacteria; Caulobacteriales; Caulobacteraceae; Brevundimonas.
- REFERENCE:** 1 (bases 1 to 899) Farias, A.R., Utges, F.M., Echeverria, M., Cuadra, P. and Fontana, G. Ferulic Biodegradation in Consortium through the Bacillus licheniformis, *Microbacterium* sp. and *Brevundimonas* sp. Unpublished
- REFERENCE:** 2 (bases 1 to 899) Farias, A.R., Utges, F.M. and Teney, M.D. Direct Submission
- JOURNAL:** Submitted (22-JUL-2020) GISTAQ, Universidad Tecnologica Nacional, Juan B. Justo 4136, Barranqueras, Chaco 3580, Argentina
- COMMENT:** #Assembly-Data-START# Sequencing Technology :: Sanger didecoy sequencing #Assembly-Data-END#
- FEATURES:** Location/Qualifiers source 1..899 /organism="Brevundimonas sp." /mol_type="genomic DNA" /strain="GISTAQ1" /isolation_source="soil sample" /db_xref="taxon:187480" c1..899 /product="16S ribosomal RNA"
- ORIGIN:** 1 ctggagtaa agagccta gggagctt tagtctag gtagatcc aggcctaac 61 ctgagctt cttgttat tggctctt gattatgag gatttatgt gattcttag 121 tctgtgtgt aatttatgt attcttag gctatgct gtagagtg actctatgt 181 tctatttga cgtgtgagc cgaagctgt agagcaaac aggtatgt accgtgtag 241 tccagctgt aagctgtgt tctgtgtt cagctgtat gctgttgtt gctgtctt 301 agatttag caactgtct gggagctgt gctcagat taactctaa agatttag 361 agagctgtc acagagctt gactgttg ttattttgt agcagagc agactctac 421 cctcttttg cttgtgtgt cctgtgtgt gctgtgtt tctctgttg gtttagaa 481 caggtatgt atgagctgt tcatgtctt tctgtgtt tgggttag tccgaagc 541 aggaacacc tgcattgt tgcctatc ttatttgg actctatgg gctgtcgt 601 gtttagag agagagct gatttatct actctctt agctcttaa aggtatgt 661 caacagctt acatagcaa ctacagag ttactctta aagttgtct cagttggt 721 tctcttttg aactagag cttgtgtgt gctgtgtt taattgttg tcatgtgt 781 gatttata cttcttcgg cttgttacc accgcttc accatagg agttgtctt 841 accagagg gttgtctaa cctagatg aggcagtc cactagagg gttgtgtc

Biofilm formation assays

Biofilm development of the assayed strains, and their combinations, expressed as absorbance values at 585 nm

A: *Brevundimonas* sp.

B: *Microbacterium* sp.

C: *Bacillus licheniformis*

<i>Brevundimonas</i>	<i>Microbacterium</i>	<i>Bacillus</i>	<i>Brevundimonas</i> + <i>Microbacterium</i>	<i>Brevundimonas</i> + <i>Bacillus</i>	<i>Microbacterium</i> + <i>Bacillus</i>	<i>Brevundimonas</i> + <i>Microbacterium</i> + <i>Bacillus</i>	Blanc
0.549	0.728	0.170	0.761	0.500	0.288	2.984	0.188
0.902	0.894	0.221	0.897	0.408	1.924	3.400	0.134
0.266	0.769	0.239	0.688	0.362	2.348	3.704	0.141
0.287	0.225	0.276	0.465	0.235	1.900	2.756	0.137
0.161	0.660	0.164	0.774	1.131	1.666	2.960	0.129
1.063	0.617	0.166	0.230	1.164	1.702	2.754	0.192

The number in red were discarded by applying a Q test.

Microorganisms	Media	Desv Est	Máx	Mín
Control	0.154	0.029	0.182	0.125
<i>Bacillus</i>	0.206	0.047	0.253	0.159
<i>Brevundimonas</i>	0.538	0.371	0.909	0.167
<i>Brevundimonas</i> + <i>Bacillus</i>	0.633	0.407	1.041	0.226
<i>Brevundimonas</i> + <i>Microbacterium</i>	0.636	0.245	0.881	0.391
<i>Microbacterium</i>	0.649	0.229	0.878	0.420
<i>Microbacterium</i> + <i>Bacillus</i>	1.638	0.705	2.343	0.933
<i>Brevundimonas</i> + <i>Microbacterium</i> + <i>Bacillus</i>	3.093	0.381	3.474	2.712

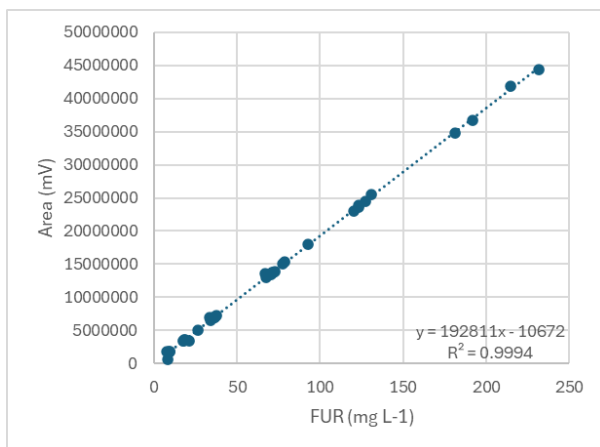
MBBR degradation tests

Furfural degradation - quebracho chips			
Time (h)	Furfural (mg L ⁻¹)	Error	Removal (%)
0	3832.56	1.91	1.98
6	3042.48	1.51	22.19
16	2765.76	1.37	29.27
20	2262.93	0.51	42.13
24	2109.66	0.47	46.05
28	385.86	0.08	90.13
40	101.28	0.01	97.41
44	93.625	0.01	97.61
48	96.12	0.01	97.54
52	76.5	0.01	98.04
64	69.32	0.01	98.23
68	12.48	0.00	99.68
72	49.3	0.00	98.74
75	24.2	0.00	99.38
87	0	0.00	100

Furfural degradation - rice husk			
Time (h)	Furfural (mg L ⁻¹)	Error	Removal (%)
0	3606	1.80	0.01
4	2779	1.38	22.94
16	1267	0.26	64.87
24	55	0.00	98.47
28	0	0.00	100
40	0	0.00	100
44	0	0.00	100
48	0	0.00	100

Analytical performance parameters of furfural quantification

Calibration curve

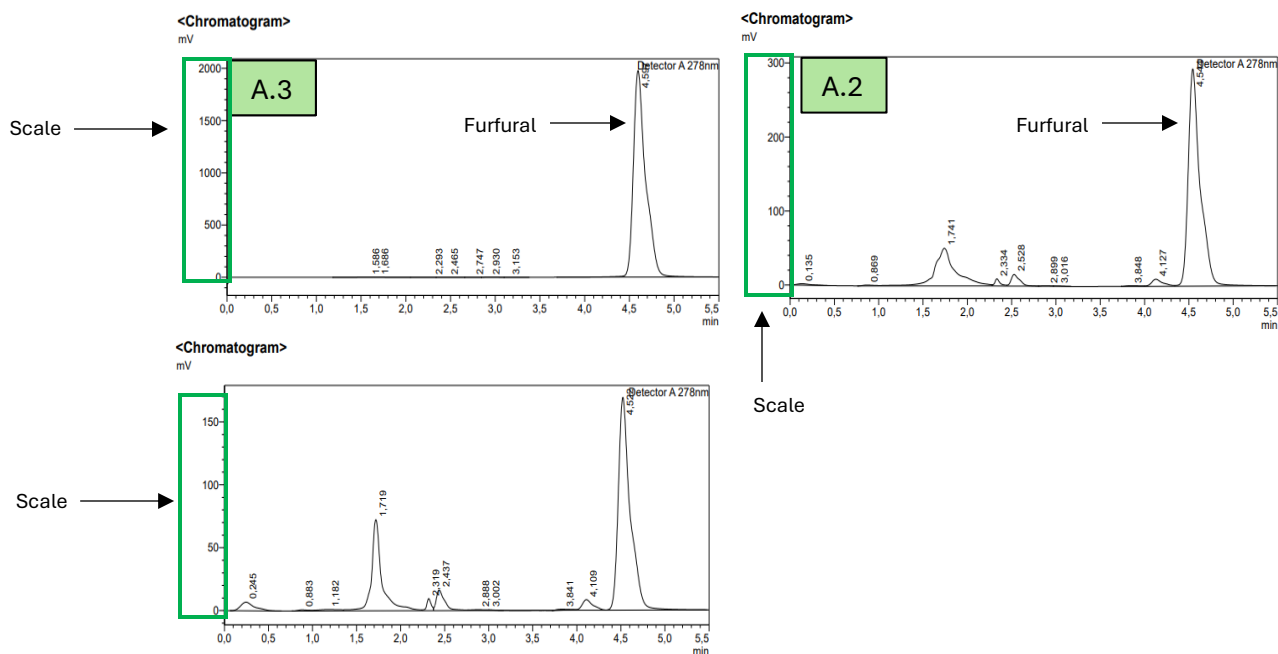


A linear range of 8 to 345 mg L⁻¹ is detected. The dynamic range is not analysed.

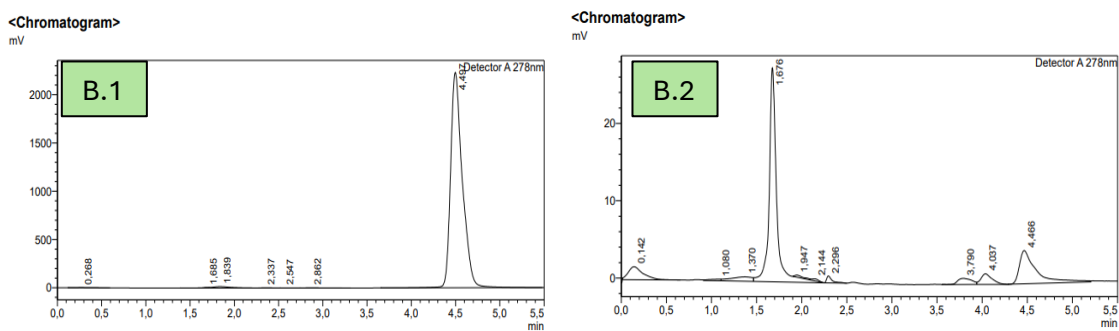
	Sensitivity (mV/ppm)		Limit of detection (LOD) mgL ⁻¹		Limit of quantification (LOQ) mgL ⁻¹
Low range	57		2.63		8.77
Middle rang	97				

Chromatographic profiles of FUR degradation

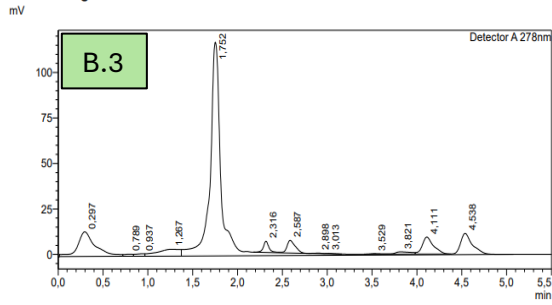
Under the test conditions indicated in materials and methods, furfural appears in a retention time of 4.5 minutes. Under the same conditions, the repetitive appearance of a retention time peak at 1.7 minutes, consistent with the disappearance of the furfural peak, would indicate the presence of furfuryl alcohol or furoic acid.



A. *Brevundimonas sp.* GISTAQ1 - 546 mg L⁻¹. A.1: Time 0, A.2: Day 1. A.3: Day 2

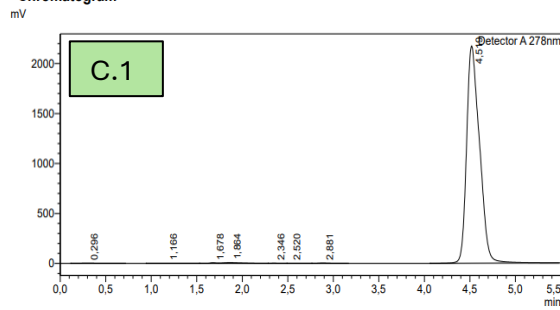


<Chromatogram>

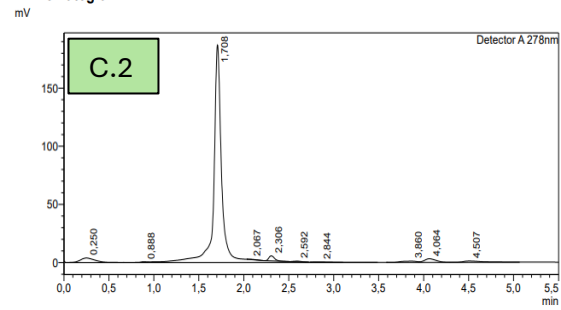


B. *Microbacterium* sp. GISTAQ2 - 720 mg L⁻¹. B.1: Time 0, B.2: Day 1. B.3: Day 2

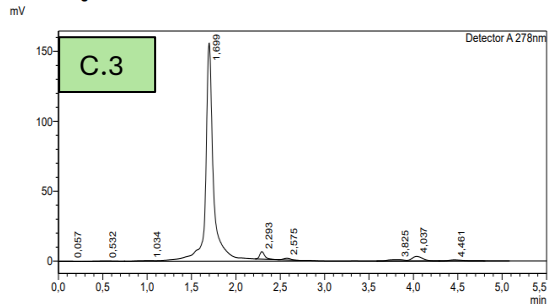
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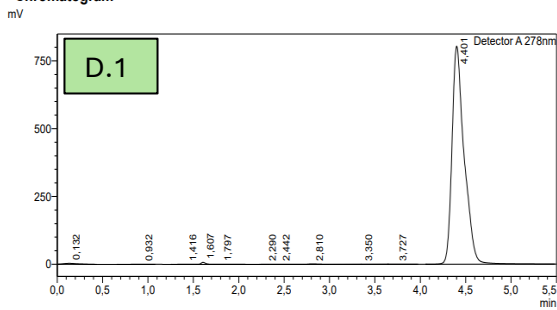


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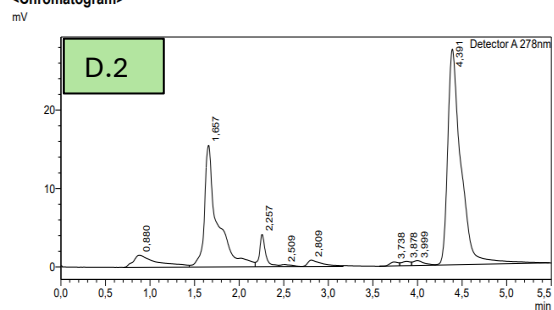


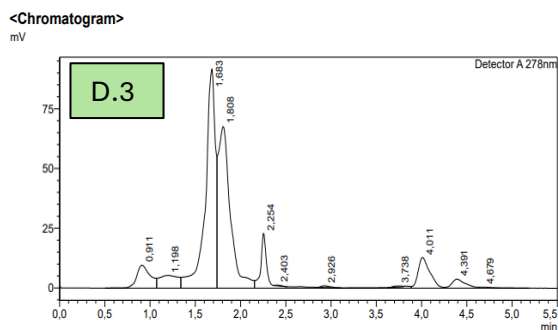
C. *Bacillus licheniformis* GTQ1 - 479 mg L⁻¹. C.1: Time 0, C.2: Day 2. C.3: Day 3.

<Chromatogram>



<Chromatogram>





D. *Bacillus licheniformis* GTQ1 + *Microbacterium* sp. GISTAQ2 + *Brevundimonas* sp. GISTAQ1 - 638
mg L⁻¹. D.1: Time 0, D.2: Day 1. D.3: Day 2

Statistical evaluation in MBBR degradation tests

FUR (mg L ⁻¹)	Media	DESVEST	CV%
9	1759166	39432	2.24
18	3453810	69107	2.00
25	12807758	40747	0.32
36	6962669	57794	0.83
72	13782219	127765	0.93
123	23773891	282840	1.19
Based on the table above, the CVs are estimated by data range.		9 a 17	2.24
		18 a 24	2.00
		25 a 35	0.32
		36 a 65	0.83
		66 a 100	0.93
		101 a 130	1.19

Dilutions are required starting at 130 mg L⁻¹. In the laboratory, dilutions are made by 1/10 for values up to 1000 mg L⁻¹, 1/20 for values up to 2500 mg L⁻¹, and 1/50 for values up to 4000 mg L⁻¹. Error propagation is calculated with an estimated uncertainty of the automatic pipettes at 1%.

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Dil 1/10	20 ul + 180 ul
Dil 1/20	10 ul + 190 ul
Dil 1/50	10 ul + 490 ul

Dil 1/10	1.81
Dil 1/20	1.90
Dil 1/50	4.90

Then, the CV of each value in % will be the result of the uncertainty due to the method (according to the corresponding range) and the uncertainty due to the dilution (according to whether it is 1/10, 1/20 or 1/50)

RICE HUSK

FUR (mg L ⁻¹)	U Method	U dil	CV final%	Error
3606	0.93	4.90	4.99	1.80
2779	0.83	4.90	4.97	1.38
1267	0.83	1.90	2.07	0.26
55	0.83	0	0.83	0.00
0	0	0	0	0

QUEBRACHO

FUR (mg L ⁻¹)	U Method	U dil	CV final%	Error
3832.56	0.93	4.90	4.99	1.91
3042.48	0.83	4.90	4.97	1.51
2765.76	0.83	4.90	4.97	1.37
2262.93	1.19	1.90	2.24	0.51
2109.66	1.19	1.90	2.24	0.47
385.86	0.83	1.81	1.99	0.08
101.28	1.19	0	1.19	0.01
93.625	0.93	0	0.93	0.01
96.12	0.93	0	0.93	0.01
76.50	0.93	0	0.93	0.01
69.32	0.93	0	0.93	0.01
12.48	2.24	0	2.24	0.00

49.30	0.83	0	0.83	0.00
24.20	2.00	0	2.00	0.00
0	0	0	0	0.00