CO_2 as a Carbon Source for Biosurfactant Production

Henrique Alves de Brito[1], Francine M. Santos[1], Amanda P. Napp[1], Lovaine S. Duarte[1], Richard S. Salvato[1], William Lautert-Dutra[1], Eduarda V. Abati[1], Daniel U. Brito[1], Clarissa L. Melo[1], and Joao Pedro T. Zielinski[1]

Search and Discovery Article #80762 (2026)**
Posted April 30, 2026

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 DOI:10.1306/80762Debrito2026

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Abstract

Objectives and Scope: Several countries have adopted carbon-neutral strategies to reduce greenhouse gas (GHG) emissions. Among these, the capture and utilization of carbon dioxide (CO_2) from industrial processes (CCU) is an effective approach. Integrating biotechnology allows CO_2 mitigation while producing value-added products. Microorganisms capable of metabolizing CO_2 offer a sustainable alternative, reducing GHGs and enabling the synthesis of bioproducts such as biosurfactants. These amphiphilic molecules have broad industrial applications, notably in Microbial Enhanced Oil Recovery (MEOR). Despite this potential, few studies have investigated biosurfactant production under CO_2-rich conditions. To address this, our collaborative project with Petronas Petróleo Brasil LTDA (PPBL) explores biosurfactant production using CO_2 as the primary carbon source.

Methods, Procedures, Process:

Twenty-eight isolates were preselected for production using a CO_2-analog molecule in two media: B medium (nutrient-rich) and C medium (restrictive and saline). Emulsification indices were assessed, and the most promising isolates were cultivated under CO_2 atmosphere in C medium. Selected isolates underwent DNA sequencing to support culture optimization and gene target identification for genetic engineering. One isolate was chosen for biosurfactant production optimization through genetic engineering and laboratory assisted evolution. Various methodologies are currently being applied to identify the biosurfactant molecule and evaluate the stability of the bioproduct under different conditions of pH, temperature, salinity, and pressure.

Results, Observations, Conclusions:

Many isolates showed a high emulsification index (>60%) in the C medium with sodium bicarbonate, which was then selected for further experiments. Three isolates were chosen for genome sequencing using Illumina and Nanopore technologies. Two represent a novel *Exiguobacterium* lineage, while the other one is a new strain of *Vreelandella zhaodongensis*. All sequenced strains grew under CO_2. Two

isolates produced emulsifying compounds even without cells and were selected for further CO_2 experiments. The isolate 253 maintained a 60% emulsification index under CO_2, which was more effective than sodium bicarbonate or glucose. The biosurfactant molecule was identified as an exopolyssacharide which is stable under different conditions of pH, temperature, salinity, and pressure.

Significance/Novelty:

This project presents a bioproduct from Brazilian biodiversity with high emulsification capacity, potential MEOR applications, and contributions to industrial innovation and CO_2 reduction.

SPE · AAPG · SEG

CCUS

Carbon Capture, Utilization, and Storage

CO_2 as a Carbon Source for Biosurfactant Production

Henrique Alves de Brito

Coordinator: João Pedro Tauscheck Zielinski

IPR Instituto do Petróleo e dos Recursos Naturais

PUCRS

PETRONAS

Introduction

How can captured CO_2 be transformed into a biotechnological product?

Introduction

Biofuel Research Journal 44 (2024) 2256-2282

Biofuel Research Journal
Journal homepage: www.biofueljournal.com

Review Paper

Third-generation biomass for bioplastics: a comprehensive review of microalgae-driven polyhydroxyalkanoate production

Rijuta Ganesh Saratale[1], Si-Kyung Cho[2], Ram Naresh Bharagava[3], Anil Kumar Patel[4], Vivekanand Vivekanand[5], Shashi Kant Bhatia[6], Luiz Fernando Romanholo Ferreira[7], Han Seung Shin[8], Mukesh Kumar Awasthi[9], Sankha Chakrabortty[10], Ramesh Kumar[11], Ganesh Dattatraya Saratale[8,*]

Review 29 November 2021

Valorisation of CO_2 into Value-Added Products via Microbial Electrosynthesis (MES) and Electro-Fermentation Technology

Marzuqa Quraishi[1,†], Kayinath Wani[2], Soumya Pandit[2,*], Piyush Kumar Gupta[2], Ashutosh Kumar Rai[3,†], Dibyajit Lahiri[4], Dipak A. Jadhav[5], Rina Rani Ray[6], Sokhee P. Jung[7] ... Ram Prasad[11,*]

foods MDPI

Foods. 2022 Dec 25;12(1):107. doi: 10.3390/foods12010107

Biotechnological Production of Sustainable Microbial Proteins from Agro-Industrial Residues and By-Products

Bojana Bajić [1], Damjan Vučurović [1,*], Đurđina Vasić [1], Rada Jevtić-Mučibabić [2], Siniša Dodić [1]

Prospective bioconversion of CO_2 and CO into fine chemicals via halophilic purple phototrophic bacteria

Mini Review | Open access | Published: 27 March 2025

Volume 24, pages 29–41, (2025) Cite this article

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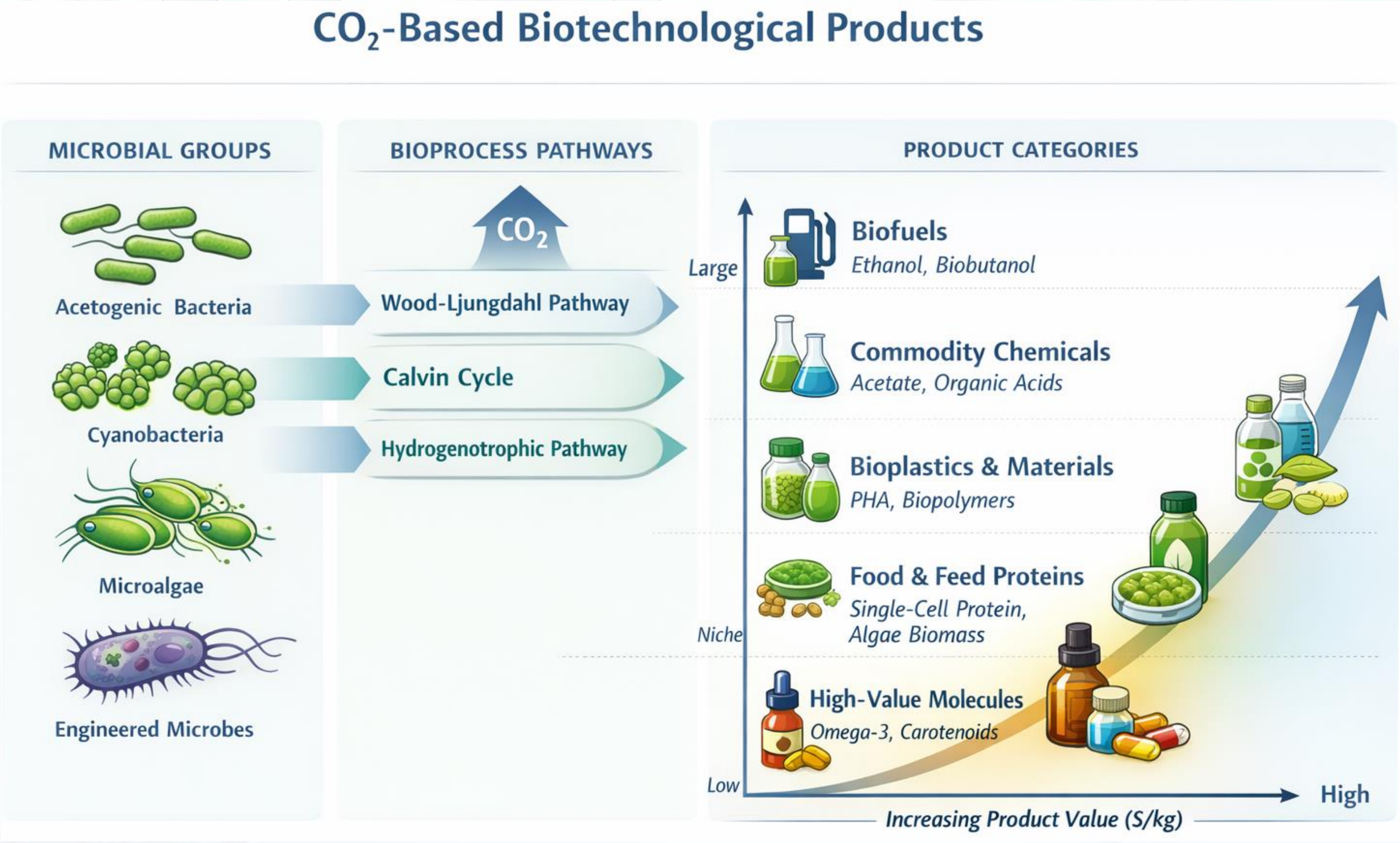
Synthetic and Systems Biotechnology
Volume 9, Issue 1, March 2024, Pages 19-25

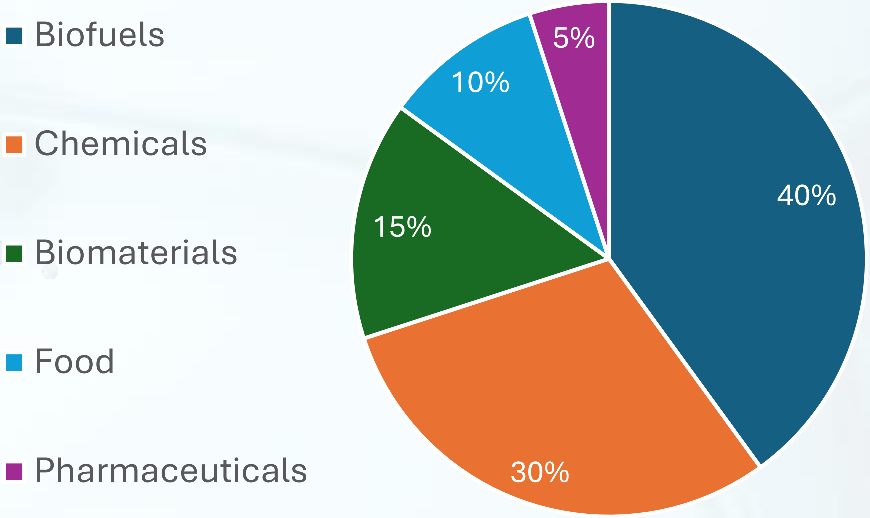
Review Article

Recent progress in engineering *Clostridium autoethanogenum* to synthesize the biochemicals and biocommodities

Sai Wan [a], Mingchi Lai [a d], Xinyu Gao [a e], Mingxin Zhou [b c], Song Yang [d], Qiang Li [e], Fuli Li [a], Lin Xia [c], Yang Tan [a]

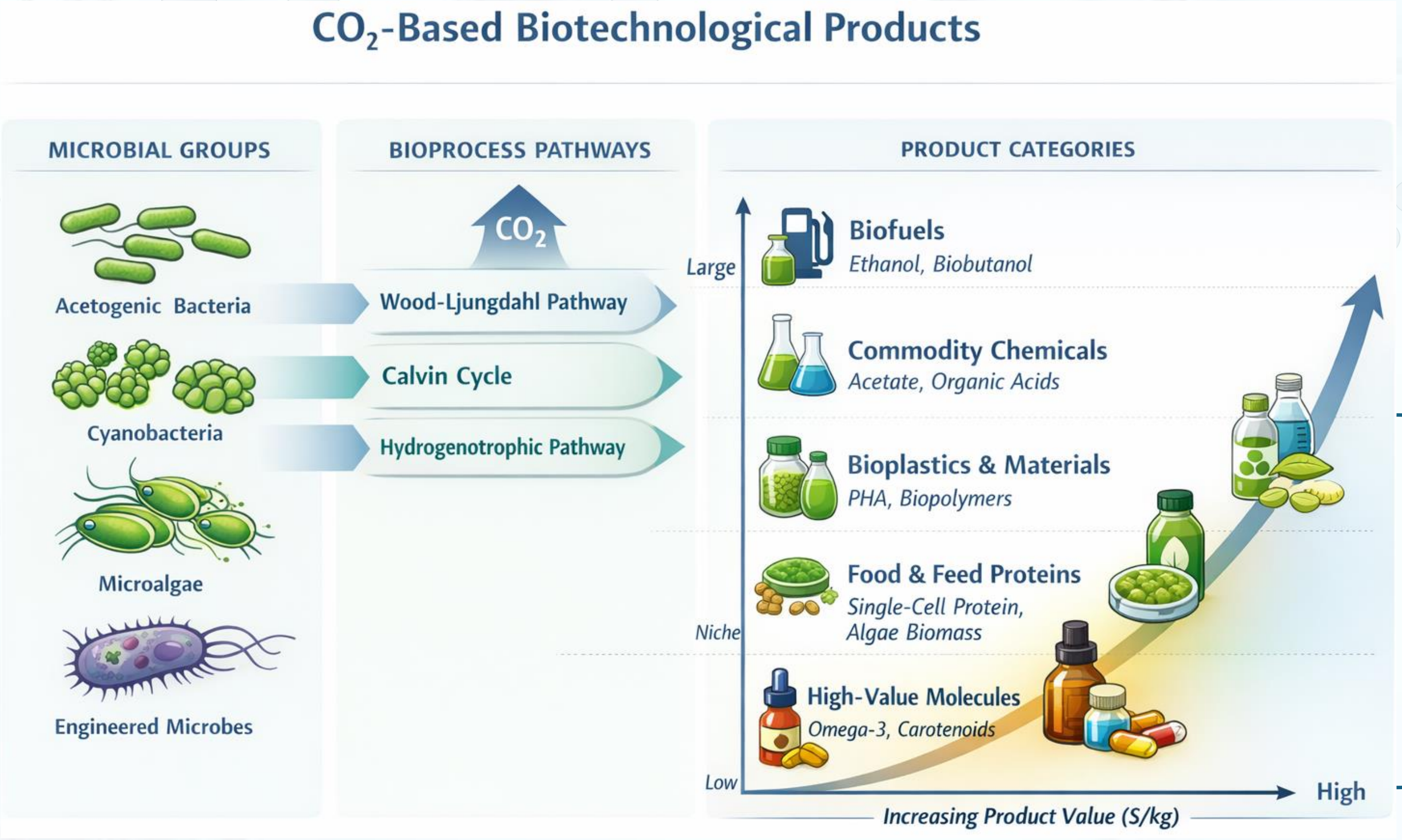
Introduction





Kumar et. al. (2026)

Introduction

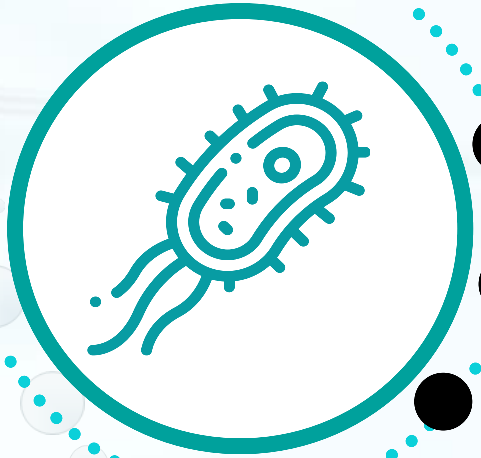


Biosurfactants

Kumar et. al. (2026)

Bioproducts - Biosurfactants

Natural compounds that can:
* emulsify
* reduce interfacial tension between oil and water



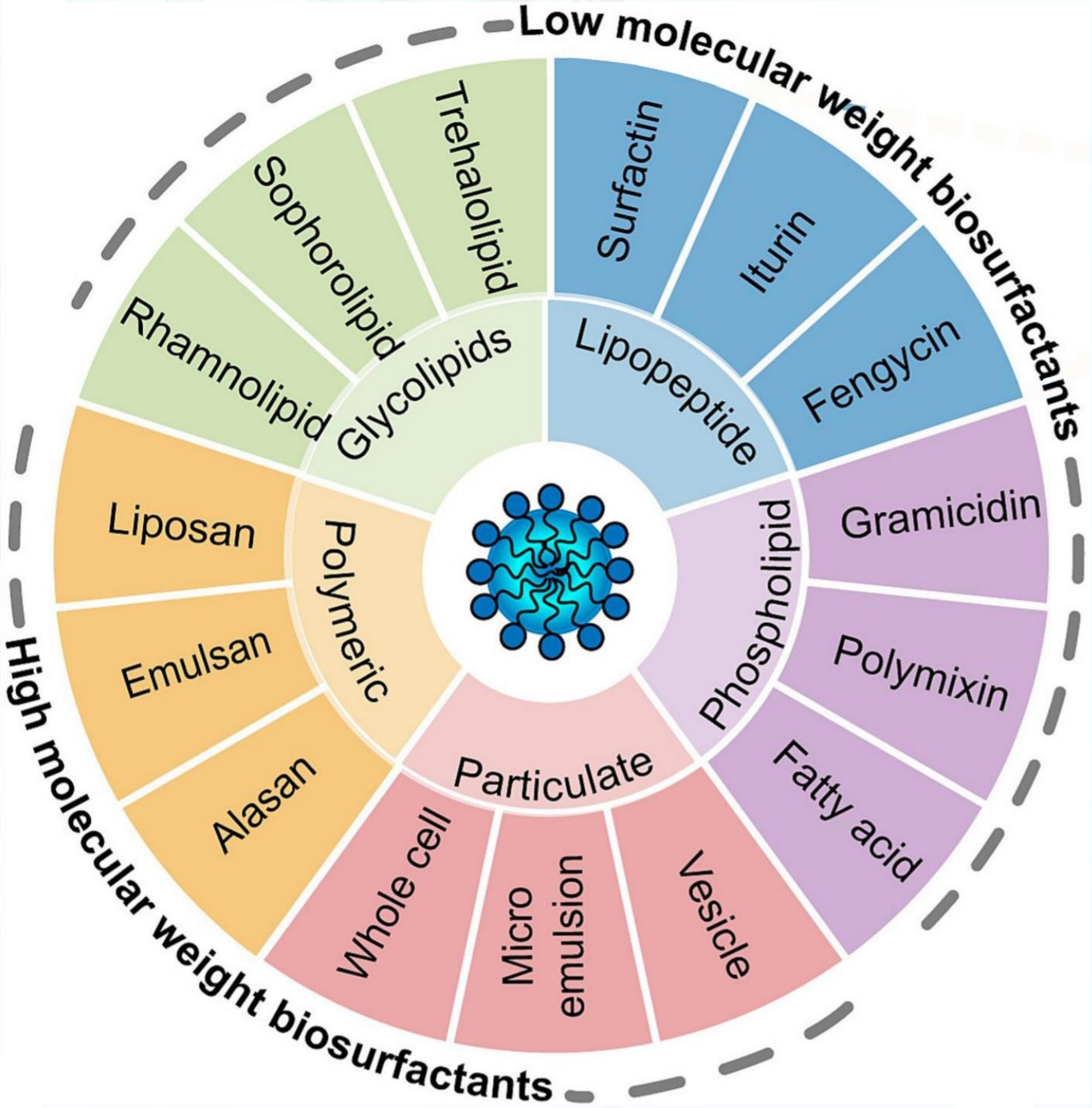
- BIODEGRADABLE
- Low toxicity
- Highly stable

Bacteria produce biosurfactants for many reasons

Biosurfactants are **more efficient and desirable** than chemical surfactants

Napp et. al. (2026)

Introduction

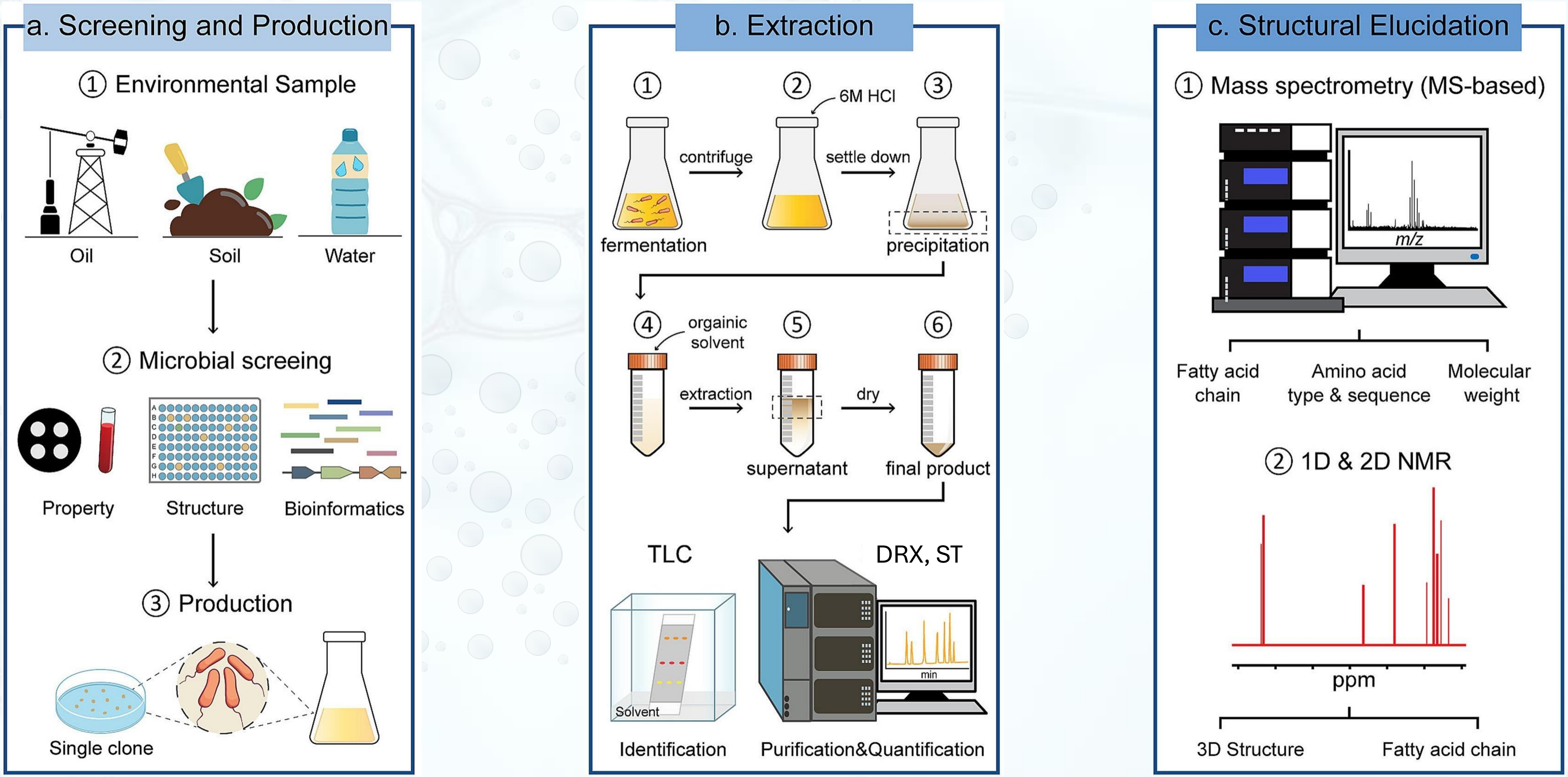


Kumar et. al. (2026)

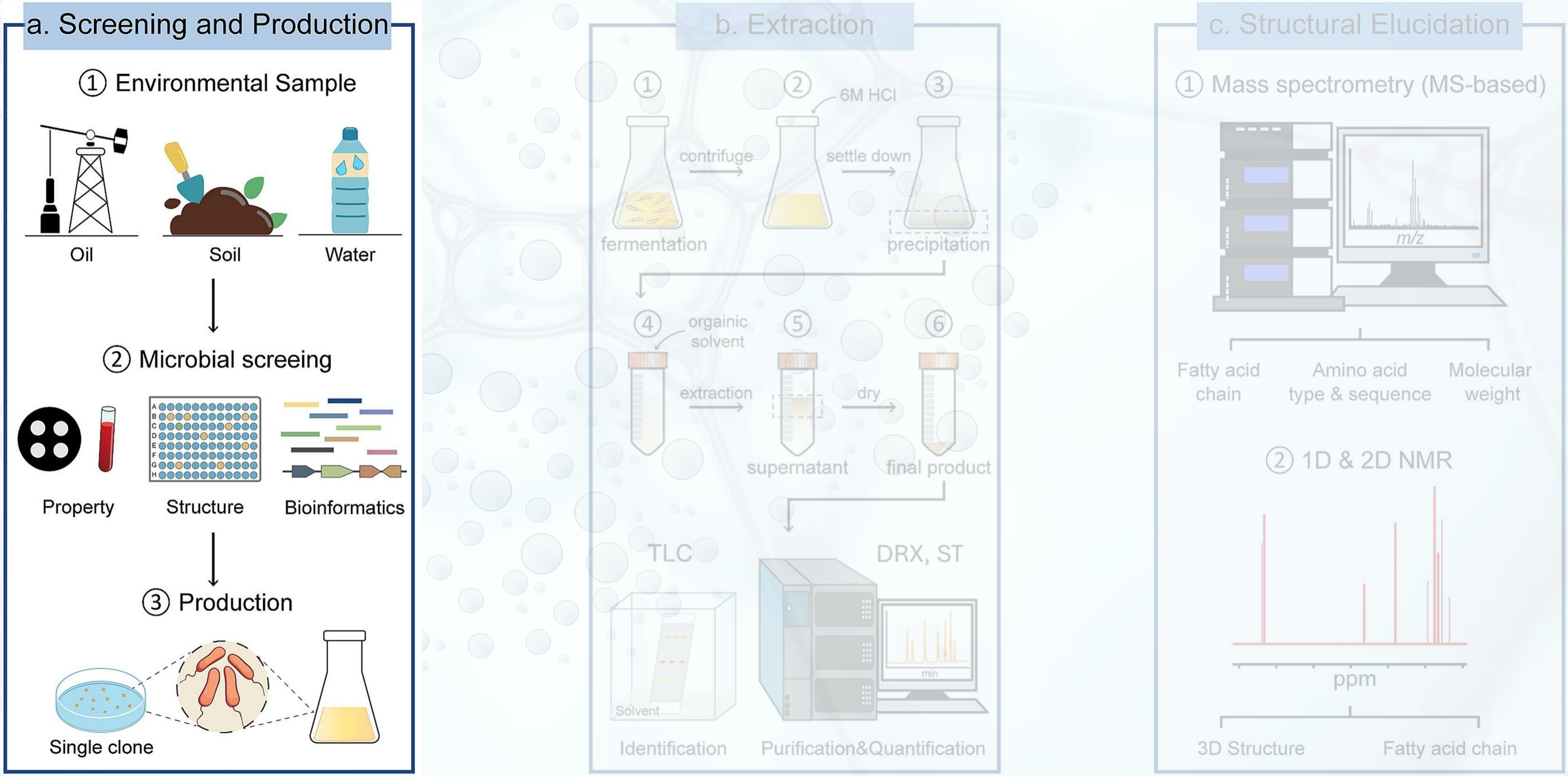
Goal

Production and characterization of biosurfactants by microorganisms through CO_2 conversion

Methods


a. Screening and Production
① Environmental Sample
Oil
Soil
Water
② Microbial screeing
Property
Structure
Bioinformatics
③ Production
Single clone
b. Extraction
①
②
6M HCl
③
contrifuge
settle down
fermentation
precipitation
④
orgainic solvent
⑤
⑥
extraction
dry
supernatant
final product
TLC
DRX, ST
Solvent
min
Identification
Purification&Quantification
c. Structural Elucidation
① Mass spectrometry (MS-based)
m/z
Fatty acid chain
Amino acid type & sequence
Molecular weight
② 1D & 2D NMR
ppm
3D Structure
Fatty acid chain

Methods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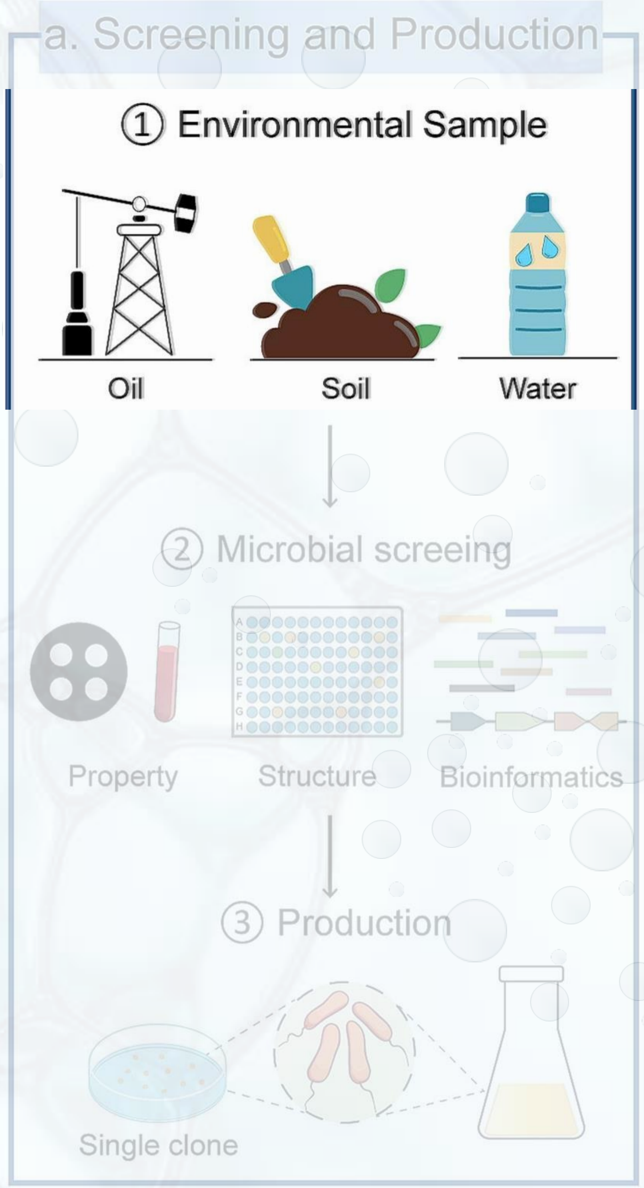
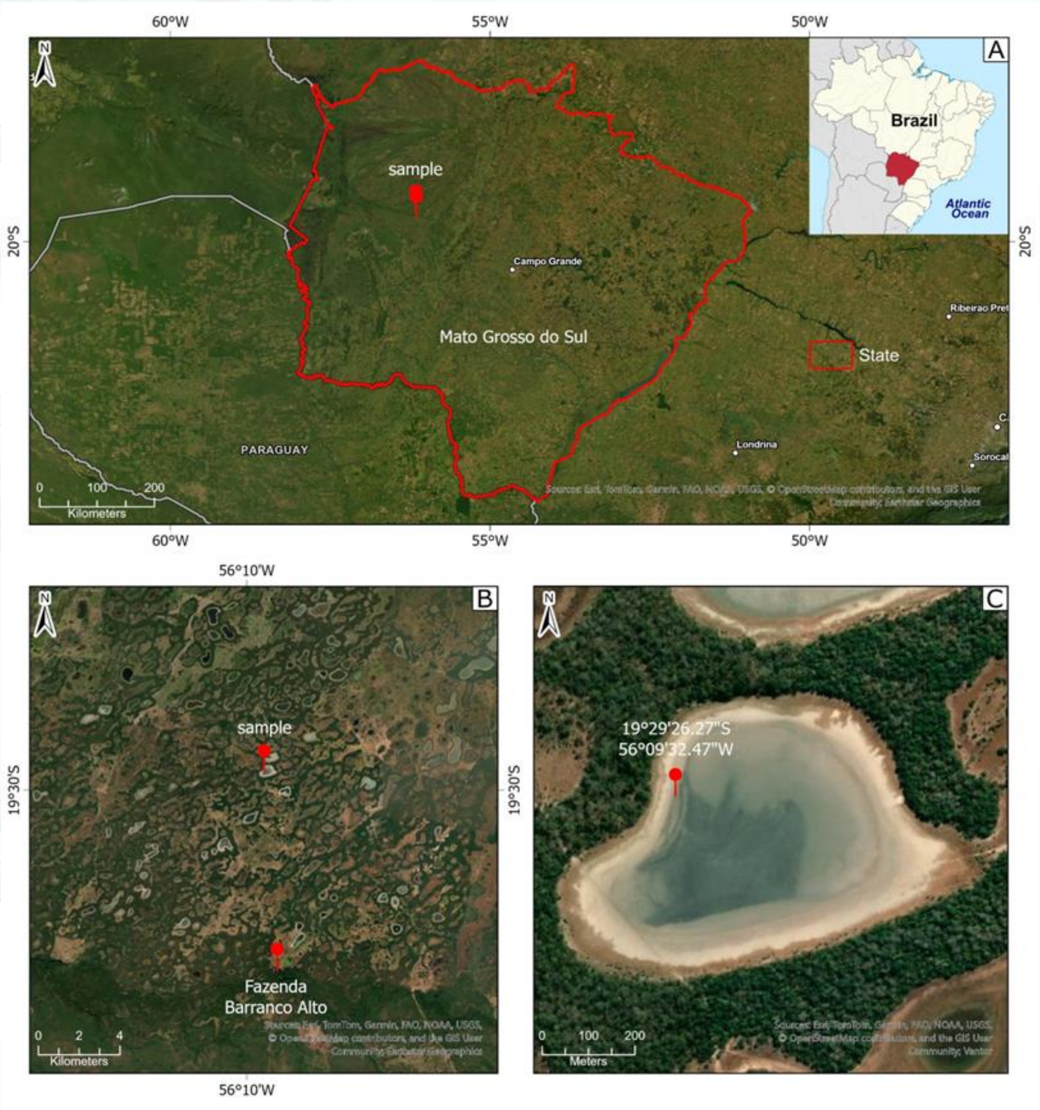
Single clone
b. Extraction
① ② ③
6M HCl
contrifuge
settle down
fermentation
precipitation
④ ⑤ ⑥
orgainic solvent
extraction
dry
supernatant
final product
TLC
DRX, ST
Solvent
min
Identification
Purification&Quantification
c. Structural Elucidation
① Mass spectrometry (MS-based)
m/z
Fatty acid chain
Amino acid type & sequence
Molecular weight
② 1D & 2D NMR
ppm
3D Structure
Fatty acid chain

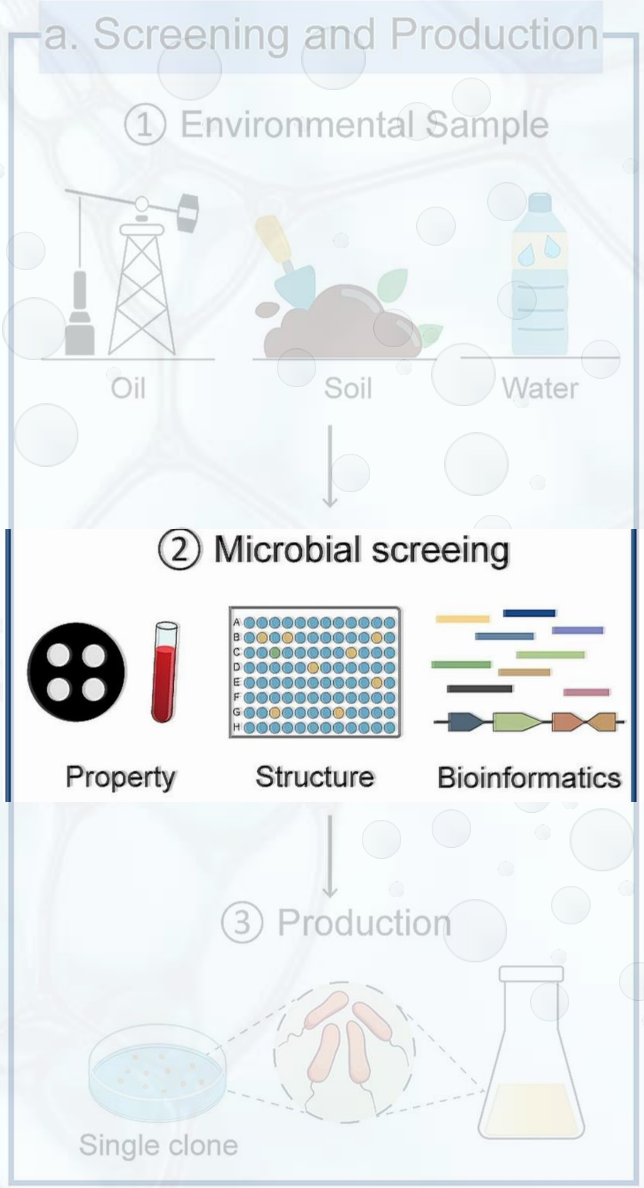
Results

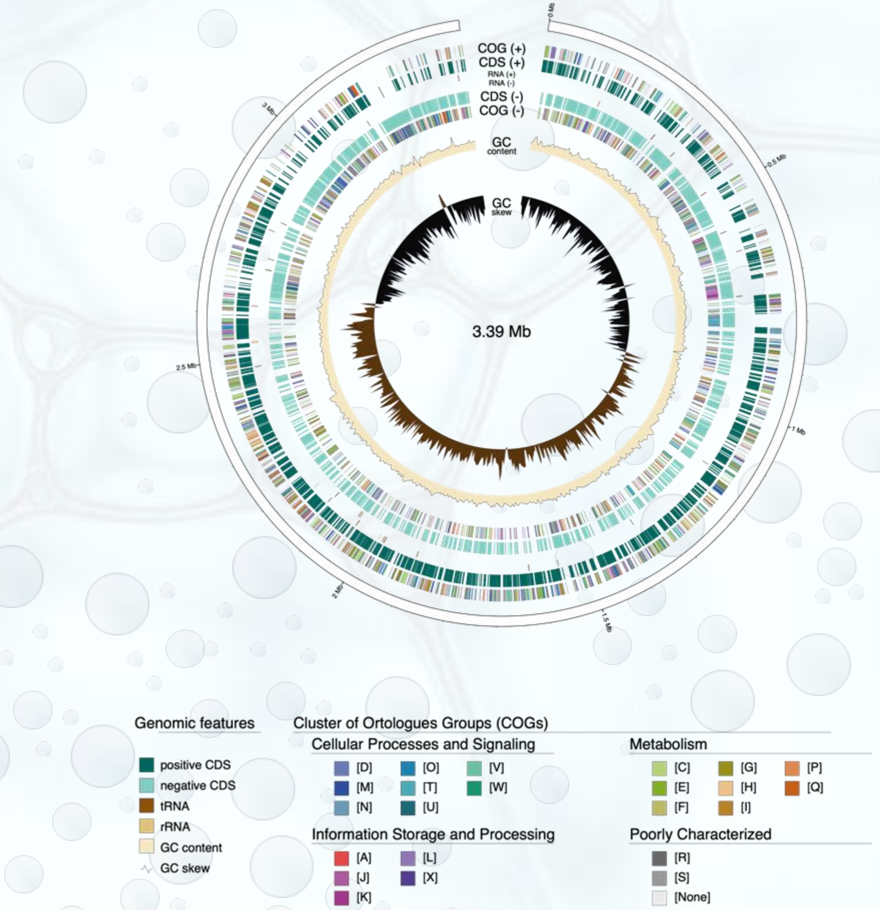


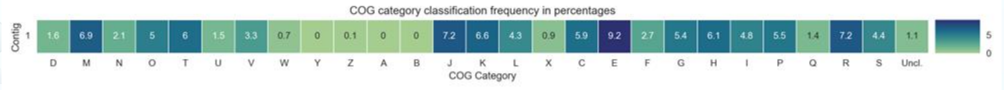


Sample collected from a saline lake in Pantanal, Brazil

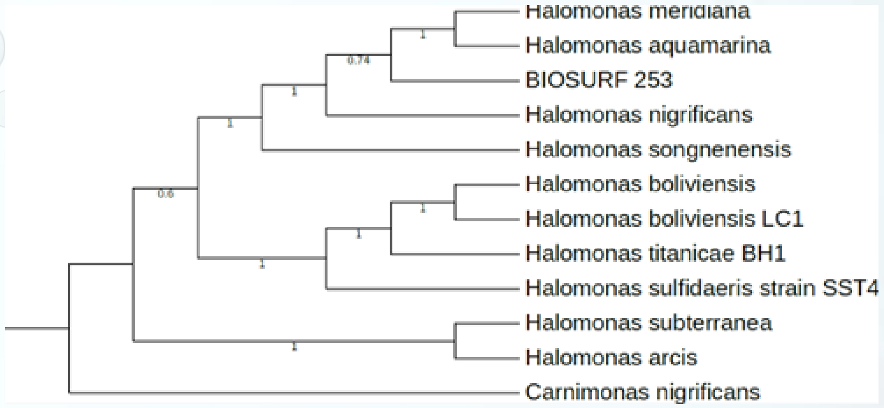
Results







General lookout of microorganism genoma.



Philogenetic tree of microrganisms

CCUS
Carbon Capture, Utilization, and Storage
SPE AAPG SEG

Results

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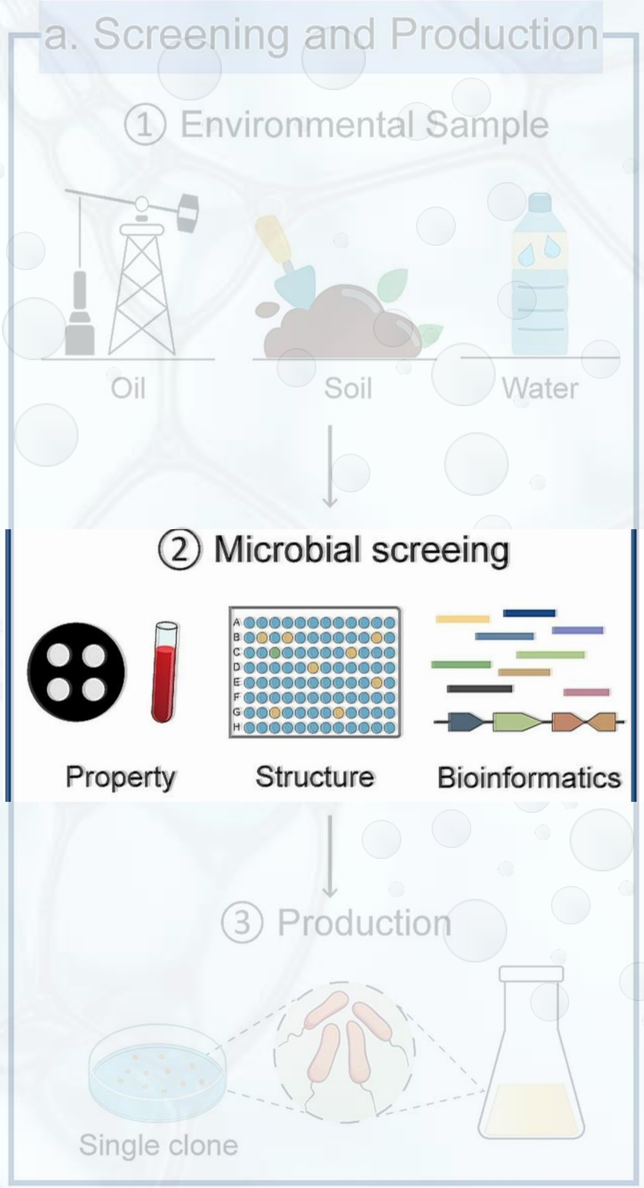

AMERICAN SOCIETY FOR MICROBIOLOGY
Microbiology Resource Announcements
GENOME SEQUENCES
November 2025 Volume 14 Issue 11 e00650-25
https://doi.org/10.1128/mra.00650-25

Complete genome sequences of two *Exiguobacterium alkaliphilum* isolates from the Brazilian Pantanal hypersaline lakes

William Lautert-Dutra, Francine Melise dos Santos, Amanda Pasinato Napp, Clarissa Lovato Melo

Environmental Monitoring and Biotechnology Laboratory, Institute of Petroleum and Natural Resources (IPR), Pontifical Catholic University of Rio Grande do Sul (PUCRS), Porto Alegre, Rio Grande do Sul, Brazil

The climate crisis has stimulated research into alternative solutions for combating climate change and environmental pollution. Extremophilic microorganisms present a valuable opportunity to detoxify and degrade pollutants. We provide the complete genome of two *Exiguobacterium alkaliphilum* isolates from a hypersaline alkaline lake and emphasize their potential as bioremediation facilitators.

KEYWORDS hybrid genome assembly, bioremediation, environmental pollution, extreme environments, Halophilic

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Complete genome sequence and metabolic features of *Vreelandella zhaodongensis* BS253:A new isolate from hypersaline lakes from Brazilian Pantanal

William Lautert-Dutra, Amanda Pasinato Napp, Eduardo Alexandre Back Sivinski, Charley Christian Staats, Francine Melise dos Santos, Clarissa Lovato Melo

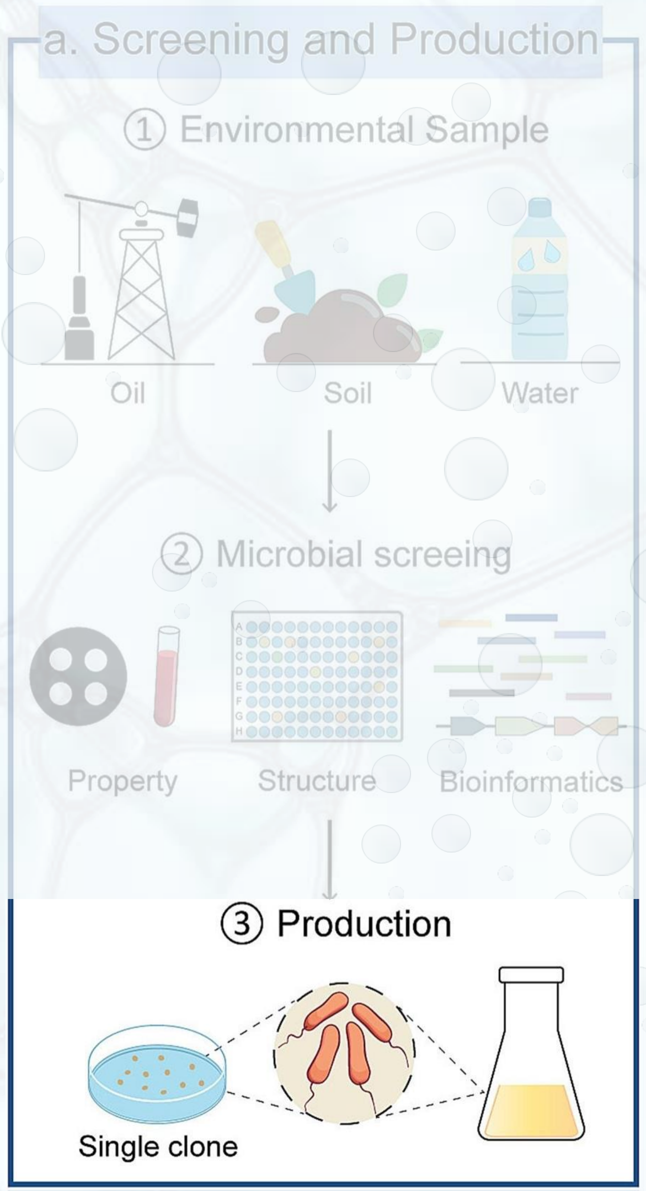
doi: https://doi.org/10.64898/2026.01.30.702823
This article is a preprint and has not been certified by peer review [what does this mean?].

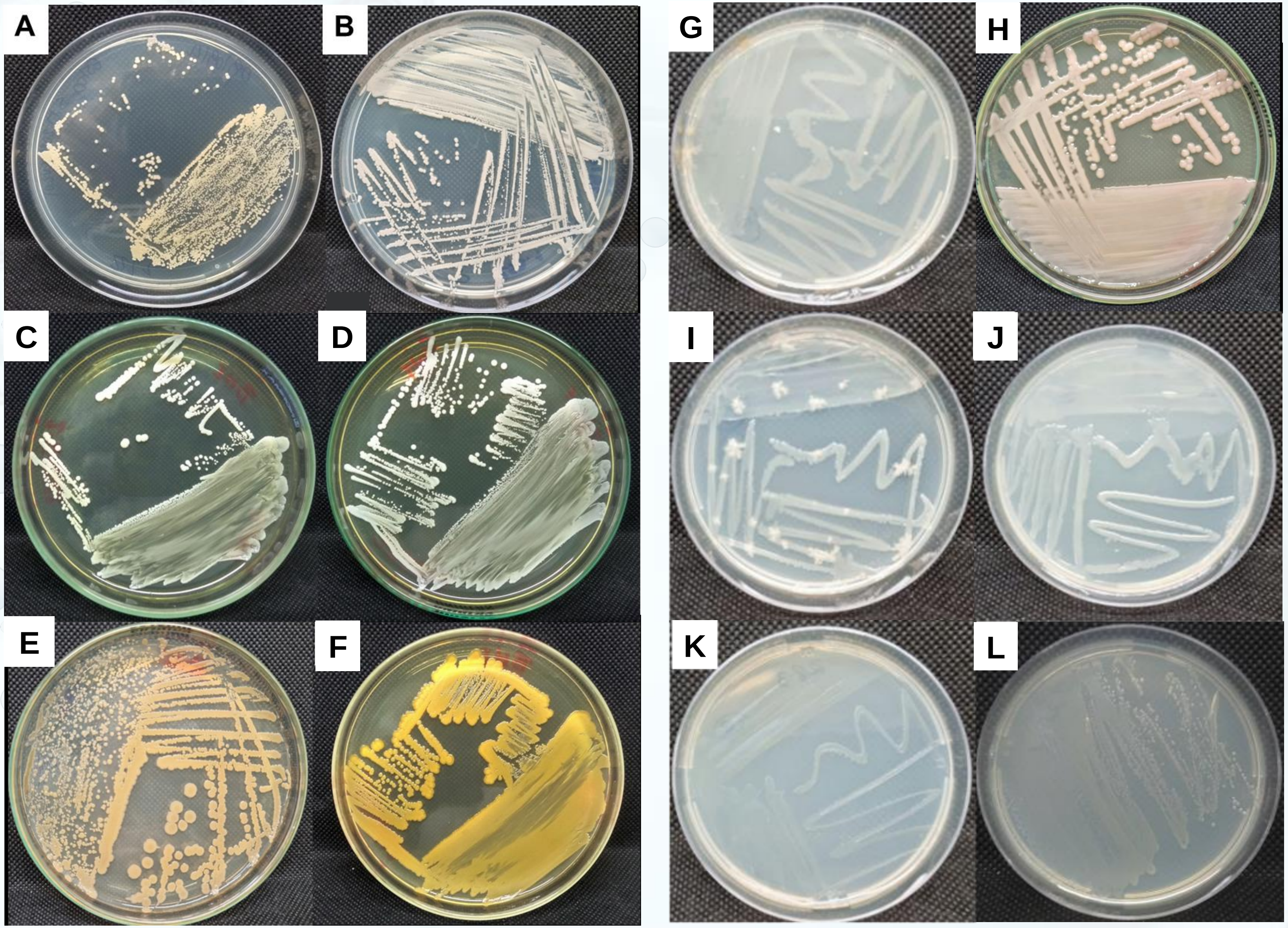
Abstract | Full Text | Info/History | Metrics | Preview PDF

Abstract

The urgent need for sustainable solutions to mitigate climate change has intensified research into carbon capture, utilization, and storage (CCUS) strategies. Biological approaches, particularly involving extremophilic microorganisms, offer promising alternatives to conventional methods due to their adaptability and potential for bioproduct synthesis. In this study, we report the complete genome sequencing and functional characterization of isolate BS253, derived from a hypersaline alkaline lake in Brazil's Pantanal region. Using a hybrid sequencing strategy combining Oxford Nanopore long reads and Illumina short reads, we assembled a circular chromosome of 3.76 Mb and identified two plasmids. Phylogenetic and comparative genomic analyses identified the isolate as *Vreelandella zhaodongensis*. Digital DNA-DNA hybridization (dDDH % = 71.4%) and ANI (96,83%) values supported the designation of BS253 as a distinct subspecies of *V. zhaodongensis*. The genome reveals genes associated with salt and alkali tolerance, hydrocarbon and plastic degradation, and the biosynthesis of secondary metabolites. Phenotypically, BS253 is a moderately halophilic, facultatively anaerobic, Gram-negative rod exhibiting biosurfactant activity, with an emulsification index of 51.7% under defined culture conditions. These findings highlight BS253 as a metabolically versatile extremophile with potential applications in different types of industries and biotechnological CCUS systems.

Results


a. Screening and Production
① Environmental Sample
Oil
Soil
Water
② Microbial screeing
Property
Structure
Bioinformatics
③ Production
Single clone


A
B
C
D
E
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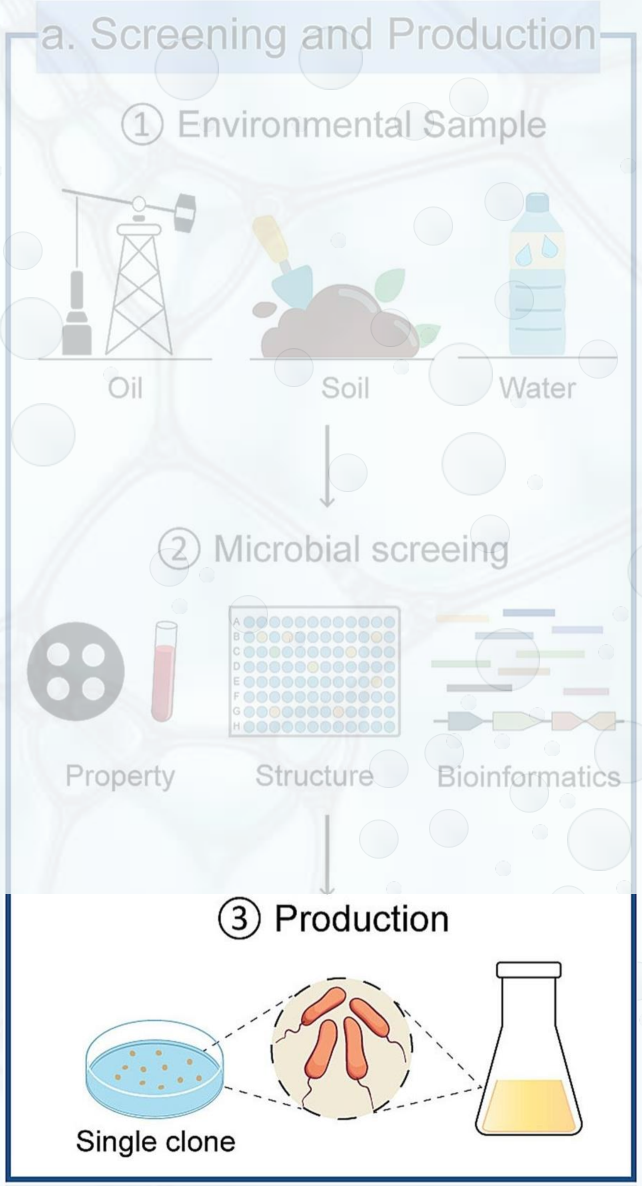
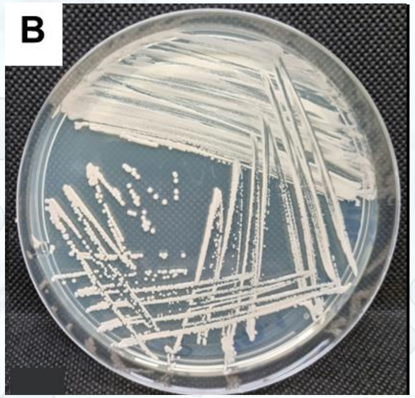
G
H
I
J
K
L

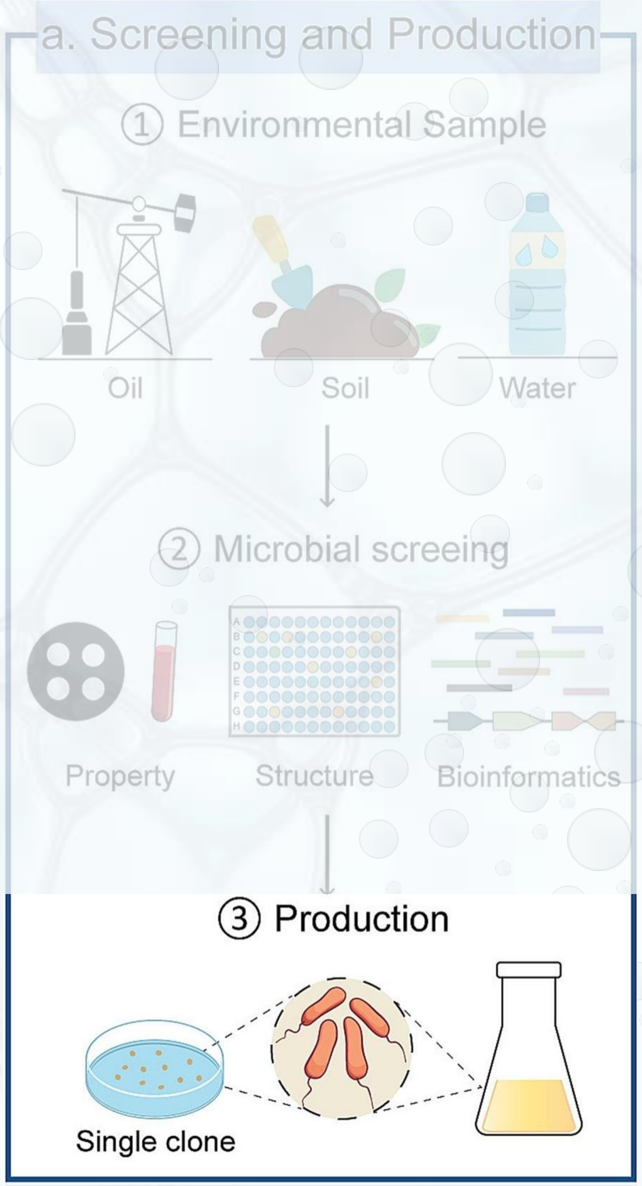
Results

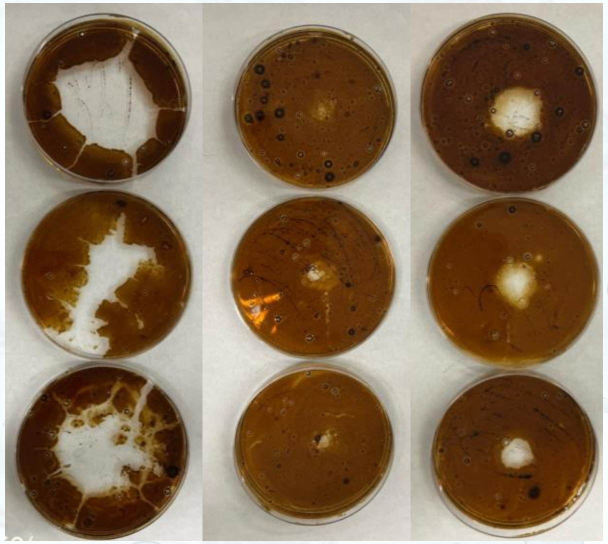




Microorganism 253

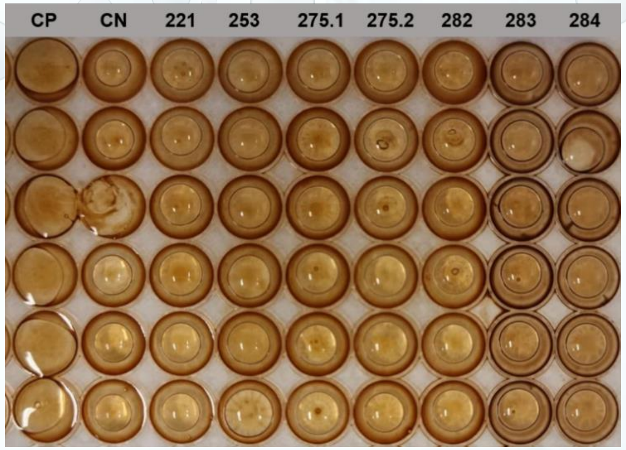
Results



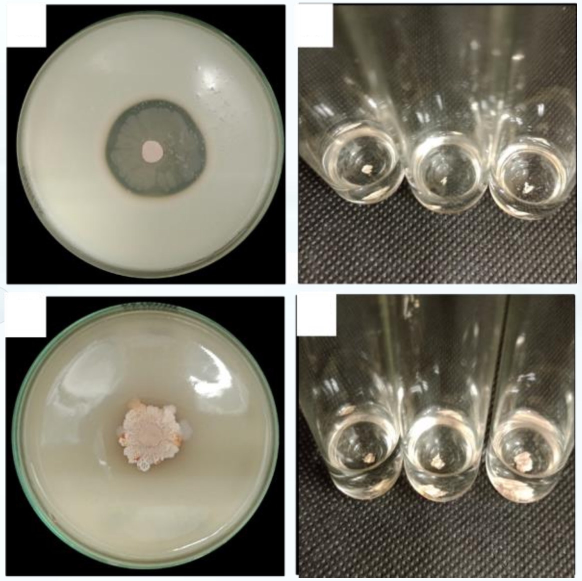


Positive Control | EPS | Surface-active

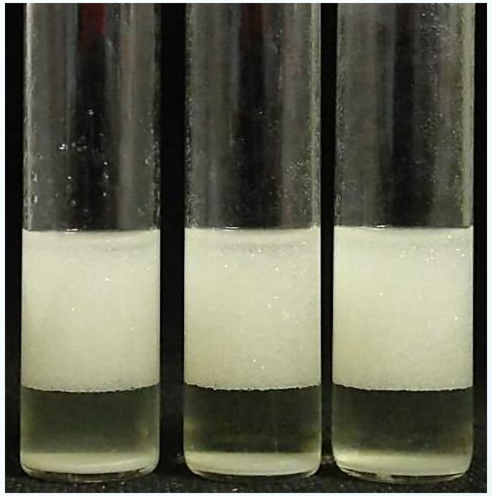
Spread oil assays



Drop colapse assays

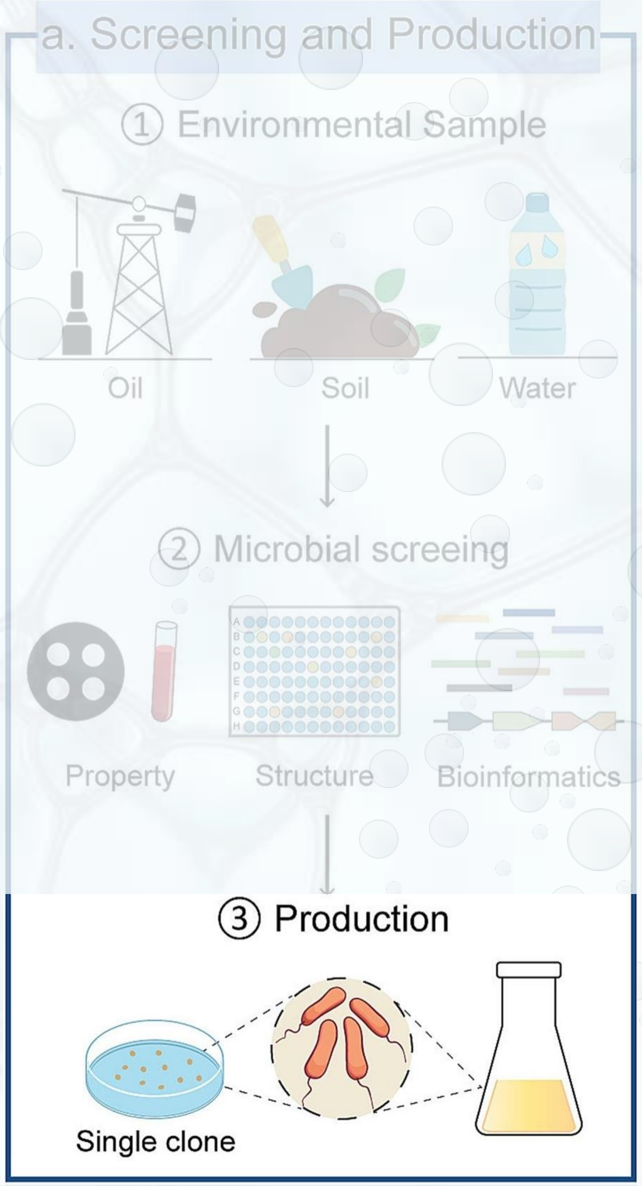


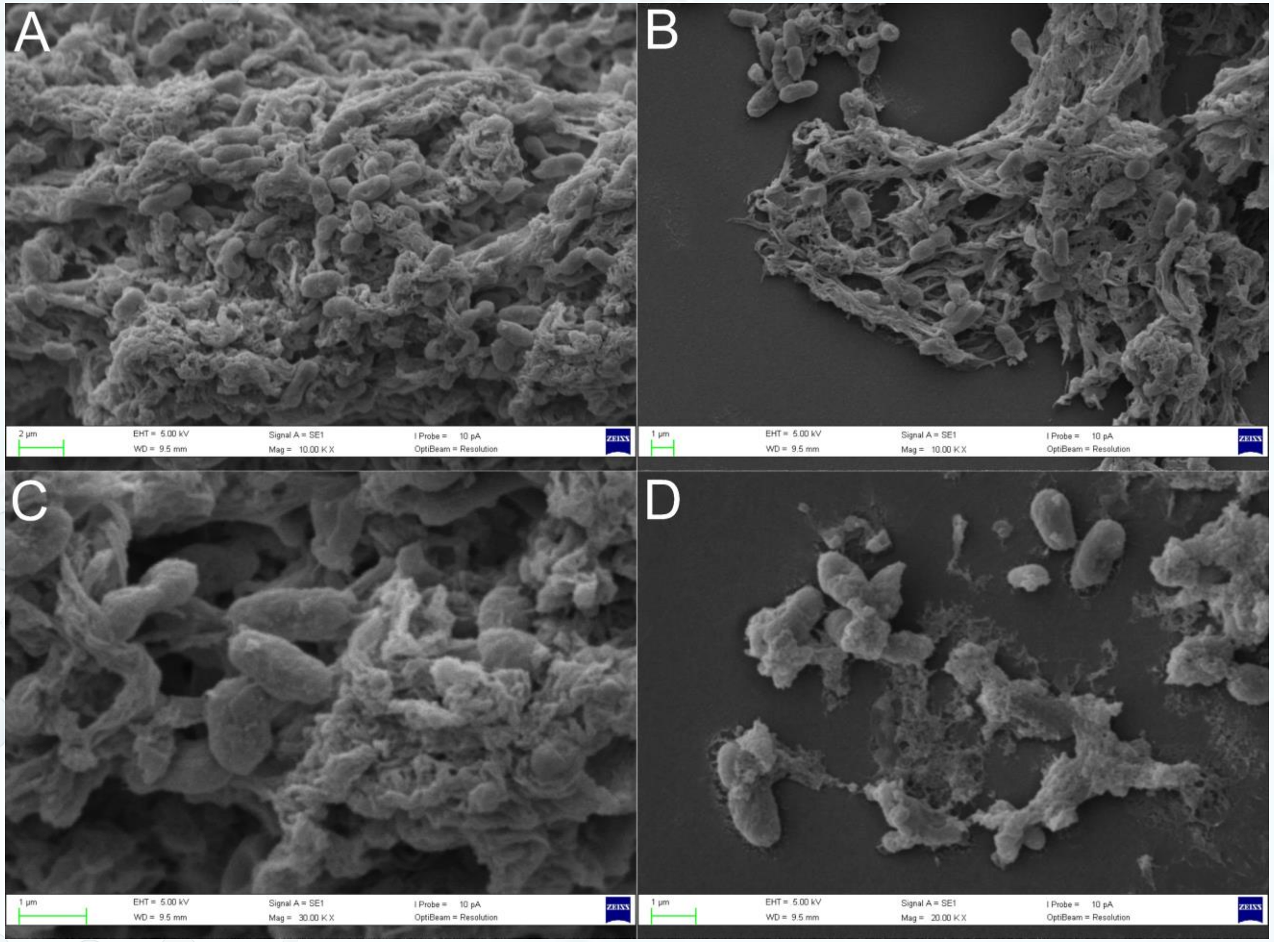
EPS formation assays



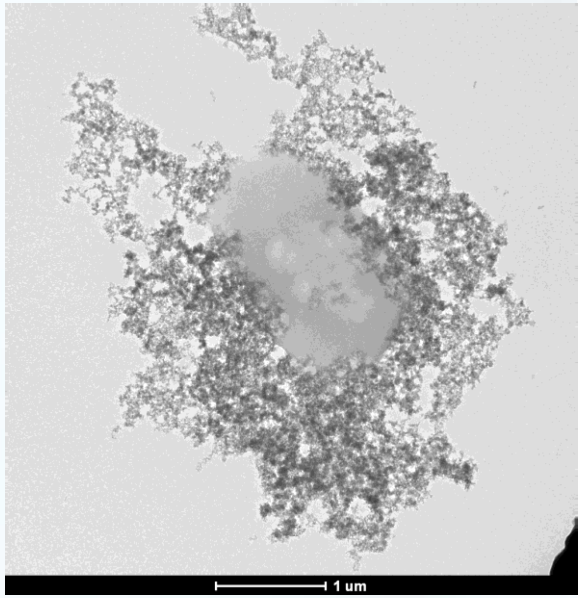
Emulsification assays

Results





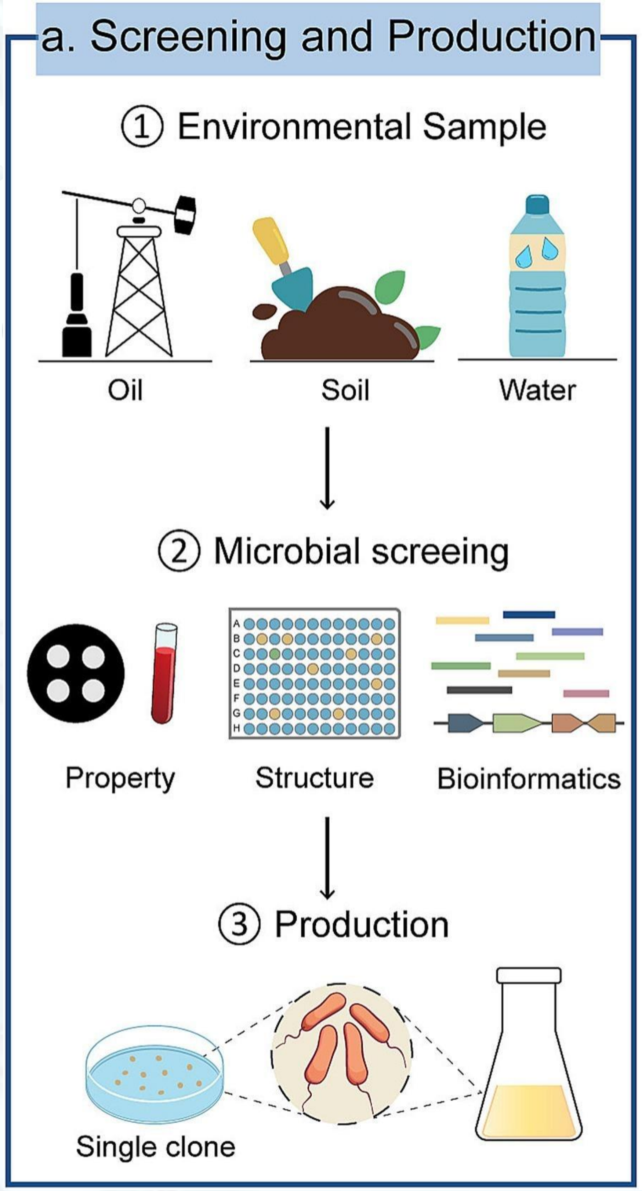
SEM from bacterial production of EPS. A, B) High EPS production connecting the bacteria. C, D) EPS is produced on the surface of the bacteria.



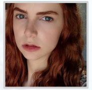
TEM from bacterial production of EPS

Results

CCUS SPE AAPG SEG
Carbon Capture, Utilization, and Storage

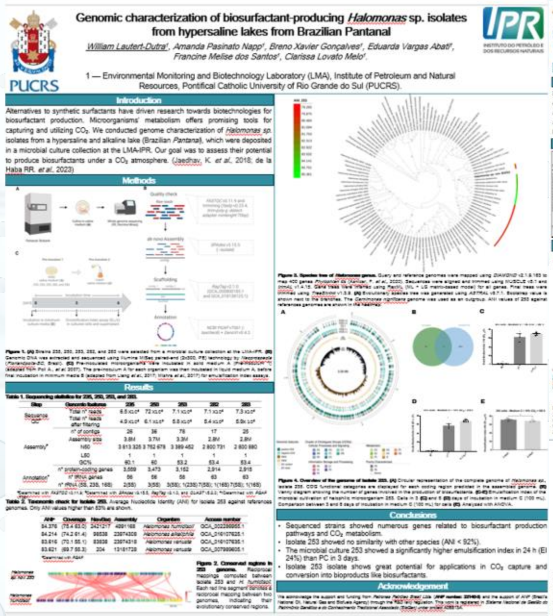


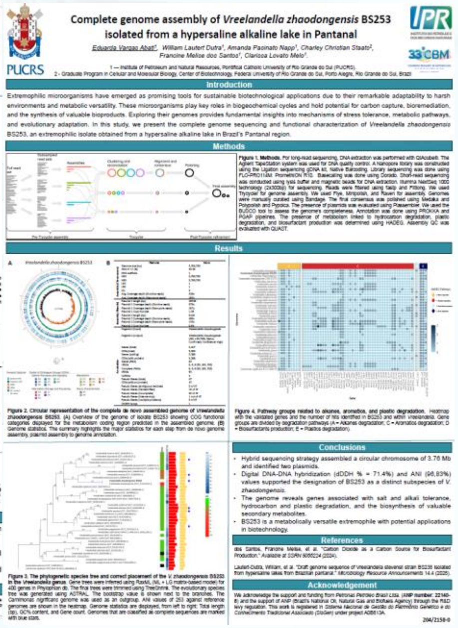
Poster presentation at Congresso Brasileiro de Genética – Campos do Jordão/ Brazil

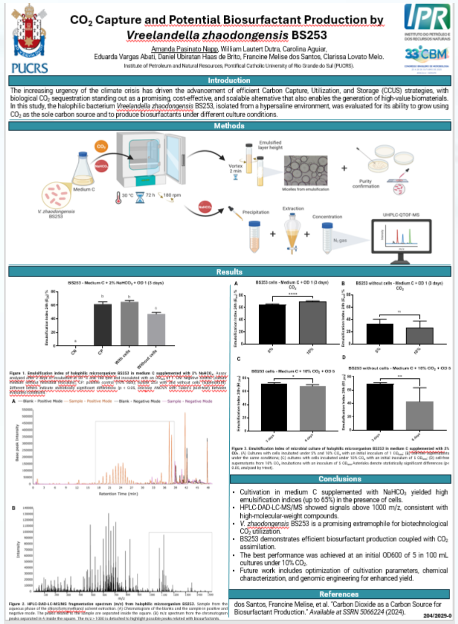


Poster presentation at 33º Congresso Brasileiro de Microbiologia – Aracaju/ Brazil

Poster presentation at 33º Congresso Brasileiro de Microbiologia – Aracaju/ Brazil







CO_2-driven biosurfactant synthesis by bacteria within CCUS

Mini Review | Open access | Published: 25 February 2026

Volume 110, article number 79, (2026) Cite this article

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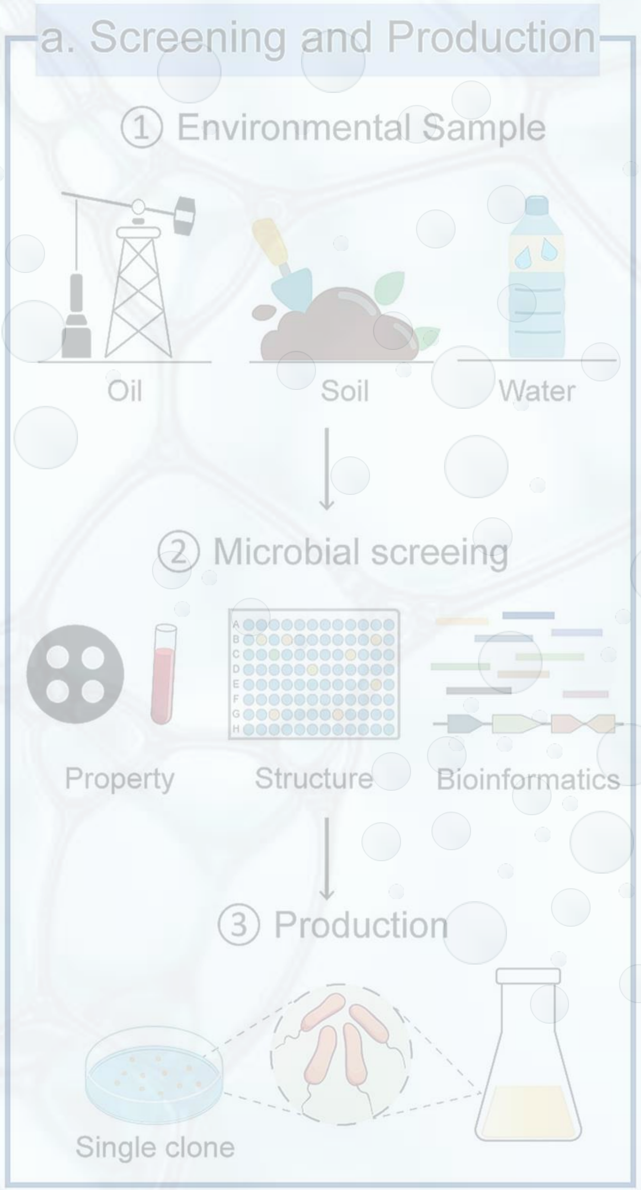
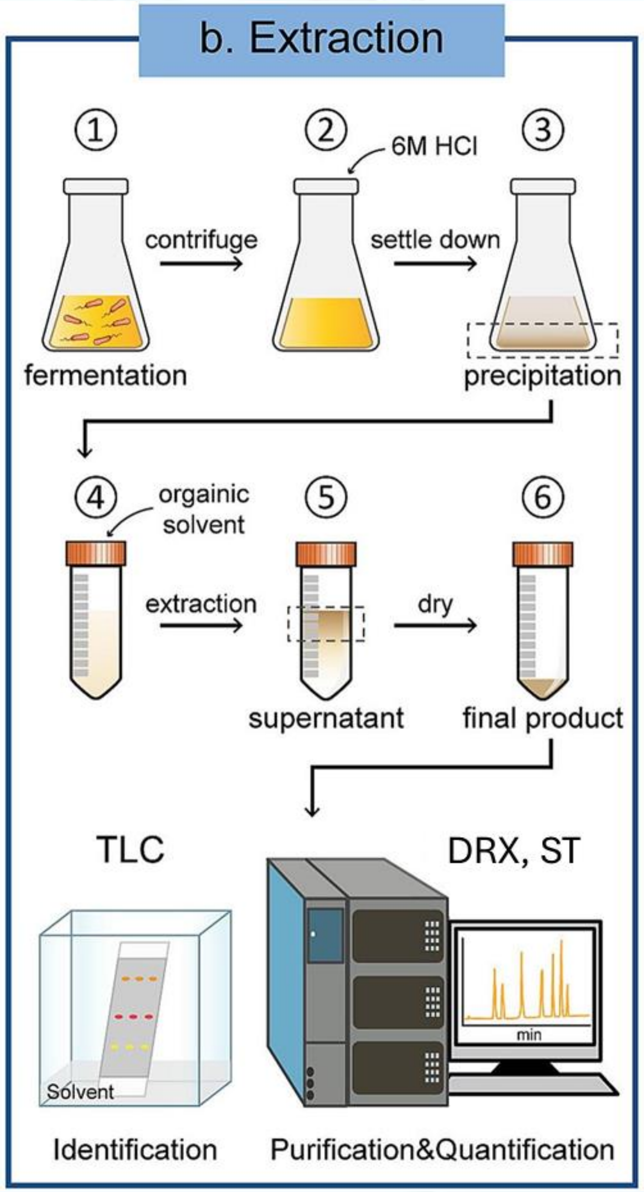
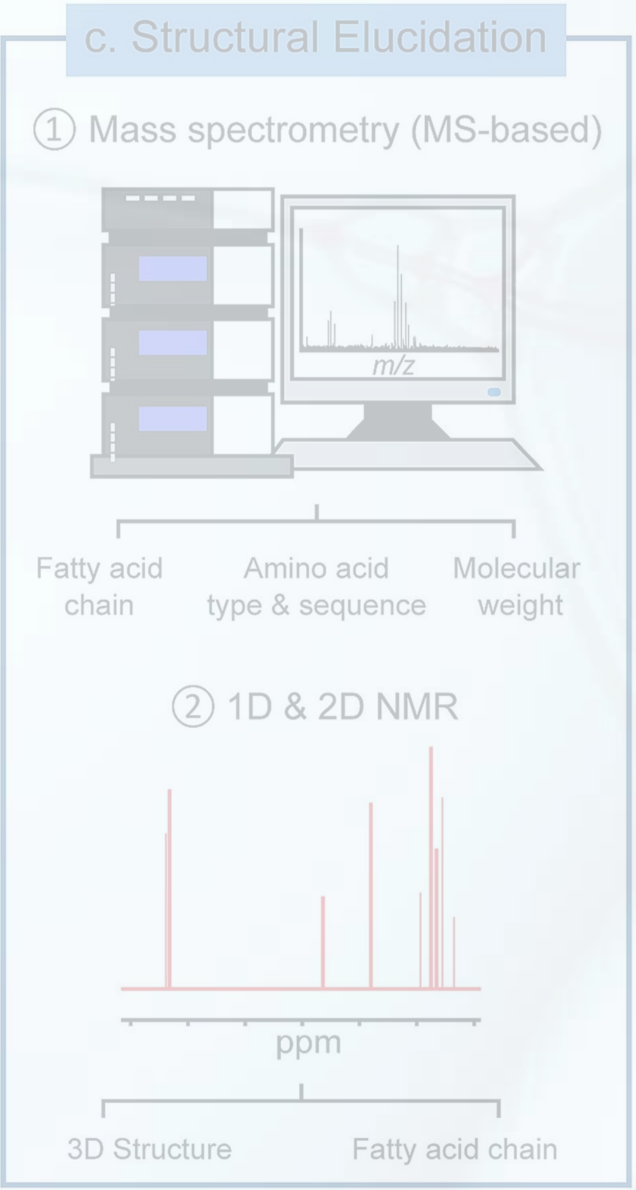
Amanda Pasinato Napp, William Lautert Dutra, Lovaine Silva Duarte, Eduarda Vargas Abati, Francine Melise dos Santos & Clarissa Lovato Melo

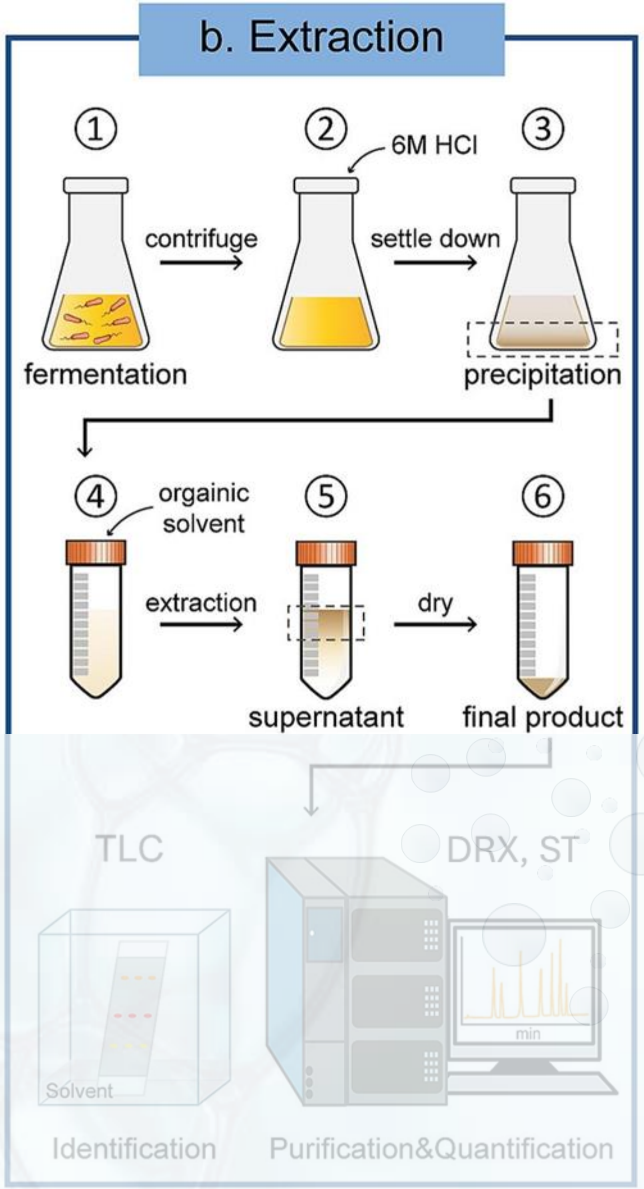
Methods

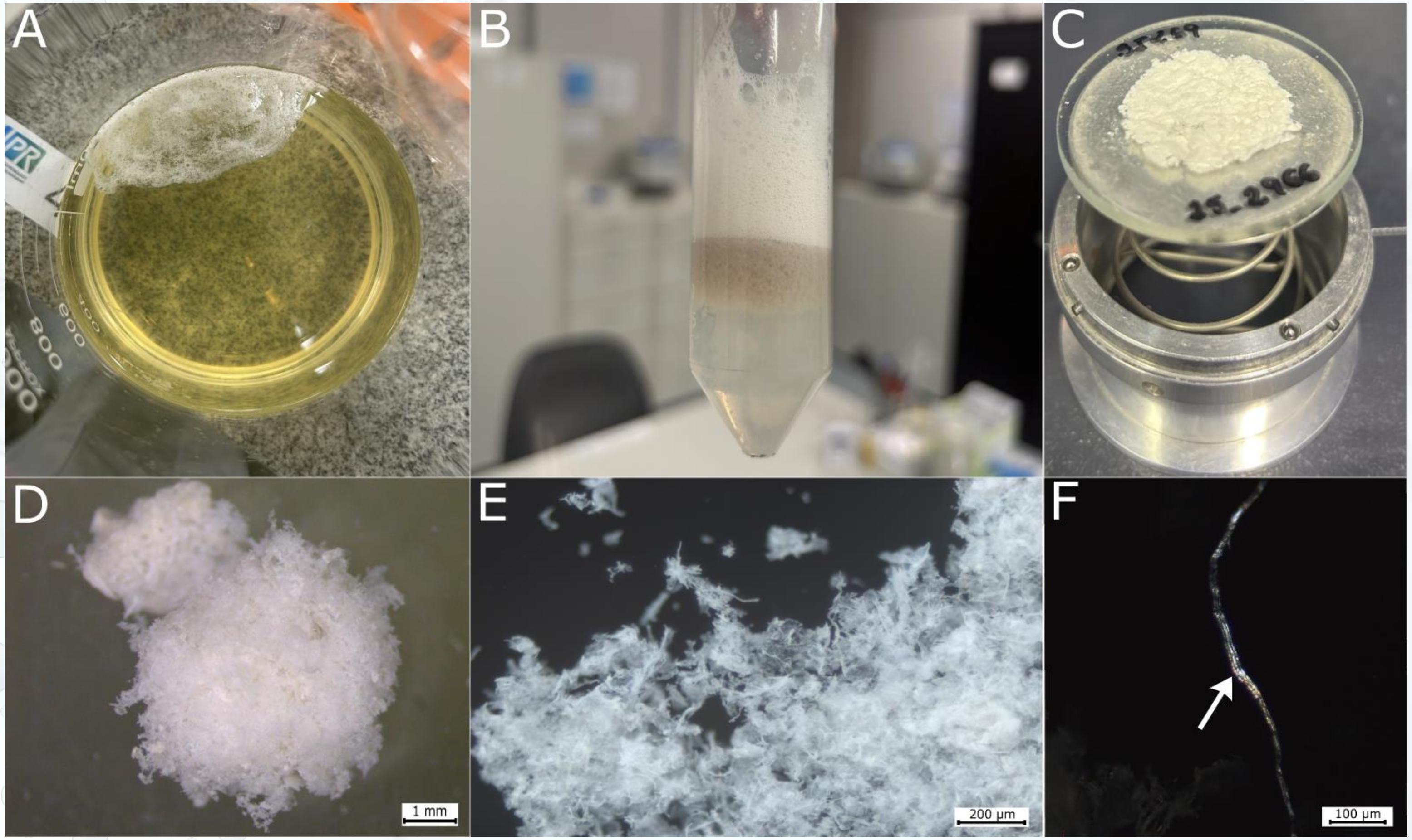

a. Screening and Production
① Environmental Sample
Oil
Soil
Water
② Microbial screeing
Property
Structure
Bioinformatics
③ Production
Single clone


b. Extraction
①
②
③
6M HCl
contrifuge
settle down
fermentation
precipitation
④
⑤
⑥
orgainic solvent
extraction
dry
supernatant
final product
TLC
DRX, ST
Solvent
min
Identification
Purification&Quantification


c. Structural Elucidation
① Mass spectrometry (MS-based)
m/z
Fatty acid chain
Amino acid type & sequence
Molecular weight
② 1D & 2D NMR
ppm
3D Structure
Fatty acid chain

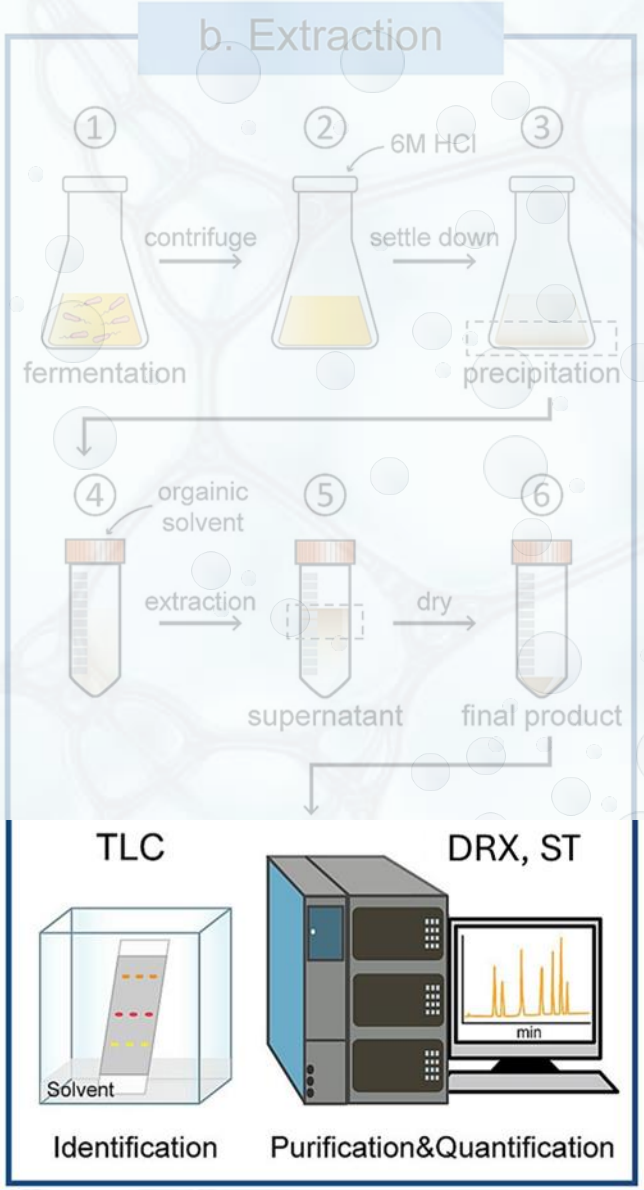
Results

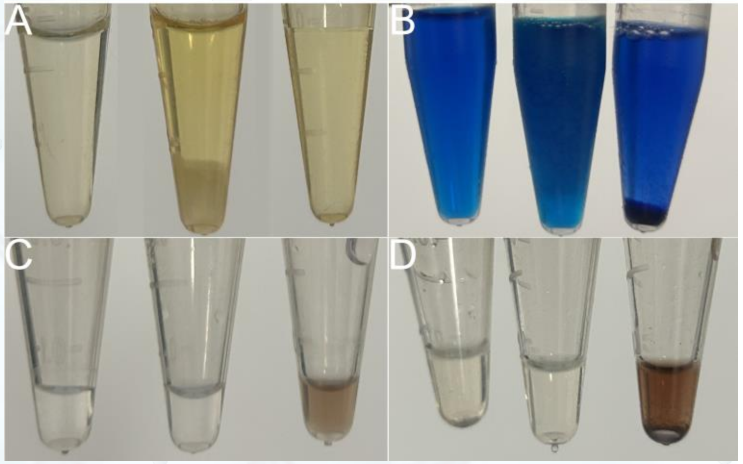


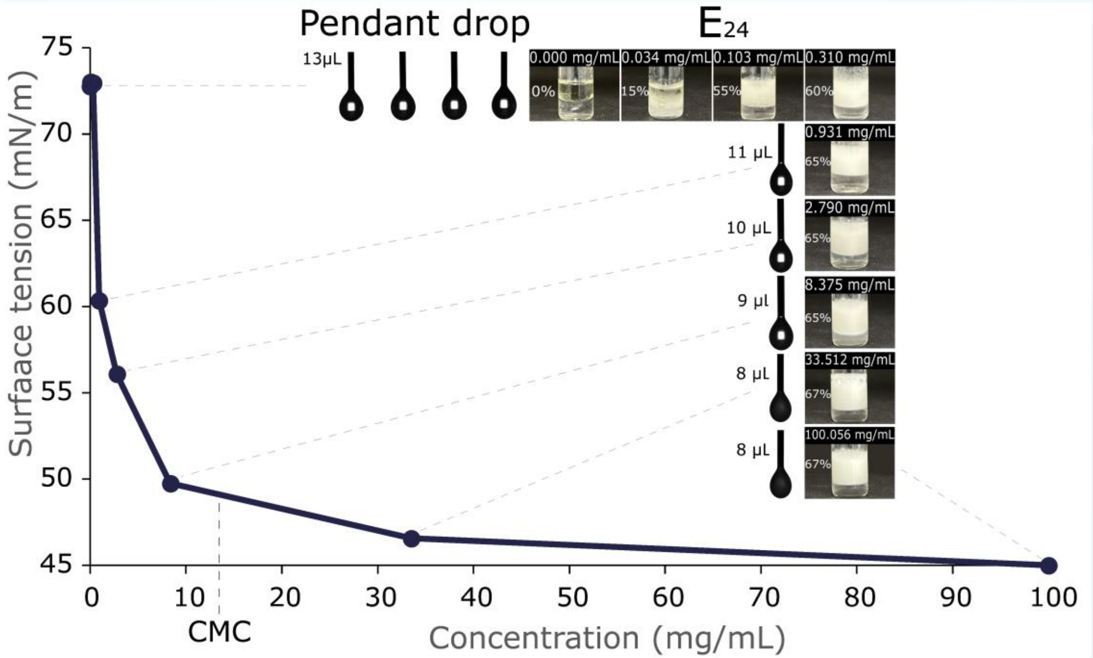


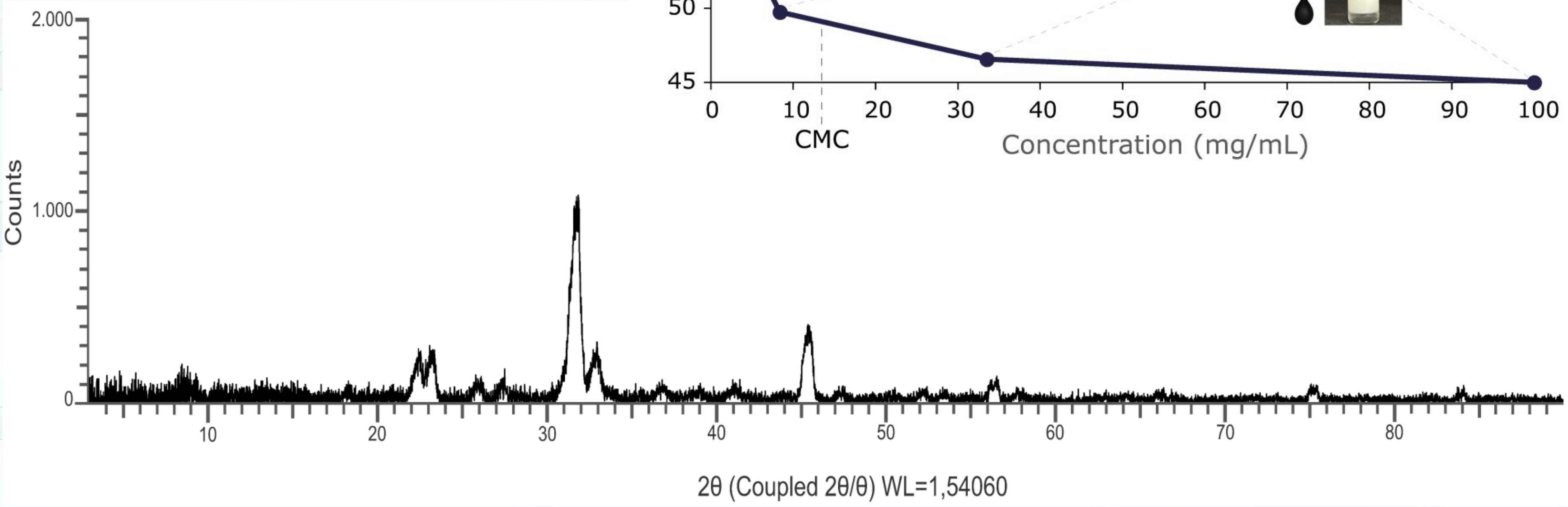
Extraction and purification of Exopolysaccharide (EPS). A) Ethanol extraction. B) Concentration by serial wash. C) EPS lyophilization. D) Optical Microscopy of EPS 1x. E) Optical Microscopy of EPS 10x. F) Polarized Microscopy of EPS 20x

Results



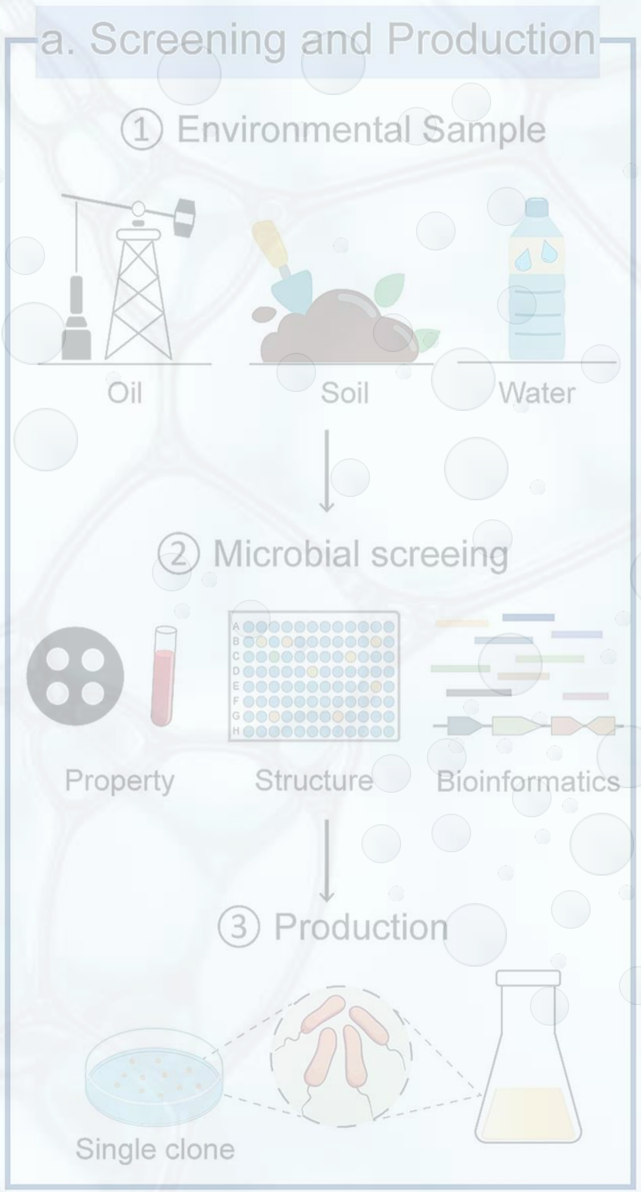






Physical-chemical characterization of EPS. Left: A, B, C, D characterize EPS as anionic and mainly glycolipidic. Right: Surface tension. Below: DRX

Methods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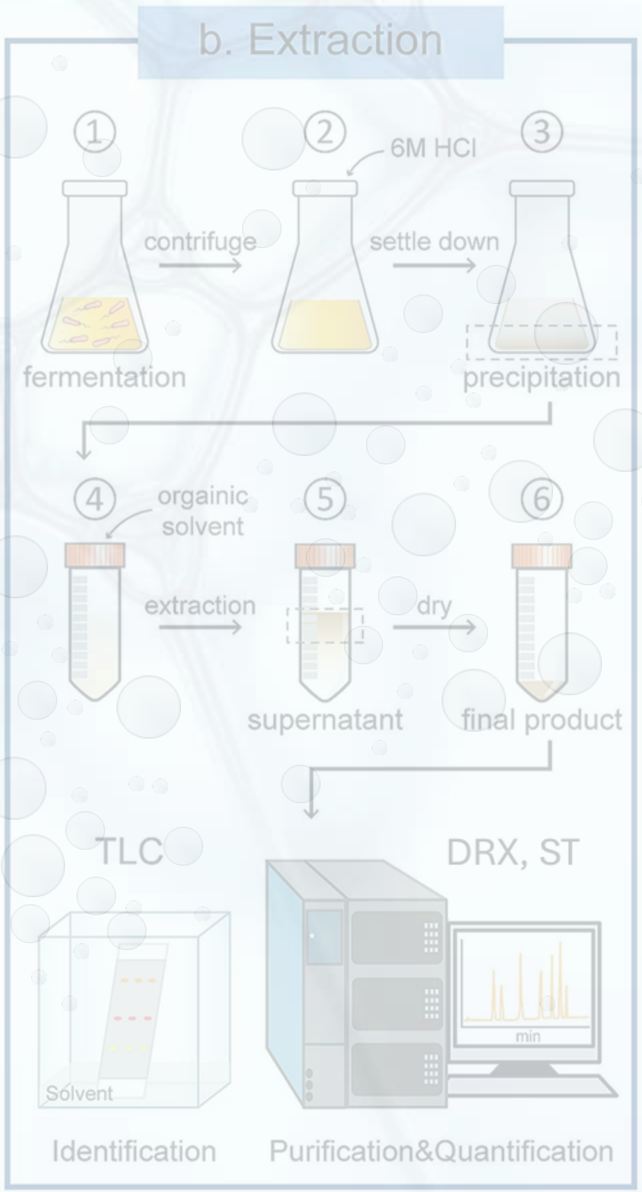
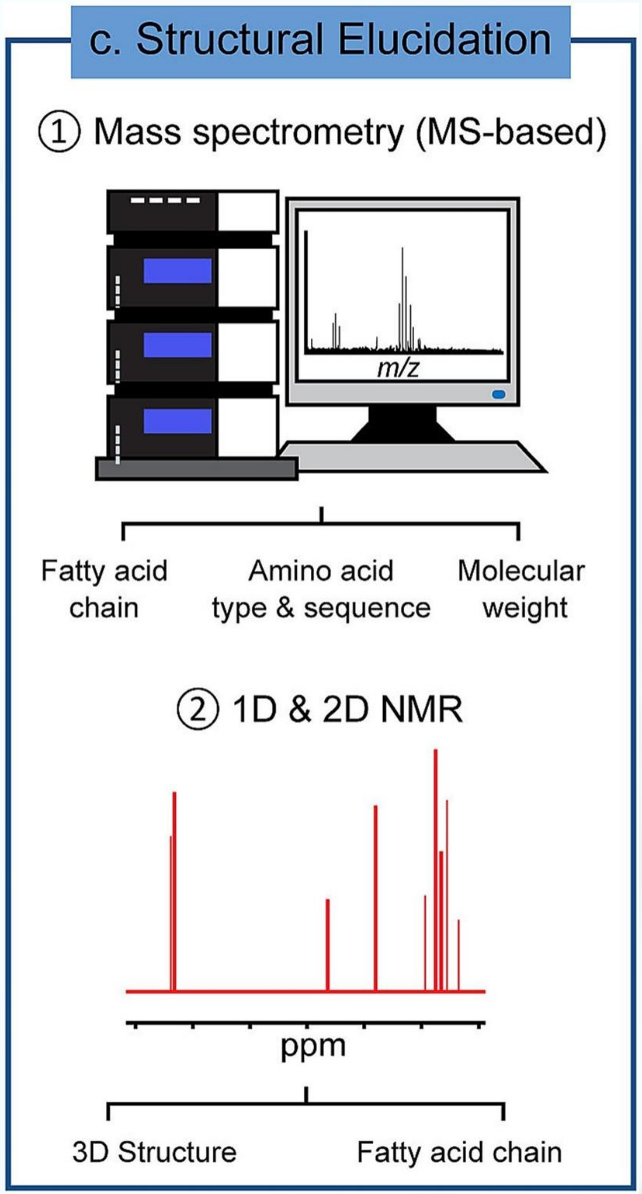
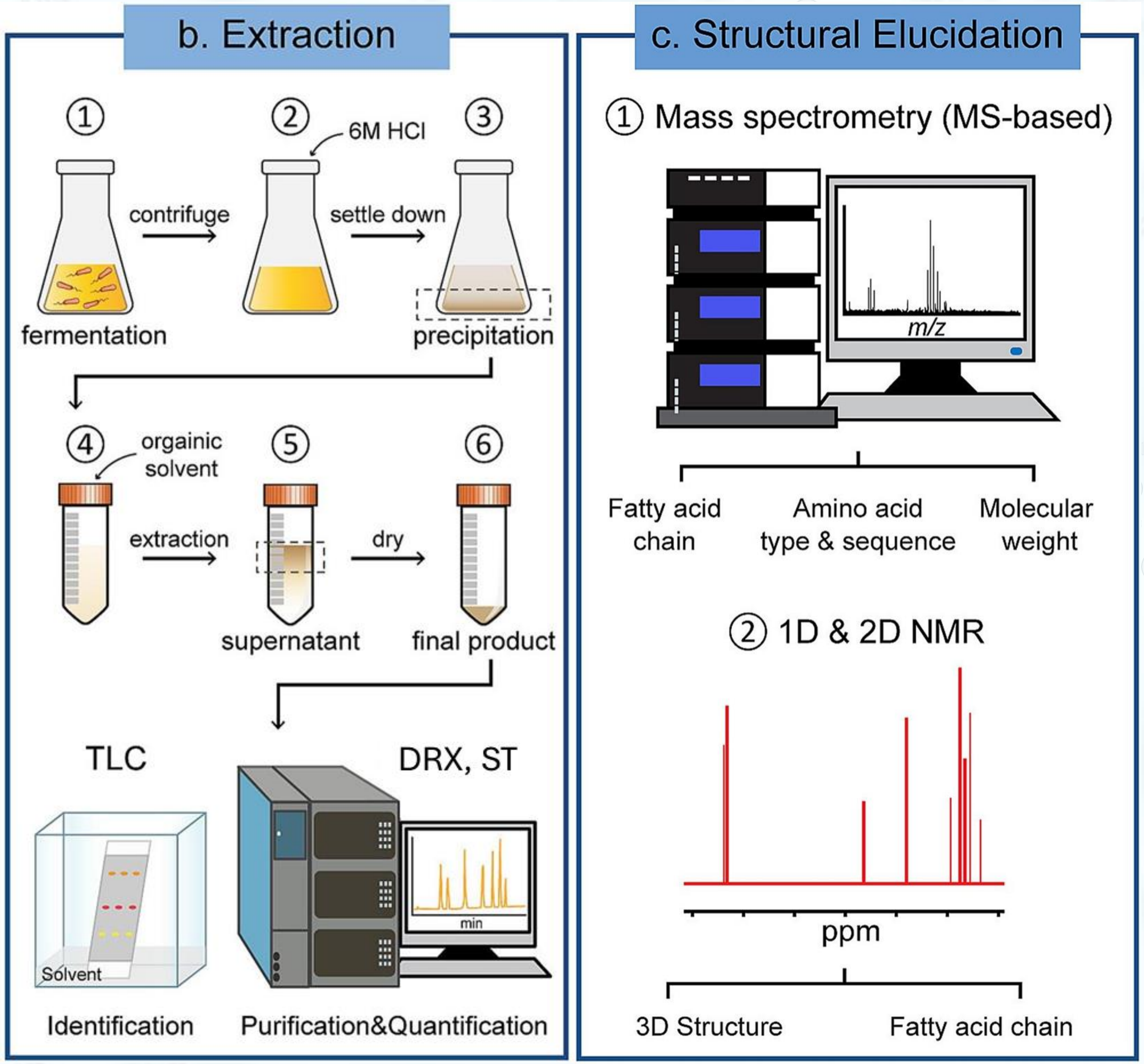
③ Production
Single clone


b. Extraction
①
②
③
6M HCl
contrifuge
settle down
fermentation
precipitation
④
⑤
⑥
orgainic solvent
extraction
dry
supernatant
final product
TLC
DRX, ST
Solvent
min
Identification
Purification&Quantification


c. Structural Elucidation
① Mass spectrometry (MS-based)
m/z
Fatty acid chain
Amino acid type & sequence
Molecular weight
② 1D & 2D NMR
ppm
3D Structure
Fatty acid chain

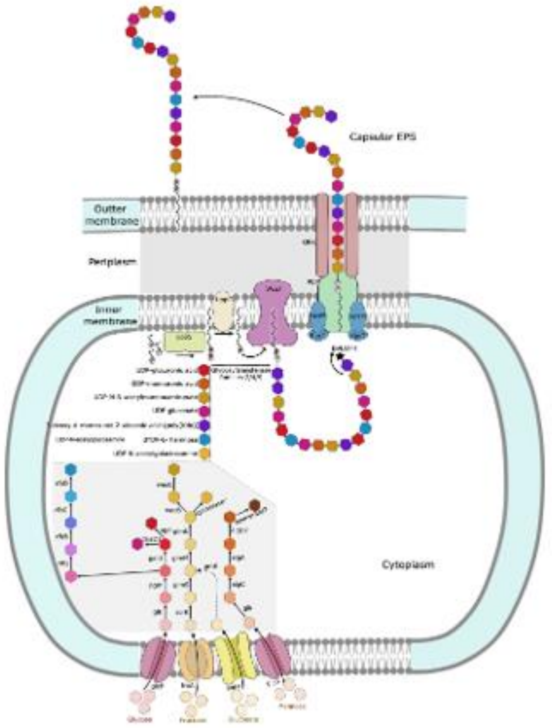
Results



Characterization and identification of emulsifying compounds produced by *Vreelandela zhaodongensis* BS253

Brito, Henrique Alves[1]; Napp, Amanda Pasinato[1]; Duarte, Lovaine Silva[1]; Salvato, Richard Steiner[1]; Brito, Daniel Ubiratan Haas[1]; Abati, Eduarda Vargas[1]; Santos, Francine Melise[1]; Melo, Clarissa Lovato[1], João Pedro Tauscheck Zielinski[1]*

[1] Pontifícia Universidade Católica do Rio Grande do Sul, Instituto do Petróleo e Recursos Naturais (IPR)



Can microbial CO_2 conversion be increased and optimize biosurfactant production?

Results

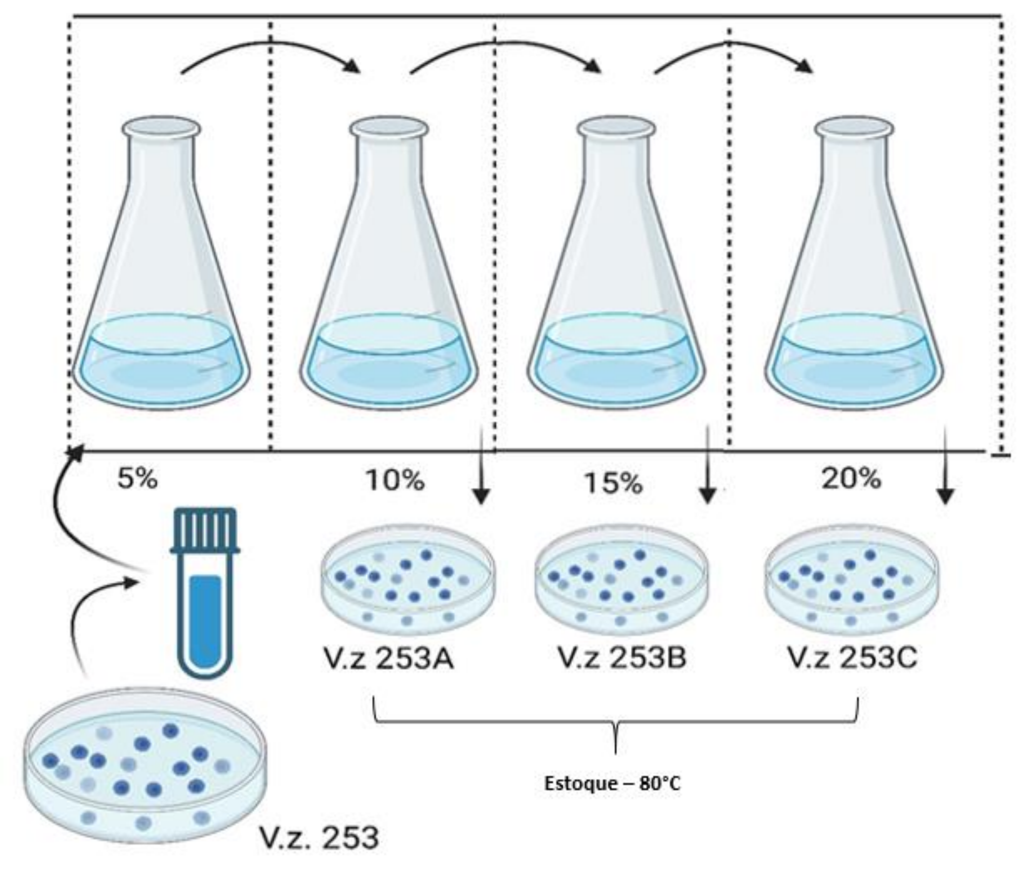
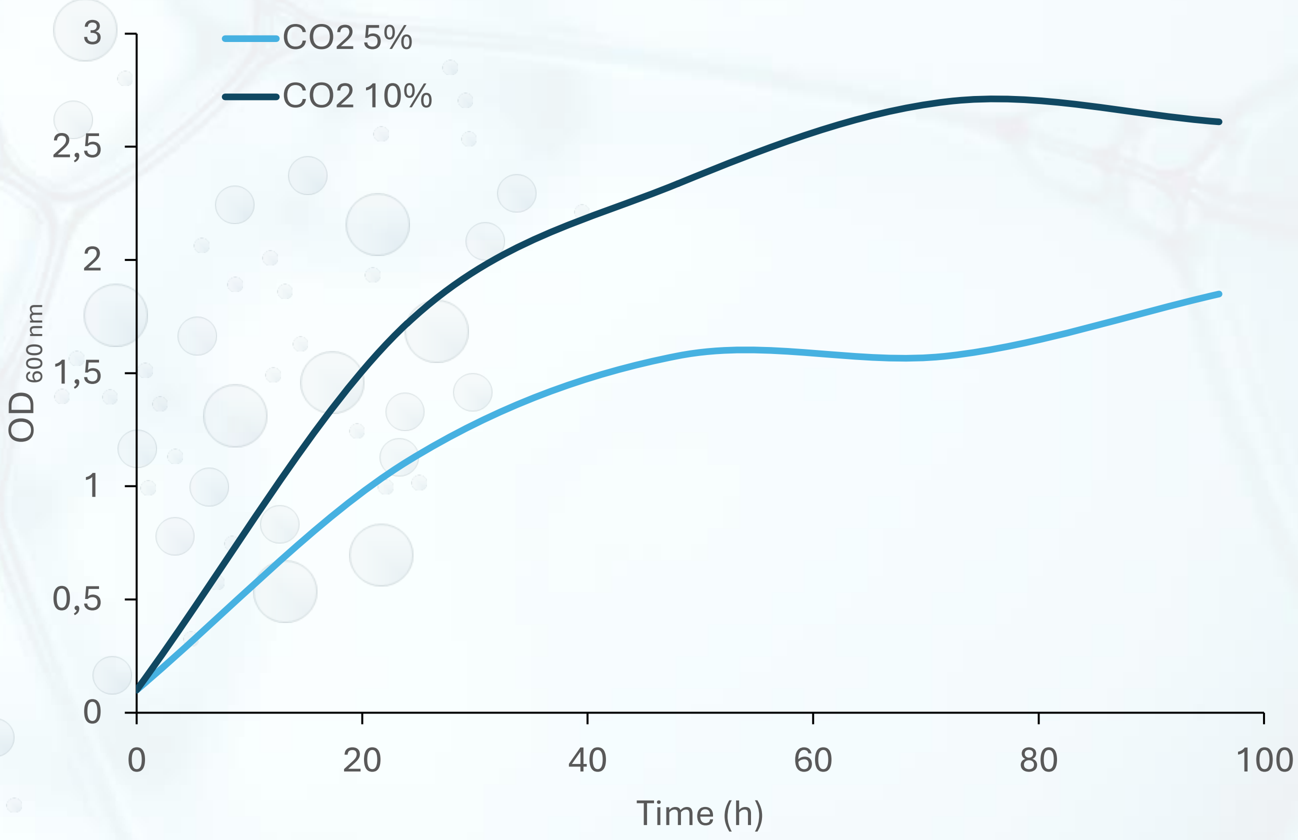
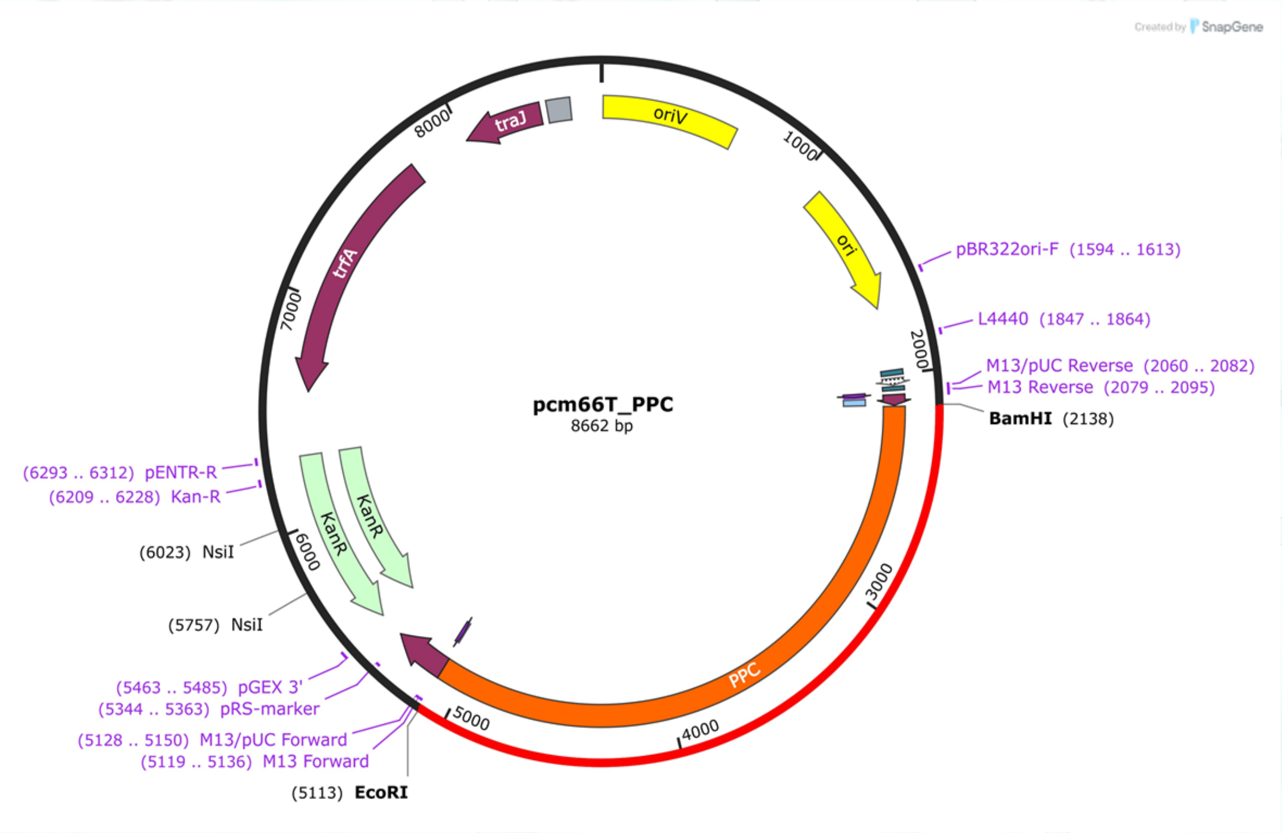


Diagram of the assisted laboratory evolution *V. zhaodongensis* BS253 under atmospheres enriched with CO_2.

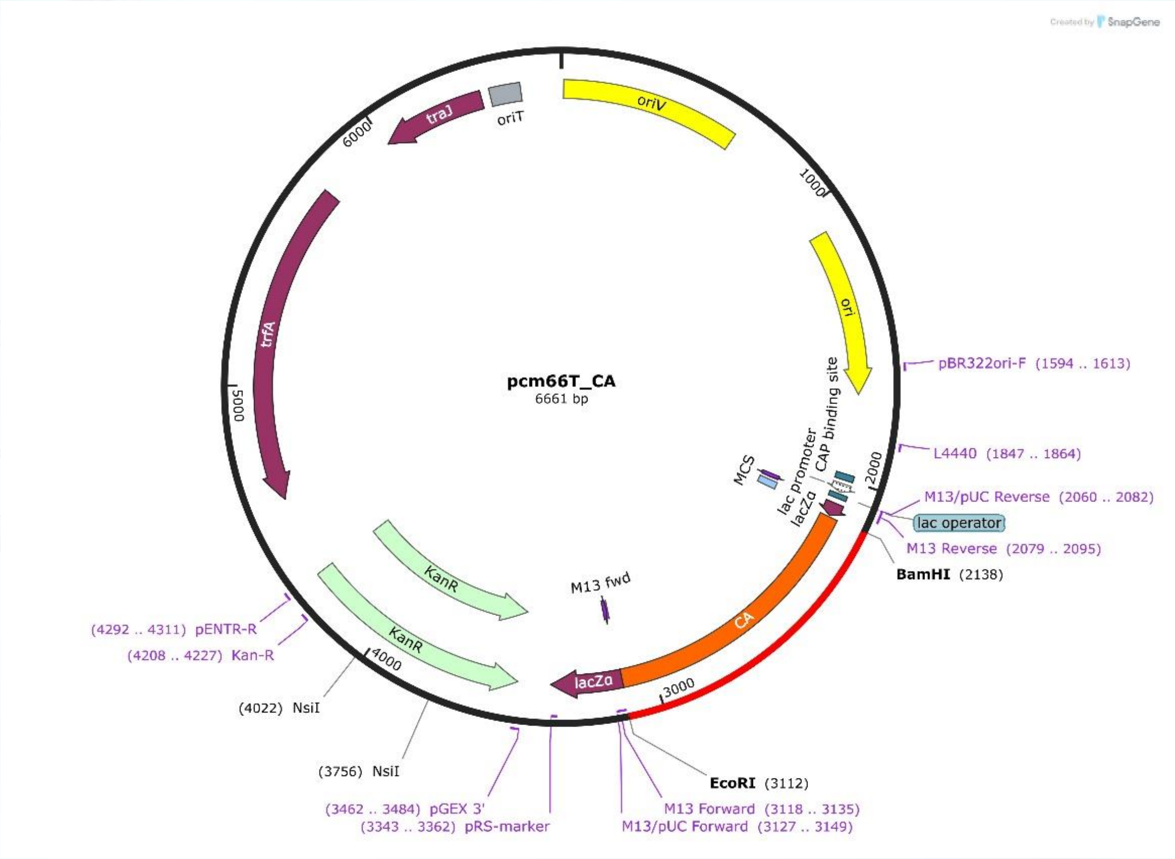


The culture exposed to 10% CO_2 showed stronger growth throughout the experiment.

Results



Physical map of the recombinant plasmid pCM66T_PPC containing Phosphoenolpyruvate carboxylase.



Physical map of the recombinant plasmid pCM66T_CA containing Carbonic Anhydrase.


João Pedro


Henrique


Lovaine


Richard


Charley


Amanda


Eduarda


Daniel

[...] accelerating the carbon cycle by enhancing nature itself. Modified organisms offer the potential to convert greenhouse gases into energy, food, fuels, materials, chemicals, nutrients, fertilizers, and other beneficial byproducts, with significantly reduced CO_2 emissions.

John Mcdougall, 2024

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Carbon Capture, Utilization, and Storage

Thank You!

Contact us:

henriqueabrito@hotmail.com

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