Screening of biosurfactant producing bacteria from offshore oil and gas platforms in North Atlantic Canada

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Introduction

Surfactant?

Surfactant = hydrophilic head (water loving) + hydrophobic tail (water repelling)

• Amphiphiles -> form micelle -> reduce interfacial tension
• Increase solubility and biosurfactability of water immiscible materials

Biosurfactants?

Biosurfactants: surface-active agents produced by microorganisms during their growth

• low toxicity + high Biodegradability
• More effective and stable even at extreme conditions
• Can be produced from various sources with simple and inexpensive procedures

Bottleneck of biosurfactant applications: less producers with high productivity + low yields and high production cost

Develop new producers?

Screening of biosurfactant producers

The current study attempted to fill the knowledge gap by isolating biosurfactant producers from crude oil, formation water, drilling mud and treated produced water samples from offshore oil and gas platforms.

The genotype and phylogenetic relation of these isolates were investigated.

The diversity of the biosurfactant producer communities in different platform samples was analyzed and compared among different samples.

The annual growth rate is significantly higher than the overall surfactant market (2%)

The current study attempted to fill the knowledge gap by isolating diverse biosurfactant producers from offshore oil and gas fields.

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Objectives

The current study attempted to fill the knowledge gap by isolating biosurfactant producers from crude oil, formation water, drilling mud and treated produced water samples from offshore oil and gas platforms.

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References

• Grabowski, A., Nercessian, O., Fayolle, F., Blanchet, D., Jeanthon, C. (2005). Microbial diversity in extreme conditions (e.g., high temperature, high pressure, and low oxygen concentration) in oil reservoirs would formulate a microbial community that distinguished from others (Grabowski et al. 2005).
• Few studies isolated biosurfactant producers from oil field, mostly from inland reservoirs. The biosurfactant producers identified from oil field samples were limited to the genera of Bacillus and Pseudomonas (Cai et al., 2015).
• Till now, very limited work has been conducted to isolate marine biosurfactant producers from offshore oil and gas fields.

Methodology

Screening of biosurfactant producing bacteria from offshore oil and gas platforms

The screening and isolation of new biosurfactant producers have been primarily conducted with terrestrial sources (Das et al., 2010).

Ocean harbors microorganisms with extraordinary metabolic and physiological features are different from their terrestrial counterparts (Satpute et al., 2010). These microorganisms are underexplored with limited published reports (Das et al., 2010; Satpute et al., 2010).

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Microbial community Diversity

The diversity of the 10 platform samples following the order of RA > SA > SB > DMA > COB > RB > COA > PWB > PWA > DMB

Raw produced water samples

Seawater samples

Treated produced water samples

Drilling mud samples

Crude oil samples

Results

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Conclusion and future work

Crude oil, formation water, drilling mud, treated produced water and seawater samples were collected in offshore oil and gas platforms in North Atlantic Canada. Through using u-hexadecane or diesel as the sole carbon source, 59 biosurfactant producers were identified and characterized. They belong to 4 genera, namely, Bacillus, Rhodococcus, Halomonas, and Pseudomonas. The 16S rRNA sequences of biosurfactant producers in the literature were combined with those of the representative strains isolated in this study to construct a comprehensive phylogenetic tree. Diverse isolates were found with featured properties such as reduction of surface tension, produce biosurfactants at high rate and stabilization of water-in-oil or oil-in-water emulsion. The possible blends of isolates or their biosurfactants and their capacities for applications were discussed and will be tested in the future studies. The diversity of biosurfactant producer communities in the platform samples followed the sequence of RA > SB > DMA > COB > RB > COA > PWB > PWA > DMB.

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