



XIV Congreso Nacional de Biotecnología y Bioingeniería



IDENTIFICATION OF CARBON DIOXIDE-PRODUCING MICROORGANISMS WITH POTENTIAL APPLICATION IN OIL RECOVERY

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MEOR, Petroleum Microbiology, CO₂ production

Introduction

Oil fields are ecosystems where interesting extremophile microorganisms can be found. Microbial metabolism generates byproducts as organic acids (acetic, butyric, lactic acid) and solvents (ethanol and butanol), generating changes in pH (1-2 units) and possibly they can also contribute to reduction of oil viscosity. Such biological products can be used to compensate the energy losses and/or to improve the properties of the rock-fluid system, such as a decreasing viscosity, reduction of interfacial tension and capillary pressures (1).

From the economic point of view, microbial oil recovery is a promising technology to enhance oil production in heavy oil reservoirs (2). Mechanisms by which bacteria can recover the trapped oil have been explored, but not completely understood. Gas production is one of the possible mechanisms. However, there are doubts about whether CO₂ can be produced microbiologically in sufficient quantities to displace oil trapped in the rock (3). Predictive study of microbial metabolism allows the efficient application of MEOR technologies under site conditions. The aim of this work was to obtain, evaluate and identify CO₂-producing microorganisms from samples of three Mexican oil reservoirs.

Methodology

Three samples from different oil reservoirs were enriched in anaerobic culture media at similar temperature reservoir conditions (70°C to 100°C). Once detected the presence of microbial activity, CO₂ production was optimized with different media formulations. Carbon dioxide was evaluated by gas chromatography (TCD).

Later microbial consortia were identified by molecular biology techniques. DNA extraction was performed followed by 16S rRNA PCR amplification using universal primers (4). The 16S genes were cloned in pJet1.2 vector and afterwards cells were transformed in *Escherichia coli*. Three libraries were obtained and RFLP selected clones were sequenced and taxonomically related.

Results

Different culture media formulations were assayed to recover and maintain fermentative microbial populations from Mexican oil reservoirs; also it was optimized culture media using formation water as nutrient diluent. It was achieved a maximum microbial CO₂ production which corresponded to 3.5 gL⁻¹ after 190 h of incubation. Fermentative species recovered were identified and belonged to *Thermotoga* and *Thermoanaerobacter* genera.

Conclusion

Fermentative microorganisms that came from oil fields samples were isolated and they were identified as *Thermotoga neapolitana*, *Thermoanaerobacter pseudoethanolicus* and *Thermoanaerobacter subterraneus*. Important amounts of CO₂ were obtained by stimulating microbial consortia. This finding is important since this microbial consortium could be proposed as an excellent candidate to MEOR applications.

Bibliography

- (1) Belyaev, SS; Borzenkov, IA; Nazina, TN; Rozanova, EP; Glumov, IF; RR, Ibatullin; Ivanov, MV. 2004. *Use of microorganisms in the biotechnology for the enhancement of oil recovery*. Microbiology, 73(5): 590-598.
- (2) Bryant, S. 2000. *Reservoir Engineering Analysis of Microbial Enhanced Oil Recovery*. SPE Annual Technical Conference and Exhibition, 1-4 October 2000. Dallas Texas.
- (3) Rafique, M.A., Ali, U. *Microbial Enhanced Oil Recovery (MEOR) with special emphasis to the "Uneconomical Reserves"*. SPE Indian oil and Gas Technical Conference and Exhibition, 4-6 March, 2008, Mumbai, India.
- (4) Relman, D. 1993. *Universal bacterial 16S rDNA amplification and sequencing*. In D. Persing, T. Smith, C. Tenover, & T. White, Diagnostic molecular microbiology: principles and applications (pp. 489-496). NY: American Society of Microbiology.