Characterization of Microbiological Communities in the Columbia River Basalts Before CO_2 Sequestration

Hiu Tung Yip[1], Brandon Briggs[2], and Rick Colwell[2]
Department of Microbiology[1], College of Oceanic and Atmospheric Sciences[2]
Oregon State University, Corvallis, OR 97331

Abstract

Global warming has become a serious environmental issue due to the high emission of carbon dioxide from various sources. One of the possible solutions is to inject supercritical carbon dioxide into subsurface geological formations. **The objective of this research is to characterize microbial communities in the Columbia River basalts prior to the pilot scale injection of CO_2 to evaluate the suitability of the formation for CO_2 sequestration and to learn how the communities will change in response to the CO_2 injection.** Water samples from 5 different depths of the injection well were collected and filtered. DNA was extracted and amplified, and then analyzed using Terminal-restriction fragment length polymorphism (T-RFLP), quantitative PCR (QPCR), and DNA sequencing. We confirmed that microbes are present at different depths in the basalts and that different depths appear to host different microbes. Bacterial DNA was extracted and amplified while the archaeal DNA did not amplify. This research will assist the development of biological indicators of CO_2 movement and diagnostic tools that can be used to account for CO_2 in place.

Objective

The objective of this research is to characterize microbial communities in the Columbia River basalts prior to the pilot scale injection of CO_2 to evaluate the suitability of the formation for CO_2 sequestration and to learn how the communities will change in response to the CO_2 injection.

Supercritical carbon dioxide - liquified carbon dioxide at 31.1°C and 72.9atm.
1000 metric tons supercritcal CO_2 = 38 tank cars.
8 million tonnes of CO_2 have been injected into the Sleipner gas field between 1996 and 2004.

Figure 1. Location of the Wallula pilot well. In Eastern Washington state.

Methods

- Samples were collected from 5 different depths. (Figure 2)
- DNA was extracted using the MoBio Kit.
- PCR reaction was carried out with universal bacterial primers (8F, 926R) and archaeal primers (21F, 958R).
- T-RFLP was done by using the restriction enzyme MspI. (Figure 3)
- QPCR was used to estimate the 16s rRNA gene concentration in the samples.
- Clone libraries and DNA sequencing identified the bacteria.

Result

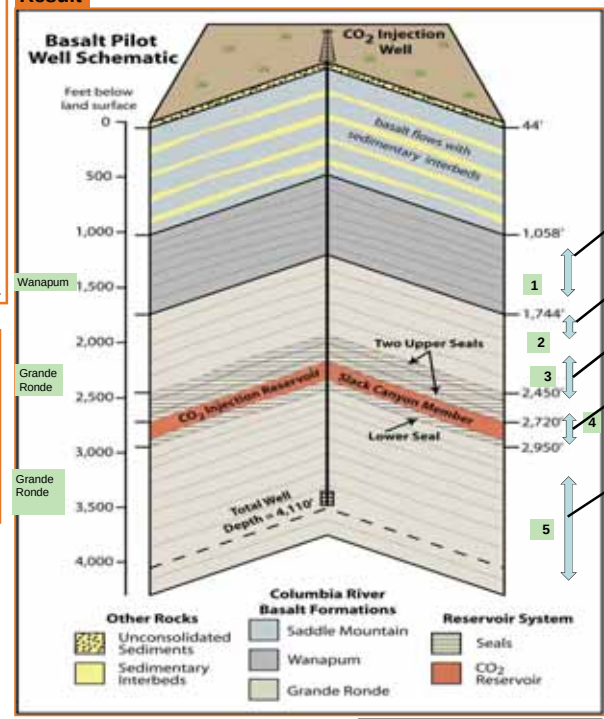

Figure 2. Columbia River Basalt Pilot Well Schematic including basalt formation identity and microbial sampling zones.

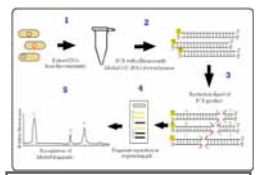

Figure 3. Generalized t-RFLP method (from Gruntzig et al. 2002. Mich. State Univ.)

Figure 4. Gel from electrophoresis after PCR with archaeal primers. Lanes 1 to 5 correspond to the samples from different depths. (Refer to figure 2 above.) +is the positive control ; - is the negative control, and B is the blank filter. And L is the 1kb DNA ladder.

Figure 5. Gel from electrophoresis after PCR with bacterial primers. Lanes 1 to 5 correspond to the samples from different depths. (Refer to figure 2 above.) +ve is the positive control; -ve is the negative control, B is the blank filter and L is the 1kb DNA ladder.

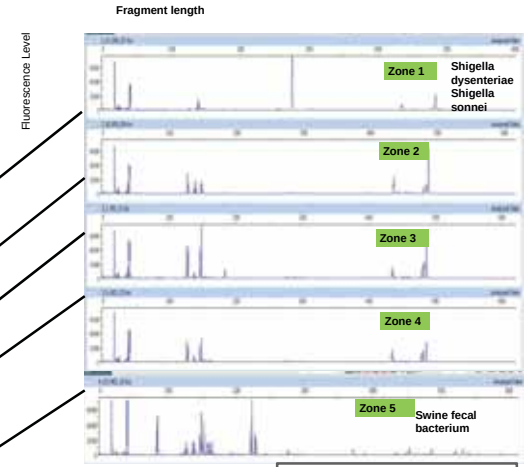

Figure 6. T-RFLP results for the microbe communities from different depth intervals.

Zone #	Depth Range (feet)	Cells/ mL	Temperature	pH	Alkalinity	Conductance
1	1108 – 1474	1.04 E 4	29.31ºC	9.1 SU	119 mg/L	314 umhos/cm
2	1700 – 1814	4.64 E 3	N/A	8.99 SU	122 mg/L	320 umhos/cm
3	1899 -2345	8.04 E 4	29.44ºC	8.95 SU	118 mg/L	320 umhos/cm
4	2520 – 2798	2.28 E 4	N/A	9.51 SU	149 mg/L	376 umhos/cm
5	3344 – 4110	9.1 5 E 5	N/A	N/A	N/A	N/A

Table 1. Cell concentration (by QPCR for 16s rRNA gene) and chemical composition for different depth intervals. Water chemistry measurements from Pacific Northwest National Laboratory.

Summary

- There are microbes in all 5 depths in the well.
- Bacterial DNA was extracted and amplified but archaeal DNA could not be amplified.
- T-RFLP suggests that microbial communities found in Wanapum and the upper Grande Ronde strata are similar to each other and distinct from microbes found in the deeper Grande Ronde and Wanapum layers.
- The bacteria found are possibly *Shigella sonnei*, *Shigella dysenteriae*, and Swine fecal bacterium.

Future directions

Continue developing the 16s rRNA clone library based on the DNA extracted from the samples. Carry out further experiments to find out how the bacteria in the basalt pilot well will react towards the injection of supercritical CO_2.

Acknowledgement

This research was supported by Portland General Electric. H. Yip was supported by an OSU Subsurface Biosphere Initiative Undergraduate Fellowship. Samples were collected by scientists from the DOE Pacific Northwest National Laboratory.