

The Importance of Coal Associated Microbes in Coal-to-Methane Consortia

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Formation water consortia from the western Surat Basin (Queensland, Australia) were enriched on native subbituminous coals; biomethane production curves were then compared to earlier water enrichments from the same area. All of the earlier well samples provided highly viable coal-to-methane microbial communities [1], whereas for the later sampling, only three of the five wells provided successful enrichments. Variability in methane production between triplicate enrichment cultures and unusually long lag phases (~70 days) suggested lower microbial numbers in the later formation water samples. Notably fewer coal fines were collected in the later well samples, leading to the hypothesis that critical community members are primarily associated with these coal fines. The attachment of primary degraders to complex solid substrates has been observed in other methanogenic systems [2]. Viable coal-to-methane enrichments were maintained over eight generations when ample coal particles were transferred with the inoculum. A 16S rDNA analysis of an enrichment culture showed the community makeup to be similar to other methanogenic communities in coal [3]. Significant microbial colonization was observed (via confocal laser scanning microscopy) on the surface of an enrichment culture coal particle. In addition, lag times were shorter and methane production rates faster when coal fines were transferred from an active enrichment culture (compared to a coal-free transfer from the same culture). These results indicate that key community members are associated with the coal surface and are required to realize the full biomethane potential of coal. Implications for field well stimulation treatments and strategies will be discussed.

[1] Papendick *et al* (2011) *Int. J. Coal Geol.* **88**, 123-134 [2] Costerton (1992) *Int. Biodeter. Biodeg.* **30**, 123-133 [3] Strapoc *et al* (2011) *Annu. Rev. Earth Plant. Sci.* **39**, 617-656