

BIOUTILISATION OF CO₂ IN COAL SEAMS

Christopher J. BOREHAM^{1,2} and Karen BUDWILL³

1. CO₂CRC, GPO Box 463, Canberra, ACT 2601, Australia
2. Geoscience Australia, GPO Box 378, Canberra, ACT 2601, Australia
3. Alberta Research Council, 250 Karl Clark Road, Edmonton, Alberta, T6N 1E, Canada

The impact of CO₂ injection on sub-surface microbial communities is not well understood and needs to be addressed as it can be both advantageous and detrimental to CO₂ storage and possible production of biogenic methane. Furthermore, it is important to develop biological, chemical and isotopic tracers for monitoring CO₂-bioassimilation at the CO₂ injection site. This study focus on the microbial activity associated with coal seams and draws on data from natural analogues and laboratory culture experiments.

In Australian coal seams, methane derived from a biological origin (biogenic methane) dominates over methane associate with petroleum generation (thermogenic methane) (Draper and Boreham, 2006 and references therein). Methanogenesis is the end-member microbial process involving a consortium of microbes that anaerobically degraded organic matter to CO₂ and methane. The two main carbon sources for biogenic methane are CO₂ and low molecular weight organic acids (eg. acetic acid). Both are the metabolic by-products of fermentative microbial degradation of higher molecular weight organic material. Additional external sources of CO₂ are from either thermal degradation of organic matter or an inorganic source (e.g. magmatic). Natural analogues studies show that both of these CO₂ sources can act as the feedstock for methanogenesis.

Laboratory experiments involve a methanogenic-enrichment culture and a sub-bituminous A coal from the Obed mine, Alberta, Canada. The free hydrocarbons in the coal are dominated by a series of conifer-derived saturated and aromatic diterpanoids with subordinate waxy *n*-alkanes (Figure 1a). There is no apparent change in the free hydrocarbon distribution before and after the culture experiment, suggesting that any carbon sources from the coal that are utilised by the microbes are associated with the solid matrix.

Within the aqueous media associated with the culture experiments a series of low molecular weight (C₂ to C₉) monocarboxylic acids (Figures 1b and c) are identified as metabolic by-products. For a healthy microbial community where carbon sources and nutrients are non-limiting, these intermediate by-products are in low abundances (Figure 1b). However, under altered conditions (e.g. absence of coal), methanogenic activity is still evident, albeit at reduced rates of methane production. Interestingly, the monocarboxylic acids are now concentrated by over 50 fold (Figures 1c). Such *in vitro* results may have

ramifications for CO₂ injection *in vivo*, where selection of a diagnostic molecular tracer will be critical for indirect monitoring of any changes to the microbial community.

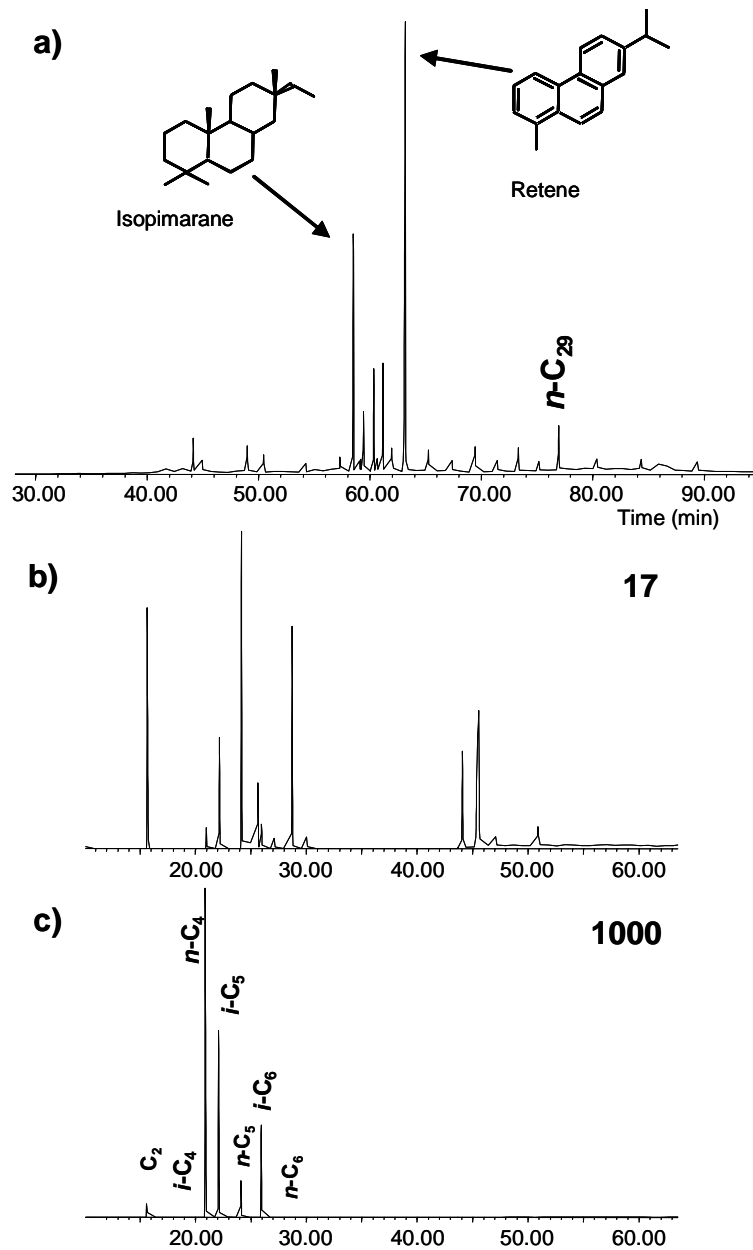


Figure 1. GCMS analyses showing a) full scan (15-550 amu) trace of the extractable organic matter from the Canadian coal, b) *m/z* 60 trace depicting the low molecular weight monocarboxylic acids for the experiment with coal, culture, mineral salts medium and tryptone (the peaks > 40 min are associated with the aqueous medium), and c) *m/z* 60 trace depicting the low molecular weight monocarboxylic acids for the experiment with culture, mineral salts medium and tryptone. Note in b) the '17' abundance is relative to an abundance of '1000' in c); the 'controls' with no added coal or culture have a relative abundance < 1.

REFERENCE

Draper, J.J. and Boreham, C.J. (2006) Geological controls on exploitable coal seam gas distribution in Queensland. *APPEA Journal*, 46(1), 343-366.