# Comparative metagenomics of in-situ and enrichment microbial communities manifesting coal biomethanation phenotypes

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Taxonomic surveys indicate a wide diversity of microbial communities exist in different coal seams around the world. Coal biomethanation is generally accepted to occur in 3 steps; initial coal depolymeriztion and solubilzation, biotransformation of coal intermediary products to methanogenesis substrates and methanogenesis. Many factors such as coal rank and pH can affect microbial community structure and function. Thus the stimulation of coal biomethanation likely requires local strategies to relieve biochemical pathway bottlenecks specific to different coal bed ecosystems.

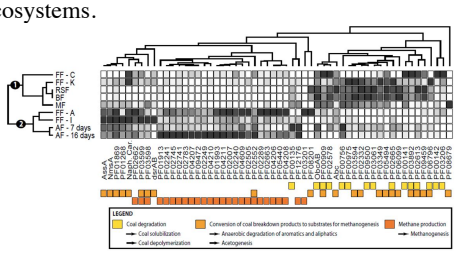


**Figure 1**. Functional screen of coal and enrichment culture metagenomes using conserved protein markers for different stages of coal biomethanation process.

Here we compare the metagenome of a methanogenic coal-degrading culture amended with a nutreint supplement to metagenomes from in-situ coal bed communities. Resulting enrichment and in-situ profiles exhibit distinct structural and functional compositions reflecting successional stages in coal biomethanation. The enrichment was more similar to stage 3 profiles identified in-situ, with over-representation of intermediate production and methanogenesis pathways. Succession in biomethanoation phenotypes has implications for the development of field deployable strategies to enhance coal conversion.