Experimental kinetic study of carbonaceous material maturation: An appraisal of pressure and time effects on vitrinite reflectance at 400°C

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Vitrinite reflectance (R_0) measurement in organic carbonaceous material-bearing rocks is of great interest in metamorphic petrology. This stems from the ability of R_0 to constrain paleotemperature conditions and maturity degree of organic matter in very low- to low-grade metamorphic terranes where recrystallization is not obvious. However, considerable discrepancy still exists concerning the role of pressure and time on R_0 evolution.

Consequently, the goal of this laboratory rate study is to understand and estimate the effects of pressure and time on the development and kinetic evolution of R_0. We conducted a series of maturation experiments at 400°C in a closed system at pressures of 2, 10 and 20 kbar employing a high-pressure piston-cylinder apparatus and cold-seal pressure vessels. Experiments were performed on dry (no water added) xylite of swamp cypress and involved run lengths from 0 second to 80 days.

The experimental results demonstrate for the first time that pressure (P) greatly enhances the elevation of R_0. Moreover, R_0 is confirmed to increase with run time (t) at each P during isobaric experiments. However, an increasing deceleration with t of the R_0 isobaric kinetic evolution at each investigated P is found despite rapid initial kinetics. Nevertheless, we clearly observe a lesser deceleration with t of the R_0 kinetic evolution with increasing P.

To quantify the relationship between R_0, P and t, we fitted our experimental R_0 results at each pressure by the method of weighted least squares to a parabolic equation of the form

$$R_0(P,t) = R_0(P,0) + k(P)\,t^{n(P)}$$

where, in contrast to the initial R_0 at $t = 0$ [$R_0(P,0)$], the rate constant $k(P)$ is found to decrease with P. This kinetic equation supports all our qualitative observations. With the exponent $n(P)$ increasing regularly with P and $0 < n(P) < 1$, our parabolic equation calls for a larger increase in R_0 and a lesser deceleration with t of the R_0 isothermal kinetic evolution with increasing P. We regard our kinetic formulation as providing a step toward a general equation describing the R_0 evolution as a function of pressure, time and temperature.

Directed proteomics applied to the detection and characterization of arsenic-transforming enzymes in complex communities from the Alvord Basin hydrothermal system

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Microorganisms have the ability to transform over forty elements on the periodic table including major, minor, and trace elements. Microbial enzymes carry out a wide variety of these transformation reactions, any of which can potentially be measured. The primary goal of this research was to apply directed proteomics to the detection and characterization of arsenic-transforming enzymes in multi-species microbial systems inhabiting a hydrothermal environment.

Microbial mat samples were collected from the Alvord Basin in southeast Oregon, USA. One laboratory isolate (*Thermus* Strain A03C), cultivated from the Alvord Basin, was used as a positive control as it is has been shown to oxidize arsenite and respire on arsenate. Proteins were sequentially extracted using detergent-aided lysis of biomass and then mechanically extracted using a vigorous glass bead-beating procedure. Microbial arsenite oxidase and arsenate reductase activities were successfully detected and resolved using zymography, an approach that allows the detection of enzyme activities among proteins and enzymes resolved by electrophoretic methods. Activity stains specific for arsenite oxidase and arsenate reductase activities were used to visualize enzymes involved in arsenic transformation. Several activity bands were effectively resolved in individual mat samples and suggest distinctive isoforms of the enzymes. Activity bands were excised from the gel, processed, and analyzed using Liquid Chromatography-Mass Spectrometry (LC/MS). The majority of peptides obtained from the LC/MS analysis had corresponding database matches for the enzyme of interest, and functional gene analysis confirmed the presence of corresponding genes. However, some samples had no peptides related to the specific activity. These sequences could signify new unidentified enzymes involved in the transformation of arsenic and can be compared to sequences in the metagenome to potentially assign a defined biological function to 'hypothetical' or unidentified proteins and their associated genes.

By combining tools commonly used in the study of microbial ecology with the most contemporary proteomic separation and analysis techniques, great strides can be made in achieving a greater understanding of microbial enzymes and their ecophysiologic roles.