

Evolution of picritic basalts in arc settings: Implication from Os isotopes of Cr-spinel and whole-rocks from Kume-jima, central Ryukyu arc

RYOKO SENDA^{1*}, KATSUHIKO SUZUKI¹, KENJI SHIMIZU¹
AND RYUICHI SHINJO²

¹IFREE, JAMSTEC (*correspondence: rsenda@jamstec.go.jp)

²Dept. Physics and Earth Sciences, Univ. Ryukyus

The Os isotope ratios of picritic basalts are commonly reported to discuss the sources of the basalts because their Os concentrations are relatively high compared with those in the other basalts. Though the picritic basalt in arc settings are uncommon, picritic basalts from the northern part of Kume-jima located at central Ryukyu arc were described [1]. Shinjo [2] suggested that they were a result of interaction between slab melts and the wedge mantle or, more likely, mixing of high-Mg andesitic magma and wedge-derived primitive magma. If they were originated in arc-trench system, their Os isotope ratios could provide geochemical information about slab-derived material and/or wedge mantle.

We tried to examine the Re-Os isotope systematics of bulk rock and Cr-spinel inclusions of Kume-jima picritic basalts. The Cr-spinel is early formed crystal during crystallization and has high Os contents. The Os isotope of the Cr-spinel holds more primitive information of magma than that of whole-rock [3]. Thus, the difference of the Os isotope between Cr-spinel and whole-rock picrites possibly provides constraints on the history of magma of Kume-jima picritic basalts. Os contents of whole-rock samples of Kume-jima picritic basalts are lower than those of picritic basalts from the other geological settings such as ocean islands and LIPs. This suggests that the origin and/or evolution of magma of picritic basalts from Kume-jima is different from those in the other geological settings.

[1] Ito & Shiraki (1999), *Jour. Geol. Soc. Japan* **105** 810-813.

[2] Shinjo (1999) *Chem. Geol.* **157** 69-88. [3] Suzuki *et al.* (2008) *Geochim. Cosmochim. Acta* **72** A919.

A comparison of approaches to model thermodynamics and maintenance energy requirements of microbial metabolism

S.S. ŞENGÖR^{1*}, C.J. BRUGATO², P. GIKAS³,
M. FLETCHER⁴ AND T.R. GINN¹

¹University of California, Davis, CA 95616, USA

(*correspondence: sssengor@gmail.com)

²Westech Engineering, Salem, OR 97302, USA

³Technical University of Crete, 73100, Chania, Greece

⁴University of South Carolina, Columbia, SC, 29208, USA

Various kinetic rate laws have been utilized to predict microbial metabolism in low energy yielding environments. For predicting microbial metabolism in such environments, the rate laws should quantitatively account for the thermodynamics of the chemical reaction. The rate laws should also consider the distinction between energy and ATP producing (catabolic) and energy and ATP consuming (anabolic) processes. Catabolic reactions associated with substrate degradation should be considered fully reversible and kinetically controlled. The catabolic and anabolic processes are stoichiometrically coupled through the ATP system. We provide a comparison of approaches for modeling microbial respiration considering thermodynamic equilibrium. We also propose a model for simulating biodegradation coupled to microbial growth for an anaerobic syntrophic coculture consisting of a butyrate degrader *Syntrophomonas wolfeii* and the hydrogen-oxidizing sulfidogen *Desulfovibrio* G11. Unlike traditional approaches, we assume that maintenance energy requirements take precedence over ATP-consuming cell synthesis reactions. Therefore, cellular growth occurs only after maintenance energy requirements are satisfied. Since the catabolic substrate utilization reactions are taken to be fully reversible and kinetically controlled, product inhibition is included and the substrate utilization rates are limited by the energetics of the system. The formulation for the reversible kinetic expressions includes product and substrate concentrations. When the catabolic reactions reach thermodynamic equilibrium with ATP formation including maintenance energy, substrate utilization stops. The end result is that the model includes the effects of product inhibition and minimum substrate thresholds. For demonstration purposes, we also compare our syntrophic model with other models that account for thermodynamic considerations in microbial metabolism.