

Baddeleyite (ZrO₂) in manganese nodules of Central Indian Ocean Basin: An evidence for low temperature mobility of zirconium

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Baddeleyite (ZrO₂) is a rare mineral that occurs in alkaline, silica-undersaturated rocks, and extra-terrestrial bodies [1,2]. While investigating some manganese nodules from Central Indian Ocean Basin (CIOB) under SEM we have recorded the occurrence of baddeleyite which has hitherto not been reported from sea-nodules. The mineral occurs either as single euhedral crystal or as clusters of very fine tabular crystals (<3µm) within the ferromanganese oxide bands. In-situ point analysis by EDS indicated 93.09 wt.% ZrO₂ and 6.91 wt.% MnO. Textural evidences indicate an authigenic origin for baddeleyite and preclude a detrital origin.

Zirconium is considered to be a highly immobile element but a number of studies indicate its mobility at low-temperatures (~ 250 °C) [3]. The authigenic formation of baddeleyite in manganese nodules of CIOB provides natural evidence for extremely low-temperature mobility of Zr in marine environment. It is inferred that Zr is released into seawater from the terrigenous sediments or the altered seafloor rocks in presence of halogens (F⁻, Cl⁻ and Br⁻) forming highly reactive fluids and subsequently crystallizing baddeleyite in the nodules under diagenetic conditions. Increased mobilization of Zr forming halogen complexes in terrestrial environment has also been conceived by others [4].

[1] Lorand, J. P., and Cottin, J. Y. (1987) *Min. Mag.* **51**, 671-676. [2] Bukovanská, M. *et al.*, (1997) *J. Geosciences*, **42**, 20. [3] Rasmussen, B. (2005) *Contrib. Mineral. Petrol.* **150**, 146-155. [4] Gao, S. *et al.*, (1998) *Geochim. Cosmochim. Acta*, **62**, 1959-1975.

Genomics and geochemistry: Promises and reality

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Since the first bacterial genome was sequenced in 1995, advances in sequencing methodology and methods of data analysis have led to rapidly accumulating data sets for both genomics and metagenomics. Never before in the history of microbiology has it been possible to gather so much information so quickly. The promise of genomics and metagenomics is so great that it is easy to believe these new methods will provide the means by which the language of the environment can be deciphered: with metagenomic and geochemical data sets in hand, one should be able to understand, and even predict, the metabolic and geochemical interactions of a complex ecosystem. This being said, it is proper to temper one's excitement with a dose of reality. On the positive side, the ability to learn about a given organism or group of organisms has been so greatly enhanced by genomics that one can now talk of the "systems biology", and metagenomic approaches have led to major advances in our understanding of some simple ecosystems. On the negative side, we are beset with many unidentified genes, with "known" genes that have different functions, and with large amounts of genomic variation between organisms identified as the same species. With regard to genomics, our own studies with the group *Shewanella* will be used to illustrate some of the "traps" that are routinely encountered. At the metagenomic level, our studies of Yellowstone Lake will be used to demonstrate how we are attempting to interface a detailed geochemical data set with metagenomic information, in an effort to interpret and even predict geochemistry by metagenomic analyses.