The noble gases isotopic compositions in the Deji ophiolites from the Yarlung Zangbo River, Tibet, SW China

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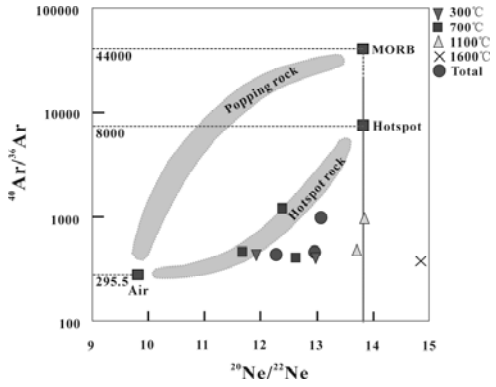
The noble gases isotopic compositions in the Deji ophiolites (one serpentinite, two altered gabbros) from the Yarlung Zangbo River, Tibet, SW China were measured by MM5400 mass spectrometer using stepwise heating method. A large amount of He was released at lower temperature for 3 samples. The R ($^3He/^4He$) value in the serpentinite was 1.19Ra (Ra = 1.400×10^{-6}, is the $^3He/^4He$ ratio in air), 0.441Ra, 2.97Ra and 1.597Ra, at 300, 700, 1100, 1600℃, respectively, lower than 8Ra, which is the typical value in MORBs. The R values in the altered gabbros were between 0.225Ra and 1.817Ra at various temperatures. As a whole, R values were decreased with increased ^4He contents, and it reflected the mark of altering. The $^{20}Ne/^{22}Ne$ values were between 12.39 and 18.50 with an average of 13.78, the $^{21}Ne/^{22}Ne$ values were between 0.02835 and 0.0513 with an average of 0.03177. The $^{40}Ar/^{36}Ar$ values were concentrated a value of about 450, and the highest value of 1215.9 was found at 700℃ in the altered gabbros. In the figure about $^{20}Ne/^{22}Ne$—$^{40}Ar/^{36}Ar$, the data points arranged along the hotspot rock zone. Summarily, the obtained data indicated that the noble gases contents and isotopic compositions in the ophiolites accorded with the characteristics of the primal mantle, although they were altered by a strong metamorphism.



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The genetics and geochemistry of microbe-selenium interactions

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Microorganisms play a major role in the global selenium cycle by catalyzing the reduction of selenium oxyanions in soils and sediments. Although bacteria have been known to reduce selenium for nearly 20 years, the molecular mechanisms that control the reduction process have remained poorly understood. In my laboratory, we have discovered essential genes that enable bacteria to catalyze selenium reduction. Insights into how microorganisms reduce selenate [Se(VI), SeO_4^{2-}] was made possible by studying genetically tractable facultative anaerobic bacteria. The establishment of a genetic system and rapid screening method allowed for the identification molecular determinants required for the reduction process. Using mutagenesis techniques, we have constructed mutant strains of the Se-reducing bacterium *Enterobacter cloacae* SLD1a-1 that have lost the ability to reduce selenate to elemental selenium [Se(0)]. Recently, we have screened the Keio Collection of systematic individual gene knockout strains of *Escherichia coli* for loss of selenate reducing activity. To date, we have identified numerous genes required for selenate reduction, including genes that encode regulatory proteins, enzyme export systems, and components in the electron transport chain. Based on this genetic data we have constructed a molecular model for microbial selenate reduction. Using genetic biomarkers, we are currently developing culture-independent methods to detect and quantify the activity of Se-reducing bacteria in contaminated environments.