The mantle neon from the Jinchuan sulfide deposit, NW China

X. R. YE [1,2] CH. A. YU [1,3] AND L. DING [2]

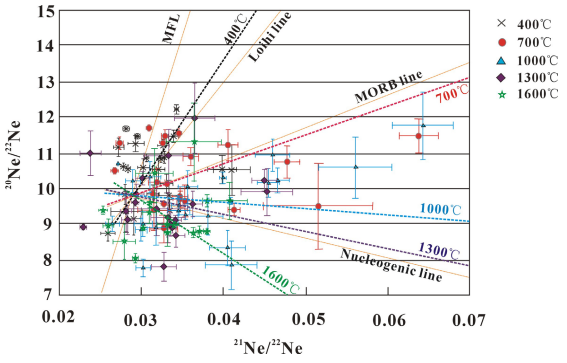
[1]Key Laboratory of Gas-Geochemistry, CAS, Lanzhou, 730000, China (xrye287@sohu.com)
[2]Institute of Tibetan Plateau Research, CAS, Beijing, 100085, China (dinglin@mail.igcas.ac.cn)
[3]Graudate University of Chinese Academy of Sciences, Beijing 100049, China (yuchuanao@eyou.com)

The noble gas isotopic compositions in the clinopyroxene, olivine, orthopyroxene and chalcopyrite from the second diggings of the Jinchuan sulfide deposits, NW China, have been determined. Stepwise heating method had been taken in order to get the noble gas isotopic compositions from the different micro-sections in a sample. The ranges of the neon contents and isotopic compositions in the samples studied were shown in the following table.

Neon data ranges in the samples studied

Temperature (ºC)	$^{20}Ne/^{22}Ne$ range (average)	$^{21}Ne/^{22}Ne$ range (average)
400	8.75—12.22 (10.58)	0.02594—0.04100 (0.03125)
700	9.39—11.705 (10.39)	0.02669—0.06380 (0.03636)
1000	7.77—11.77 (9.64)	0.02649—0.06430 (0.03795)
1300	7.81—11.97 (9.62)	0.02292—0.04530 (0.03275)
1600	8.04—11.30 (9.22)	0.02536—0.04070 (0.03289)
Total	9.00—11.368 (10.02)	0.02697—0.04400 (0.03361)

Apparently, the neon isotopic compositions of the samples were different from atmospheric. Higher $^{20}Ne/^{22}Ne$ values were found at 400ºC and 700ºC with an average of 10.58 and 10.39, respectively. In the three isotopes diagram of neon, the data points are dispersive, which shows a characteristic mixed on multi-member fluid. However, the data points are concentrated or show a correlation between $^{20}Ne/^{22}Ne$ and $^{21}Ne/^{22}Ne$ at every temperature step. It is noticeable that the line at 400ºC closed to Loihi line, the line at 700ºC trends to MORB line, and the lines at 1000ºC, 1300ºC and 1600ºC shown an addition of radiogenic neon. The fluids released at lower temperature were mainly come from fluid inclusion, so it is surmisable that the mineral captured mantle fluid during crystallization.



Acknowledgements

This work was supported by NSFC (Grant No. 40573012), and the West Light (the Talent Training Plans) of CAS.

A molecular model for microbial Se(VI) reduction

NATHAN YEE[1], JINCAI MA[1] AND DONALD. Y. KOBAYASHI[2]

[1]Department of Environmental Sciences, Rutgers, The State University of New Jersey; New Brunswick NJ, USA (nyee@envsci.rutgers.edu)
[2]Department of Plant Biology & Pathology, Rutgers, The State University of New Jersey; New Brunswick NJ, USA (kobayashi@aesop.rutgers.edu)

Background

The redox cyling and mineralization of selenium is largely controlled by microbial processes. Phylogentically diverse species of *Bacteria* and *Archaea* are able to reduce soluble selenate oxyanions [Se(VI), SeO_4^{2-}] to insoluble elemental selenium [Se(0)]. Although Se-reducing bacteria are known to govern the redox transformation of selenium in a broad range of terrestrial and aquatic environments, the mechanisms of microbial selenate reduction remain poorly understood. In this study, we apply molecular techniques to identify the genes involved in selenate reduction pathway.

Methods

Transposon mutagenesis and direct cloning techniques were used to identify genetic regions in the Se-reducing bacterium *Enterobacter cloacae* SLD1a-1 associated with selenate reductase activity. The mini-Tn5 transposon system was used to produce mutants that have lost the ability to reduce selenate. *E. cloacae* mutants and genomic library clones heterologously expressed in *E. coli* S17-1 were screened for activity on LB agar supplemented with sodium selenate. The rate of selenate reduction by the clones was measured in liquid minimal media, and the Se(0) minerals formed by the clones were examined using XANES and SEM.

Results and Discussion

Essential genes required for microbial selenate reduction were identified. The experiments showed that mutation of the Fumurate Nitrate Reduction regulator gene, menaquinone biosynthesis operon, and twin-arginine translocation operon produces derivative strains that are deficient in selenate reductase activity. Complementation by the wild-type sequences restores the ability of mutant strains to reduce Se(VI). These results demonstrate that: 1) oxygen sensing molecules regulate the expression of selenate reductase genes; 2) selenate reduction activity is dependent on the secretion of the reductase enzyme to the periplasmic space; and 3) anaerobic electron carriers are involved in the shuttling of electrons to the terminal selenate reductase protein. We propose a molecular model to describe microbial Se(VI) reduction.