Investigating the biogenic synthesis of chalcogenide-based nanomaterials

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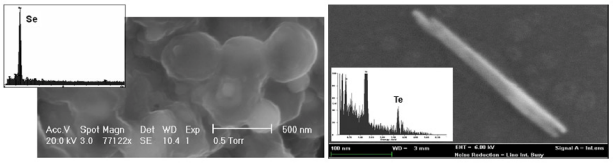
The future of materials science is closely linked to nanotechnology and, as such, there is a need to improve the manufacture of nanomaterials in terms of environmental and economic impact. Using the capability of microbes to manufacture potentially useful bionanominerals offers new methods of material synthesis that eliminate toxic organic solvents, minimize expensive high-temperature processing and can involve the use of industrial waste as the starting material, thereby incorporating a remediation step.

This research involves (i) identification of biomolecules associated with different bacterial strains that act as templates to direct bionanomineral nucleation and growth; (ii) investigation of enzyme-mediated electron transfer reactions resulting in precipitation of nanoparticles; (iii) harnessing and scaling up these processes for biomimetic materials synthesis.

The biotransformation of selenium and tellurium oxyanions by four diverse organsims (*Veillonella atypica, Bacillus selenitireducens, Geobacter sulfurreducens* and *Geobacillus stearothermophilius*) has been selected as a model system to study bionanomineral formation by a range of reduction processes. These organisms produce size- and shape-constrained Se/Te nanoparticles with different structural and spectral characteristics to their chemically formed counterparts (Fig. 1)[1].

Figure 1: Biogenic Se and Te nanoparticles



The elemental Se/Te is then further reduced to form reactive selenide/telluride, which is precipitated to produce chalcogenide-based fluorescent nanoparticles, such as CdSe.

Reference

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Factors controlling ^{14}C contents of organic compounds in oceans and sediments

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Fourteen years ago, Hayes published a review entitled "Factors controlling ^{13}C contents of sedimentary organic compounds: Principles and evidence" (Hayes, 1993). It described four processes governing the distribution of the stable isotopes of carbon in individual molecules: "(1) the carbon source utilized, (2) isotope effects associated with assimilation of carbon…, (3)…effects associated with metabolism and biosynthesis, and (4) cellular carbon budgets". To a first-order approximation, only the first of these would apply in an analogous discussion of "factors controlling ^{14}C". The ^{14}C content of organic samples is reported in terms of fractionation-normalized values of $\Delta^{14}C$ or f_m (fraction modern). This practice erases all of the biosynthetic fractionations discussed above. Compound-specific ^{14}C (CSRA) approaches were developed in part because of this apparent simplicity: values of $\Delta^{14}C$ for individual compounds should depend only on the ^{14}C content at $t = 0$ and radioactive decay since then. Calibration records determine $^{14}C/^{12}C$ ratios at $t = 0$, in principle allowing calculation of absolute chronologies. However, this applies only to organic matter produced directly from fixation of atmospheric CO_2; biosynthetic reactions that draw upon other pools of the carbon cycle automatically begin with the imprint of a "reservoir correction". In practice, this means that the value of $\Delta^{14}C$ rarely = 0 at $t = 0$. Now, after more than ten years of CSRA, it is becoming apparent that reservoir correction is just one of several challenges facing the application of individual-compound measurements. These challenges can be classified broadly as *analytical* or *interpretational*. Problems of analysis include: (1) difficulty obtaining adequate quantities of sample, (2) tedious laboratory separations, (3) ballooning uncertainties in values of $\Delta^{14}C$ at small sample sizes, and (4) the difficulty of obtaining authentic standards and measuring realistic processing blanks. Nearly all obstacles to interpretation are due to the problem of heterogeneous mixing: there can be (1) multiple sources of the same compound, each having a different initial reservoir age but mixed in the same terminal reservoir, (2) a single source for a compound, but scrambling of its age by post-depositional mixing, and (3) in the case of prokaryotic metabolism, uncertain contributions of presumed planktonic molecules by deep-pelagic or benthic populations. Despite the challenges, there have been numerous, successful applications of CSRA. Here I will show several recent examples from the literature and discuss how further work promises to illuminate new information about fluxes and residence times throughout the global carbon cycle.

Reference

Hayes, J.M. (1993) *In*: R.J. Parkes, P. Westbrook, and J.W. de Leeuw (Editors), Marine Sediments, Burial, Pore Water Chemistry, Microbiology, and Diagenesis. *Mar. Geol.*, **113**: 111-125.