Influence of boundary condition of diffusion test method on migration parameter in compacted bentonite

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Observation of Boundary Effect

Effective diffusion coefficient, D_e, of radionuclides in compacted bentonite is the key parameter for safe high-level nuclear waste repository. The De is usually derived from flux of target element in test specimen caused by given concentration gradient in experimental configuration. Thus, precise control or accurate understanding of the boundary concentration are essential. Mass transfer resistance in filter on D_e measurement has been pointed out in previous researches [1]. Besides, there still exist uncertainties with less interpretative diffusion behavior in compacted clay system. According to Donnan equilibrium and Poisson-Boltzman theories, partition of mobile ions will be induced at reservoir solution-compacted clay boundary in media with fixed charge, due to electric potential (ϕ) produced by the fixed charge [2]. This boundary condition is a potential influence on D_e measurement because concentration gradient of ions in the media varies with the partition. We measured $\Delta\phi$ at the boundary in compacted clay system by two Pt-electrodes method to investigate partition of mobile ions and its influence on D_e measurement with theoretical basis as a function of salinity and compaction density of clay (ρ).

Salinity (NaCl [M])	$\Delta\phi$ [mV]
0.01	14.0
0.1	3.0
0.5	0.2

Table 1: The $\Delta\phi$ at solution-clay boundary (clay:Smectite (Kunipia P, ρ=0.9g/cm^3).

Discussion of Results

Potential difference observed depending on the salinity indicates that the partion of mobile ions was produced under low salinity condition, which may cause an over estimation of D_e in the compacted system.

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[1] Loon *et al*. (2008) *J. Cont. Hydrol.* **97**, 67-74. [2] Davies (1961) *Interfacial Phenomena*, Academic Press, Inc.

Protein-stable isotope probing (Protein-SIP) for simultaneous identification of bacterial species and determination of metabolic activity

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We developed a concept for analysing carbon and nitrogen fluxes in microbial communities by employing protein-based stable isotope probing (Protein-SIP) in metabolic labelling experiments with stable isotope labelled substrates. In a Protein-SIP experiment microbial pure or mixed cultures are grown on substrates containing ^{13}C or ^{15}N and subsequently the incorporation of the heavy isotopes into proteins is determined by mass spectrometry of proteins or peptides. The mass spectrometric analysis of peptides yields the identification of the protein and the species of origin whereas incorporation of ^{13}C or ^{15}N can be used as a measure for metabolic activity.

The identification of species can be further supported by intact protein profiling (IPP), by making use of reference mass spectra from known microbial species. The best results for simultanous species identification and determination of metabolic activity were obtained by shotgun mass mapping (SMM). Here the protein extracts of microbial cultures are digested with trypsin before the peptides are measured by MALDI-MS. The identification rate was increased and the determination of incorporation showed a detection limit of about 5% which is superior to nucleotide based SIP-approaches and allows to detect the early stages of consumption of isotope labelled substrates in pure cultures and microbial communities.