Environmental Mineralogy Group and Geomicrobiology Network Joint Research in Progress Meeting

Dates: 8th – 9th September 2026

Theme: Geo-Bio-Interfaces

Location: British Geological Survey, Keyworth, Nottingham

Organising committee

Luke Townsend	Nuclear Waste Services
John Moreau	University of Glasgow
Kevin Murphy	Mineralogical Society
Laura Kelly	Manchester Metropolitan University
Richard Kimber	University of Manchester
Katherine Rothwell	University of Stirling
Thomas Neill	University of Manchester

Event Information

Location: British Geological Society, Keyworth, Nottinghamshire, Nicker Hill, NG12 5GG

It is recommended to stay in central Nottingham as the site can be easily accessed by bus and car. Further information can be found here: https://www.bgs.ac.uk/about-bgs/contact-us/locations/keyworth-accessibility/

Bus: Keyworth is served directly from Nottingham city centre (Broadmarsh bus station) via the Keyworth bus service operated by Trent Barton. The bus runs every 20 minutes, with the journey from city centre taking approximately 30 minutes.

- Arrival: the nearest bus stop is Covert Close on Wolds Drive. The Covert Close bus stop is about a one to two-minute walk (50 metres) from the main entrance
- Departure: for the fastest route back to Nottingham city centre, take the bus from the bus stop at Green Close on Station Road. The Green Close bus stop is about a three to five-minute walk (300 metres) from the main entrance and is sheltered

Car: Car parking and bicycle shelters are available on site. A member of the security team will direct you to the designated areas. There is a marked drop-off area and three accessible parking bays near the Hercules statue. If you are arriving by car, please notify the conference organiser and a free parking space can be made available.

During the meeting, the following locations will be used. Upon arrival on the first day, please register your attendance with the Organisers in the foyer. The meeting will be held throughout the following areas:

Main Conference Room: Conference Suite, First Floor

Coffee / Lunch: Exhibition Area, Ground Floor

Poster Session: Exhibition Area, Ground Floor

Information for presenters

Oral Presentations:

If you have an oral presentation, please ensure you have uploaded your talk to the meeting room computer before your session begins. There will be EMG Committee members on-hand to help with this.

Poster Information:

Poster boards will be provided and will accommodate the standard A0 size of poster. We will announce when to put up posters at the opening of the meeting.

Online Presentations & Remote Attendees:

The meeting will use Microsoft Teams and a link to join will be circulated the day before the event (Monday 7th September).

Evening meal: In line with recent RiP meetings, an informal evening meal will be arranged for the evening of Tuesday 8th September. Please contact the organising committee if you wish to attend this meal. The costs of the meal are not covered by EMG or GMBN.

Agenda

Tuesday 8th September

Session	**Time**	**Presenter**
Arrival and lunch	12:00–13:00	
Welcome	13:00–13:10	
Session 1	13:10–13:25	**James Gusek** (Online) *Revisiting Bactericides: a 40-Year-Old (and Counting) Technology to Suppress Acid Rock Drainage*
	13:25–13:40	**Megan Barnett** *Stimulating natural microbial communities in beach sand to aid coastal defence*
	13:40–14:10	**Piyush Sriwastava** (Keynote) *Organic matter decay controls clay authigenesis: from postmortem mineral formation to secular trends in Earth's clay record*
Coffee break	14:10–14:30	
Session 2	14:30–14:45	**Lucian Staicu** (Online) *On the allotropic transition of biogenic* Se^0
	14:45–15:00	**Oliver Moore** *Probing the mechanisms controlling N-transformation pathways in agricultural soils under anoxia*
	15:00–15:15	**Shane O'Reilly** (Online) *Effects of peatland disturbance on peat soil microbial diversity and composition*
	15:15–15:30	**Mohammed Rehmanji** *Elucidation of links between genomic variation and calcium carbonate biomineralization in Sporosarcina pasteurii*
	15:30-15:45	**Max Barclay** *Impact of biomolecules on iron (oxyhydr)oxide transformations*
Poster Session	15:45–16:30	
Informal evening meal	19:00–21:00	

Wednesday 9th September

Session	Time	Presenter
Arrival	08:30–09:30	
Session 3	09:30–09:45	**Sujata Dabolkar** (Online) *Geomicrobiology of Indian Caves: Microbial Diversity, Microbe–Mineral Interactions and Future Metagenomic Perspectives*
	09:45–10:00	**Paloma Núñez-Munoz** *Towards Seawater-Based Chalcopyrite Bioleaching: Microbial Adaptation and Copper Recovery*
	10:00–10:15	**Hannah Koepnick** *Biofilm-based bioleaching for recovery of metals from electronic waste*
	10:15–10:30	**Flora Reid** *Fate of double-stranded RNA at goethite surfaces*
	10:30-10:45	**Tom Neill** *Environmental chemistry of actinides under nuclear legacy conditions*
Coffee break	10:45–11:15	
Session 4	11:15–11:30	**Aimae Jean Lunsayan** *Bioprospecting Acidophilic Microbial Communities from Philippine Acid Mine Drainage: Genomic and Cultivation-Based Characterization Toward Biotechnological Applications*
	11:30–11:45	**Chris Wort** *Geomicrobiological controls on radionuclide speciation and fate during the geodisposal of radioactive waste*
	11:45–12:00	**John Moreau** *Abiotic and biotic controls on hexavalent chromium mobility in urban waterways with legacy chromium contamination*
	12:00–12:15	**Philip Vixseboxse** *Characterisation of decay in filamentous cyanobacteria reveals a predictable, broadly conserved taphonomic pathway*
	12:15–12:30	**Luca Stigliano** *Cyanobacterial influence on carbonate mineralization under varying geochemical conditions: insights from high-throughput correlative imaging and Raman spectromicroscopy*
Close & prizes	12:30–12:45	
BGS Core Store tour	13:00–13:40	

Abstracts

Oral presentation abstracts

Revisiting Bactericides: a 40-Year-Old (and Counting) Technology to Suppress Acid Rock Drainage

James J. Gusek,[1] Jamie Robinson[2]

[1]Retired Mining Influenced Water Consultant; Lakewood, CO USA

[2]Technical Director, Hydrology & Hydrogeology. SLR Consulting Limited, Bradford-on-Avon, Wiltshire, United Kingdom

Email: jrobinson@slrconsulting.com

Patented controlled-release bactericide pellets formulated in the 1980s, coupled with surfaceapplied bactericide, were used at dozens of acid rock drainage (ARD) prone sites across the USA and internationally. In the late-1990s, usage of this technology virtually ceased when the sole vendor of the bactericide products closed its doors. The primary goal of these products was facilitating revegetation on acid generating mine wastes; decreases in ARD flow, metals/acidity loading, and sulphate were secondary benefits. At the time, state agencies in the US and mining companies alike viewed bactericide applications as temporary remedies. In hindsight, were they right? This presentation considers available data for selected sites to assess the long-term conditions two or more decades after bactericide applications as well as data from more-recent research projects.

The presentation will also examine several promising 21st century technologies that might capitalize on this earlier work and be combined with bactericides to fashion a practical one-timeapplication remedy for ARD prevention. For mining companies and government agencies which are saddled with ARD treatment in perpetuity, this 40-plus-year-old technology could be a gamechanger.

Keywords: acid rock drainage prevention; Acidithiobacillus ferrooxidans

Stimulating natural microbial communities in beach sand to aid coastal defence

Megan Barnett[1], Simon Gregory[1], Jessica Mackie[1], MARCUS DOBBS[1], Finn Sabin[1,2], Ed Bruce[1], Shayne Bessler[1,3], Gráinne El Mountassir[4]

[1]British Geological Survey, [2]University of Warwick University, [3]University of Nottingham, [4]University of Strathclyde

The microbial production of carbonates has been used for a variety of geotechnical applications. Most commonly, this involves addition of the bacterium *Sporosarcina pasteurii* to induce carbonate precipitation via breakdown of urea (urease pathway). This produces ammonia and carbon dioxide ultimately leading to pH increase and calcium carbonate precipitation if calcium ions are also added. The stimulation of natural microbial communities reduces the need for on-site cultivation of *Sporosarcina* or the introduction of non-native microorganisms. Previous work has focused on comparing *Sporosarcina* to the native microbial community in coastal material from a single site in Norfolk. Experiments focussed on changes in geochemical and microbial community in batch experiments. Conductivity and pH increased and then stabilised within three days and increase in relative proportion of *Sporosarcina* which continued to increase in up to day 9. Recent work used sands from Cornwall and East Lothian as well as Norfolk and the focus was looking at geochemical and geophysical properties in column experiments. The results demonstrated that bio-cementation can significantly increase the compressive strength of sand columns, with values up to roughly 1MPa achieved after treatment. Samples with at least a two-day initial microbial growth period displayed greater cementation capacity than those with only one day, highlighting the importance of the initial growth period. The relationship between added calcium carbonate content and compressive strength was weak, suggesting other factors, such as the distribution of carbonate, may be more important than the total amount. Overall, our results show that stimulating natural communities in a beach environment may be a viable alternative to adding model organisms to natural systems.

On the allotropic transition of biogenic Se^0

Lucian C. Staicu[1,2,*], Axel Schippers[2], Julie Cosmidis[3]

[1]Institute of Microbiology, Leibniz University Hannover, Hannover, Germany

[2]Federal Institute for Geosciences and Natural Resources (BGR), Hannover, Germany

[3]Department of Earth Sciences, University of Oxford, Oxford, UK

*lucian.staicu@ifmb.uni-hannover.de; https://staiculab.com/

Biogenic Se^0 is produced by bacteria through the reduction of selenium (Se) oxyanions (selenate, SeO_4^{2-}, and selenite, SeO_3^{2-}) under oxic and anoxic conditions via a biomineralization process [1-2]. In addition, biogenic Se^0 displays colloidal stability that is not pH-sensitive. Visually, Se^0 is red and has an amorphous structure. However, red Se^0 is not stable and undergoes allotropic transition to the black allotrope. This process is not well understood, as biogenic Se^0 displays different transition rates as a function of inoculum (pure cultures vs mixed microbial communities) and culturing conditions (oxic vs anoxic). In this study, biogenic red Se^0 was produced by a selenate-respiring bacterial culture, *Shewanella* sp. O23S [2-3], and a mixed microbial community (anaerobic granular sludge) collected from a full-scale bioreactor in North Carolina, USA. The red Se^0 produced by the mixed community using both Se oxyanions lost colloidal stability and turned black within two months, whereas the red Se^0 biominerals produced by *Shewanella* sp. O23S partially retained their colloidal stability and did not undergo allotropic transition during the same interval. This process is being investigated using a wide range of analytical techniques including mineralogy (Raman spectroscopy), electron microscopy (SEM and TEM), protein analysis, surface charge (zeta potential) and others. Understanding this transition will help better understand the fate of Se^0 in aquatic ecosystems and may provide knowledge for the synthesis and functionalization of commercially relevant nanoparticles.

Keywords: Biogenic Se^0, biominerals, anaerobic respiration, allotropic transition, mixed microbial communities.

References:

[1] Staicu LC et al. (2025) Microbial respiration - A biomineral perspective. FEMS Microbiol Ecol 101: fiaf093. 10.1093/femsec/fiaf093 (link)

[2] Staicu LC, Barton LL (2024) Geomicrobiology: Natural and Anthropogenic Settings. Cham: Springer, 978-3-031-54305-0 (link)

[3] Staicu LC et al. (2022) Interplay between arsenic and selenium biomineralization in *Shewanella* sp. O23S. Environ Pollut 306:119451 (link)

[4] Staicu LC et al. (2022) Bioremediation of a polymetallic, arsenic-dominated reverse osmosis reject stream. Lett Appl Microbiol 75(5):1084-1092 (link)

Organic matter decay controls clay authigenesis: from postmortem mineral formation to secular trends in Earth's clay record

Piyush Sriwastava[1], Nicholas J. Tosca[2], Julie G. Cosmidis[1], Ross P. Anderson[1]

[1] *University of Oxford, UK*

[2] *University of Cambridge, UK*

Organic matter decay is a major, yet underconstrained, control on authigenic clay mineral formation in sedimentary environments. As organisms decompose, shifting pH and the release of metabolic byproducts can drive local supersaturation of aluminosilicate phases, coupling biological decay directly to mineral authigenesis. Here, we use geochemical modelling and controlled precipitation experiments in shale pore-fluid analogue solutions to show that organic acids released during early decay, specifically lactic and acetic acid, complex aluminium and elevate Al^{3+} activity into the kaolinite supersaturation window at pH 4.5–5.5. Subsequent ammonia release during protein degradation, simulated via ammonium carbonate sublimation, buffers the system toward neutral pH, spatially confining Al-silicate precipitation to the immediate zone of decay. Notably, only lactic acid produced detectable Al-silicate among the acids tested, pointing to a biochemical specificity in kaolinite nucleation that has not previously been recognized. This decay-mineral coupling offers a mechanistic explanation for the association of kaolinite with exceptionally preserved soft tissues, such as in Burgess Shale-type fossils, where early clay authigenesis may inhibit decay and template biomolecule polymerization. More broadly, we propose that variation in organismal biochemistry, and the resulting diversity of postmortem organic acid signatures, represents an unrecognized control on clay authigenesis through geologic time. This mechanism may contribute to the Proterozoic–Palaeozoic transition in clay mineral sourcing, when authigenic marine clay production gave way to terrestrially-derived clays; a shift classically attributed to intensified continental weathering following land plant and animal colonisation, but which our results suggest may also reflect increased clay formation from decaying terrestrial biomass.

Probing the mechanisms controlling N-transformation pathways in agricultural soils under anoxia

Oliver C Moore[1,4], Aurélien Saghaï[1], Tobias Rütting[2,3], Christopher Jones[1], Sara Hallin[1]

[1]Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden

[2]Department of Earth Sciences, University of Gothenburg, Gothenburg, Sweden

[3]Soil and Plant Systems, Brandenburg University of Technology Cottbus-Senftenberg, Cottbus, Germany

[4]School of Geographical and Earth Sciences, University of Glasgow, Glasgow, UK

Globally, it is estimated that around 50% of nitrogen (N) added to agricultural soils as fertiliser is lost as nitrous gases and by leaching (Lassaletta *et al.,* 2014), highlighting the need to improve understanding of nitrogen use efficiency (NUE). In nitrate-based fertilisation systems common in northern Europe, the fate of added nitrate (NO_3) is broadly determined by two competing reductive pathways: denitrification (producing N_2 and N_2O gases) and dissimilatory nitrate reduction to ammonium (DNRA; producing NH_4). From an agronomic and climate change perspective, DNRA is the desired outcome as it improves N-retention and crop yields, and any denitrification should be complete (to minimise N_2O emissions) (Hallin and Saghai, 2023). The microbial and biogeochemical controls on the competition between denitrification and DNRA remain unclear, with much research having focused on the role of C/NO_3 ratios, and a recent field-based study suggesting that NO_3 loadings are the controlling factor (Saghai *et al.,* 2025).

To probe the mechanisms behind these competing pathways, we conducted anoxic incubations using soils from two long-term field experiments in Sweden, subjecting them to contrasting C/NO_3 loadings and ratios. We quantified the changes in N-cycling gene abundances using qPCR (*nrfA* for DNRA, *nir* for denitrification, and *nosZ* for N_2O reduction), and measured N-transformation pathways using ^{15}N-tracing assays.

In contrast to the recent field-based findings at the same sites (Saghai et al., 2025), we found that under anoxic conditions, high loadings of exogenic bio-labile C (regardless of NO_3 loadings) promoted incomplete denitrification, indicated by higher N_2O production and decreased *nrfA/nir* and *nosZ/nir* ratios. Conversely, low (exogenic bio-labile) C and NO_3 loadings promoted complete denitrification and DNRA, indicated by higher *nrfA/nir* and *nosZ/nir* ratios, lower N_2O production, and $^{15}NO_3 \rightarrow {}^{15}NH_4$ recovery. Overall, these results provide new insights into the fundamental biogeochemical controls governing nitrate fate in agricultural soils, which are often obscured by complex field dynamics, but could be crucial for predicting NUE – especially during soil saturation events.

References

Lassaletta, L., Billen, G., Grizzetti, B., Anglade, J., Garnier, J., 2014. 50 year trends in nitrogen use efficiency of world cropping systems: the relationship between yield and nitrogen input to cropland. Environ. Res. Lett. 9, 105011. https://doi.org/10.1088/1748-9326/9/10/105011

Hallin, S., Saghaï, A., 2023. Can nitrate-reducing ammonifiers increase nitrogen retention in soil and support ammonium-based cropping systems? J. Sustain. Agric. Environ. 2, 541–545. https://doi.org/10.1002/sae2.12073

Saghaï, A., Moore, O.C., Jones, C.M., Hallin, S., 2025. Microbial controls of nitrogen retention and N2O production in cropping systems supporting soil carbon accrual. Soil Biol. Biochem. 208, 109858. https://doi.org/10.1016/j.soilbio.2025.109858

Effects of peatland disturbance on peat soil microbial diversity and composition

Mupamhadzi, TL[1], Moffat, A[2], Bartley, M[1], Li, Y[4], Buttimer, H[1], Jordan, S.F[3], Kelleher, B[3], Zhang, C[4], Caruso, T[2], Schmidt, O[2], O'Reilly, S.S[1]

[1]School of Chemical and Biopharmaceutical Sciences, Technological University Dublin, Dublin, Ireland

[2]School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland

[3]School of Chemical Sciences, Dublin City University, Glasnevin, Dublin, Ireland

[4]School of Geography, Archaeology and Irish Studies, Geography, Ryan Institute, University of Galway, Ireland

Microbial communities are integral to peatland carbon storage and ecosystem functioning, yet their responses to long-term peatland disturbance, particularly peat extraction for fuel and drainage for agriculture, remain poorly understood. This knowledge gap will limit broader policy goals such as recently adopted EU Nature Restoration Regulations and the Soil Monitoring Directive. This study investigated bacterial and fungal diversity, community composition, and biomass across 31 Irish peatland sites representing a gradient of disturbance and management conditions. Bacterial and fungal communities were characterised using 16S rRNA gene and ITS amplicon sequencing, respectively, while microbial biomass was quantified using ester-linked fatty acid methyl ester (EL-FAME) analysis.

Across all sites, 41 bacterial phyla (686 genera) and 15 fungal phyla (566 genera) were identified. Soil pH was the strongest environmental predictor of microbial diversity and community composition, explaining up to 30% of variation in richness and Shannon diversity. In contrast, peatland condition, water content, and total organic carbon were not significant predictors of microbial diversity. Although disturbed and semi-natural peatlands exhibited comparable microbial diversity, disturbed sites showed significantly lower bacterial and fungal biomass. Several taxa demonstrated strong habitat specificity and may serve as potential indicators of peatland condition, including the fungal genera *Dactylonectria*, *Pyrenochaetopsis*, and *Tricellula*, and the bacterial genera *Psychrobacillus* and *Fimbriiglobus*.

These findings suggest that microbial biomass and community composition may provide more sensitive indicators of peatland disturbance than diversity metrics alone and highlight the potential of genomic approaches for peatland health assessment, monitoring, and restoration programmes.

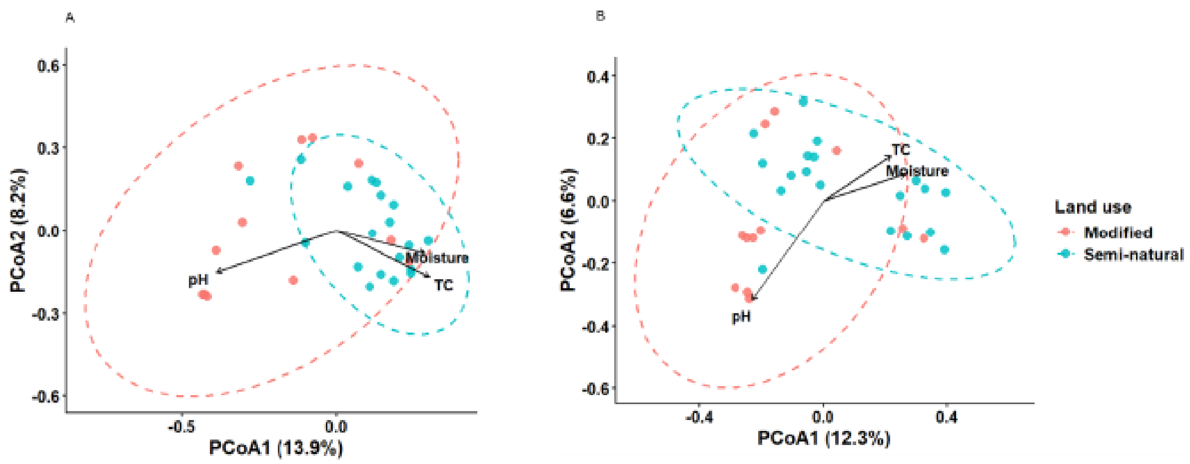

Figure 1. Principal Component Analysis plots based on Bray–Curtis dissimilarity showing variation in (a) bacterial ASV composition and (b) fungal ASV composition across peatland soils. Each point represents an individual soil sample, coloured according to peatland group. Ellipses indicate 95% confidence intervals around each peatland group. Environmental vectors show fitted soil physicochemical gradients associated with community composition.

Elucidation of links between genomic variation and calcium carbonate biomineralization in *Sporosarcina pasteurii*

<u>Rehmanji M.</u>[1] Stigliano L[1] and Cosmidis J.[1]

[1]Department of Earth Sciences, University of Oxford, Oxford UK

Email: mohammed.rehmanji@earth.ox.ac.uk

Microbially induced carbonate precipitation (MICP) by *Sporosarcina pasteurii* provides a model system for investigating how microbial activity controls carbonate mineral formation. While the role of urease in *S. pasteurii* based MICP is well established, the contribution of other genes involved in this process remains poorly understood. More broadly, the genetic mechanisms linking mineral phenotypes remains poorly resolved. Here, we developed a high-throughput screening platform combining microscopy, automated image analysis, machine learning, and Raman spectroscopy to examine *S. pasteurii* mutant library for altered biomineralization. The screen revealed substantial phenotypic diversity, including mutants producing predominantly calcite (M5.7, M5.9, M5.10, M6.3, M6.6, M6.9) and mutants producing predominantly vaterite (M6.14, M6.15). Whole-genome sequencing and annotation identified variants in genes linked to membrane function, pH homeostasis, EPS and cell wall biogenesis, transport, motility, and urease regulation. Calcite-associated mutants carried missense mutations in *fliP*, *nri*, and *nhaC* genes, as well as a stop-gained mutation in UDP-glucose 4-epimerase, suggesting altered flagellar assembly, nitrogen regulation, ion homeostasis, and EPS synthesis. Vaterite-associated mutants showed mutations in an aspartate/glutamate racemase family protein, a putative nickel-responsive regulator, a colanic biosynthesis transferase, and membrane/ABC transporter proteins, pointing to changes in cell envelope structure and surface chemistry. Together, these findings link distinct genetic changes to carbonate polymorph outcome and provide a high throughput screening platform for exploring microbial genetic control of biomineralization.

Geomicrobiology of Indian Caves: Microbial Diversity, Microbe–Mineral Interactions and Future Metagenomic Perspectives

Sujata Dabolkar

Department of Botany, Government College of Arts Science and Commerce Quepem Goa India

E-mail: sujatadabolkar@gmail.com

Indian caves represent unique subterranean ecosystems characterized by darkness, low nutrient availability, high humidity and relatively stable physicochemical conditions. These environments harbour diverse microbial communities that contribute to mineral transformation, biomineralization, organic matter degradation and biogeochemical cycling. This review synthesizes available research on the geomicrobiology of Indian caves, with emphasis on bacterial and fungal diversity, cave sediments, speleothems, moonmilk, microbial mineral weathering and microbe–mineral interactions. Studies from Sahastradhara, Meghalaya, Borra and other Indian caves have demonstrated diverse microbial communities and the ability of several bacterial isolates to induce calcium carbonate precipitation, supporting an important biological contribution to speleothem formation. Existing investigations have primarily employed culture-dependent isolation, microscopy, 16S rRNA gene sequencing, MALDI-TOF identification, FISH and mineralogical techniques such as XRD, SEM–EDX and spectroscopy. Metagenomic studies can extend these approaches by extracting total environmental DNA directly from cave sediments, mineral surfaces, biofilms and speleothems, followed by shotgun sequencing, quality filtering, taxonomic profiling, functional gene annotation and comparative analysis of microbial metabolic pathways. This culture-independent approach can reveal uncultured microorganisms and genes associated with biomineralization, carbon, nitrogen, sulfur and iron cycling. Integrating metagenomics with mineralogy, geochemistry and experimental biomineralization will provide a more comprehensive understanding of cave ecosystem functioning. Future studies can establish microbial–mineral relationships, identify novel extremophiles and biomolecules, improve cave conservation strategies and explore applications in biomining, bioremediation, biotechnology and astrobiology. Thus, Indian caves offer promising natural laboratories for understanding microbial contributions to geological processes and subterranean biogeochemical cycling.

Keywords: Indian caves; geomicrobiology; microbial diversity; metagenomics; microbe–mineral interactions; biomineralization; speleothems; biogeochemical cycling; mineral weathering; astrobiology.

Towards Seawater-Based Chalcopyrite Bioleaching: Microbial Adaptation and Copper Recovery

Paloma Núñez Muñoz[1], Luis Salinas-Farran[1], Stephen J. Neethling[1], Maria Magliulo[2], Ana Santos[2], and Pablo R. Brito-Parada[1]

[1] *Department of Earth Science and Engineering, Imperial College London, London SW7 2AZ, United Kingdom*

[2] *Natural History Museum, Cromwell Road, London SW7 5BD, UK*

Declining ore grades and aggravating freshwater scarcity in arid regions, which hold much of the world's copper reserves, are placing increasing pressure on the copper industry. These constraints call for extraction methods capable of reducing freshwater consumption and environmental impact while remaining economically viable. Bioleaching has emerged as a promising alternative in this regard, offering reduced water and reagent requirements compared to conventional hydrometallurgical processes. Nonetheless, its large scale implementation is still constrained by slow reaction kinetics, chalcopyrite surface passivation, and operational limitations.

This study investigates the adaptation of two acidophilic microbial consortia, a natural consortium obtained from a mine site and a synthetic consortium comprising conventional sulfur and iron oxidising microorganisms, to increasing seawater concentrations from 5 to 100%. The aim was to enhance chalcopyrite bioleaching under saline conditions. Following adaptation, the best performing consortia were evaluated in controlled bioreactor experiments to assess bioleaching performance and compare their behaviour with freshwater controls, providing a basis for subsequent column experiments and pilot scale validation.

Early results show that during adaptation, the natural consortium showed greater resilience to increasing seawater salinity, maintaining microbial activity and iron oxidation at high seawater concentrations, whereas the synthetic consortium experienced a more substantial decline in activity. However, this behaviour was reversed in the bioreactors, where the seawater adapted synthetic consortium achieved the highest and most sustained copper recovery, while the natural consortium showed a more variable leaching response. This shift suggests that adaptation may have selected a more competitive microbial community within the synthetic consortium under favourable reactor conditions. In contrast, the natural consortium may have prioritised survival and community stability during adaptation, with interactions among its microbial populations contributing to its subsequent leaching behaviour. These results demonstrate that salinity tolerance does not necessarily translate directly into bioleaching performance and highlight the importance of microbial community interactions and microbe-mineral interactions in determining copper recovery.

Overall, these findings suggest that microbial community composition and interactions, together with their response to process conditions, could influence copper recovery. This work supports further development of seawater based bioleaching as a more water efficient approach to copper production in water scarce regions.

Biofilm-based bioleaching for recovery of metals from electronic waste

Koepnick, H.R.; Byrne, J.M.

School of Earth Sciences, University of Bristol

Microbiological approaches to recovering metals from waste are increasingly being investigated to support a circular economy, as they are less environmentally impactful than chemical leaching approaches.[1] Direct contact mechanisms, facilitated by biofilm formation, are essential for effective bioleaching of metals from mine waste materials.[2] Despite this, relatively little research has explicitly investigated the role of biofilms in leaching metals from electronic wastes.[3] Biofilms of acidophilic iron oxidisers enhance leaching via increased synthesis of extracellular polymeric substances (EPS), which facilitate extracellular electron transfer between Fe(III) ions and solid phase metals.[4] Additionally, biofilms have increased metal resistance compared to planktonic microbes, potentially allowing for higher waste loading in bioleaching systems.[5] On the other hand, EPS can bind metal ions and make recovery of leached metals more challenging.[3] We are investigating the effectiveness of biofilm reactor systems for bioleaching of e-waste.

In this presentation, we report ongoing experiments into bioleaching using biofilm-forming environmental isolates of *Acidithiobacillus ferrivorans* and *Acidithiobacillus ferriphilus*. Shake flask experiments have been conducted with both strains for initial evaluation of leaching potential. Biofilm assays have also been performed to assess the ability of these strains to colonise the e-waste and their interactions with different types of materials present in the waste. Ongoing and future work is focused on designing and optimising a biofilm reactor system.

References

1. Jadoun, S.; Chinnam, S.; Jabin, S.; Upadhyay, Y.; Jangid, N. K.; Zia, J. Recovery of Metals from E-Waste: Facts, Methods, Challenges, Case Studies, and Sustainable Solutions. *Environ. Sci. Technol. Lett.* **2025**, *12* (1), 8–24. https://doi.org/10.1021/acs.estlett.4c00696.

2. Salas, B.; Díaz, M.; Vera, M. Understanding Biofilm Formation in Acidophilic Bioleaching Microorganisms: Advances and Challenges. In *Advances in Applied Microbiology*; Elsevier, 2026; Vol. 133, pp 1–35. https://doi.org/10.1016/bs.aambs.2026.04.003.

3. Mathivanan, K.; Zhang, R.; Chandirika, J. U.; Mathimani, T.; Wang, C.; Duan, J. Bacterial Biofilm-Based Bioleaching: Sustainable Mitigation and Potential Management of e-Waste Pollution. *Waste Management* **2025**, *193*, 221–236. https://doi.org/10.1016/j.wasman.2024.12.010.

4. Kinzler, K.; Gehrke, T.; Telegdi, J.; Sand, W. Bioleaching—a Result of Interfacial Processes Caused by Extracellular Polymeric Substances (EPS). *Hydrometallurgy* **2003**, *71* (1–2), 83–88. https://doi.org/10.1016/S0304-386X(03)00176-2.

5. Harrison, J. J.; Ceri, H.; Turner, R. J. Multimetal Resistance and Tolerance in Microbial Biofilms. *Nat Rev Microbiol* **2007**, *5* (12), 928–938. https://doi.org/10.1038/nrmicro1774.

Fate of double-stranded RNA at goethite surfaces

Reid, F.[1], Singh, V. V.[2], Krämer, S. M.[2], Coker, V. S.[1], and Kimber, R. L.[1]

[1] Department of Earth and Environmental Sciences, School of Natural Sciences, Faculty of Science and Engineering, The University of Manchester, Manchester, M13 9PL, UK
Email: flora.reid@postgrad.manchester.ac.uk

[2] Department of Environmental Geosciences, Centre for Microbiology and Environmental Systems Science, University of Vienna, 1090 Vienna, Austria

RNA interference (RNAi) biopesticides are pest control products which use double-stranded RNA (dsRNA) designed to target specific organisms as their active pesticidal ingredient. Compared to traditional chemical pesticides, RNAi biopesticides provide increased specificity for target pests and are presumed to rapidly biodegrade in soil systems via microbial uptake and enzymatic degradation.

However, abiotic factors have also been found to influence dsRNA stability in the environment. For example, while metal-catalysed hydrolysis of dsRNA in solution has been found to be limited [1], adsorption at iron (oxyhydr-)oxide mineral surfaces can enhance dsRNA hydrolysis [2]. Uncovering the role that geochemical processes play in controlling the environmental fate of dsRNA is crucial to accurately assess environmental risk and develop guidance for safe and sustainable use of RNAi biopesticides.

In this work, batch equilibrium tests were performed to assess how pH and the presence of environmentally relevant metal cations impacted dsRNA adsorption to goethite and stability of dsRNA at the surface of goethite was also assessed through analysis of dsRNA fragment size by automated gel electrophoresis. Adsorption of dsRNA to goethite was found to decrease with increasing pH but an increase in adsorption was observed with increasing metal cation concentration at all pH levels tested.

Despite evidence of some goethite-catalysed hydrolysis occurring over the experimental period, a broad size distribution of dsRNA was found to persist even after 2 weeks, suggesting that hydrolysis may induce fragmentation but not complete degradation of dsRNA polymers. Preliminary work assessing the impact of polymer size on stability of dsRNA adsorbed to goethite through reverse-transcriptase quantitative PCR and automated gel electrophoresis also indicated smaller fragments may persist longer than larger dsRNA fragments. These findings suggest that dsRNA may exhibit greater persistence under a range of geochemical conditions than previously recognised, offering a foundation for mechanistic understanding of the factors regulating its environmental fate in soils.

References:

[1] Chatterjee et al. (2022) Environ Sci Technol 56(6):3564-3574

[2] Zhang et al. (2023) Environ Sci Technol 57(22):8280-8288

Impact of biomolecules on iron (oxyhydr)oxide transformations

Max Barclay[1], Victoria S. Coker[1] and Richard L. Kimber[1]

[1] Department of Earth and Environmental Sciences, School of Natural Sciences, Faculty of Science and Engineering, University of Manchester, Manchester, M13 9PL, UK.

Email: max.barclay@manchester.ac.uk

Ferrihydrite, an iron oxyhydroxide, is a widely occurring environmental mineral that plays a key role in controlling pollutant and nutrient mobility through surface binding. However, as a metastable phase, ferrihydrite readily transforms into a variety of secondary mineral phases via processes including recrystallization, topotactic nucleation, and dissolution-reprecipitation, often altering its surface reactivity and sorption capacity. These transformation processes are heavily influenced by the presence of adsorbed organic and inorganic species including phosphate and organic acids. However, the role and impact of biomolecules, including ubiquitous nucleic acids, on these processes is not known.

This work aims to identify the impact of nucleic acids (DNA) on the structural evolution and phase development of ferrihydrite during Fe(II)-catalysed transformation. The effect of DNA polymer length, DNA loading, and aqueous Fe(II) concentration on ferrihydrite transformation was quantitatively assessed with X-Ray Diffraction (XRD). Quantitative Phase Analysis (QPA) was performed by assigning 'crystallinity' to ferrihydrite via the Partial or Not Known Crystal Structure (PONKCS) method, followed by assigning phase % weighting using Rietveld Refinement. DNA adsorption was found to impact the extent of ferrihydrite transformation as well as the secondary minerals formed, relative to systems lacking DNA or containing adsorbed phosphate. These effects were further influenced by DNA polymer length and starting aqueous Fe(II) concentration. Differences observed in lattice plane diffraction peaks may also indicate preferential orientation when secondary mineral nucleation is occurring in the presence of DNA, potentially influencing the stability and reactivity of the transformation products.

Alongside QPA, transformation products were also characterised using transmission electron microscopy (TEM). TEM confirmed the presence of phases identified via QPA but may suggest an overestimation of the remaining ferrihydrite component by QPA. This could be explained by XRD's inability to distinguish between amorphous minerals and secondary nanophases that may be present. For resolving these initial conclusions, further work and in-depth analysis, such as Mossbauer and 4D-STEM, is planned. These results suggest that the presence of nucleic acids can strongly influence secondary crystal nucleation processes, such as preferential orientation, transformation pathways, and resulting phase composition. These effects may drive downstream differences in nutrient and pollutant binding, with consequences for mineral reactivity and biogeochemical cycling.

Bioprospecting Acidophilic Microbial Communities from Philippine Acid Mine Drainage: Genomic and Cultivation-Based Characterization Toward Biotechnological Applications

Aimae Jean B. Lunsayan[1,2], Mylah Villacorte-Tabelin[1], Ana Santos[2]

[1] Department of Biological Sciences, College of Science and Mathematics, Mindanao State University–Iligan Institute of Technology, Iligan City 9200, Philippines

[2] Natural History Museum, London, UK

*aimaejean.lunsayan@g.msuiit.edu.ph

Acid mine drainage (AMD) environments support microbial communities that persist under low pH and elevated metal concentrations, where their activities can strongly influence iron, sulfur, and other geochemical cycles. These communities therefore represent not only important drivers of AMD biogeochemistry, but also a potential source of microorganisms and metabolic functions that could be explored for environmental biotechnologies. This ongoing PhD project investigates acidophilic microbial communities from AMD-impacted mining environments in the Philippines and examines how their diversity, metabolic capabilities, and interactions may contribute to AMD bioremediation.

Water and sediment samples were collected from four mining areas representing different stages of mining and environmental management: an active mine, a mine undergoing rehabilitation, an abandoned mine, and a legacy mine. This range of sites provides contrasting geochemical and ecological settings in which AMD-associated microbial communities can be examined. Geochemical and mineralogical characterisation is used to establish the environmental context of each site, while 16S rRNA gene sequencing and selected metagenomic analyses are being used to explore microbial taxonomic and functional diversity. In parallel, cultivation approaches target microorganisms involved in key AMD processes, particularly iron oxidation, sulfur oxidation, and sulfate reduction.

Rather than examining these functional groups independently, the project ultimately aims to bring selected microorganisms and enriched communities together into microbial consortia. Their interactions and performance will be evaluated using synthetic AMD microcosms, allowing changes in water chemistry, microbial communities, and mineral formation to be followed over time. By linking microorganisms with the geochemical environments from which they originate, this work aims to identify indigenous microbial communities and functions with potential application in the development of biologically based AMD treatment strategies.

Keywords: acid mine drainage; acidophilic microorganisms; geomicrobiology

Geomicrobiological controls on radionuclide speciation and fate during the geodisposal of radioactive waste

Christopher T. Wort[1], Jon R. Lloyd[1], Katherine Morris[1], Samuel Shaw[1]

[1] Radioactive Waste Disposal and Environmental Remediation National Nuclear User Facility and Williamson Research Facility, Department of Earth and Environmental Sciences, The University of Manchester, Manchester, M13 9PL U.K.

Email: Christopher.wort@postgrad.manchester.ac.uk

The internationally accepted pathway for management of intermediate and high heat generating radioactive wastes is via deep geological disposal. Building on past work that has identified geomicrobiological processes as potentially significant in radioactive waste disposal [1], this project seeks to define how geomicrobial processes will contribute to the long-term biogeochemical evolution of a Geological Disposal Facility (GDF) in conditions relevant to lower strength sedimentary rocks, and how that impacts radionuclide mobility. This is an interdisciplinary research project combining geomicrobiology, microbial genomics, radiochemistry and mineralogy. Research so far has focused on understanding the microbial ecology native to Oxford Clay, a representative lower strength sedimentary rock of international relevance [2]. Preliminary geochemical and nucleic acid extraction data will be presented exploring the stimulated indigenous microbial communities in Oxford Clay samples. Additionally, the methodology for future work expected during the research project will be discussed. Both batch and dynamic flowthrough systems will be used and interrogated using state of the art techniques including microbial analysis (DNA and culture-based), advanced imaging techniques including Confocal Microscopy, Environmental Scanning Electron Microscopy, Transmission Electron Microscopy, X-ray Absorption Spectroscopy and X-ray Refraction Tomography, alongside geochemical, mineralogical and radiochemical characterisation.

References:

[1] Butterworth, S. J., Barton, F., & Lloyd, J. R. (2023). Extremophilic microbial metabolism and radioactive waste disposal. In *Extremophiles* (Vol. 27, Issue 3). Springer. https://doi.org/10.1007/s00792-023-01312-4

[2] Sellin, P., Livier, O., & Leupin, X. (2013). The use of clay as an engineered barrier in radioactive-waste management — a review. https://doi.org/10.1346/CCMN.2013.0610601

Abiotic and biotic controls on hexavalent chromium mobility in urban waterways with legacy chromium contamination

Elisa Davancens[1, (4)], Mathew P. Watts[2, (3)], Eric Hanssen[3], Erin Bleakley[4], Liam Brunton[(4)], Ethan Barsauckas[(4)], Samantha Pirie[(4)] and John W. Moreau[(3), 4;]

(superscript) = "formerly at" when contributing to this work

[1]Département des science biologiques, Université de Québec à Montréal

[2]Environmental Protection Agency, Victoria (AUS)

[3]Ian Holmes Imaging Centre, Bio21 Institute, University of Melbourne

[4]School of Geographical and Earth Sciences, University of Glasgow

Glasgow's long industrial history includes over a century of legacy hexavalent chromium contamination in urban soils, sediments and groundwater. Despite over a decade of repeated chemical treatments in an ongoing effort to remediate Cr(VI), serious Cr pollution problems remain, especially during warmer summer months where some urban waterways show the characteristic yellow-green hue of elevated Cr(VI) concentration. The Moreau Geomicrobiology Group has been investigating various aspects of this problem in the context of abiotic and biotic physical and chemical factors influencing Cr biogeochemical cycling, including local hydrological forcing, Cr partitioning into suspended minerals, redox interactions with poorly crystalline manganese (IV) phases, and reduction by Cr(VI)-respiring microorganisms. The studies described below were produced by 1 postdoc, 5 graduate students and 2 principal investigators over the past 12 years and will be discussed in the context of processes controlling Cr speciation and mobility both in East Glasgow and similar legacy hexavalent Cr-polluted sites.

Variations in water chemistry along the Cr-contaminated Polmadie Burn (stream) that roughly correlate with salinity suggest that a large weir on the River Clyde does not completely prevent the influence of tides on the migration of hexavalent chromium in this small local tributary. Chromium contaminated surface waters were collected, filtered and analysed with XRD; results support the partitioning of at least some Cr(III) into a poorly soluble ferrous-chromite phase ($FeCr_2O_4$), although it was unclear as to whether this phase represents primary Cr ore-processing residue (COPR) or a secondary Cr-bearing phase produced by either repeated injection of calcium polysulfide solution or microbial reduction of Cr(VI). To investigate interactions between poorly crystalline (i.e. biogenic) Cr(III) and Mn(IV) phases, δ-MnO2 and $Cr(OH)_3$ were synthesized and reacted in the presence and absence of selected organic species, including low molecular weight organic acids and humic acids. Throughout the reaction, solution chemistry was monitored, and cryo-TEM imaging and EELS analysis were used to investigate nano-scale changes in Cr and Mn redox states. Finally, groundwater from the East Glasgow site was used to inoculate anoxic cultures for enrichment of anaerobic Cr(VI)-respiring microorganisms, using acetate as the sole electron donor. After several weeks, enrichment cultures of Cr(VI)-reducing bacteria were grown, and community genomic DNA was extracted for sequencing and phylogenetic analysis.

Characterisation of decay in filamentous cyanobacteria reveals a predictable, broadly conserved taphonomic pathway

Philip B. Vixseboxse[1] & Sean McMahon[2]

[1]School of Geosciences, Grant Institute, University of Edinburgh, Edinburgh EH9 3FE

[2]School of Physics and Astronomy, James Clerk Maxwell Building, University of Edinburgh, Edinburgh EH9 3FD

Filamentous cyanobacteria are a major component of biofilms, occupying, and often delineating, the interface between solid substrates and fluids. Modification of this interface can occur via numerous mechanisms, with both *in* and *ex vivo* processes resulting in substrate-organic interactions, and mineral(oid) precipitation, dissolution, or transformation. While the sedimentological consequences of most cyanobacterial life processes are well-characterised, those that occur after death are less well-understood. Here, utilising a novel taphonomic well slide protocol, we characterise the decay pathways of individual cyanobacterial filaments for multiple strains of cyanobacteria, including representatives of Oscillatoriales, Nostocales, and Pseudanabaenales. We explore the impact of heterotrophic microorganisms on decomposition, finding both commonalities and dissimilarities between taxa, which we present and discuss here. Building upon these results, we intend to introduce solutes and minerals, to investigate their effects upon decay rates and taphonomic pathways.

Cyanobacterial influence on carbonate mineralization under varying geochemical conditions: insights from high-throughput correlative imaging and Raman spectromicroscopy

Luca Stigliano[1], Mohammed Rehmanji[1] and Julie Cosmidis[1]

[1] University of Oxford, Department of Earth Sciences, Oxford, United Kingdom

luca.stigliano@earth.ox.ac.uk

Microorganisms influence mineral precipitation across a range of natural and engineered environments, affecting mineralogy, morphology and growth rates of the mineral products. Microbially mediated minerals often display features that distinguish them from abiotic precipitates, including complex morphologies, metastable phases, and close associations with organic matter. These characteristics influence mineral reactivity, stability, and the cycling of elements within biogeochemical systems, and may also provide potential biosignatures preserved in the geological record. Understanding how these features arise requires disentangling the complex interplay between microbial metabolism, extracellular polymeric substances (EPS) and surrounding geochemical conditions. This requires rapid, scalable, in situ and non-destructive approaches capable of probing mineral growth across broad geochemical and biological parameter spaces under physiologically relevant aqueous conditions.

Here, we leverage a high-throughput correlative imaging and Raman spectromicroscopy workflow that we recently developed [1] to investigate carbonate precipitation in the presence of three cyanobacterial strains (*Synechococcus elongatus* PCC 11901, *Synechococcus* sp. PCC 11901, and *Cyanobacterium aponinum* UTEX 3222) across a range of Ca^{2+}, Mg^{2+} and SO_4^{2-} concentrations. Cyanobacterial experiments were conducted at room temperature under 12-hour light/12-hour dark cycles, alongside abiotic controls. Time-resolved bright-field and cyanobacterial autofluorescence imaging were combined with targeted Raman spectromicroscopy to simultaneously track the spatial and temporal development of microbial and mineral populations.

Results show that, under the investigated conditions, calcite emerged as the dominant precipitated phase and preferentially formed in spatial proximity to dense cyanobacterial clusters. In particular, under conditions where Ca^{2+} was in large excess relative to carbonate, cyanobacteria-associated precipitates displayed pronounced anisotropic growth and complex aggregation textures compared with abiotic systems. This was particularly pronounced for *Cyanobacterium aponinum* UTEX 3222, which produced dense, spatially complex microbial growth patterns associated with large calcite aggregates displaying branched and intricate textures. In contrast, dark control experiments, in which cyanobacterial growth was strongly limited, did not produce these characteristic complex carbonate structures, suggesting that the observed distinct morphologies are linked to active cyanobacterial growth rather than simply to the presence of cellular material.

Together, these observations indicate that cyanobacterial growth patterns can spatially guide carbonate precipitation. We propose that growing cyanobacteria populations generate localised geochemical microenvironments favourable to calcite formation, potentially through photosynthetically driven increases in pH and consequent increase in carbonate saturation. The resulting coupling between microbial and mineral growth may generate complex mineral textures that preserve information about the spatial organisation and activity of microbial communities, with potential implications for the interpretation of mineral biosignatures in the geological record.

Reference

[1] Stigliano, L. & Cosmidis, J. (2026). *High-throughput mineralogical characterization using*

automated in situ microscopy and Raman spectroscopy [preprint]. https://doi.org/10.21203/rs.3.rs-9233635/v1

Poster presentation abstracts

Root oxygen and water table control CO_2 – CH_4 trade-offs in tropical peatlands

Shaun M. Allingham[1], Simon P. Gregory[2], Eleanor J. Burke[3], Yanxin Liu[3], Richard Betts[4], Rachel Collin[5], Sofie Sjögersten[1]

[1] School of Biosciences, University of Nottingham, Sutton Bonington, Loughborough, LE12 5RD, UK

[2] British Geological Survey, Keyworth, Nottingham, NG12 5GG, UK

[3] Department of Geography, University of Exeter, Exeter, UK

[4] Met Office Hadley Centre, Exeter, UK [5] Smithsonian Tropical Research Institute, Ancón 0801, Panama

Tropical peatlands store vast carbon stocks but are also major sources of methane (CH_4), creating uncertainty in climate feedbacks. We conducted a field manipulation experiment in a Panamanian peatland to test how root activity and water table position regulate greenhouse gas emissions. By altering root presence, oxygen supply, and hydrology, we created gradients in peat oxygenation and redox conditions. Lower water tables and intact root systems increased oxygen availability, promoting CO_2 emissions while suppressing CH_4. In contrast, root exclusion and high water tables reduced oxygen availability, enhancing CH_4 emissions. These shifts were strongly linked to changes in the abundance of methane-cycling microorganisms. Our findings demonstrate that small changes in hydrology and vegetation can fundamentally alter carbon loss pathways in tropical peatlands. This highlights a critical trade-off for peatland management and restoration, where interventions that reduce CO_2 emissions may increase CH_4, and vice versa, with important implications for climate mitigation strategies.

Using limits of life to predict microbial activity and survival in engineered barrier systems

Jessica Mackie[1], Simon Gregory[1], Megan Barnett[1]

[1] British Geological Survey, Keyworth, Nottingham, NG12 5GG, UK

Potential for microbial activity within a geological disposal facility (GDF) needs to be considered by waste management organisations because microorganisms consume and produce gases, corrode metals, breakdown organic wastes and mobilise radionuclides, amongst other processes relevant to safety planning. The environment in and around a GDF, in particular the engineered barrier system (EBS), produces harsh conditions for microbial life. However, numerous studies have demonstrated that microbial communities have a remarkable ability to survive in extreme conditions, thus changing their local environment. Understanding what limits life within the EBS will give a better indication of when and where microbial activity is more or less likely.

The limits to microbial activity and survival were reviewed for the following relevant variables: temperature, pH, radiation, salinity, saturation, and availability of nutrients and energy sources. Where data allowed, limits were given specific to EBS materials or specific to microbial groups of interest.

Using predictions of how each environmental variable changes during the post-closure phase, we outlined the times and locations when microbial activity is expected to be limited. A range of repository concepts relevant to high heat generating waste and lower heat generating waste in lower strength sedimentary rocks, higher strength rocks and in evaporites were considered. Finally, we suggest how data from multiple variables can be combined to improve our understanding of the potential for microbial activity to occur within the EBS.

We propose that these “limits to life” be combined with existing or new EBS environmental condition evolution models to give a better understanding of the activity and survival of microorganisms. This could be integrated into safety planning to identify the potential for microbial impacts on the containment of waste. It can also be used to identify gaps in knowledge of microbiology within the EBS and inform the design of future research programmes.

Biogeochemical Interactions Associated with LSSR Relevant to Geological Disposal of Radioactive Waste in Highly Saline Environments

Rose, M. N.[1], Morris, K.[1], Shaw, S.[1], Lloyd, J.R.[1]

[1]RAdioactive waste Disposal and Environmental Remediation (RADER) National Nuclear User Facility and Williamson Research Facility for Molecular Environmental Science, Department of Earth and Environmental Sciences, The University of Manchester, Oxford Road, Manchester, M13 9PL, UK

Worldwide nuclear power generation and other nuclear fission related activities have generated high- and intermediate-level radioactive waste and spent nuclear fuel. Globally, the accepted route for disposal of these wastes is deep geological disposal in a geological disposal facility (GDF). Microbial/mineral interactions are ubiquitous in engineered and natural environments in the presence of suitable electron donors and acceptors. Low-strength sedimentary rock (LSSR) formations are appropriate candidates for geological disposal of radioactive waste. Representative LSSRs may feature groundwaters with elevated salinity, often due to the presence of evaporate minerals, in turn these extreme salinity conditions may present energetic constraints to microbial metabolism. Previous work has demonstrated that microbial communities adapted to high salinity conditions (e.g., soda lakes, brine pools) are able to reduce electron acceptors including nitrate, ferric iron (e.g. ferrihydrite), and sulfate in-situ [1]. The capacity for such high salinity tolerant microbial communities to reduce priority radionuclides including uranium has also been demonstrated [2]. Here, we examine the fundamental biogeochemical processes associated with core samples from the Mercia Mudstone Group (MMG) and its microbial communities in relevant high-salinity conditions, as well as communities from an analogous high salinity environment (Cheshire Brine Springs). Microcosm experiments were undertaken containing disaggregated rock samples and high salinity groundwaters relevant to MMG formations, incubated over timescales of up to 1 year. The experiments included suitable electron donors for microbial activity, and where applicable added nitrate and ferrihydrite, to probe terminal electron accepting processes and their impacts on radionuclide fate (e.g., U) in conditions relevant to the MMG lithology.

[1] Foti et al. (2007) Appl. Environ. Microbiol. 73(7): 2093-2100

[2] Nevin et al. (2003) Appl. Environ. Microbiol. 69(6): 3672-3675

Mixed-Valence Iron Mineral Controls on Phosphorus Cycling Under Anoxic Ferruginous Conditions

Pragya Singh, Yijun Xiong, Benjamin J.W. Mills, Simon W. Poulton

School of Earth, Environment and sustainability, University of Leeds, Leeds LS2 9JT, UK

Elemental scavenging during precipitation of iron minerals exerts a fundamental control on nutrient cycling in ferruginous basins. The drawdown and retention of phosphorus (P) — the ultimate limiting nutrient on geological timescales — is of particular significance, as P bioavailability directly regulates marine primary productivity, organic carbon burial, and the net oxygen flux to the ocean-atmosphere system. Under the pervasively ferruginous ocean conditions that characterised much of the Precambrian, the metastable mixed-valence mineral green rust has been proposed as a kinetically favoured precipitate at the iron redoxcline. However, the extent of P uptake by green rust, its sensitivity to pH, and whether sequestered P is retained or released upon subsequent transformation to the stable iron oxides and carbonates preserved in banded iron formations, remain largely unexplored.

Here, we investigate phosphate partitioning during coprecipitation with carbonate green rust and its subsequent transformation under strictly anoxic conditions. Sealed serum bottle experiments were aged for 1–6 months across a matrix of pH (7.5–9.5) and P concentrations (0.05–0.50 mM), complemented by constant-pH stirred reactor experiments sampled over hours to days. Precipitates were characterised by XRD, and aqueous Fe and P concentrations were determined by spectrophotometry and ICP-OES. Our results demonstrate that carbonate green rust exhibits strong P uptake across the entire pH range tested. Phosphate inhibits green rust transformation to magnetite and siderite in a dose-dependent manner, consistent with kinetic control via surface passivation of crystal growth sites. Upon complete transformation of carbonate green rust into stable iron oxide and carbonate minerals, dissolved phosphate does not increase appreciably, indicating that sequestered P is substantially retained within the transformed mineral assemblage. These findings provide new experimental constraints on the role of green rust in mediating P drawdown and retention in Precambrian ferruginous oceans.

Opportunities for Research and Innovation in Geomicrobiology at the UK Geoenergy Observatories

Mike Spence[1*], Vanessa Starcher[2]

[1] British Geological Survey, Nicker Hill, Keyworth, NG12 5GG

[2] British Geological Survey, The Lyell Centre, Research Avenue South, Edinburgh, EH14 4AP

*mspen@bgs.ac.uk

The UK Geoenergy Observatories in Glasgow and Cheshire are highlighted as uniquely well-characterised facilities for research and innovation in geomicrobiology. Observatory users benefit from a wide range of open-access geological characterisation data, the opportunity to access preserved core material, and extensive in-situ monitoring capabilities. They can also heat or cool the Observatory rock volume, vary groundwater flow velocity and collect groundwater samples from bedrock piezometers, multilevel groundwater monitoring wells and abstraction wells.

Background monitoring at the Observatories has highlighted strong variation in groundwater chemistry with depth, rock type and the presence of anthropogenic features such as mine workings. The Observatories are real instrumented geological systems and so provide readily transferrable knowledge of how microbially driven reactions can affect groundwater quality, aquifer properties and the lifetime of subsurface infrastructure.

A complete set of 21 borehole data packs is now available for the Cheshire Observatory alongside a BGS drilling report that provides the detailed as-built design. Further Cheshire datasets are being prepared for release including BGS reports detailing the hydrogeology, hydrochemistry and first 2 years of groundwater monitoring data.

Potential geomicrobiology research and innovation areas include: the relationship between aquifer redox zonation, microbial ecology and biochemical transformation capability; the potential for aquifer heating or cooling to affect biogeochemical processes; the relationship between the attached and mobile aquifer microbial community using frozen/refrigerated core material, and the development and testing of novel in-situ sensors to monitor microbial ecosystems.

If you would like to know more about the Observatory capabilities and the potential for geomicrobiology research please visit the UKGEOS website (www.ukgeos.ac.uk) or email enquiries@bgs.ac.uk

Keywords: Aquifer microbiology, biogeochemical processes, thermal energy storage, Sherwood Sandstone, Scottish Coal Measures