دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ایران
کتابخانه دانشکده بهداشت

Mineralization

1-Extreme soil salinity reduces N and P metabolism and related microbial network complexity and community immigration rate

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By Yang, C (Yang, Chao) [1] , [2] , [3] ; Chen, YT (Chen, Yitong) [1] ; Sun, WY (Sun, Wenyao) [1] ; Zhang, Q (Zhang, Qian) [1] ; Diao, MM (Diao, Mengmeng) [1] , [2] , [3] ; Sun, J (Sun, Juan) [1] , [2] , [3]

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Abstract

Soil microbiomes are well known to suffer from the effects of rising salinity. There are, however, no current understandings regarding its specific effects on microbial metabolic functions associated with nitrogen (N) and phosphorus (P) cycling, particularly in the Yellow River Delta (YRD), one of the largest estuaries in the world. This research examined soil microbiomes at 50 sites in the YRD region to analyze their co-occurrence networks and their relationship with N (nitrification, denitrification, dissimilatory, assimilatory, fixation, and mineralization) and P (solubilization, mineralization, transportation, and regulation) metabolism processes. Our findings indicate a notable reduction in soil multifunctionality as salinity levels increase, with Halofilum-ochraceum playing a significant role in nitrification, whereas Bacteroidetes-SB0662-bin-6 helps solubilize inorganic P in highly saline areas. High soil salinity negatively affected the amoA gene involved in nitrification and increased the nosZ gene involved in denitrification in extreme salinity soil with 8.2 g/kg salt content. Extreme salinity significantly reduced the expression of genes involved in inorganic P solubilization, such as ppa and ppx. Additionally, the alkaline P gene phoD exhibited significant decreases in extremely saline soils, thereby impeding the mineralization of organic P. The neutral community models indicated that microbial community immigration rate showed a linear negative relationship with soil EC in the six N and four P processes. Salinization, however, displayed a nonlinear pattern with clearly defined thresholds on the community of microbes involved in N and P cycling. Reduced microbial diversity and interactions are causing a decline in soil multifunctionality, and the soil multifunctionality and network edges jointly limited the microbial community immigration rate involved in N and P cycling. It is crucial to preserve soil microbial functions to support nutrient cycling and predict the ecological effects of soil salinization.

Keywords

Author Keywords

Extreme salinityNutrient cyclingN and P-cycling genesNetwork complexityNeutral community modelsYellow River Delta

Keywords Plus

COMPLETE NITRIFICATIONDYNAMICSBIODIVERSITYDIVERSITYBACTERIALECOLOGYGENE

Mineralization

2-Micro-pressure promotes endogenous phosphorus release in a deep reservoir by favouring microbial phosphate mineralisation and solubilisation coupled with sulphate reduction

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By Zhuo, TY (Zhuo, Tianyu) [1] ; He, LX (He, Lixin) [2] , [4] ; Chai, BB (Chai, Beibei) [2] , [4] ; Zhou, SL (Zhou, Shilei) [5] ; Wan, Q (Wan, Qiong) [3] ; Lei, XH (Lei, Xiaohui) [6] ; Zhou, ZM (Zhou, Zhenming) [7] ; Chen, B (Chen, Bin) [8] (provided by Clarivate) Source WATER RESEARCH Volume 245 DOI 10.1016/j.watres.2023.120647 Article Number 120647 Published OCT 15 2023 Early Access SEP 2023 Indexed 2024-02-10 Document Type Article

Abstract

Deep reservoirs vary in their hydrostatic pressure owing to artificial water level control. The potential migration of phosphorus (P) in reservoir sediments raises the risk of harmful algal blooms. To ascertain the mechanisms of endogenous P release in reservoirs, we characterised aquatic microbial communities associated with coupled iron (Fe), P and sulphur (S) cycling at the sediment-water interface. The responses of microbial communities to hydrostatic pressures of 0.2-0.7 mega pascals (MPa; that is, micro-pressures) were investigated through a 30-day simulation experiment. Our findings unravelled a potential mechanism that micro-pressure enhanced the solubilisation of Fe/aluminium (Al)-bound P caused by microbially-driven sulphate reduction, leading to endogenous P release in the deep reservoir. Although the vertical distribution of labile Fe was not affected by pressure changes, we did observe Fe resupply at sediment depths of 2-5 cm. Metagenomic analysis revealed increased abundances of functional genes for P mineralisation (phoD, phoA), P solubilisation (pqqC, ppx-gppA) and sulphate reduction (cysD, cysC) in sediments subjected to micro-pressure, which contrasted with the pattern of S oxidation gene (soxB). There was a tight connection between P and S cycling-related microbial communities, based on significant positive correlations between labile element (P and S) concentrations and functional gene (phoD, cysD) abundances. This provided strong support that Fe-P-S coupling processes were governed by micro-pressure through modulation of P and S cycling-related microbial functions. Key taxa involved in P and S cycling (for example, Bradyrhizobium, Methyloceanibacter) positively responded to micro-pressure and as such, indirectly drove P release from sediments by facilitating P mineralisation and solubilisation coupled with sulphate reduction.

Keywords
Author Keywords
P releaseHydrostatic pressureMicrobial driversDiffusive gradients in thin filmsMetagenome
Keywords Plus
HYDROSTATIC-PRESSUREGENE-EXPRESSIONN2O EMISSIONSSULFIDEINTERFACEVIRULENCEOXIDATIONSEDIMENTSRESPONSESOCEAN

Mineralization

3-Effect of degradable microplastics, biochar and their coexistence on soil organic matter decomposition: A critical review

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By Lin, JJ (Lin, Junjie) [1] ; Cheng, QT (Cheng, Qitai) [1] ; Kumar, A (Kumar, Amit) [2] ; Zhang, WL (Zhang, Wenling) [3] ; Yu, ZG (Yu, Zhiguo) [2] ; Hui, DF (Hui, Dafeng) [4] ; Zhang, CA (Zhang, Changai) [1] ; Shan, SD (Shan, Shengdao) [1] (provided by Clarivate) Source TRAC-TRENDS IN ANALYTICAL CHEMISTRY Volume 183 DOI 10.1016/j.trac.2024.118082 Article Number 118082 Published FEB 2025 Early Access DEC 2024 Indexed 2024-12-18 Document Type Review

Abstract

Biodegradable plastics often degrade into microplastics within the natural environment, where they interact with soil organic matter (SOM). Concurrently, biochar is applied to soil as a photosynthesis-derived negative carbon technology. However, the efficacy of biochar in carbon sequestration may be compromised by the priming effect triggered by the presence of degradable microplastics. This review critically examines the interaction between degradable microplastics and soil organisms and their collective impact on SOM dynamics. It synthesizes current knowledge on the influence of biochar and degradable agricultural films on SOM, the mineralization processes of degradable microplastics, and the resulting stability of SOM. Special attention is given to the priming effect induced by microplastics and the implications of their coexistence with biochar on SOM decomposition. The review underscores the need for further research to elucidate the long-term carbon budget implications of biochar application and the fate of microplastics on carbon pools within biochar-amended soils.

Keywords

Author Keywords

MicroplasticsSoil organic matterBiocharEmerging pollutantsCarbon neutrality

Mineralization

4-Numerical simulation and evaluation of residual oil saturation in waterflooded reservoirs

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By Deng, R (Deng, Rui) [1] , [2] ; Dong, JJ (Dong, Junjie) [1] , [3] ; Dang, LX (Dang, Lixia) [1] (provided by Clarivate) Source FUEL Volume 384 DOI 10.1016/j.fuel.2024.134018 Article Number 134018 Published MAR 15 2025 Early Access DEC 2024 Indexed 2025-03-07 Document Type Article

Abstract

This study focuses on the evaluation of residual oil saturation in waterflooded reservoirs, a critical parameter for optimizing fuel recovery in enhanced oil recovery processes. Neutron lifetime logging technology is widely used to assess residual oil saturation, but variations in water injection methods and production techniques introduce complexities in underground fluid dynamics and reservoir properties, leading to uncertainties in logging interpretations. To address these challenges, we employ numerical simulations to investigate the errors and key factors influencing logging interpretation accuracy across different degrees of waterflooding. A threedimensional geological reservoir model consistent with neutron lifetime logging principles was constructed, and simulated logging processes were integrated with theoretical parameters to calculate residual oil saturation. The results reveal that thermal neutron time spectra are closely related to the capture cross-section and are influenced by various environmental and operational factors. Multiple linear regression analysis of pure water and oil layers within the same reservoir block effectively determines interpretation parameters. Using a standard volumetric model, residual oil saturation interpretation errors were reduced to below 15 % for mineralization levels exceeding 15.5 x 104 ppm, demonstrating high accuracy and practical applicability. This method provides a robust theoretical framework for residual oil saturation evaluation, contributing to more reliable logging interpretations and enhancing the optimization of fuel recovery in waterflooded oil reservoirs.

Keywords

Author Keywords

Volumetric modelMineralizationResidual oil saturationNeutron loggingFuel Recovery Optimization

Keywords Plus

MONTE-CARLO-SIMULATION

Mineralization

5-Technology status to treat PFAS-contaminated water and limiting factors for their effective full-scale application

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By Tshangana, CS (Tshangana, C. S.) [1] ; Nhlengethwa, ST (Nhlengethwa, S. T.) [1] ; Glass, S (Glass, S.) [2] ; Denison, S (Denison, S.) [2] ; Kuvarega, AT (Kuvarega, A. T.) [1] ; Nkambule, TTI (Nkambule, T. T. I.) [1] ; Mamba, BB (Mamba, B. B.) [1] ; Alvarez, PJJ (Alvarez, Pedro J. J.) [2] ; Muleja, AA (Muleja, A. A.) [1] , [2] (provided by Clarivate) Source NPJ CLEAN WATER Volume 8 Issue 1 DOI 10.1038/s41545-025-00457-3 Article Number 41 Published MAY 15 2025 Indexed 2025-05-21 Document Type Review

Abstract

Per- and polyfluoroalkyl substances (PFAS) are a class of synthetic chemicals that are highly resistant to degradation because of the strong C-F bond and their unique physico-chemical properties. Several techniques, both destructive and non-destructive, have been explored for removing PFAS from contaminated water. However, the most desirable techniques, ideally capable of effective separation and complete PFAS destruction and mineralization, have not progressed beyond bench-scale testing. This paper provides an overview of the existing treatment techniques demonstrated at laboratory, pilot, and industrial scales, and their associated treatment mechanisms. Insufficient data on pilot-scale and full-scale applications for PFAS remediation has limited the optimization and advancement of these systems at a large scale. Most research related to PFAS-remediation is based on laboratory-scale studies under ideal conditions that do not represent the complexity of PFAS-contaminated media. Factors such as inhibition by competing background compounds and secondary water or air pollution limit the application of some PFAS removal techniques at full-scale. Additionally, high energy intensity, cost, and inappropriate reactor design restrict the scalability of some proposed innovations. Here, we propose integrated systems and treatment trains as potential approaches to effectively remove and destroy PFAS from contaminated waters. This review also offers and contextualizes implementation barriers and scalable approaches for PFAS treatment.

Keywords

Keywords Plus

GRANULAR ACTIVATED CARBONPOLYFLUOROALKYL SUBSTANCES PFASSPERFLUOROOCTANE SULFONATE PFOSPERFLUOROALKYL SUBSTANCESDRINKING-WATERPHOTOCATALYTIC DECOMPOSITIONELECTROCHEMICAL DEGRADATIONPERFLUOROHEXANOIC ACIDPERFLUORINATED COMPOUNDSINITIAL CONCENTRATION

Mineralization

6-Land conversion to agriculture induces taxonomic homogenization of soil microbial communities globally

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By Peng, ZH (Peng, Ziheng) [1] ; Qian, X (Qian, Xun) [2] ; Liu, Y (Liu, Yu) [1] ; Li, XM (Li, Xiaomeng) [1] ; Gao, H (Gao, Hang) [1] ; An, YN (An, Yining) [1] ; Qi, JJ (Qi, Jiejun) [1] ; Jiang, L (Jiang, Lan) [2] ; Zhang, YR (Zhang, Yiran) [2] ; Chen, S (Chen, Shi) [1] ; (provided by Clarivate) **Source NATURE COMMUNICATIONS Volume 15 Issue 1 DOI 10.1038/s41467-024-47348-8 Article Number 3624 Published APR 29 2024 Indexed 2024-06-22 Document Type Article**

Abstract

Agriculture contributes to a decline in local species diversity and to above- and below-ground biotic homogenization. Here, we conduct a continental survey using 1185 soil samples and compare microbial communities from natural ecosystems (forest, grassland, and wetland) with converted agricultural land. We combine our continental survey results with a global meta-analysis of available sequencing data that cover more than 2400 samples across six continents. Our combined results demonstrate that land conversion to agricultural land results in taxonomic and functional homogenization of soil bacteria, mainly driven by the increase in the geographic ranges of taxa in croplands. We find that 20% of phylotypes are decreased and 23% are increased by land conversion, with croplands enriched in Chloroflexi, Gemmatimonadota, Planctomycetota, Myxcoccota and Latescibacterota. Although there is no significant difference in functional composition between natural ecosystems and agricultural land, functional genes involved in nitrogen fixation, phosphorus mineralization and transportation are depleted in cropland. Our results provide a global insight into the consequences of land-use change on soil microbial taxonomic and functional diversity.

Agricultural land-use change affects belowground biodiversity. Here, the authors compare soil microbial communities from natural ecosystems and agricultural systems, finding that agricultural conversion leads to taxonomic and functional homogenisation.

Keywords

Keywords Plus

BIOTIC HOMOGENIZATIONUSE INTENSIFICATIONBETA-DIVERSITYBIODIVERSITYBACTERIALFORESTCONSEQUENCESCONSERVATIONALIGNMENTPH

Mineralization

7-Efficient photocatalytic degradation of antibiotics using Z-scheme MIL-88 (Fe)/Ti3C2/MoO3: Mechanistic insights and toxicity assessment

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By Li, Q (Li, Qiang) [1] ; Zhou, H (Zhou, Hao) [5] ; Li, ZH (Li, Zhiheng) [1] ; Liu, AX (Liu, Aoxiang) [1] ; Wang, E (Wang, Erpeng) [2] ; Wu, YL (Wu, Yanling) [1] ; Tang, XJ (Tang, Xiujuan) [1] ; Du, H (Du, Hao) [1] ; Jin, LM (Jin, Limin) [1] ; Zhu, HY (Zhu, Huayue) [3] ; (provided by Clarivate) **Source JOURNAL OF HAZARDOUS MATERIALS Volume 486 DOI 10.1016/j.jhazmat.2024.137051 Article Number 137051 Published MAR 15 2025 Early Access JAN 2025 Indexed 2025-01-25 Document Type Article**

Abstract

Antibiotic residues cause water contamination and disrupt aquatic ecosystems. Herein, we reported the fabrication of a novel Z-scheme heterojunction, MIL-88A(Fe)/Ti3C2/MoO3 (MTO), for safe and efficient removal of antibiotics. Ti3C2 was introduced into the MIL-88A(Fe)/MoO3 (MO) heterojunction as an electronic mediator to accelerate charge separation. Consequently, the ternary MTO achieved a tetracycline (TC) degradation rate 2.5 times higher than that of MO. Notably, the MTO heterojunction maintained high TC degradation efficiency over 36 consecutive hours without significant decline. Photogenerated holes, hydroxyl radicals, and superoxide radicals synergistically led to efficient and deep mineralization of TC. Furthermore, toxicity assessments were performed using Toxicity Estimation Software Tool (T.E.S.T.), bacteria (S. aureus and E. coli) cultivation, wheat germination and cultivation. The results all confirmed the safe degradation of TC. Therefore, this study provides a promising strategy for photocatalytic removal of antibiotics and promotes sustainable water purification technologies.

Keywords

Author Keywords

AntibioticsPhotocatalysisZ -schemeEcotoxicity

Keywords Plus

ABSORPTION

Mineralization

8-Stem Cells Recruited from Multifunctional Tetrahedral Framework Nucleic Acids Induce Vascularized Osteogenesis to Repair Bone Defects

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By Shi, SR (Shi, Sirong) [1] , [2] ; Liao, H (Liao, Hang) [4] ; Lu, WT (Lu, Weitong) [1] ; Chen, TY (Chen, Tianyu) [1] ; Sun, Y (Sun, Yue) [1] ; Lin, YF (Lin, Yunfeng) [1] , [2] , [3] (provided by Clarivate)

Source ADVANCED FUNCTIONAL MATERIALS Volume 35 Issue 40 DOI 10.1002/adfm.202421993
Published OCT 1 2025 Early Access MAY 2025 Indexed 2025-05-10 Document Type Article

Abstract

Repairing and reconstructing massive bone defects remains a critical clinical challenge. Recruiting early stem cells, and promoting their angiogenesis and osteogenesis are crucial for the initiation of efficient in situ bone regeneration and repair. This study aims to promote bone regeneration and reconstruct massive bone defects using tetrahedral framework nucleic acids (tFNAs) with Apt19S, microRNA-21 (miR21), and bone morphogenetic protein 2 (BMP2) (Apt19S-tFNAs-miR21/BMP2 [ATMB]). ATMB promotes the proliferation, migration, and recruitment of bone mesenchymal stem cells (BMSCs), alkaline phosphatase activity, and osteogenesis-related mRNAs and proteins in vitro. The angiogenesis-related genes and proteins of HUVECs are effectively enhanced by ATMB. Furthermore, chitosan hydrogel fills bone defects and extends the duration of drug action, combining with ATMB to form ATMCB. ATMCB is highly efficient at recruiting BMSCs, matrix mineralization, and new bone formation in rat calvarial defects of critical size in vivo. This study demonstrates a promising in situ bone regeneration approach for bone defect repair that overcomes the traditional limitations of cell-delivery therapy.

Keywords

Author Keywords
angiogenesisbone regenerationosteogenesisstem cell recruitmenttetrahedral framework nucleic acid
Keywords Plus
SCAFFOLD DESIGNAPTAMERCONTRIBUTESCURCUMINDELIVERY

Mineralization

9-Simplified microbial network reduced microbial structure stability and soil functionality in alpine grassland along a natural aridity gradient

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By Zhang, C (Zhang, Chao) [1] , [2] ; Lei, SL (Lei, Shilong) [1] ; Wu, HY (Wu, Hongyue) [1] ; Liao, LR (Liao, Lirong) [2] ; Wang, XT (Wang, Xiangtao) [3] ; Zhang, L (Zhang, Lu) [1] ; Liu, GB (Liu, Guobin) [1] , [2] ; Wang, GL (Wang, Guoliang) [1] , [2] ; Fang, LC (Fang, Linchuan) [1] ; Song, ZL (Song, Zilin) [4] , [5] (provided by Clarivate) Source SOIL BIOLOGY & BIOCHEMISTRY Volume 191
DOI 10.1016/j.soilbio.2024.109366 Article Number 109366 Published APR 2024 Early Access
FEB 2024 Indexed 2024-03-24 Document Type Article

Abstract

Increasing aridity is known to influence the diversity and function of soil microbiome. However, how it affects the microbial co-occurrence network are poorly understood, particularly in alpine ecosystem, which is one of the most vulnerable ecosystems. Here, we investigated the co-occurrence networks of soil microbiomes based on 60 sites along a natural aridity gradient across the Tibetan Plateau and evaluated their relationship with soil functionality. We hypothesized that increasing aridity could lead to a reduction in the complexity of microbial networks (e.g., the decreased number of nodes and edges, lower connectance, average degree, clustering coefficient and centralization degree), and this changed network complexity is strongly relate to microbial structure stability (network robustness and vulnerability) and soil functionality. Our results supported the hypothesis that the network complexities of bacteria, fungi and protists decreased along the aridity gradient. Microbial network complexity was significantly correlated with network robustness and vulnerability, suggesting that soil network complexity supports structure stability. Bacterial and fungal network complexities were strongly related to community functional traits (e.g., enzymes activities, carbohydrate and amino acid metabolism, C degradation genes), soil processes (e.g., CO2 and CH4 emission, N mineralization) and multifunctionality. This suggests a key relationship of microbial networks to alpine soil functionality, with a more significant impact observed in semiarid and arid habitats than that in humid and semi-humid habitats. Plants played key roles in driving microbial network through altering soil organic C, with plant diversity having a greater impact in humid habitats, while plant biomass was more influential in semi-arid and arid habitats. Our results indicate that aridity-induced simplification of microbial communities can potentially weaken community stability and alpine soil functionality. Therefore, preserving the complexity of belowground communities is critical for ecosystem management and for predicting the ecological consequences of future aridification.

Keywords
Author Keywords
Microbial structureEcosystem functionalityClimatic aridityAlpine ecosystem
Keywords Plus
COMPLEXITYECOLOGY