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Depth heterogeneity of lignin-degrading microbiome alters organic carbon processing in mangrove sediments

Jijuan Ding[a], Cheng Wang[a,*]

[a] Environmental Microbiomics Research Center, School of Environmental Science and Engineering, Sun Yat-sen University, Guangzhou, Guangdong, China

Abstract: Mangrove ecosystems have gained global prominence with their blue carbon (C) sequestration capacity. The C input to mangrove sediments is dominated by lignocellulosic detritus, but how microbes control on the bioconversion of lignocellulosic detritus sequestered in the mangrove sediments remains elusive. Through lignocellulosic analysis and metagenomic sequencing, we found a consistent high proportion of lignin (95.0%–97.7%) in lignocellulosic biomass and a minor fraction (1.24%–1.98%) of lignin-degrading genes in CAZyme genes across five 100-cm mangrove sediment columns. Genes and microbes for depolymerizing lignin and mineralizing lignin monomer derivatives (LMDs) showed a significant depth stratification. Genes for aerobically depolymerizing lignin and mineralizing LMDs were enriched in the surface sediments (0–20 cm). The surface-enriched Pseudolabrys and Burkholderiales showcased proficiency in converting LMDs into intracellular C storage compounds (i.e., polyhydroxyalkanoate) via multiple O_2-adaptive strategies. However, genes for anaerobically mineralizing LMDs were enriched in the subsurface sediments (20–100 cm). The subsurface-enriched microbes tend to employ a “slow processing” strategy to decelerate lignin derived C degradation and biomass production, i.e., Zixibacteria, growing slowly and only relying on anaerobic ATP-dependent LMDs’ mineralization pathway with energy provided by dissimilatory sulfate reduction or tetrathionate respiration. Further microbe-centered analyses of biomass production rates and adaptive metabolism revealed a diminished microbial C use efficiency potential and an augmented “enzyme latch” with increasing sediment depths. Collectively, these findings significantly contribute to our comprehension of the spatial intricacies governing sedimentary organic C sources and storage within coastal blue C ecosystems.

Future climate scenarios aggravate health risks of soil microbiome by reshaping resistome and pathogenome

Zhiguo Zhang[a], Feng Ju[a,*]

[a] Key Laboratory of Coastal Environment and Resources Research of Zhejiang Province, Westlake University, Hangzhou, Zhejiang, China

Abstract: Antibiotic resistance has become a global health challenge owing to its rapid dissemination between microbes in humans, animals, and the environment. This crisis is being aggravated by global climate warming, as indicated by the significant correlation between elevated ambient temperature and increased antibiotic resistance prevalence in clinical pathogenic isolates. However, the impacts of long-term experimental warming on soil resistomes, regarding antibiotic resistance gene (ARG) mobility and host pathogenicity, are poorly understood. By examining the dynamics of cropland and grassland soil resistomes in a six-year (2014–2019) climate warming experiment through metagenomic sequencing, this study revealed that simulated warming (+0.6°C) and extreme summers (+2.2°C during 2018–2019) significantly altered the soil resistomes, leading to a reduction in the diversity of antibiotic resistance genes (ARGs). Extreme summers significantly exacerbate the abundance of ARGs conferring resistance to novobiocin (52.7%–72.8%), tetracycline (32.5%–53.0%) and vancomycin (31.5%–62.9%), thereby amplifying their health risks under future climate scenarios. Importantly, simulated warming significantly increased the proportion of mobilizable ARGs, potentially resulting from the SOS response of soil microbes stimulated by warming-induced drought. However, extreme summers decreased the mobility potential by dramatically filtering the hosts (e.g., γ-Proteobacteria) of mobilizable ARGs. Climate warming and extreme summers also offer a worrisome competitive advantage for specific soil-dwelling antibiotic-resistant phytopathogens (e.g., Clavibacter michiganensis and Rhodococcus fascians) and human pathogens (e.g., Staphylococcus aureus and Mycobacterium tuberculosis), which escalates the risk of outbreaks for specific plant and human infectious disease. Overall, our findings emphasize the urgent need for continuous monitoring of soil ARGs and pathogens under the on-going global change. Such efforts are crucial for safeguarding human health and ensuring the sustainability of modern agriculture within a global One-Health framework.

New insights into the degradation of perfluoroalkyl carboxylic acids by dielectric barrier discharge plasma: Performance, dominant active substance and degradative pathways

Min Song[a,*], **Chengye Song**[a]
[a] School of Energy and Environment, Southeast University, Nanjing, Jiangsu, China

Abstract: Low-temperature plasma technology holds great promise for decomposing perfluoroalkyl substances (PFAS) due to its effectiveness and eco-friendly nature. In this study, we utilized a self-designed disk-type dielectric barrier discharge (DBD) plasma apparatus to degrade five PFAS compounds with varying carbon chain lengths. Our findings revealed the exceptional degradation performance of the DBD device, achieving up to 96% degradation of PFOA within 30 minutes and a defluorination rate of 48%. Notably, the degradation rates of different PFAS compounds showcased an inverse relationship with carbon chain length. Although hydroxyl radicals, superoxide radicals, and reactive nitrogen species could participate in the degradation of PFAS, the primary driving force was free electrons at the gas-liquid interface rather than hydrated electrons. As a result, the primary degradation pathway of PFAS was reductive defluorination via HF elimination. Additionally, owing to PFAS salt-out phenomena, the plasma system demonstrated high efficiency in PFAS removal from complex aqueous environments. This study underscored the crucial role of free electrons, offering valuable insights for the continued development and refinement of plasma-based technologies for PFAS treatment.

Source, transport, and fate of perfluoroalkyl acids (PFAAs) in turbid coastal environments: Significant roles of suspended sediment and water column stratification

Jianwei Dong[a,*]
[a] College of Marine Science and Engineering, Nanjing Normal University, Nanjing, Jiangsu, China

Abstract: The coastal area was the major region receiving pollution from land-based sources into the sea. Perfluoroalkyl acids (PFAAs) in famous estuaries or bays had aroused wide concern, but the importance of underdeveloped or small coastal environments with notable levels of PFAAs were often neglected. Understanding of characteristics and transport of PFAAs in heterogeneous estuarine environments as well as roles of suspended sediment (SPS) and water column stratification on PFAA behaviors were limited. This study explores the multiphase distribution process and mechanism of PFAAs controlled by SPS across surface and bottom layers in five underdeveloped estuaries and four bays with different types. Higher PFAA concentrations in surface water/SPS than bottom layer occur only in strongly stratified estuaries, not in well-mixed estuaries. The urban bays had higher PFAA contamination and posed a greater threat of short-chain PFAAs in water-SPS-sediment system than the island bays. The water-SPS partitioning of some short-chain PFAAs (PFBS, PFHxA, and PFHpA) is influenced by environmental factors (pH, depth, temperature, and salinity) due to electrostatic interactions, while the sorption of some long-chain PFAAs (PFOA, PFOS, and PFNA) is controlled by SPS and dissolved organic carbon, driven by hydrophobic interactions. SPS plays a dominant role in PFAA partitioning in both surface and bottom water-SPS systems ($p<0.05$), and salinity only significantly affects PFBS in bottom layer ($p<0.01$). The major source of PFAAs in water and SPS was domestic sewage in urban bays and was rainfall-runoff in island bays. Water column stratification with higher PFAA partition in water-SPS system in the surface layer than bottom layer was only found in the urban bays due to the higher human activity intensity. These findings are critical for understanding the drivers of PFAA partitioning and the roles of SPS in different layers, underscoring the necessity of considering particle-associated PFAA fractions in future coastal environmental management.

Quorum sensing signal molecule C6-HSL enhanced the cometabolic removal of sulfadiazine by ammonia oxidizing bacteria

Yaqin Wang[a], Bingzheng Wang[a], Ziheng Feng[a], Jiali Fang[a], Haoxing Hu[a], Ji Li[a],*
[a] School of Environment and Ecology, Jiangnan University, Wuxi, Jiangsu, China

Abstract: Ammonia-oxidizing bacteria (AOB) can efficiently remove antibiotics via cometabolic degradation. N-acyl-homoserine lactones (AHLs)-based quorum (QS) sensing has been reported to be capable of enhancing the performance of wastewater treatment functional microorganisms. Yet few reports investigated the effect of exogenous AHLs on cometabolic degradation of antibiotics by AOB. In this study, a typical AHL, C6-HSL, and a typical antibiotic, sulfadiazine (SDZ), were selected, and the long-term experiment were conducted in a sequencing batch reactor to explore the effects of C6-HSL on AOB's cometabolism in removing low-concentration (1 mg/L) and high-concentration (10 mg/L) SDZ. The results showed that C6-HSL enhanced the cometabolic removal of SDZ by AOB. With the addition of exogenous C6-HSL, the removal rates of SDZ with low and high concentrations were 0.11 mg/(L·h) and 0.54 mg/(L·h), respectively, which were significantly higher than those without exogenous C6-HSL (0.08 mg/(L·h) and 0.43 mg/(L·h), respectively). The existence of SDZ resulted in the decrease of ammonia oxidation efficiency, amoA gene abundance, ammonia monooxygenase activity and cellular ATP concentration, while the content of extracellular polymeric substances increased to resist the biotoxicity induced by SDZ. On the other hand, the addition of C6-HSL alleviated the adverse effects caused by SDZ by increasing the activity and abundance of AOB, amoA gene abundance, the activity of ammonia monooxygenase and the concentration of cellualr ATP. Based on metagenomics analysis, it was found that the relative abundance of the functional genes related to nitrogen metabolism significantly decreased under SDZ stress, especially the genes related to ammonia oxidation process, such as hao, amoA, amoB and amoC, while the relative abundance of the functional genes related to QS increased. However, with the addition of exogenous C6-HSL, the functional genes related to nitrogen metabolism was up-regulated, and the functional genes related to QS was down-regulated.

Environmental photochemical behavior of liquid crystal monomers

Chao Li[a,*]
[a] School of Environment, Northeast Normal University, Changchun, Jilin, China

Abstract: Liquid crystal monomers (LCMs), a wide range of synthetic chemicals, are being widely used in liquid crystal displays. LCMs with potential persistence, bioaccumulation, toxicity and ubiquitous occurrence, are considered as a kind of new pollutants. However, their transformation and fates are rarely reported so far. In this study, we reported the transformation behaviors and toxicity evolution of typical LCMs in multiple media by experiment and computational simulation. The results show that the photolytic half-lives of three phenylbenzoate LCMs are in the range of 12.0–29.6 min in water, indicating they can be rapidly eliminated via photolysis in water. Dissolved organic matter can significantly inhibit their photolysis because of the light-shielding effect. Their direct photolysis reactions occur via their excited triplet states, and the dissolved oxygen can promote their degradation due to the generation of ·OH, $^1O_2$ and ·O^{2-}. Their main photolysis pathways are ester bond cleavage. The photolysis solutions of three LCMs exhibit no obvious toxicity on vibrio fischeri, which may be attributed to the low exposure concentrations of LCMs and their photolysis products. We selected the appropriate calculation methods for the gaseous reactions of ·OH with phenylbenzoate LCMs (ωB97/6-311+G(3df, 2p)//M06-2X/6-311+G(d, p)) and with biphenyl ethynylenes LCMs (M06-2X/6-311+G(3df, 2p)//ωB97/6-311+G(d, p)). The calculated ·OH reaction rate constants and half-lives for the three phenylbenzoate LCMs and biphenyl ethynylene LCMs at 298 K were in the range of (0.9~1.4) ´ 10–12, (1.3 ~ 8.0) ´ 10–12 cm^3 molecule^{-1} s^{-1}, and 5.7–8.9, 1.0–6.2 days, respectively. These results indicated that the investigated LCMs (except 1, 2, 3-trifluoro-5-(2-(4-propylphenyl)ethynyl)benzene) have atmospheric persistence and potential for long-distance atmospheric transport. Additionally, some degradation products exhibited enhanced aquatic toxicity compared with the parent LCMs, suggesting that much attention should be also paid to the environmental risk of atmospheric transformation products besides the parent LCMs in the future.

Soil metabolome impacts the formation of the eco-corona and adsorption processes on microplastic surfaces

Yang Song[a,*]

[a] State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, Nanjing, Jiangsu, China

Abstract: The eco-corona on microplastics refers to the initial layer of biomolecular compounds adsorbed to the surface after environmental exposure. The formation and composition of the eco-corona in soils has attracted relatively little attention; however, this has important implications on the fate and impacts of microplastics, and their associated chemical additives, in the terrestrial environment. To this end, black polyethylene film microplastics, white polyethylene film microplastics and pure polyethylene microplastic granules were selected as typical polyethylene (PE) microplastic, which is one of the most abundant microplastics in soil. Three types of soil, including mollisol soil, fluvo-aquic soil, and red soil, were collected to obtain different soil metabolomes. Both the non-targeted and targeted metabolomics, along with several spectroscopic techniques, were used to test the formation of eco-corona on microplastics based on soil metabolites. The sorption of dibutyl phthalate (DBP) as a proxy for a soil contaminant on the microplastics with or without eco-corona was investigated. Here we demonstrate a fast formation of eco-corona on polyethylene microplastics exposed to water-extractable soil metabolites (WESMs) via two pathways: direct adsorption of metabolites on microplastics and bridging interactions mediated by macromolecules. The main eco-corona components were identified as lipids and lipid-like molecules, phenylpropanoids and polyketides, nucleosides, nucleotides and their analogues. The WESMs were found to reduce sorption of organic contaminants on microplastics by two pathways: reduced adsorption to the eco-corona surface and co-solubilization in the surrounding water. The impact of eco-corona formation should be considered an integral part of environmental fate and risk assessments of terrestrial emissions of microplastics and associated contaminants.

Identification and characterization of a biodegradable plastic mulch film degrading bacteria strain PBAT-1 in the soil

Chen Tu[a], **Yongming Luo**[a,*]

[a] State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, Nanjing, Jiangsu, China

Abstract: Plastic mulch film can increase temperature, keep soil moisture and increase crop yield, widely used in agricultural production. However, due to the low recovery rate of mulch film recycling, the residual mulch film in the soil is easily fragmented or degraded into microplastics under light exposure, mechanical shear force and biological actions. Thus, plastic mulch film has become one of the essential sources of microplastics in soil. Polyadipate/butylene terephthalate (PBAT) is a biodegradable plastic polymer with ideal ductility, heat resistance, tear resistance and biodegradability. PBAT is one of the most active and best biodegradable materials in the research of biodegradable plastics, which has been widely applied to make biodegradable mulch films in recent years. However, studies have shown that PBAT only exhibits a good degradation effect under specific conditions, and the limited existing PBAT degrading strains are difficult to degrade PBAT mulching film effectively under mild environmental conditions. In this study, a few PBAT degrading bacterial strains were screened and isolated from the agricultural soil in Shandong province, which has a long history of plastic mulching film utilization. With a comprehensive analysis of the indicators, such as OD value of the bacterial cultures, the morphologic changes and weight loss rate of PBAT films, an efficient PBAT degrading bacterial strain was successfully isolated. The morphological, physiological and molecular identification of the strain were also carried out. Finally, the dynamic degradation of PBAT by the isolated strain was characterized, including the changes of molecular weight, roughness, chemical functional groups, hydrophobicity, surface morphology and biofilm composition characteristics of PBAT microplastics. The results of this study will provide a new bioresource for the biodegradation of PBAT plastics, and will provide a scientific basis for revealing the degradation mechanism of biodegradable plastic mulching films.

Distribution characteristics and ecological risk of microplastics in Karst ecological fragile area, southwest China

Fudong Zhang[a], **Zhenming Zhang**[a,*]
[a] College of Resources and Environmental Engineering, Guizhou University, Guiyang, Guizhou, China

Abstract: The occurrence, sources, effects, and risks of microplastics (MPs) in farmland soils have attracted considerable attention. However, the pollution and ecological characteristics of MPs in farmland soils at different levels of rocky desertification remain unclear. We collected and analyzed farmland soil samples from rocky desertification areas in Guizhou, China, ranging from no to heavy risks. We explored differences and migration of MPs across these areas, unveiled the relationship between diversity, niche, and risks of MPs, and determined influencing factors. The average abundance of soil MPs was 8721 ± 3938 item/kg, and the abundance and contamination factor (CF) of MPs escalated with the increase in rocky desertification level. Diversity, niche, and risk of soil MPs in different rocky desertification areas were significantly different. Rocky desertification caused both MP community differences and linked MP communities at different sites. Diversity and niche significantly affected MP risk ($p < 0.05$). Environmental factors with significant correlations ($p < 0.05$) with the abundance and ecological characteristics of MPs varied significantly in soils of different rocky desertification areas. This study advances our comprehension of MP pollution in farmland soils within rocky desertification areas, offering essential data and theoretical insights for the development of control strategies.

Uptake and translocation of perfluorooctanoic acid and perfluorooctane sulfonate in crops

Lei Xiang[a], Peng-Fei Yu[a], Hai-Ming Zhao[a], Yan-Wen Li[a], Quan-Ying Cai[a], Ce-Hui Mo[a,*]
[a] Guangdong Provincial Research Center for Environment Pollution Control and Remediation Materials, Department of Ecology, Jinan University, Guangzhou, Guangdong, China

Abstract: Perfluorooctanoic acid (PFOA) and perfluorooctane sulfonate (PFOS) are perfluorinated alkyl substances (PFASs) widely used in industrial and domestic products. They are highly bioaccumulative in crops, posing risk to human health. Cultivation of low-accumulating crop varieties has been considered as a practical solution to ensure the food safety via reducing pollutant accumulation in edible parts of crops. We identified the PFAS low-accumulating lettuce varieties that are loose-leaf lettuces. PFOA/PFOS concentrations of the low-accumulating lettuce were 3.7–5.5-fold lower than those of high-accumulating lettuce. Rhizospheric activation, uptake, translocation, and compartmentalization of PFOA/PFOS are the key factors governing low accumulation. Root exudates, especially oxalate can effectively reduce PFOA/PFOS sorption to soils by decreasing hydrophobic force, electrostatic attraction, ligand exchange, and cation-bridge effect, because oxalate enhances dissolution of metallic ions, iron/aluminum oxides, and organic matters from soils and forms oxalate−metal complexes. PFOA/PFOS root uptake is governed by the transporter-mediated processes that are related to aquaporin and rapid-type anion channel genes. Concentrations of oxalate in root exudates and expression of these genes are directly related to root uptake of PFOA/PFOS into lettuce. Furthermore, low-accumulating lettuce varieties showed the characteristics of high deposition of PFOA/PFOS in the root cell walls and low root-to-shoot translocation of PFOA/PFOS in comparison with the high-accumulating ones. These findings provide new insights into the uptake and accumulation of PFASs, and reveal the multi-process mechanisms underlying absorption and translocation of PFASs in vegetables, which is of significance in ensuring food safety and protecting human health.

Distribution and transport mechanisms of microplastics in the Caohai Basin, Guizhou, China

Yongcheng Jiang[a], Zhenming Zhang[a,*]

[a] College of Resources and Environmental Engineering, Guizhou University, Guiyang, Guizhou, China

Abstract: The use and disposal of plastic products in manufacturing and living practices exacerbate the risk of microplastic accumulation in the environment. Microplastics are transported in different environments under external conditions such as runoff, wind and agricultural and biological activities. Taking the Caohai lakes in Caohai Guizhou as the study object, the results showed that MPs contamination existed in the lakes, sediments and surrounding farmland soils of Caohai. The relative abundance of MPs in the order of largest to smallest was farmland soils, inlet sediments, lake sediments, and the inlet water body was larger than the lake water body. Local residential areas have a greater influence on the abundance of MPs in the Caohai watershed. Sewage irrigation and plastic film are the two main sources of local farmland soils. The correlation between MPs and physicochemical indicators in farmland, lake inlets and water bodies was weak, and land use practices had a greater influence on the distribution of microplastics in the Caohai Basin. In soil, water and air, microplastic aging cannot be simply considered as a result of weathering or sunlight exposure, and the role of microbial-driven microplastic aging should not be ignored. As time passes, the aging degree of microplastics gradually deepens, and microstructural changes are mainly reflected in the generation of depressions, cracks and voids in the fibres, which increase the specific surface area of microplastics, thus increasing the number of attachment sites for microbial communities, and the abundance of microbial communities increases dramatically; microbial reproduction also promotes the aging of microplastics.

Extracellular antibiotic resistance genes in the environment: Identification, fate and risk mitigation

Qingbin Yuan[a,*]

[a] Environmental Science, Nanjing University, Nanjing, Jiangsu, China

Abstract: Antibiotic resistance genes (ARGs) have been widely detected in various environmental media, becoming a highly concerning new pollutant. Compared to intracellular ARGs, research on other forms, particularly extracellular ARGs, has been relatively lacking due to the limitations of detection methods. We have developed an efficient and selective extraction method for extracellular resistance genes in complex environments, investigated their environmental behavior in environmental and water treatment processes, and established a molecular imprinting-based selective degradation strategy.

Legacy and emerging poly- and perfluoroalkyl substances in typical marine mammals from east China sea: Temporal trends and tissue-specific accumulation

Bo Zhang[a], Tao Zhang[a,*]
[a] School of Environmental Science and Engineering, Sun-Yat Sen University, Guangzhou, Guangdong, China

Abstract: Poly- and perfluoroalkyl substances (PFASs) are diverse and their contamination characteristics are unclear. Perfluoroalkyl sulfonates (PFSAs), perfluoroalkyl carboxylates (PFCAs), and emerging alternatives and precursors of these compounds were determined in tissues of stranded finless porpoise and whales collected from East China Sea. The results showed that hepatic concentrations of emerging PFASs and some precursors, including chlorinated polyfluorinated ether sulfonates (Cl-PFESAs) as well as fluorotelomer carboxylates (FTCAs) and fluorotelomer sulfonates (FTSAs) were frequently detected in marine mammals. Study on temporal trend indicate The concentrations of 6:2 Cl-PFESA and some short-chain PFASs increased with time between 2009−2010 and 2018−2019. Further, concentrations of legacy PFAS perfluorooctanoate (PFOA) showed a declining trend in finless porpoise, whereas perfluorooctanesulfonate (PFOS) and its precursor (i.e., perfluorooctane sulfonamide [FOSA]) showed an increasing trend with time between 2009−2010 and 2018−2019. Analysis of PFASs in nine different tissues/organs of marine mammal revealed a similar distribution pattern between 6:2 Cl-PFESA and PFOS; however, the tissue distribution patterns differed between PFOA and their alternatives. The estimates of body burdens of PFASs in marine mammals suggested comparable accumulation of PFAS alternatives and legacy PFSAs and PFCAs. This study provides novel information on temporal trends and tissue distribution of emerging PFASs in marine mammals in China.

Selective succession of biofilms on microplastic particles: Implications for persistent pollutant enrichment and pathogen risks

Jinping Cheng[a,*]
[a] Department of Science and Environmental Studies, The Education University of Hong Kong, Hong Kong, China

Abstract: Plastic debris in the aquatic environment has become a significant concern due to its role as a habitat and hotspot for persistent pollutants. Understanding the dynamics between plastic surfaces, microbial biofilms, and the emergence of persistent pollutants is crucial for comprehending the ecological effects of plastic pollutants in the coastal waters. This study focuses on the selective succession of biofilms on environmentally deployed microplastic particles and its implications for the enrichment of persistent pollutants and pathogen risks. Field experiments and microcosm incubations were conducted to compare the community composition of biofilms on microplastic particles with the bacteria in the surrounding seawater. Scanning electron microscopy was used to observe the temporal succession of these biofilms. Screening potential pathogens using an aquaculture pathogen database demonstrated a correlation between pathogen abundance and the production of extracellular polymeric substances within the biofilms. Pseudomonas and Pseudoaltermonas were identified as dominant contributors to the abundance of potential pathogens. Additionally, chemical treatment influenced the formation of potential pathogens during biofilm development. Preliminary data revealed that the diversity of biofilm communities is influenced by spatial variation, and bacterial colonizers may influence subsequent eukaryotic components during biofilm succession. The findings highlight that biofilms on plastic surfaces play a crucial role in the recruitment, enrichment, and dissemination of pollutants in aquatic environments. This study contributes to our knowledge of the ecological effects and risks of plastic pollution in coastal waters. Understanding the selective biofilm succession on microplastic particles enhances our understanding of the fate and impact of persistent pollutants, ultimately aiding in the development of effective mitigation strategies to address plastic pollution.

Accumulation and growth toxicity mechanisms of fluxapyroxad revealed by physiological, hepatopancreas transcriptome and gut microbiome analysis in Pacific white shrimp (Litopenaeus vannamei)

Xizhi Shi[a], Ningbo Wang[a,b], Zeming Zhang[a,b,*]

[a] State Key Laboratory for Managing Biotic and Chemical Threats to the Quality and Safety of Agro-products, School of Marine Sciences, Ningbo University, Ningbo, Zhejiang, China

[b] Laboratory of Marine Biotechnology of Zhejiang Province, School of Marine Sciences, Ningbo University, Ningbo, Zhejiang, China

Abstract: Fluxapyroxad (FX), a typical succinate dehydrogenase inhibitor fungicide, is causing increased global concerns due to its fungicide effects. However, the accumulation and grow toxicity of FX to *Litopenaeus vannamei* (*L. vannamei*) is poorly understand. Therefore， the accumulation pattern of FX in *L. vannamei* was investigated for the first time in environmental concentrations. FX accumulated rapidly in shrimp muscle. Meanwhile, growth inhibition was observed and the mechanism derived by primarily accelerated glycolipid metabolism and reduced glycolipid content. Moreover, exposure to environmental concentrations of FX induced significant growth inhibition and oxidative stress and inhibited oxidative phosphorylation and TCA cycle in *L. vannamei*. The endocytosis signaling pathway genes were activated, thereby driving growth toxicity. Oxidative phosphorylation and cytosolic gene expression were further rescued in elimination experiments, demonstrating the mechanism of growth toxicity by FX exposure. The results revealed that FX persistently altered the gut microbiome of *L. vannamei* using gut microbiome sequencing, particularly with increased Garcinia Purple *Pseudoalteromonas luteoviolacea* for organic pollutant degradation. This study provided new insights into the potential toxicity of FX to marine organisms, emphasizing the need for further investigation and potential regulatory considerations.

Assessing in-silico tools for precise physicochemical property prediction of novel organophosphate esters

Changyue Xing[a], Ying Zhu[a,*]
[a] School of environmental science and engineering, Shanghai JiaoTong University, Shanghai, China

Abstract: Organophosphate esters (OPEs) are widely used in various industries, but some well-studied OPEs have been linked to environmental and health issues, leading to restrictions in some regions. Therefore, novel OPE substitutes have been adopted prevalently, but relevant research on their environmental behavior and human exposure is limited. Precise physicochemical property data are essential for thorough assessments of environmental behavior, exposure and risks of these substances, leading to the deployment of in-silico tools to bridge information gaps. Our study evaluates how effectively four in-silico tools can predict the properties of OPEs, with the purpose of identifying the most accurate techniques to deepen the understanding of OPEs properties. In this study, we have screened out the in-silico tools with excellent predictive performance for OPEs with different chemical substituent groups, and the predicted physicochemical properties by these tools can be used as a reference for novel OPEs for which experimental data are lacking. Based on the screening results, we provide appropriate physicochemical property predictions for novel OPEs, which improve the accuracy of prediction of the physicochemical properties of novel OPEs, thus reducing the uncertainty in environmental risk assessment.

Plasticizers in the mariculture ecosystem: Environmental occurrence, bioaccumulation and risk assessments

Zeming Zhang[a,b], Xizhi Shi[a,b,*]

[a] State Key Laboratory for Managing Biotic and Chemical Threats to the Quality and Safety of Agro-products, Ningbo University, Ningbo, Zhejiang, China

[b] Laboratory of Marine Biotechnology of Zhejiang Province, School of Marine Sciences, Ningbo University, Ningbo, Zhejiang, China

Abstract: As emerging pollutants, microplastics (MPs) have attracted worldwide attention and recently become a research focus in aquatic environmental science. Plasticizers, a common endocrine disruptor and key plastic additive, worsens the environmental and organismal harm of MPs through its exposure and release from them. Phthalate esters (PAEs) and organophosphate esters (OPEs) are recognized as significant constituents of plasticizers, and have emerged as pervasive pollutants in the mariculture environment, posing threats to both biosecurity and human health via the food chain. Herein, we investigated the environmental occurrence, bioaccumulation, and risks of PAEs and OPEs in seawater, sediment, and aquaculture organisms from a typical mariculture area in China. Di-nbutylphthalate (DnBP), diisobutyl phthalate (DiBP), and di(2-ethylhexyl) phthalate (DEHP) were the dominant PAE congeners in all media. For OPEs, chlorinated OPEs were the predominant congeners detected in seawater, whereas alkyl-OPEs were the leading contributors in sediment and biological samples. Both PAEs and OPEs occurrence were heavily influenced by the mariculture activities, e. g., the input of nutrients, the leakage from aquaculture facilities and the influence on hydrodynamic conditions. The bioaccumulation of PAEs demonstrated benthic feeding fishes with relatively high trophic levels concentrated high levels of phthalates, while OPEs' lgKOW is a crucial physicochemical characteristic in determining OPE bioaccumulation in aquatic organisms. DEHP, DiBP and DnBP had various degrees of ecological risks in the aquatic environment, whereas only the DiBP posed potential risks in sediments. The current assessment of PAEs carcinogenic and noncarcinogenic risks posed by fish consumption were within acceptable limits for humans. Meanwhile, indices of ecological and health risks of OPEs were lower than their risk threshold, indicating that the OPEs detected in this study posed a low risk to the aquatic environment and human health. Ultimately, this study aimed to provide new insights into the plasticizers fate and risks in a specific eco-environment.

Catalytic hydrolysis of contaminants by minerals under water-unsaturated conditions

Cheng Gu[a,*]
[a] School of Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Surface properties of minerals play important roles on mediating the migration and transformation of contaminants in the environment. However, the prior studies relating to the mineral-water interfacial processes were mostly investigated in aqueous conditions, without considering the water unsaturated surface moisture conditions. The transformation behaviors of contaminants on the mineral surface under the water unsaturated conditions are of great concern. In the previous studies, we have found that various minerals, such as kaolinite, montmorillonite, iron minerals, aluminum oxides, exhibited exceptional catalytic hydrolysis activities when exposed to moderate atmospheric humidity levels (i. e., 33%-76%), resulted in degradation of antibiotics (i. e., chloramphenicol, CAP) and phthalate esters with orders of magnitude faster rates than those observed in aqueous phase. It is also worth noting that the catalytic mechanism is specific for each mineral and contaminant. For instance, the hydrolysis of CAP on kaolinite surface relayed on the strength of hydrogen-bonding interaction with the alumina octahedral sheet of kaolinite. The hydrolysis of CAP on montmorillonite surface correlated to the interlayer exchange cations, whose polarization capability determines the surface Brönsted acidity of montmorillonite. While the surface Lewis acid catalytic mechanism was mainly responsible for the hydrolysis of CAP on iron minerals. Further investigation showed that the catalytic performance of hematite is also facet-dependent, related to the atomic array of surface undercoordinated Fe on each facet. Taking dimethyl phthalate (DMP) as an example, the {012} and {104} facets of hematite with the proper neighboring Fe-Fe distance of 0.34-0.39 nm could bidentate coordinate with DMP, thus induce much stronger Lewis-acid catalysis. All these phenomena strongly supported the specific catalytic activities of minerals under the water-unsaturated conditions. Except the hydrolysis processes, the catalytic redox reactions on mineral surface might be also of great interest, while still far from clear regarding to the influence of surface moisture.

Exposure to 6 ppd quinone at environmentally relevant concentrations inhibits both lifespan and healthspan in C. elegans

Hua Xin[a], **Dayong Wang**[b,*]

[a] School of Public Health, Southeast University, Nanjing, Jiangsu, China

[b] Medical School, Southeast University, Nanjing, Jiangsu, China

Abstract: N-(1,3-Dimethylbutyl)-N′-phenyl-p-phenylenediamine (6-PPD), one of the most common additives used in rubber industries. 6-PPD quinone (6-PPDQ) is an important derivative of 6-PPD after ozonization with wide distribution in the environment, such as runoff water and soil. We here used Caenorhabditis elegans as animal model to examine the effect of 6-PPDQ exposure on lifespan and healthspan and underling mechanism. Firstly, the accumulation of 6-PPDQ was observed in the body of nematodes. In addition, exposure to 6-PPDQ (1 and 10 μg/L) significantly shorted the lifespan of nematodes. Meanwhile, during aging process, 6-PPDQ (0.1-10 μg/L) could decrease both pumping rate and locomotion behavior reflected by head thrash and body bend, suggesting the adverse effect of 6-PPDQ exposure on healthspan. Accompanied with the observed 6-PPDQ toxicity, exposure to 1-10 μg/L 6-PPDQ increased expressions of daf-2 encoding insulin receptor, age-1, akt-1, and akt-2 and decreased expression of daf-16 encoding FOXO transcriptional factor in insulin signaling pathway. The toxicity of 6-PPDQ on lifespan, pumping rate, and locomotion behavior could be suppressed by RNAi of daf-2, age-1, akt-1, and akt-2, and enhanced by RNAi of daf-16. Genetic interaction analysis indicated that DAF-2 inhibited function of downstream DAF-16, and DAF-16 further activated downstream targets of SOD-3 and HSP-6 to control 6-PPDQ toxicity on lifespan and healthspan. Moreover, exposure to 6-PPDQ could increase expressions of genes encoding insulin peptides (INS-1, INS-6, INS-7, and DAF-28), which further activated corresponding receptor DAF-2. Molecular docking analysis suggested the binding potential of 6-PPDQ with both insulin peptides (INS-1, INS-6, INS-7, and DAF-28) and DAF-2. Therefore, our findings suggested that chronic exposure to 6-PPDQ at surrounding concentrations that are ecologically relevant causes damage on lifespan and healthspan by activating insulin signaling in organisms.

Evaluation of potential ecological risk of soil microplastics and its modelling under high geological background values

Fupeng Li[a], Zhenming Zhang[a,*]

[a] College of Resources and Environmental Engineering, Guizhou University, Guiyang, Guizhou, China

Abstract: Soils with high geological backgrounds are usually more ecologically vulnerable and thus have higher ecological risks. The study investigated microplastic abundance as well as microplastic properties in different prefecture-level cities and ecologically vulnerable areas in Guizhou. The results showed that the characteristic shapes of microplastics in the study area were fibers and particles, black in color, with particle sizes of 0-0.5 mm, and the polymer type of PP. The environmental risks were evaluated by modelling, and the stability of the model, R^2, was greater than 0.97. The microplastics in each area showed higher risks, and the higher the ecological fragility, the higher the risk. The results of structural equation modelling showed that TP and AK were highly significantly correlated with microplastic abundance ($p<0.01$), and Pb (5.53%) had the highest contribution to microplastic abundance. The use of agricultural energy and materials such as mulch, fertilizers and pesticides also increased the abundance of microplastics, which in turn increased the environmental risk.

From rubber antioxidants to toxins: Elucidating the acute toxicity and mechanisms of emerging PPD-Qs on aquatic bacterium

Wei Wang[a,*], **Zongwei Cai**[a]
[a] State Key Laboratory of Environmental and Biological Analysis, Hong Kong Baptist University, Hong Kong, China

Abstract: Substituted para-phenylenediamines (PPDs) are synthetic chemicals used globally for rubber antioxidation, with their quinone derivatives (PPD-Qs) raising particular environmental concerns due to their severe toxicity to aquatic organisms reported by Science. Emerging research has identified a variety of novel PPD-Qs ubiquitously detected in the environment, yet experimental proof for the toxicity of PPD-Qs has not been forthcoming due to the unavailability of bulk standards, leaving substantial gaps in the prioritization and mechanistic investigation of such novel pollutants. Here, we first studied the acute toxicity of 18 PPD-Qs and PPDs to the aquatic bacterium V. fischeri using synthesized chemical standards and investigated the underlying mechanisms through in vitro biological response assays and in silico simulations. Bioluminescence inhibition EC50 of PPD-Qs ranged from 1.76 to 15.6 mg/L, with several emerging PPD-Qs demonstrating significantly higher toxicity than the well-studied 6PPD-Q. Comparatively, PPDs exhibited pronounced hazards with the EC50 ranging from 0.02 to 7.07 mg/L, assigning these emerging contaminants as harmful to very toxic pollutants in the aquatic environment. Such observations suggest a broad toxicological threat that PPDs and PPD-Qs pose to the aquatic bacterium, other than 6PPD-Q. Biological response assays revealed that PPDs and PPD-Qs can reduce the esterase activity, cause cell membrane damage, and induce intracellular oxidative stress. These effects collectively contributed to the acute toxicity of such emerging contaminants. Molecular docking unveiled multiple interactions of PPD-Qs with the luciferase in V. fischeri, suggesting their potential functional impacts on proteins through competitive binding. It is worth noting that the emerging ecotoxicity of PPD-Qs to aquatic bacteria was identified for the first time. Our results provided crucial toxicity benchmarks for PPD-Qs, prioritized these novel pollutants, and shed light on the potential toxicological mechanisms. The broad toxicity of novel PPD-Qs is unveiled, and the toxicological mechanisms can help comprehend their toxicities to other species.

Environmental fate and biofouling impacts of reticulated microplastics: A comparative study with disposable masks

Lujian Lin[a], Bo Yuan[a], Hualong Hong[a], Chongling Yan[a,]*

[a] College of Environment and Ecology, Xiamen University, Xiamen, Fujian, China

Abstract: The post-treatment phase is a critical component in the transformation of plastic raw materials into everyday products. Among these, reticulated plastic products are a significant category that has not received adequate focus regarding their environmental interactions. The study utilizes disposable masks as a case study to investigate the characteristics and environmental implications of reticulated microplastics. These microplastics exhibit a substantial surface area due to their porous nature and roughness, which is distinct from that of conventional plastic films or powders. Our research indicates that the aging process enhances the adsorption capacity of these microplastics for various pollutants, primarily due to the increased presence of oxygen-containing functional groups on their surfaces. Intriguingly, even without fragmentation, reticulated microplastics demonstrate a comparable or superior adsorption affinity for metallic pollutants compared to other forms of microplastics. The biofouling of reticulated microplastics results in augmented surface roughness, adhesion properties, moisture retention, and composite density. Notably, biofouled reticulated microplastics exhibit a more rapid sinking rate compared to biofouled films, highlighting that the three-dimensional structure of the microplastics, beyond size and shape, significantly influences their sinking dynamics in aquatic environments. Furthermore, biofouling-impacted reticulated microplastics display a markedly higher desorption potential for toxic metals. These findings underscore the significance of the reticulated structure in microplastics and its implications for environmental studies. The insights gained from this research contribute to the foundation for developing comprehensive environmental inventories and strategies for effective plastic pollution control in the future.

Exposure to 6:2 chlorinated polyfluorinated ether sulfonate (6:2 Cl-PFESA) during lactation induces neurobehavioral impairments in weaned offspring mice by affecting amino acid transport

Ruiyuan Zhang[a,b], **Yongjie Liu**[b], **Jun Zhang**[a,b,*]

[a] School of Public Health, Shanghai Jiao Tong University School of Medicine, Shanghai, China

[b] Ministry of Education-Shanghai Key Laboratory of Children's Environmental Health, Xinhua Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai, China

Abstract: To investigate whether exposure to 6:2 Cl-PFESA via maternal milk during lactation induces neurobehavioral impairments in weaned mice. Dam C57BL/6J mice were treated with distilled water containing 5‰Tween20 or 6:2 Cl-PFESA at doses of 0.3 mg/kg/day or 3 mg/kg/day through daily oral gavage during lactation from postnatal day 1(PND1) to PND21. The weaned mice were evaluated for changes in neurobehavioral battery. Hematoxylin and eosin staining and transmission electron microscope were used to observe the pathological and ultrastructure changes of cortex and hippocampus. Concentrations of 22 amino acids in the brain were determined using targeted gas chromatography-mass spectrometry(GC/MS) analysis. The expression levels of genes and proteins related to tryptophan and glutamate transporters and tight junctions were measured in the cortex and hippocampus. Our findings showed that exposure to 6:2 Cl-PFESA via maternal milk during lactation significantly affected depression- and anxiety-like behavior, short-term working memory, and locomotor balance in weaned offspring. 6:2 Cl-PFESA exposure also caused pathological and ultrastructure damage in the cortex and hippocampus and significantly decreased body weight at PND21($P<0.05$). The concentrations of neurotransmitter-related amino acids, such as tryptophan, glutamine, glycine, and proline, were significantly decreased in the brains of 6:2 Cl-PFESA exposed weaned mice($P<0.05$). The mRNA expression of glutamine transporters Slc6a19 in the cortex and Slc7a8 and Slc6a14 in the hippocampus was significantly upregulated($P<0.05$). Additionally, the mRNA expression of tight junction Claudin12 in the cortex was significantly downregulated, while Zo2 and Occludin in the hippocampus were significantly upregulated in 6:2 Cl-PFESA exposed weaned mice. Our study sheds light on neurodevelopmental impairments induced by exposure to 6:2 Cl-PFESA through maternal milk, characterized by significant alterations in brain tight junction, neurotransmitter-related amino acid concentrations, and the expression of tryptophan and glutamine transporters. These findings provide animal experimental evidence for health risk assessments related to 6:2 Cl-PFESA exposure via maternal milk.

Soil microbial response to multi-pollutants exposure in megacity parks: A real-world study in Beijing

Yajing Qu[a,*]

[a] State Key Laboratory of Environmental Criteria and Risk Assessment, Chinese Research Academy of Environmental Sciences, Beijing, China

Abstract: In megacities, the combined exposure of multiple pollutants will have an important impact on the structure and function of soil microorganisms, but there is still a lack of empirical studies. Hence, we conducted a real-world study in Beijing urban parks. The results showed bacteria were abundant in the soil of Beijing parks, showing the same dominant groups and different rare groups, the dominant groups were Actinobacteria and Proteobacteria, the same as in other studies, and candidate phyla radiation (CPR) was the main specialists. Under the combined exposure of multiple pollutants, the structure of soil microbial community in different parks tended to be similar. The explanation of community change by pollutants (31%) was much higher than that by natural factors (2.4%). It was interesting to find that, among multi-pollutants, the organophosphate esters (OPEs) led by DBP had the greatest influence on microbial abundance distribution, and the increase of DBP decreased the abundance of Firmicutes, while the abundance of Synergistota may increase. The interaction between different pollutants was different, BEHP and Nap were synergistic, BEHP and Yb were antagonistic. In addition, BCEP, Ni, and BghiP can also influence microorganisms by working with OPEs. High-molecular-weight PAHs (BaP and BghiP) mainly act on functional genes and thus affect multiple biogeochemical cycles. And BaA, BCEP and As were the main pollutants affecting metabolic pathways. Our research will help to further deepen the understanding of the impact of urban environmental pollution on soil microorganisms.

DNA damage, neurotoxicity, oxidative stress, hematological response, gut microbiota dysbiosis, and behavioral alteration in zebrafish (Danio rerio) exposed to Polyvinylchloride (PVC) microplastics: An analysis of microplastics toxicity in model organism

Muhammed Sinan Malik P. C[a,*]
[a] Zoology, Periyar University, Salem, Tamilnadu, India

Abstract: The aquatic environment is alarmingly polluted with resin pellets and plastic particles that can endanger the health of aquatic species. The current study looked at the effects of polyvinyl chloride (PVC) microplastics on acetylcholinesterase, DNA fragmentation, blood parameters, behavior, gut microbiota, and the antioxidant system (brain, liver, and gill) in zebrafish (*D. rerio*). The zebrafish is a freshwater indicator animal that is frequently used as a model for ecotoxicological tests. Fish were subjected to PVC microplastics (145.6 4.23 nm) for 20 days with a control diet; blood and tissues were taken every 10 days for haematology and antioxidant enzymes assays. The findings demonstrated that PVC was responsible for the significant changes in haematological indices. In groups exposed to MPs, the activities of superoxide dismutase, glutathione-S-transferase, lipid peroxidation, and DNA fragmentation increased in a dose-dependent manner compared to the control group. The gut microbiota isolates demonstrated microbial deterioration using a culture-dependent approach. Acetylcholinesterase activity in the brain was suppressed, while glutathione peroxidase activity was significantly changed as exposure duration increased. Neurotoxicity and behavioral perturbation were shown to have significant and positive correlation, suggesting that disruption of cholinergic function, impaired detoxification, locomotory and swimming performance using Toxtrac software. The present study fosters multi level toxicological data toward elucidating and quantifying the impacts of PVC microplastics on freshwater organisms.

Naproxen chiral enantiomers promote horizontal transfer of antibiotic resistance genes and its health risk assessment

Yingying Wang[a,*]

[a] College of Environmental Science and Engineering, Nankai University, Tianjin, China

Abstract: Antibiotic resistance is a global threat to public health. Recent studies have showed the contribution of non-antibiotic pharmaceuticals to the transmission of ARGs. This study revealed the comprehensive profile, horizontal gene transfer potential, hosts and public health risks of antibiotic resistomes in the chiral NAP-exposed river ecosystems. The results showed that stress of NAP led to the selective enrichment of ARGs and MGEs, thereby increasing the resistance of bacterial communities to specific antibiotics. The spatial difference of NAP chiral enantiomers led to the enantioselectivity of bacterial resistance to antibiotics. (S)-NAP and (R)-NAP promoted the horizontal transfer potential in different degree. (S/R)-NAP facilitated the aggregation and DNA transport between microorganisms through T4SS-related functional genes, and promoted the conjugation of sul1. Chiral NAP induced pathogens to obtain ARGs and accelerated the enrichment of Burkholder. ARG-Rank results showed that the risk of (R)-NAP exposure was higher than that of (S)-NAP, and the risk of mixed presence was the highest. This study revealed the horizontal transfer and transmission mechanism of ARGs under the stress of NAP chiral enantiomers, highlighting the potential health risks of NAP chiral enantiomers.

Foliar uptake of nanoplastics and related mechanisms

Chunguang Liu[a,*], Yuting Li[a], Rui Zhang[a], Lei Wang[a], Lei Sun[a]
[a] College of Environmental Science and Engineering, Nankai University, Tianjin, China

Abstract: In order to investigate the mechanism of nanoplastic uptake by plant leaves, three plants with different properties of leaves were selected for foliar exposure using amino-modified, carboxyl-modified and unmodified polystyrene nanoplastics to analyze the pathways of nanoplastic uptake in the foliage of different plants as well as the distribution of nanoplastics in the leaves. It was found that all three plant leaves were able to absorb through the cuticle and transport nanoplastics through the plasmodesmata. Corn leaves could absorb nanoplastics through stomata, and cucumber leaves could absorb nanoplastics through trichomes. The absorbed nanoplastics were mainly distributed in the cuticle, cell interstitial space and vascular tissues, and a small amount of nanoplastics were internalized into the chloroplasts or transported to the phloem.

6PPD-quinone affects the photosynthetic carbon fixation in cyanobacteria by extracting photosynthetic electrons

xiuqi You[a], weiling Sun[a,*]

[a] Environmental Science and Engineering, Peking university, Peking, China

Abstract: Photosynthetic carbon fixation by cyanobacteria plays a pivotal role in the global carbon cycle but is threatened by environmental pollutants. Quinones with the electron shuttling property exert as-yet unknown impacts on cyanobacterial photosynthesis. Here, we presented the first study investigating the effects of an emerging quinone pollutant, i. e., 6PPD-Q, on the cyanobacterium Synechocystis sp. over a 400-generation exposure period. Synechocystis sp. exhibited distinct sequential phases, including hormesis, toxicity, and eventual recovery, throughout this exposure. Extensive evidence, including thylakoid membrane morphology, photosynthetic responses, carbon fixation rates, and key genes/proteins, strongly indicates 6PPD-Q as a potent disruptor of photosynthesis. It accepts photosynthetic electrons at QB site in PSII and A1 site in PSI, leading to a sustained decrease in the carbon fixation of cyanobacteria after an ephemeral increase. This work uncovers the specific mechanism through which 6PPD-Q interfered with photosynthetic carbon fixation in cyanobacteria, which is of great importance to global carbon cycle.

Antibiotic-like activity of antibiotic intermediates for the induction of multiple antibiotic resistance

Sun Miao[a], Jiane Zuo[a,*]

[a] College of the Environment, Tsinghua University, Beijing, China

Abstract: Antibiotic resistance (AR) is one of the most challenging public health issues. Antibiotic intermediates (AIs) in the production of antibiotics have similar bioactive structures as antibiotics while the effects of AIs and their interactive effects with antibiotics on the emergence of AR are unknown. In this study, antibiotic-sensitive E. coli K12 was exposed to 5 β-lactam AIs and their parent antibiotic ampicillin (AMP). The results indicated that β-lactam AIs can inhibit bacterial growth, stimulate the production of reactive oxygen species (ROS), as well as induce AR like the parent β-lactam antibiotic AMP. Among the 5 β-lactam AIs tested, 6-APA exhibited higher resistance and persistence induction potential than the other four AIs tested, which was consistent with its oxidative stress and inhibition effect on bacteria growth. Moreover, combined exposure of 6-APA and AMP synergistically stimulated the induction of multiple AR and the combination index reached up to 1326.5, which might be attributed to their combined effect on promoting ROS generation and inhibiting bacterial growth. Phenotypic and genotypic analyses revealed that overproduction of ROS, enhanced stress response signature, stimulation of efflux pump expression, and increased persistence were associated with increased AR induced by AIs and AMP. Together, the findings provide evidence and mechanic insight into the induction of AR by AIs.

Discovering novel organophosphorus compounds in wastewater treatment plant effluents through suspect screening and nontarget analysis

Jingrun Hu[a], Yitao Lyu[a], Mingzhen Li[b], Lei Wang[c], Yi Jiang[d], Weiling Sun[a,*]

[a] College of Environmental Science and Engineering, Peking University, Beijing, China

[b] College of Safety and Environmental Engineering, Shandong University of Science and Technology, Qingdao, Shandong, China

[c] School of Agriculture, Shenzhen Campus of Sun Yat-sen University, Shenzhen, Guangdong, China

[d] Department of Civil and Environmental Engineering, The Hong Kong Polytechnic University, Kowloon, Hong Kong, China

Abstract: Limited knowledge on the structure of emerging organophosphorus compounds (OPCs) hampers our comprehensive understanding of their environmental occurrence and potential risks. Through suspect and nontarget screening, combining data-dependent acquisition, data-independent acquisition, and parallel reaction monitoring modes, we identified 60 OPCs (17 traditional and 43 emerging compounds) in effluents of 14 wastewater treatment plants (WWTPs) in Beijing and Qinghai, China. These OPCs comprise 26 organophosphate triesters, 17 organophosphate diesters, 6 organophosphonates, 7 organothiophosphate esters, and 4 other OPCs. Notably, 14 suspect OPCs were newly identified in WWTP effluents, and 16 nontarget OPCs were newly discovered in environmental matrices. Specifically, the cyclic phosphonate, (5-ethyl-2-methyl-1,3,2-dioxaphosphorinan-5-yl)methyl dimethyl phosphonate P-oxide (PMMMPn), consistently appeared in all WWTP effluents, with semi-quantitative concentrations ranging from 44.4 to 282 ng/L. Its analogue, di-PMMMPn, presented in 93% of wastewater samples. Compositional differences between the WWTP effluents of two cities were mainly attributed to emerging OPCs. Hazard and ecological risk assessment underscored the substantial contribution of chlorinated organophosphate esters and organothiophosphate esters to overall risks of OPCs in WWTP effluents. This study provides the most comprehensive OPC profiles in WWTP effluents to date, highlighting the need for further research on the occurrence, fate, and risks, particularly for chlorinated OPCs.

Phytoeffects and phytoremediation of aquatic micro/nanoplastics

Wenke Yuan[a], Yuyi Yang[a,*]
[a] Aquatic Plant Research Center, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan, Hubei, China

Abstract: Plastic pollution and its potential risks have been arousing public concern as a global environmental issue. Our study indicates that micro/nanoplastics can enter the roots and leaves of various aquatic plants, but the toxic effects they cause can be ignored. Floating plants have a much higher bioaccumulation of nanoplastics than other types of plants. An interesting discovery is that duckweed, which has absorbed microplastics, can release nanoparticles after returning to a clean environment. Single-cell transcriptome sequencing was conducted to explore the molecular responses of duckweed to micro/nanoplastics and found that vascular cells play a crucial role in responding to and adapting to micro/nanoplastic exposures. Global plastic waste may double by 2030, posing a significant challenge to the remediation of environmental plastics. In addition to finding alternative products and managing plastic emission sources, effective removal technologies are crucial to mitigate the negative impact of plastic pollution. However, current remediation strategies, including physical, chemical, and biological measures, are unable to compete with booming amounts of plastics entering the environment. Here we propose that phytoaccumulation, phytostabilization, and phytofiltration can be applied to reduce the concentration of micro/naoplastics in terrestrial, aquatic, and atmospheric environments, as well as to prevent the transport of microplastics from sources to sinks. Phytoremediation can be an excellent strategy to alleviate global micro/nanoplastic pollution because of the cost-effectiveness and environmental sustainability of green technologies.

Chronic exposure to environmental concentrations of HFPO-TA causes intergenerational toxicity in zebrafish offspring

Shao Ying[a,*], Yulin Zhang[a], Yanghao Zhou[a]

[a] College of Environment and Ecology, Chongqing University, Chongqing, China

Abstract: Hexafluoropropylene oxide trimer acid (HFPO-TA, $C_7HF_{13}O_4$) which is reported to have high capability of bioaccumulation, widespread environmental distribution, and multiple toxicities, has been used as an alternative of perfluorooctanoic acid (PFOA) in the fluoropolymer industry for several years . Their negative effects on parental fish are investigated while intergenerational effects at environmentally relevant concentrations remain unclear. In this study, F0 zebrafish was exposed to HFPO-TA (0, 500, and 5000 μg/L) for 90 days to investigate the intergenerational effects. HFPO-TA affected F0 zebrafish fecundity and gonadal development, with accumulations found in F0 Liver, muscles and ovaries and F1. In F1 generation, maternal exposure to HFPO-TA also significantly reduced survival rate, hatching rate, malformation rate, and especially lead to bone curvature. Metabolomics analysis revealed that arachidonic acid metabolism, steroid hormone biosynthesis, pantothenate and coa biosynthesis, purine metabolism and folate biosynthesis related pathways in HFPO-TA groups were significantly enriched in F1 offspring. Among them, arachidonic acid is an important nutrient for young fish to maintain optimal growth, reproduction, overall health and bone development. The findings indicated that prolonged maternal exposure to HFPO-TA could severely cause intergenerational toxicity, resulting in developmental toxicity effects in zebrafish offspring.

High level of selenium exposure in the strong heart study: A cause for incident cardiovascular disease?

Di Zhao[a,*]

[a] College of Resources and Environmental Sciences, Nanjing Agricultural University, Nanjing, Jiangsu, China

Abstract: Increasing evidence suggests that high selenium (Se) exposure is associated with adverse health effects. However, limited evidence exists on the association of Se exposure with cardiovascular disease (CVD), especially in communities affected by high naturally occurring Se in environmental media. We evaluated the prospective association between urinary Se levels and CVD incidence and mortality for 2727 American Indian adults who participated in the Strong Heart Study, with urinary Se levels measured at baseline (1989–1991) and CVD outcomes ascertained through 2017. The median (interquartile range) of urinary Se was 49. 0 (36.7–67.4) μg/g creatinine. The multivariable adjusted hazard ratios (95% confidence interval) of incident CVD, coronary heart disease, and stroke comparing the 75th versus 25th percentile of urinary Se distributions were 1.11 (1.01–1.22), 1.05 (0.94–1.17), and 1.08 (0.88–1.33), respectively. In flexible dose–response models, increased risk for CVD incidence was only observed when the urinary Se level exceeded 60 μg/g creatinine. For CVD mortality, a nonstatistically significant U-shaped relationship was found across urinary Se levels. There was no evidence of effect modification by other urinary metal/metalloid levels. Our observation leads to the hypothesis that elevated Se exposure is a risk factor for CVD, especially in Se-replete populations.

New insights into Hg-Se antagonism: Minor impact on inorganic Hg mobility while potential impacts on microorganisms

Yang Zhou[a], Huan Zhong[a,*], Wenli Tang[a]

[a] School of Environment, Nanjing University, Nanjing, Jiangsu Sheng, China

Abstract: Selenium (Se) is a crucial antagonistic factor of mercury (Hg) methylation in soil, with the transformation of inorganic Hg (IHg) to inert mercury selenide (HgSe) being the key mechanism. However, little evidence has been provided of the reduced Hg mobility at environmentally relevant doses of Hg and Se, and the potential impacts of Se on the activities of microbial methylators have been largely ignored. This knowledge gap hinders effective mitigation for methylmercury (MeHg) risks, considering that Hg supply and microbial methylators serve as materials and workers for MeHg production in soils. By monitoring the mobility of IHg and microbial activities after Se spike, we reported that 1) active methylation might be the premise of Hg [single bond] Se antagonism, as higher decreases in MeHg net production were found in soils with higher constants of Hg methylation rate; 2) IHg mobility did not significantly change upon Se addition in soils with high DOC concentrations, challenging the long-held view of Hg immobilization by Se; and 3) the activities of iron-reducing bacteria (FeRB), an important group of microbial methylators, might be potentially regulated by Se addition at a dose of 4 mg/kg. These findings provide empirical evidence that IHg mobility may not be the limiting factor under Se amendment and suggest the potential impacts of Se on microbial activities.

Ambient levels, sources, and source-specific health risks of $PM_{2.5}$-bound organophosphate flame retardants in Hong Kong atmosphere

Xuemei Wang[a], **Di Hu**[a,b,c,*]
[a] Chemistry, Hong Kong Baptist University, Hong Kong, China
[b] HKBU Institute of Research and Continuing Education, Shenzhen Virtual University Park, Shenzhen, Guangdong, China
[c] State Key Laboratory of Environmental and Biological Analysis, Hong Kong Baptist University, Hong Kong, China

Abstract: Organophosphate flame retardants (OPFRs) are emerging organic pollutants in $PM_{2.5}$, which have caused significant public health concerns in recent years, given their potential carcinogenic and neurotoxic effects. However, studies on the sources, occurrence, and health risk assessment of $PM_{2.5}$-bound OPFRs in Hong Kong are lacking. To address this knowledge gap, we characterized thirteen OPFRs in one-year $PM_{2.5}$ samples using gas chromatography-atmospheric pressure chemical ionization tandem mass spectrometry. Our findings showed that OPFRs were present at a median concentration of 4978 pg m^{-3} (range from 1924 pg m^{-3} to 8481 pg m^{-3}), with chlorinated-OPFRs dominating and accounting for 82.7% of the total OPFRs. Using characteristic source markers and positive matrix factorization, we identified one secondary formation and five primary sources of OPFRs. Over 94.0% of $PM_{2.5}$-bound OPFRs in Hong Kong were primarily emitted, with plastic processing and waste disposal being the leading source (61.0%), followed by marine vessels (14.1%). The contributions of these two sources to OPFRs were more pronounced on days influenced by local pollution emissions (91.9%) than on days affected by regional pollution (44.2%). Our assessment of health risks associated with human exposure to $PM_{2.5}$-bound OPFRs indicated a low-risk level. However, further source-specific health risk assessment revealed relatively high noncarcinogenic and carcinogenic risks from chlorinated-OPFRs emitted from plastic processing and waste disposal, suggesting a need for more stringent emission control of OPFRs from these sources in Hong Kong.

Nanobody-functionalized two-dimensional material sandwich-based immunosensor for field detection of virus transmission chain

Wenjin Hu[a], Yi Luo[a,*]
[a] School of Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: The pathogen virus spreads through the fecal-oral route, infecting individuals via contaminated food and water sources, as well as through the transmission of viral particles in the feces of infected patients. This mode of transmission is observed in various viruses, such as SARS-CoV-2, norovirus, adenovirus, and hepatitis B virus, among others. Early detection of pathogens enables prompt intervention and effective management before large-scale community transmission occurs, particularly in the context of the ongoing pandemic. However, current detection tools suffer from labor-intensive procedures, high costs, and error-prone. Although immunosensors provide cost-effective and portable detection modules, many rely on susceptible antibodies and exhibit limited tolerance. In this study, we employed multivalent nanobodies as stable substitutes for the traditional antibodies that require cumbersome preparation and are labile. By employing a sandwich strategy, we synthesized an enhanced two-dimensional material composed of MXenes@CNTs@AuNPs with a large specific surface area to facilitate the enrichment and immobilization of nanobodies. This material was coupled with catalase-modified dual-functional magnetic probes to amplify signals. We constructed a novel immunosensor by utilizing a nanobody-functionalized nanomaterials sandwich for accurate and sensitive detection of rotavirus in rectal swabs and wastewater samples. Notably, our proposed novel sensor achieved a remarkable detection limit of 0.0207 pg/mL for VP6 antigen, which was 2.6538×10^5 fold more sensitive than commercially available antigen kits (with a detection limit of 78 ng/mL). The outstanding performances of this novel sensor also included specificity, repeatability, stability, and accuracy for detecting various samples, underscoring it is a promising tool for on-site detection of rotavirus. Collectively, our work provides a practical strategy for developing an ultrasensitive analytical platform that addresses the urgent need for efficient and reliable virus detection methods across various settings.

Organosulfur compounds in ambient fine particulate matter in an urban region: Findings of a nontargeted approach

Ailin Li[a], Xinghua Qiu[a,*]

[a] College of Environmental Sciences and Engineering, Peking University, Beijing, China

Abstract: Organosulfur compounds (OSCs) are important components of fine particulate matter ($PM_{2.5}$); however, little information is available on OSCs in urban regions due to their chemical complexity, especially for novel species such as aromatic sulfonates. To supplement the detection technique and systematically identify OSCs, in this study we developed a nontargeted approach based on gas chromatography and high-resolution mass spectrometry (GC-HRMS) to screen OSCs in $PM_{2.5}$ of urban Beijing and provide field evidence for their source and formation mechanism. 76 OSCs were found through mass difference of sulfur isotopes and characteristic sulfur-containing fragments. 6 species were confirmed as aromatic sulfonates by authentic standards. 32 OSCs showed higher levels in the heating season, presumably because of the intensive emission, especially from coal combustion. While certain species, with 2-sulfobenzoic acid as the representative, were 2.6-times higher in the non-heating season than in the heating season. Such species were significantly correlated with ozone and aerosol liquid water content ($r = 0.2–0.8$, $p < 0.05$), implying an oxidation-involved aqueous-phase formation in the atmosphere. In addition, with an average proportion of ~95% of the total sulfobenzoic acids, the predominance of the 2-substitution product over its isomers of 3- or 4-sulfobenzoic acid suggests a more plausible mechanism of radical-initiated reaction of phthalic acid followed by sulfonation, with atmospheric reactivity indicated by ozone and temperature as the determining factor. This study provided not only a nontargeted approach for OSCs in ambient $PM_{2.5}$, but also field evidence on their secondary formation proposed in previous simulation studies, which could help further research on their health effects.

Impact of mercury exposure on reproductive health and early childhood development

Mengwei Yuan[a], Tsz Ki Tsui[a,*]
[a] School of Life Sciences, The Chinese University of Hong Kong, Hong Kong, China

Abstract: Mercury (Hg), a heavy metal with widespread distribution, has been implicated in a host of adverse health outcomes affecting individuals across different life stages. Animal studies indicated that exposure to Hg could induce DNA rupture in sperm and lead to a decrement in sperm motility and dysfunction, although the exact mechanisms by which various forms of Hg influence sperm morphology and fertilizing capacity remain uncertain. Methylmercury (MeHg), an organic form of Hg, can readily cross placenta and blood-brain barrier, potentially harming the fetal brain during pregnancy, while the selective transport mechanisms at the placental barrier are still unidentified. Examining the impact of Hg on human reproductive health could offer valuable insights for medical interventions. Moreover, the daily interactions with household items that contain Hg and the inadvertent ingestion of MeHg contaminated food sources insidiously contribute to the body's cumulative exposure. The developing brains and bodies of children are disproportionately affected by the neurotoxic effects of MeHg, which may manifest in developmental delays and a range of cognitive and behavioral challenges. Therefore, a comprehensive understanding of environmental and dietary exposures to Hg is essential for protecting children's health. Address on these knowledge gaps, we collaborated with hospitals to collect different human samples. Advanced techniques like cold vapor atomic fluorescence spectroscopy (CVAFS), Inductively coupled plasma mass spectrometry (ICP-MS), stable mercury isotope analysis will be used to illustrate the Hg toxicity and Hg transition in human body.

Pollution characteristics and potential health effects of airborne microplastics and culturable microorganisms during urban haze in China

Jiahui Jiang[a],*, Bingfeng Liu[a]
[a] Environment School, Harbin Institute of Technology, Harbin, Heilongjiang, China

Abstract: Airborne microplastics (MPs) and bioaerosols have been reported in many typical coastal and inland cities and pose a potential threat to public health, however, there is limited information on their pollution characteristics during haze days in cold cities. In this study, active sampling technology was used to collect MPs and microorganisms simultaneously on haze days in Harbin, China. Airborne MPs concentrations in Junior high school (162.4 ± 44.6 particles/m^3) with high vehicular and pedestrian traffic was higher than those in University (63.2 ± 21.8 particles/m^3) and Park (12.8 ± 5.5 particles/m^3). More airborne MPs were detected in the night samples than in the morning and noon samples. The majority (69.06%) of airborne MPs measured less than 100 μm, with fibers (69.4%) being the predominant form. Polyesters, polyethylene and polyamide were the dominant polymers. In addition, the average concentration of bacteria was higher than that of fungi, and the bacteria and fungi concentration at night was higher than that in the morning. Five opportunistic bacteria genus and four opportunistic fungi genus were detected on hazy days. The airborne MPs concentrations were positively correlated with microorganisms and PM_{10} concentrations, and the health hazards associated with microorganisms and MPs exposure via inhalation far exceeded those associated with skin contact, which can serve as a theoretical foundation for considering MPs as indicators of air quality in the future.

Prenatal exposure to metal mixtures, body mass index trajectories in early life and effect modifiers: Insights from a prospective birth cohort study

Chenhui Yang[a], Yuanyuan Li[a,*]

[a] Wuhan Children's Hospital, Huazhong University of Science and Technology, Wuhan, Hubei, China

Abstract: Background: Prenatal metal exposures are ubiquitous and may affect infant growth, but the effects of metal mixtures on early life growth trajectories were not well understood. Objectives: We aimed to evaluate specific relationships between prenatal exposure to metal mixtures and infant growth trajectories, and explore the potential modifiers. Methods: This study included 7, 118 mother-infant pairs from a Chinese birth cohort. Concentrations of 18 metals in third-trimester urine samples were quantified, and standardized body mass index (BMI) trajectories from birth to 24 months were identified using Latent class growth models. A three-phase analytical framework was applied to calculate the risk ratio (RR) and 95% confidence interval (95% CI) of single and co-exposure to metal mixtures on growth trajectories, along with potential effects modification by pre-pregnancy BMI and infant sex. Results: Five growth trajectory groups were identified. Exposure to metal mixtures driven by thallium (Tl, 34.8%) and aluminum (Al, 16.2%) was positively associated with the risk of low-rising trajectory (RR = 1.58, 95% CI: 1.25, 2.00); mixtures driven by strontium (Sr, 49.5%) and cobalt (Co, 41.8%) exhibited an inverse correlation (RR = 0.81, 95% CI: 0.67, 0.97). Additionally, infants with higher Tl or Al levels and lower maternal pre-pregnancy BMI had a significantly higher risk of low-rising trajectory than others, whereas infants with higher Sr or Co levels and normal pre-pregnancy BMI demonstrated a lower risk. In addition, infant girls with higher Tl levels also had a higher risk of low-rising trajectory than others. Our findings provided insight into the complex effects of metal mixtures with the risk of low-rising trajectory characterized as catch-up growth in early life and identified the metals needing more attention. Pre-pregnancy BMI and infant sex may exert modifying effects on metal-trajectory associations.

Stable isotope-assisted mass spectrometry reveals in vivo distribution, metabolism, and excretion of tire rubber-derived 6PPD-quinone in mice

Jing Zhang[a], **Zongwei Cai**[b,*]

[a] Chemistry, Hong Kong Baptist University, Hong Kong, China

[b] Chemistry, Hong Kong Baptist University, Hong Kong, China

Abstract: N-1,3-dimethylbutyl-N'-phenyl-p-phenylenediamine quinone (6PPD-Q), has been identified as a ubiquitous environmental contaminant in our surrounding locality including air particles, roadside soils, dust, and water, which may enter the human body via various exposure routes. Recently, the prevalence of 6PPD-Q in human urine has accentuated the urgency for investigating its biological fate and health implications. To address this, we conduct a comprehensive investigation using stable isotope-assisted high-resolution mass spectrometry (HRMS) to uncover the distribution, metabolism, excretion, and toxicokinetic properties of this contaminant in a mouse model. In this study, we first detected the levels of 6PPD-Q in human serum samples with concentrations ranging from 0.11 to 0.43 ng/mL, and mice were fed with deuterated 6PPD-Q-d5 at human-relevant exposure levels. Our findings revealed rapid assimilation and distribution of 6PPD-Q into the bloodstream and major organs of mice, with concentrations peaking under 1 h following administration. In addition, 6PPD-Q was determined to be more likely to accumulate in adipose, lung, kidney, testis, and spleen. Moreover, our measurement demonstrated that 6PPD-Q can penetrate the blood-brain barrier of mice within 30 minutes. The half-lives ($t_{1/2}$) of 6PPD-Q in serum, lung, kidney, and spleen were measured at 12.7 ± 0.3, 20.7 ± 1.4, 21.6 ± 5.3 and 20.6 ± 2.8 h, respectively, while a relatively shorter $t_{1/2}$ of 6.7 ± 0.6 h was observed in the liver. Using HRMS combined with isotope tracing techniques, two novel hydroxy-metabolites of 6PPD-Q in mice liver were identified for the first time, which provides new insights into its rapid elimination in vivo. Furthermore, we determined fecal excretion to be the primary pathway for eliminating 6PPD-Q and its hydroxylated metabolites. Collectively, our findings extend the current knowledge on the biological fate and exposure status of 6PPD-Q in a mouse model, which has the potential to be extrapolated to humans.

Exposure risks of volatile organic compounds from personal care products

Nan Lin[a,*]
[a] Department of Environmental Health, Shanghai Jiao Tong University, Shanghai, China

Abstract: Volatile organic compounds (VOCs), including both traditional priority pollutants such as benzene and emerging contaminants such as 1, 4-dioxane can induce irritation, adverse effects on the liver and kidney and cancer. Exposure to VOCs from personal care products (PCPs) is noteworthy but sorely understudied. Via developing sensitive detection methods, we identified toxic VOCs in 110 PCPs of 9 categories. VOC composition depended on the product type, manufacturer and brand. Products labels such as "organic" did not necessarily indicate lower concentrations. Inhalation exposure to VOCs emitted from PCPs could cumulate 80% in 8-10 hours. Reasonable upper bound exposure scenario estimations suggested a large non-cancer risk due to n-heptane and a notable cancer risk due to benzene and 1,4-dioxane. The emission of 1,4-dioxane from PCPs may be larger than its industrial emission. Via measuring urinary VOC concentrations of reproductive-aged women, we found that higher n-nonane, benzene, and toluene in products were associated with higher urinary concentrations in women. A physiologically based toxicokinetic (PBTK) model finally unveiled the toxicokinetic of VOCs in human body and stated that using urinary concentration as an exposure biomarker may lead to bias because of accumulation difference in various tissues. Our results show that both health risks and environmental burden of toxic VOCs in PCPs are high enough to warrant additional attention and possibly corrective measures. More follow-up studies, particularly addressing the kinetics of exposure process via skin and secondary pollutants, are warranted. The release process and multi-media distribution of emerging chemicals from PCPs, e.g., 1,4-dioxane also need disclosure.

Prenatal organophosphate esters exposure and neurodevelopment trajectory in infancy: Evidence from the Shanghai Maternal-Child Pairs Cohort

Yuhan Zhou[a], **Yunhui Zhang**[b,*]
[a] Exercise and Health, Shanghai University of Sport, Shanghai, China
[b] Environmental Epidemiology, Fudan University, Shanghai, China

Abstract: Concerns remain about neurotoxic properties of the ubiquitous organophosphate esters (OPEs), the replacement of the toxicant polybrominated diphenyl ethers. We examined the associations of prenatal exposure to OPEs and their mixtures with early-life neurodevelopment trajectories. Totally 1276 mother-child pairs were recruited from the Shanghai Maternal-Child Pairs Cohort. A high-performance liquid chromatography-triple quadrupole mass spectrometer was used to measure the levels of 7 OPEs in cord serum. Ages and Stages Questionnaires was used to examine children's neuropsychological development at 2, 6, 12, and 24 months of age. Group-based trajectory models were applied to derive the neurodevelopmental trajectories. Multiple linear regression and logistic regression models were performed to assess the relationships between OPEs exposure and neurodevelopment and trajectories. Mixtures for widely detected OPEs (n=4) were investigated using quantile-based g-computation. Tributyl phosphate (TBP), tris (2-butoxy ethyl) phosphate (TBEP), tris(1,3-dichloro-2-propyl) phosphate (TDCPP), and 2-ethylhexyl diphenyl phosphate (EHDPP), had detection rates greater than 50%. TDCPP had the highest median concentration (1.02 μg/L) in cord serum. EHDPP concentrations were negatively associated with scores in most domains at 12 months of age, with effect values (β) ranging from -1.89 to -0.57. EHDPP could negatively affect the total ASQ (OR=1. 07, 95% CI: 1, 1.15) and gross-motor (OR=1.09, 95% CI: 1.02, 1.17) trajectory in infancy. Joint exposure to OPEs was associated with decreased scores in the total ASQ, gross-motor, fine-motor and problem-solving domain of 12-month-old infants, with β ranging from -5.93 to -1.25. In addition, the qgcomp models indicated significant positive association between the concentrations of OPEs mixtures and risks of the persistently low group of the total ASQ, gross-motor and fine-motor development in early childhood. The impact of OPEs was more pronounced in boys. Our findings suggested OPEs, especially EHDPP, had a persistently negative effect on neurodevelopment during the first 2 years.

Specific soil microbes drive methylmercury formation and health risks

Xiao Zhang[a], **Huan Zhong**[a,*], **Wenli Tang**[a]

[a] School of the Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Emerging global concerns about the accumulation of neurotoxic methylmercury (MeHg) in rice is due to the importance of rice in food security being a staple food for more than half of the world's population. MeHg in rice derives from conversion of inorganic mercury (Hg) by diverse microorganisms in soil; however, the key microbial taxa driving MeHg formation remain unclear, causing high uncertainty in predicting MeHg concentrations in rice and thus human exposure. Here, we identify the diversity and relative importance of Hg methylating communities in the soil from 67 cropland ecosystems, stretching across 3600 km from north to south in China. Our continental-scale assessment reveals that Geobacteraceae is the most abundant methylating assembly, and its relative abundance strongly and positively correlates to soil MeHg content. Inhibiting the activity of Geobacteraceae significantly reduces soil MeHg formation. Furthermore, our biogeochemical model shows that rice MeHg concentration is 1.3-1.7 times more sensitive to changes in the relative abundance of Geobacteraceae compared with variations in Hg input, being recognized as the primary parameter in controlling MeHg exposure. These findings demonstrate that Geobacteraceae drives MeHg formation in rice paddy soil and predicts the subsequent bioaccumulation, which opens a window to mitigate negative human health effects through regulating soil microbiome.

Neonicotinoids and elevated cardiometabolic risk in rural Chinese: A prospective cohort study combing mendelian randomization study

Xueyan Wu[a], Dandan Wei[a], Zhiwei Chen[a], Wenqian Huo[a], Chongjian Wang[a], Zhenxing Mao[a,*]
[a] College of Public Health, Zhengzhou University, Zhengzhou, Henan, China

Abstract: Neonicotinoid insecticides are extensively dispersed across the environment and commonly occur in people due to their widespread usage worldwide. However, there is a scarcity of epidemiological research on the impact of neonicotinoid insecticides on cardiometabolic risk. In this prospective cohort study from the Henan Rural Cohort Study, 2315 participants were involved at baseline, and 1841 participants completed cardiometabolic risk predictors determinations during the 3-year follow-up. Each neonicotinoid pesticide was normalized to imidacloprid (IMIeq) using the relative potency factor approach. Quantile-based g-computation (Qgcomp) regression was used to evaluate the effect of the mixtures of neonicotinoids Mediation analysis was employed to explore whether inflammatory markers levels and platelet traits mediated these relationships. Mediation analysis was employed to explore whether inflammatory markers levels and platelet traits mediated these relationships. Finally, a two-sample MR study was further used to causal association. Qgcomp regression found statistically positive relationships between neonicotinoids mixture exposure and cardiometabolic risk score at baseline and follow-up over 3 years. Notably, linear relationships of IMIeq with cardiometabolic risk at baseline (p_overall < 0.001; p_nonlinearity = 0.628) and follow-up over 3 years (p_overall < 0.001; p_nonlinearity = 0.335) were observed. Both NEUT/MONO and PLT were mediators in the relationship between IMIeq and cardiometabolic risk score at baseline and follow-up over 3 years. The causal risk effect of pesticide exposure were (2.5 (0.05, 4.95)) and (5.24 (1.28, 9.19)) for cardiometabolic risk indicators including insulin resistance and TG, respectively. Nevertheless, there was no correlation discovered between pesticide exposure and other markers of cardiometabolic risk. Neonicotinoid insecticides exposure was connected to an increased cardiometabolic risk, especially for individuals with T2DM. Furthermore, inflammatory markers and PLT seemed to be two vital mediators of the associations. Additionally, genetic evidence on pesticide exposure and cardiometabolic risk still needs to be validated by multiregional and multiethnic GWAS studies.

Decoding chemical exposome of a typical regionally prevalent disease: esophageal squamous cell carcinoma in China

Shenxi Deng[a,b], Linwei Tian[b], Qian Liu[a,*], Guibin Jiang[a]

[a] State Key Laboratory of Environmental Chemistry and Ecotoxicology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, China

[b] Faculty of Medicine, The University of Hong Kong, Hong Kong, China

Abstract: Esophageal squamous cell carcinoma (ESCC), marked by stratified geographical disparities in incidence, presents a long-standing unresolved challenge in etiological exploration. Efforts have been made to investigate genomic mutations and external environmental risks, yet a comprehensive analysis of both synthetic and natural chemicals as potential hazards in ESCC's internal environment remains scant. We address this plight here by profiling inorganic elements, endogenous and exogenous compounds to outline ESCC patients' chemical exposome. The components of the chemical exposome could act as mediators in the relationship between factors related to ESCC specific diet/lifestyle habits and health status. The evolution trajectory of ESCC chemical exposome, as delineated by the disease progression, indicates that the most drastic alterations in the internal environment occur at the disease's initiation phase. Concurrently, two panels of chemical components in plasma are discovered as non-invasive predictive biomarkers to discriminate esophageal premalignant lesions (EPL) versus ESCC and health control (HC). Among them, the emerging typical environment pollutant, perfluorooctanesulfonic acid (PFOS) endows attention on the qualification of per- and polyfluoroalkyl substances (PFASs). In addition, ESCC chemical exposome is deciphered with a clear geographical pattern with more evident variations in high-incidence, geographically narrow areas than in broader, low-incidence regions. Fashioning machine learning algorithms to ESCC chemical exposome further reveals its significant predictive power for regional disease risk. Taken together, our work provides technical feasibility and knowledge expansion on exposome paradigm, suggests the chemical exposome could inform large-scale retrospective cohort studies on chemical and disease causality, lay a foundation of early ESCC detection therapeutic strategies, and aid public health decisions through disease risk stratification based on geographical patterns.

Examining the effects of prolonged phthalate exposure on gender-related traits and identity in Chinese children: Insights from a 3.5-year longitudinal study

Jieyu Liu[a,*], Yanhui Dong[a], Zhiyong Zou[a], Jun Ma[a]
[a] School of Public Health, Peking University, Beijing, China

Abstract: Phthalate esters (PAEs) are a group of chemicals that are ubiquitous in the environment. Gender identity refers to the sense of self as male or female, or neither, which is a central construct of mental health. We aimed to investigate the associations between prolonged PAEs exposure, gender traits and identity in children. A total of 571 children (278 boys) aged 8.33 ± 0.93 years completed the follow-up from Oct 2017 to 2020 in a cohort in Xiamen, China. PAEs metabolites were classified into two groups according to their sex-specific 50th percentiles. The Children's Sex Role Inventory scale was used to assess gender traits and identity (masculinity, femininity, androgyny, undifferentiated). Generalized linear models were applied to estimate long-term PAEs exposure, and gender trait scores, and the log-binomial regressions were used to assess the relationships between persistent PAEs exposure and gender identity. Sensitivity analyses were conducted when we only restricted to children with early pubertal onset during the follow-up. Overall, the concentration of most PAEs in more than 90% of participants was above the limit of detection values. Long-term exposure to MEHP was significantly related with increased femininity trait ($\beta = 1.32$, 95%CI = 0.31, 2.32) and masculinity trait ($\beta = 1.17$, 95%CI = 0.24, 2.09) in boys with earlier puberty onset, and exposure to MEHHP ($\beta = 1.02$, 95%CI = 0.01, 2.04) and MEOHP ($\beta = 1.34$, 95%CI = 0.21, 2.48) were also related with the increased femininity trait. In addition, persistent exposure to LMWP was negatively associated with undifferentiated type among boys entering puberty earlier (RR = 0.18, 95%CI = 0.05, 0.75, $P < 0.05$); and a majority of PAEs metabolites exposure showed RRs > 1 for boys' femininity. Long-term exposure to PAEs were positively related with the increased scores of femininity trait in boys with early pubertal onset. Strengthening industry legislation are of great public health importance.

Ferroptosis is critical for BBP to impair blood-testis barrier by targeting ceruloplasmin

Yu Dong[a], Xiaobing Shen[a], Yongquan Yu[a,*]
[a] School of Public Health, Southeast University, Nanjing, Jiangsu, China

Abstract: The increasing risk of male infertility is a growing concern for the global population. Testicular function is largely dependent on Sertoli cells, which maintain the blood-testis barrier (BTB) and contribute to the process of spermatogenesis. Butyl benzyl phthalate (BBP, CAS No. 85-68-7) is a common phthalate that requires attention due to its widespread use and high potential for human exposure. In vivo and in vitro experiments were conducted to investigate whether BBP causes reproductive damage in males and the mechanisms involved. In vivo experiments showed that exposure to BBP did not alter body weight, organ weights of the testes and epididymis, serum testosterone and estradiol levels. BBP significantly affects reproductive outcomes in male mice, mainly in the form of reduced sperm quantity and quality. Pathological examination showed testicular vacuolization and reduced sperm density in the epididymis after exposure to BBP. Biotin tracer assays showed increased accumulation of biotin in the testis and epididymal lumen of BBP-treated mice. Western blot analysis showed decreased levels of ZO-1 and Occludin, suggesting that BBP induced a disruption of BTB integrity. In addition, exposure to BBP increased Ptgs2 levels and decreased Gpx4 and ceruloplasmin (Cp) levels. These findings were confirmed by in vitro experiments in which TM4 cells showed decreased levels of ZO-1, Occludin, Gpx4, and Cp, increased levels of Ptgs2, and increased levels of Fe^{2+} after exposure to BBP. Moreover, ferroptosis inhibitors (DFOM and Fer-1) as well as overexpression of Cp were effective in attenuating BBP-induced ferroptosis and BTB damage by modulating Fe^{2+} and lipid peroxidation levels. Exposure to BBP may disrupt the intracellular iron homeostasis of Sertoli cells by down-regulating Cp, leading to ferroptosis. This disruption ultimately damages the structural and functional integrity of Sertoli cells, leading to BTB injury.

Light-independent phytoplankton degradation of methylmercury in water

Jin Zhang[a], **Huan Zhong**[a,*], **Pei Lei**[b]
[a] School of Environment, Nanjing University, Nanjing, Jiangsu, China
[b] School of Environment, Nanjing Normal University, Nanjing, Jiangsu, China

Abstract: Phytoplankton serves as a key entry point for the trophic transfer and bioaccumulation of the neurotoxin methylmercury (MeHg) in aquatic food webs. Trace levels of MeHg in water (at picomolar to low nanomolar concentrations) enter the aquatic food web predominantly via biological uptake by phytoplankton, which can be bioaccumulated and biomagnified up to ten-million-fold, reaching toxic levels in fish. However, it is unclear whether and how phytoplankton itself may degrade and metabolize MeHg in the dark. Here, using several strains of the freshwater alga Chlorella vulgaris, the marine diatom Chaetoceros gracilis and two cyanobacteria (or blue-green algae), we report a light-independent pathway of MeHg degradation in water by phytoplankton, rather than its associated bacteria. About 36%-85% of MeHg could be degraded intracellularly to inorganic Hg(II) and/or Hg(0) via dark reactions. Endogenic reactive oxygen species, particularly singlet oxygen, were identified as the main driver of MeHg demethylation. Given the increasing incidence of algal blooms in lakes and marine systems globally, these findings underscore the potential roles of phytoplankton demethylation and detoxification of MeHg in aquatic ecosystems and call for improved modelling and assessment of MeHg bioaccumulation and environmental risks.

Epigenetic down-regulation of ERO1α via the DNA methylation mechanism contributed to hepatic endoplasmic reticulum stress was inhibited by zinc, selenium and chromium in female offspring of gestational diabetes rat

Xueqiong Yao[a,*]

[a] School of Public Health, Hengyang Medical School, University of South China, Hengyang, Hunan, China

Abstract: Epigenetic changes caused by gestational diabetes mellitus (GDM) may be one of the mechanisms contributing to the increased risk of diabetes mellitus in offspring. We previously reported zinc, selenium and chromium supplementation improved hepatic endoplasmic reticulum (ER) stress in GDM rats. However, it is relatively unknown whether the epigenetic molecular mechanism is involved in this improvement. Here, female Sprague Dawley rats were fed with either a high-fat and sucrose (HFS), to induce the GDM model, or a low-fat (LF) diet for three consecutive generations (F0, F1, and F2), with zinc, selenium and chromium supplemented by gavage daily. Glucose homeostasis, hepatic ER stress and insulin signaling pathway were analyzed. Global DNA methylation levels as well as methylation levels of CpG island in the promoter regions of ER stress-related genes were evaluated by pyrosequencing. Glucose intolerance, insulin resistance, hepatic ER stress and increased global DNA methylation were exhibited in F1 and F2 female neonates of GDM. Pyrosequencing identified a hypermethylated promoter region in ERO1α that regulated ER stress, which was associated with reduced gene expression and activation of ER stress. Efficient zinc, selenium and chromium supplementation with GDM conferred significant protection against hypermethylation status of the ERO1α gene promoter region in F1 and F2 female neonates, thus alleviating the ER stress and insulin resistance. The results showed a novel role of ERO1α in the transgenerational effect of regulating both glucose homeostasis and ER stress in female offspring of GDM. Zinc, selenium, and chromium supplementation was efficient to protect glucose intolerance and ER stress via modifying the abnormal methylation modifications, which might be the underlying molecular mechanisms of hyperglycemia in GDM offspring.

Revealing the link: Unraveling the association between pesticide exposure and hypertension, exploring the role of lipids in different glycemic statuses

Zhiwei Chen[a], Dandan Wei[a], Erbao Han[a], Yumeng Yan[a], Guozhen Han[a], Zhenxing Mao[a,*]
[a] College of Public Health, Zhengzhou University, Zhengzhou, Henan, China

Abstract: Considering the widespread use of organophosphorus pesticides（OPs） and the global prevalence of hypertension(HTN), and given studies indicating that different glucose glycemic statuses may respond differently to the biological effects of OPs. Therefore, this study, based on the Henan rural cohort, investigates the association between OPs exposure and HTN, and further explores whether lipids mediate these associations. The plasma levels of OPs in 2775 participants under different glycemic statuses were measured using gas chromatography-triple quadrupole mass spectrometry (GC-MS/MS). A generalized linear model, Quantile g-computation (QGC), adaptive elastic net (AENET), and Bayesian kernel machine regression (BKMR) models were used to assess OP exposure's impact on HTN, with LASSO penalty regression identifying main OPs. Mediation models evaluated blood lipids' intermediary role in the OPs-HTN relationship. Detection rates for all OPs were high, spanning from 76.35% to 99.17%. In the NGT population, single exposure models revealed that malathion and phenthoate were associated with an increased incidence of HTN (P-FDR < 0.05), with corresponding odds ratios (ORs) and 95% confidence intervals (CIs) of 1.624 (1.167, 2.260) and 1.290 (1.072, 1.553), respectively. QGC showed a positive association between OP mixtures and HTN, with malathion and phenthoate being the major contributors. Moreover, according to the ERS constructed in the AENET model, the risk of HTN increases with higher ERS (P<0.001). Furthermore, BKMR revealed that co-exposure to OPs increases HTN risk, with phenthoate having a significant impact. Additionally, TG mediated 6.55% of the association between phenthoate and HTN. However, no association was found in IFG and T2DM populations. Our study found that in the NGT population, OPs may play a significant role in the development of HTN, suggesting TG as a novel approach to preventing HTN.

Interdisciplinary research of exposure of endocrine disruptors damaging intestinal barrier via SLC39A9/ERK/Claudin1 axis and promoting the formation of prostate cancer immune suppressive microenvironment

Shi Qiu[a,*], Zilong Zhang[a], Fang Qi[b]
[a] Department of Urology, West China Hospital, Chengdu, Sichuan, China
[b] Department of Burns and Plastic Surgery, Affiliated Hospital of Zunyi Medical University, Zunyi, Guizhou, China

Abstract: Recent studies have demonstrated that the dysbiosis of microbiota plays a vital role in the progression of cancer, which generally carries an unfavorable prognosis with unsatisfactory therapeutic effects. However, the contribution of commensal fungi to the occurrence of cancer is understudied. Here, we found that *Candida glabrata* (*C. glabrata*) infections are often undiagnosed in prostate cancer (Pca). Oral administration of *Candida glabrata* (*C. glabrata*) to the mice with high Environmental Endocrine Disruptors (EDC) accelerated Pca progression. Mechanistically, EDCs exposure increases intestinal permeability via non-canonical androgen receptor SLC39A9, resulting in the leakage of *C. glabrata* from gut to the tumor. Intriguingly, intratumoral *C. glabrata*-derived mannans activates DECTIN2-SYK pathway in polymorphonuclear myeloid-derived suppressor cells (PMN-MDSCs), which not only enhances its immunosuppressive and migration ability, but also triggers the activation of immune-endocrine axis. In addition, the endocrine hormone Activin A produced by PMN-MDSCs facilitates Pca progression by upregulating androgen related genes in tumor cells. Taken together, these results reveal that the gut-to-tumor transmission of commensal fungi contributes to Pca progression by boosting the immunosuppressive tumor microenvironment (TME) and pro-tumor hormone produced by PMN-MDSCs.

Hidden demethylation pathway in crop plants removes mercury from human food web

Mengjie Wu[a], Wenli Tang[a], Huan Zhong[a,*]
[a] School of the Environment, Nanjing University, Nanjing University, Jiangsu, China

Abstract: Chronic exposure to methylmercury (MeHg) from the consumption of contaminated food causes irreversible damage to human cognition, leading to deficits in the intelligence quotient (IQ). The risk of MeHg exposure is largely mitigated by its demethylation in the environment through photolysis and microbial degradation, while the processes following uptake and bioaccumulation in complex organisms remain unknown. Here, we report the discovery of a new MeHg demethylation process in crop plants, including rice, which is a primary dietary source of human MeHg exposure. The novel MeHg demethylation process is shown to be induced by reactive oxygen species (primarily singlet oxygen) generated in vivo. Following demethylation, Hg evaporates from plants as elemental Hg, a previously unidentified process estimated to account for a global release of 14.7-19.3 tons/year. Using a health risk model, we predict the rice MeHg concentration would increase by 2.4- to 4.7-fold without MeHg demethylation, which leads to IQ losses of 0.01-0.51 points per newborn in major rice-consumption countries, corresponding to annual economic benefits of US$30.7-84.2 billion globally. This discovered pathway effectively removes Hg from human food webs, playing an important role in exposure mitigation and global Hg cycling.

Spatiotemporal distribution, source appointment, and risk assessment of polycyclic aromatic hydrocarbons in sediments from highly urbanized river

Yu Ma[a], Ling Chen[a,*], Chunzhao Chen[b]
[a] College of Environmental Science and Engineering, Tongji University, Shanghai, China
[b] Advanced Interdisciplinary Institute of Environment and Ecology, Beijing Normal University, Zhuhai, Guangdong, China

Abstract: Taipu River, as an important drinking water source, has dense human population density and intensive industrial activities. This study investigated the impacts of human activities on polycyclic aromatic hydrocarbons (PAHs) contamination in sediments from the Taipu River during three hydrological seasons. The spatial distribution of PAHs between the mainstream and its tributaries were also examined to fully assess the potential risks of PAHs to water sources. The total concentrations of 16 PAHs spanned two orders of magnitude (244-24616 ng/g dw) with an average of 2097 ± 2673 ng/g dw. High molecular weight (4-ring to 6-ring) PAHs were the dominant PAH components, accounting for 90%. The spatial distribution of PAH in sediments varied in this order: midstream > downstream > upstream in the Taipu River, since the midstream connects with several small lakes favoring the inflow of contaminants. PAH showed highest concentrations in rainy season, which consistent with the seasonal variations of local industrial production capacity and river transportation. Multiple statistical analyses revealed that 88% of PAHs originated from coal combustion and diesel combustion, while the remaining 12% derived from shipping activities, including diesel combustion and oil leakage. Sediment quality guidelines and risk quotient suggested that PAHs in the Taipu River Network presented ecological risks, even in areas near drinking water sources. The incremental lifetime cancer risk indicated that ingestion through drinking water posed health risks to local adults and children. Overall, this study underscored the influence of human activities and hydrodynamic forces on PAH distribution, providing insights for local drinking water safety and corporate green development.

Association of long-term $PM_{2.5}$ and its component exposure with lung function level and the potential role of body weight change

Zhenzhen Li[a], Weihong Qiu[a], Weimin Ye[a,*]

[a] Department of Epidemiology and Health Statistics, School of Public Health, Fujian Medical University, Fuzhou, Fujian, China

Abstract: The adverse effects of long-term exposure to $PM_{2.5}$ and its components on lung function and the role of long-term body weight changes remain unclear. A total of 14,111 participants aged 35-75 years from the Fuqing Cohort were enrolled. The lung function of each participant was determined and four parameters (FVC, FEV1, FVCperc, and FEV1perc) were selected. $PM_{2.5}$ and its five components (SO_4^{2-}, NO_3^-, NH_4^+, OM, and BC) during the study period were collected from the Tracking Air Pollution (TAP) in China. All participants' current body weights were determined by precision scales and their weights at the age of 20 were gathered through face-to-face questionnaire surveys. Generalized linear models (GLM) were conducted to assess the association between $PM_{2.5}$ and its five components (SO_4^{2-}, NO_3^-, NH_4^+, OM, and BC) and lung function, as well as assess the combined effects of $PM_{2.5}$ and its components and long-term weight changes on lung function. After adjusting for the covariates, we found that for each 1 $\mu g/m^3$ increase in $PM_{2.5}$ and its five components (SO_4^{2-}, NO_3^-, NH_4^+, OM, and BC), FVC, FEV1, FVCperc and FEV1perc decreased, and similar results, except OM and BC, were found for each 1% increase in SO_4^{2-}, NO_3^-, NH_4^+ (all $P < 0.05$). In addition, we found that each unit increase in weight change was associated with a 111.34 mL decrease for FVC, an 66.79 mL decrease for FEV1, a 3.59% decrease for FVCperc, and a 2.61% decrease for FEV1perc (all $P < 0.05$). We found that long-term weight changes have joint effects with $PM_{2.5}$ and its five components on lung function decline, particularly in individuals experiencing weight gain. Long-term exposure to $PM_{2.5}$ and its components may decrease lung function. Long-term weight changes can exacerbate the negative impacts of PM on lung function.

Human impact on the different occurrences of antimony and arsenic in a typical urban river system of southern China

Chenqi Guo[a], Haiyan Zhang[a,*]
[a] School of Environment, Hangzhou Institute for Advanced Study, University of Chinese Academy of Sciences, Hangzhou, Zhejiang, China

Abstract: Antimony (Sb) and arsenic (As) are both group-V elements with similar chemistry, toxicity and binding properties. Various human activities would cause Sb and As contamination, whereas their occurrence differences in non-mining urban environment and anthropogenic sources are still not clear. Herein we investigated the distributions and exposure risks of Sb and As, and their associations with multiple socioeconomic variables in the Qiantang River basin, a typical urban river system. Concentrations of Sb (maximum 25.3 μg L^{-1}, mean 2.58 μg L^{-1}) in river water was much higher than those of As (2.15 μg L^{-1}, 1.15 μg L^{-1}). A positively correlation was observed between Sb concentrations and industrial wastewater emission in the basin, while As concentrations showed positive correlations with other three variables (population density, gross industrial output, and energy consumption) ($p < 0.05$). Structural equation models also showed that industrial wastewater emissions directly influenced Sb levels in the river water, while the As levels were affected by gross industrial output and population density. These results suggested that Sb was mainly influenced by the point source emissions (i.e., wastewater discharge), while As was influenced by both industrialization and urbanization. The emission fluxes estimation of wastewater treatment plants further demonstrated that textile printing and dyeing industries were the major contributor for Sb pollution in this basin. Health risk assessment based on Monte Carlo simulation showed that the non-carcinogenic and carcinogenic risks of residents were in the acceptable range. Nevertheless, compared to background areas, the non-carcinogenic health risks significantly increased by 67% and 312% for the residents lived in urban areas and industrial areas, respectively. Our findings highlight the key anthropogenic factors and increased health risks of Sb and As pollution in urban river systems, providing valuable support for priority management and control strategy of Sb pollution in industrial areas.

Associations between short-term exposure of $PM_{2.5}$ metal components and cardiovascular system during pregnancy

Jiufeng Li[a,*]

[a] Public Health, Fudan University, Shanghai, China

Abstract: Cardiovascular diseases during pregnancy are important factors affecting the health of mother and child. Environmental factors such as particulate matter $PM_{2.5}$ have been proved to be closely related to the incidence of cardiovascular diseases. However, there are few studies on the impact of metal components of $PM_{2.5}$ on the cardiovascular system of pregnant women, and the potential mechanism is not yet clear. Based on the Shanghai parent-child cohort, 329 pregnant women were recruited from February 2017 to October 2018. We found that the mixture of $PM_{2.5}$ metal components was negatively correlated with Left Ventricular Posterior Wall Thickness at Diastole (LVPWd) and A peak value, but positively correlated with LVPWd, right ventricular diameter (RVD), pulmonary artery orifice blood flow velocity (PV). Ni and Ba exhibited an interaction on RVD, with bile acid metabolites playing a crucial role. Al and V interacted with each other on the mitral valve orifice area (MVA), with carnitine metabolites playing a significant role. We observed $PM_{2.5}$ exposure induced 43 metabolites and 63 metabolites changed significantly in the first trimester and in the third trimester, respectively. The enrichment analysis revealed that fatty acid biosynthesis substantially altered in the first trimester while arginine and proline pathway predominantly modified in the third trimester. This study revealed that Short-term exposure to $PM_{2.5}$ metal components can affect the structure and function of the cardiovascular system, and there is an interaction between components. Bile acids and carnitine metabolites were found to play a key role in the interaction. Aberrant lipid metabolism and perturbations in arginine and proline metabolism appear to be significant metabolic pathways underlying the impact of $PM_{2.5}$ metal components on cardiovascular indicators. This study will play a suggestive role in pollution prevention and control and prevention of cardiovascular diseases.

Disinfectant-induced ammonia oxidation disruption in microbial N-cycling process in aquatic ecosystem after the COVID-19 outbreak

Lutong Yang[a,*]

[a] State Key Laboratory of Environmental Aquatic Chemistry, Research Centre for Eco-Environmental Sciences, Beijing, China

Abstract: Anthropogenic activities significantly impact the elemental cycles in aquatic ecosystems, with the N-cycling playing a critical role in potential nutrient turnover and substance cycling. We hypothesized that measures to prevent COVID-19 transmission profoundly altered the nitrogen cycle in riverine ecosystems. To investigate this, we re-analyzed metagenomic data and identified 60 N-cycling genes and 21 host metagenomes from four urban reaches (one upstream city, Wuhan, and two downstream cities) along the Yangtze River. Our analyses revealed a marked decrease in the abundance of bacterial ammonia monooxygenase genes, as well as in the host, ammonia-oxidizing autotrophic Nitrosomonas, followed by a substantial recovery post-pandemic. We posited that discharge of sodium hypochlorite (NaOCl) disinfectant may be a primary factor in the reduction of N-cycling process. To test this hypothesis, we exposed pure cultures of Nitrosomonas europaea to NaOCl to explore the microbial stress response. Results indicated that NaOCl exposure rapidly compromised the cell structure and inhibited ammonia oxidation of N. europaea, likely due to oxidative stress damage and reduced expression of nitrogen metabolism-related ammonia monooxygenase. Using the functional tagging technique, we determined that NaOCl directly destroyed the ammonia monooxygenase protein and DNA structure. This study highlights the negative impacts of chlorine disinfectants on the function of aquatic ecosystems and elucidates potential mechanisms of action.

Exposure to acrylamide and risk of type 2 diabetes mellitus: Relationship, mediation, and gene-environment interaction analyses in a general population in China

Bin Wang[a,*], Jiahao Song[a], Linling Yu[a], Wei Liu[a], Yongfang Zhang[a], Yueru Yang[a], Shuhui Wan[a], Weihong Chen[a]

[a] Department of Occupational and Environmental Health, School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, Hubei, China

Abstract: The health risk of acrylamide, a pollutant ubiquitous in daily life, has become one of the major global public health problems, attracting worldwide attention. We aimed to evaluate the relationship between acrylamide exposure and type 2 diabetes (T2DM), the underlying role of heme oxygenase-1 (HO-1) activity, and the interaction between acrylamide exposure and T2DM genetic susceptibility. Urinary acrylamide metabolites (N-Acetyl-S-(2-carbamoylethyl)-L-cysteine [AAMA] and N-Acetyl-S-(2-carbamoyl-2-hydroxyethyl)-L-cysteine [GAMA], biomarkers of acrylamide exposure) and exhaled carbon monoxide (eCO, biomarker of HO-1 activity) were measured for 3522 Chinese adults from the Wuhan-Zhuhai cohort to assess the relationship of acrylamide exposure with T2DM (logistic model) and the underlying mediation role of HO-1 activity (mediation analysis). The polygenic risk score (PRS) was constructed based on 137 T2DM-associated single nucleotide polymorphisms to further assess the gene-environment interaction on additive scale. Urinary acrylamide metabolites were significantly and dose-dependently associated with T2DM. The odds ratio was 1.29 (95% confidence interval: 1.08, 1.55), 1.27 (1.03, 1.55), or 1.30 (1.08, 1.57) associated with each 3-fold increase in AAMA, GAMA, or AAMA+GAMA, respectively. eCO significantly mediated the associations between AAMA, GAMA, and AAMA+GAMA and T2DM with mediated proportions of 11.07%, 11.54%, and 11.34%, respectively. Gene-environment interactions on additive scale were further found between PRS and AAMA (relative excess risk due to interaction: 0.99; 95% confidence interval: 0.17, 1.82) and AAMA+GAMA (0.99; 0.14, 1.85) rather than GAMA (0.10; -1.22, 1.42), and higher odds ratio of T2DM was observed in participants with higher levels of both PRS and urinary acrylamide metabolites. Exposure of the general population to acrylamide was related to increased risk of T2DM, which was mediated by HO-1 activity and aggravated by T2DM genetic susceptibility.

Infantile internal and external exposure to neonicotinoid insecticides: A comparison of levels across various sources

Henglin Zhang[a], Tao Zhang[a,*]
[a] School of Environmental Science and Engineering, Sun Yat-sen University, Guangzhou, Guangdong, China

Abstract: Little is known about exposure of infants to neonicotinoid insecticides (NEOs). In this study, concentrations of six parent NEOs (p-NEOs) and N-desmethyl-acetamiprid (N-dm-ACE) were measured in urine and whole blood samples from infants, in addition to breast milk, infant formula and tap water collected in South China. The p-NEOs with the highest median concentration in urine (0.25 ng/mL) and blood (1.30) samples was dinotefuran (DIN), while imidacloprid (IMI) was abundant in breast milk (median: 0.27 ng/mL), infant formula (0.22) and tap water (0.028). The older infants (181-360 days) might face higher NEOs and N-dm-ACE exposure than younger infants (0-180 days). Blood samples contained significantly ($p < 0.01$) higher median concentration of $\sum 6$p-NEOs (2.03 ng/mL) than that of urine samples (0.41), similar to acetamiprid (ACE), IMI, thiacloprid (THD), DIN and N-dm-ACE, suggesting that NEOs readily partition into blood. Furthermore, breast-fed infants tend to have higher exposure levels than formula-fed infants. Infant formula prepared with tap water augmented the daily intake (DI) of $\sum$NEOs. The external sources contributed 80% of the total dose to IMI and clothianidin (CLO) exposure, while other unknown sources contributed to ACE, THD and DIN exposure, in infants. To the best of our knowledge, this is the first study to assess levels and sources of infantile exposure to NEOs through internal and external exposure assessment.

Impact of easing COVID-19 restrictions on antibiotic usage: A longitudinal study in Eastern China using wastewater-based epidemiology

Jinxin Zang[a], Lufang Jiang[a], Yingying Wang[a], Yue Chen[b], Chaowei Fu[a], Na Wang[a,*], Barbara Kasprzyk Hordern[c], Helen S Lambert[d], Qingwu Jiang[a]

[a] School of Public Health, Fudan University, Shanghai, China

[b] Faculty of Medicine, University of Ottawa, Ottawa, Canada

[c] Faculty of Science, University of Bath, Bath, United Kingdom

[d] Bristol Medical School, University of Bristol, Bristol, United Kingdom

Abstract: Coronavirus Disease 2019 (COVID-19) emerged in December 2019 and zero-COVID policy was implemented in Mainland China during the first two years of the pandemic. The policy was eased in December 2022, resulting in a nationwide wave of COVID cases. We used wastewater-based epidemiology (WBE) to compare the antibiotic levels in wastewater before and after the easing of the zero-COVID policy. Wastewater samples were repeatedly collected from five wastewater treatment plants (WWTPs) in Eastern China in January and February of 2021 and 2023, respectively. 27 antibiotics were quantified and estimated via WBE, and obtained estimates were compared with catchment specific prescription data. The results revealed a substantial increase (531%-3734%) in antibiotics consumption via WBE in 2023 compared with 2021, featuring a different combination of antibiotic types. Macrolides and quinolones were more likely to coexist in 2023 ($r = 0.67$-0.94, $p < 0.05$). This study highlights the significant surge in antibiotic consumption during the period of increased COVID cases. The catchment specific prescription data showed similar trends. The implication of overuse or misuse of antibiotics during the COVID-19 pandemic warrants further investigation.

Association of exposure to multiple organic pollutants in early pregnancy with gestational diabetes mellitus

Gaga Mahai[a], **Shunqing Xu**[a,*]
[a] School of Life and Health Sciences, Hainan University, Haikou, Hainan, China

Abstract: Ubiquitous organic pollutants including pesticides, parabens, volatile organic compounds, phenols, and biocides have received a growing global concern over their adverse health effects. This study aimed to assess the associations of exposure to multiple organic pollutants including eight neonicotinoid, six organophosphate, and three pyrethroid insecticides, 2, 4-dichlorophenoxyacetic acid, carbendazim, seven paraben derivatives, pentachlorophenol, triclosan, and triclocarban in early pregnancy with gestational diabetes mellitus (GDM) and the mediation roles of oxidative DNA damage, RNA damage, and lipid peroxidation in the associations. With a prospective nested case-control study, 519 GDM cases and 519 controls were matched on the infant's sex and maternal age. Urinary biomarkers of organic pollutants' exposure and oxidative stress were measured in early pregnancy. We estimated the associations of single and the mixture of the pollutants above with GDM by conditional logistic regression and quantile g-computation models, respectively. The mediating roles of oxidative stress were evaluated by the structural equation model. The odds of GDM significantly increased by 13% to 49% in each unit increment of ln-transformed concentrations of urinary organic pollutants, respectively. Exposure to the mixture of NNIs was associated with increased odds of GDM (adjusted OR: 1.76; 95 %CI: 1.45, 2.13). Advanced maternal age enhanced the associations of 5-hydroxy-IMI, DN-IMI, and IMI-olefin with GDM ($P < 0.05$), and being overweight/obese before pregnancy strengthened the effects of IMI, IMI-olefin, and THM on GDM ($P < 0.05$). In the association of NNIs exposure and GDM, the proportions mediated by oxidative DNA damage, RNA damage, and overall oxidative stress were 9.8%, 11.8%, and 14.5%, respectively ($P < 0.05$). Exposure to multiple organic pollutants were associated with GDM, and maternal age and pre-pregnancy BMI may modify the association. The possible mechanism underlying the association between NNIs and GDM may involve oxidative damage to nucleic acids.

Hydrostatic pressure drives microbe-mediated biodegradation of microplastics in surface sediments of deep reservoirs: Novel findings from hydrostatic pressure simulation experiments

Beibei Chai[,*], Kehong Yu[a], Qingfeng Tang[b], Lixin He[a], Xiaohui Lei[c], Bin Chen[d]

[a] School of Water Conservancy, Hebei University of Engineering, Handan, Hebei, China

[b] Beijing Center for Physical & Chemical Analysis, Beijing Center for Physical & Chemical Analysis, Beijing, China

[c] State Key Laboratory of Simulation and Regulation of Water Cycle in River Basin, China Institute of Water Resources and Hydropower Research, Beijing, China

[d] School of Environment, Beijing Normal University, Beijing, China

Abstract: Microplastics originate from the physical, chemical, or biological degradation of plastics in the environment. Once ingested by organisms at the bottom of the food chain, microplastics are passed on to organisms at higher trophic levels, posing a threat to human health. The distribution of microplastics and the metabolic pathways involved in their microbial degradation in surface sediments of drinking water reservoirs are still poorly understood. This study analyzed the occurrence patterns of microplastics and microbial community structure associated with microplastic biodegradation in surface sediments from a deep reservoir at various hydrostatic pressures. Based on the results of Fourier-transform and laser direct infrared spectroscopy, elevating the pressure resulted in altered sizes and shapes of microplastics in sediment samples with the presence of microorganisms. The influence of hydrostatic pressure on small-sized microplastics (20–500 μm) was pronounced. For instance, high pressure accelerated the breakdown of fibers, pellets, and fragments into smaller-sized microplastics. In particular, the mean size of polyethylene terephthalate microplastics decreased from 425.78 μm at atmospheric pressure to 366.62 μm at 0.7 Mpa. Metagenomic analysis revealed an increase in the relative abundances of plastic-degrading genera, such as *Rhodococcus*, *Flavobacterium*, and *Aspergillus*, in response to elevated pressures. Eight functional genes for biodegradation of polystyrene, polyethylene, and polyethylene terephthalate microplastics were annotated, including paaK, ladA, tphA3. Of these, tphA3 gene abundance was negatively influenced by hydrostatic pressure, providing direct evidence for the pathway by which microbial metabolism of polyethylene terephthalate led to decreased microplastic size under high pressure conditions. This study presents novel insights into hydrostatic pressure-driven microbial community structure, functional gene abundance, and key metabolic pathways associated with biodegradation of microplastics in reservoir sediments.

Associations between maternal urinary concentrations of volatile organic compound metabolites and child neurocognitive development at two years of age

Xi Qian[a,b], Yanjian Wan[c], Juxiao Li[a], Gaga Mahai[a], Aizhen Wang[a], Yan Wang[a], Jiaolong Ma[a], Yuanyuan Li[a], Shunqing Xu[a], Wei Xia[a,*]

[a] Key Laboratory of Environment and Health (HUST), Ministry of Education & Ministry of Environmental Protection, and State Key Laboratory of Environmental Health (Incubation), School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, Hubei, China

[b] Center for Reproductive Medicine, Women and Children's Hospital of Chongqing Medical University, Chongqing, China

[c] Center for Public Health Laboratory Service, Institute of Environmental Health, Wuhan Centers for Disease Control & Prevention, Wuhan, Hubei, China

Abstract: Neurotoxicity of exposure to volatile organic compounds (VOCs) has been documented in animal studies, but related epidemiological investigations are very limited; particularly, that based on biomonitoring data are not available yet. This study aimed to evaluate the trimester-specific association between urinary concentrations of multiple VOC metabolites (mVOCs) and child neurodevelopment. Twenty mVOCs were measured in urine samples repeatedly collected at the first, second, and third trimesters from 1023 pregnant women in Wuhan, China. The Bayley Scales of Infant Development (Chinese Revision) was used to assess children's neurocognitive development [mental development index (MDI) and psychomotor development index (PDI)] at two years old. General linear models, generalized estimating equation models, and weighted quantile sum (WQS) regression were used to evaluate the associations between urinary concentrations of mVOCs and Bayley scores. Lower child MDI score was found to be associated with higher urinary concentration of 2-aminothiazoline-4-carboxylic acid (ATCA, a metabolite of cyanide) at the first trimester, especially among boys (P-FDR < 0.05). Each interquartile ratio (IQR)-fold increase in the urinary concentration of ATCA was associated with a decrease of 4.42 points (95% confidence interval: −6.82, −2.01) in boys' MDI score. Additionally, WQS regression analyses with repeated holdout validation suggested that the mVOC mixture at the first trimester was significantly and negatively associated with boys' MDI score, and the association was mainly driven by ATCA (45%). Prenatal exposure to certain VOC even at environmentally relevant dose may impact child neurodevelopment. Further studies are needed to confirm these findings and clarify underlying mechanisms. Corresponding measures need to be taken to reduce gestational exposure to cyanide.

Microplastics in human lung tissues: Relationship with clinical indicators

Cui-Lan Bai[a], **Ying Guo**[a,*]

[a] College of Environment and Climate, Jinan University, Guangzhou, Guangdong, China

Abstract: Since microplastics (MPs) are abundant in indoor and outdoor air, human ingestion of MPs through inhalation is inevitable. Historical studies indicated respiratory symptoms and illnesses, including dyspnea, coughing, wheezing and decreasing lung capacity were occurred following exposure to MPs in occupation environment. Currently, evidence of ingested MPs posing a substantial health risk to human health is far from confirmed. In this study, the accumulation and characteristics of MPs in human lung tissues from 71 participants with lung disease were determined by using Raman spectroscopy. Microplastics were detected in human lung tissue samples with an average of 1.43 ± 2.95 (median: 0.28) items g^{-1}, supporting that MPs are accumulated in human lungs through inhalation. Seven types of MPs were detected in 71 lung samples. Polyethylene terephthalate (42%) was the most abundant, followed by poly (1,4-phenylene sulfide) (34%) and polypropylene (18%), with the majority being < 30 μm (87%) in with and < 250 μm (33%) in length. Our study demonstrated that the abundance of MPs in lung tissue negatively correlated with indicators of blood routine examination, including plateletcrit and monocyte percentage, which can help in the diagnosis of inflammation and immune-related diseases. In addition, generalized linear model analysis showed that increased MPs abundance in lung tissue may significantly affect monocyte percentage levels in blood ($\beta = -0.186$, 95% CI: −0.0337 to −0.035, $p = 0.016$). Our results indicated that exposure to certain doses of airborne MPs may be disrupt clinical indicators and associated with the immune damage and inflammatory response. The relative mechanisms and the detailed potential health risks warrant further investigation. This study provides a reference for further research on the relationship between exposure to MPs and respiratory diseases in the future.

Conversion of PET to active hydroxyl-terminated oligomers with 98.4% recycling efficiency and their potential application in functional composites

Xing Zhou[a,*]

[a] State Key Laboratory of Eco-hydraulics in Northwest Arid Region of China, Xi'an University of Technology, Xi'an, Shaanxi, China

Abstract: Developing a highly efficient and one-pot strategy for upcycling post-consumer waste polyethylene terephthalate (PET) into feedstock for the production of valuable products at scale remains a formidable challenge through chemical recyclability. Here we present the chemical degradation of waste PET sheets at scale via a one-pot process, which yields active hydroxyl terminated oligomers with 98.4% recycling efficiency by a degree of polymerization of 4-7. The recycling oligomers hold the great potential application in synthesis of polyurethane, preparation of functional composites and sensors. Notably, the oligomers can also be directly used as raw materials for preparing organic pigments. The combination of these two renewable and valuable materials (e. g. polyurethane and pigments) enables the creation of multi-colored coatings boasting remarkable brightness, exceptional hiding power, and impressive coloring strength. In essence, our work establishes a simple closed-loop recycling system for waste PET into useful and environment-friendly chemical products at scale in high efficiency.

Gut microbiota mediates ambient $PM_{2.5}$ exposure-induced abnormal glucose metabolism via short-chain fatty acids

Wenpu Shao[a], Zhouzhou Li[a], Haidong Kan[a], Zhekang Ying[b], Yanyi Xu[a,*]
[a] Environmental Health, Fudan University, Shanghai, China
[b] Medicine Cardiology, University of Maryland, Baltimore, Maryland, United States

Abstract: Exposure to $PM_{2.5}$ has been found to impair glucose homeostasis and cause gut dysbiosis in human and animal models. Despite of its critical role in regulating glucose metabolism, few studies have investigated the mediation effect and biological importance of gut microbiota in $PM_{2.5}$ exposure-induced glucose metabolic abnormalities. Mice were exposed to concentrated ambient $PM_{2.5}$ (CAP) or filtered air (FA), and gut microbiota depletion and faecal microbiota transplantation experiments were performed to explore the role of gut microbiota. The composition of gut microbiota and levels of short-chain fatty acids (SCFAs) in mice were assessed by 16S rRNA sequencing and targeted SCFAs profiling, respectively. Finally, the identified differential SCFA was supplied to FA/CAP-exposed mice to check its potential prevention effect on $PM_{2.5}$-induced abnormal glucose metabolism. Microbiota depletion by antibiotics treatment significantly alleviated CAP-induced glucose intolerance and insulin resistance, as indicated by the intraperitoneal glucose tolerance test (IPGTT), glucose-induced insulin secretion (GIIS), insulin tolerance test (ITT) and insulin-induced phosphorylation levels of Akt in insulin sensitive tissues. In addition, faecal microbiota transplantation (FMT) from CAP-exposed donor mice successfully remodelled the glucose metabolism abnormalities in recipient mice, while the transplantation of autoclaved faecal materials did not. Faecal microbiota analysis demonstrated that the composition and alpha diversity of the gut bacterial community were altered by CAP exposure and in FMT recipient mice. Furthermore, SCFAs levels analysis showed that the circulating acetate was significantly decreased in CAP-exposed donor and FMT recipient mice, and supplementation of sodium acetate successfully improved the glucose metabolism abnormalities induced by $PM_{2.5}$ exposure. These results suggest that gut microbiota plays a critical role mediating $PM_{2.5}$-induced abnormal glucose homeostasis potentially through influencing SCFAs, thereby indicating the possibility that manipulating the gut microbiota or its metabolites could be a potential strategy for preventing the adverse health effects of ambient $PM_{2.5}$.

Refractory dissolved organic matters in sludge leachate trigger the combination of anammox and denitratation for advanced nitrogen removal

Ben Dai[a], Siqing Xia[a,*]

[a] State Key Laboratory of Pollution Control and Resource Reuse, College of Environmental Science and Engineering, Tongji University, Shanghai, China

Abstract: It is estimated that globally, over 300 million tons of waste sludge are produced annually from sewage treatment plants. Over the years, landfilling has been the conventional method for municipal sludge treatment due to its simplicity and cost advantage in handling large quantities of sludge. However, such a disposal process has led to a new issue of the production of sludge leachate (SL) in aged landfill, posing adverse risks to the ecological environment and human health. The SL in landfills exhibited a high enrichment of ammonia and refractory dissolved organic matters (rDOM), originating from the hydrolysis of extracellular polymeric substances and biomass decay. Therefore, the cost-effective treatment of SL with high nitroganen content d rDOM has drawn increasing attention. This study employed, for the first time, a rDOM triggered denitratation-anammox continuous-flow process to treat landfill SL. Moreover, the mechanisms of exploiting rDOM from SL as an inner carbon source for denitratation were systematically analyzed. The results demonstrated outstanding nitrogen and rDOM removal performance without any external carbon source supplement. In this study, effluent concentrations of 4.27 ± 0.45 mg TIN/L and 5.58 ± 1.64 mg TN/L were achieved, coupled with an impressive COD removal rate of 65.17% ± 1.71%. The abundance of bacteria with rDOM degradation functionality increased from 18.23% to 35.62%. As a result, various types of rDOM were utilized to different extents, with proteins being the most notable, except for lignins. Metagenomic analysis revealed a preference for directing electrons towards NO_3^--N reductase rather than NO_2^--N reductase, indicating the coupling of denitratation bacteria and anammox bacteria (*Candidatus Brocadia*). Overall, this study introduced a novel synergy platform for advanced nitrogen removal in treating SL using its inner carbon source. This approach is characterized by low energy consumption and operational costs, coupled with commendable efficiency.

Effect of clay mineral particles on uptake of microplastics in wheat seedlings

Jie Yang[a], Chen Tu[a], Yongming Luo[a,*]

[a] State key laboratory of soil & sustainable agriculture, Institute of soil science, Chinese academy of sciences, Nanjing, Jiangsu, China

Abstract: Anthropogenic microplastics contaminate global terrestrial ecosystems. The effects of microplastics on crop plants have attracted growing attention. Studies have indicated that many terrestrial plant species can take up and transport microplastics to the aboveground tissues. However, little is known about the effect of clay minerals on the uptake of microplastics by crop plant. This study investigated the influence of two common clay minerals (kaolin and montmorillonite) on the uptake and transport of polystyrene (PS) microplastics by wheat seedlings in hydroponic solutions. Fluorescent labeling and scanning electron microscopy revealed that microplastics enter root steles at lateral root emergence sites, followed by transport to shoots. Clay minerals can limit the uptake of microplastics in wheat by forming heterogeneous aggregates with microplastics or competing for uptake pathways in new lateral root cracks of wheat. Europium (Eu)-marked PS was used to quantitatively assess the effect of clay minerals on the uptake of microplastics by wheat. Compared with kaolin, montmorillonite (larger size and specific surface area) has a more significant limiting effect on plant uptake of microplastics. By comparing the transfer factors (TFs) of microplastics in wheat, it was found that clay minerals promoted the transfer of microplastics from roots to shoots. These findings provide compelling evidence for the negative effect of clay mineral on the uptake of microplastics in crop plants. This study opens new avenues for research on the interactions between mineral particles and plants in terrestrial ecosystems and provides a new scientific basis for assessing the agricultural product safety and environmental risk of microplastics in plant-soil systems.

Elevational trends of mercury bioavailability and vegetation controls on methylmercury distribution in upland soils

Xizi Yang[a], **Tsz Ki Tsui**[a,*]
[a] Life Science, Chinese University of Hong Kong, Hong Kong, China

Abstract: The distinct physical and chemical properties of mercury enable its long-distance transport among continents and remote ecosystems. Its highly toxic organic form, methylmercury, is produced in situ in reducing environments such as wetlands, which have been widely identified as hotspots of methylmercury production. However, our understanding on the production of methylmercury in largely oxic terrestrial upland landscapes remains relatively limited. Here, we investigated mercury distribution and speciation in soils along an elevational gradient in Hong Kong, China and Sichuan, China. The soil methylmercury levels can reach up to 2 ng/g at certain altitudes in both study areas, Tai Mo Shan (TMS) and Gongga Mountain (Mt. Gongga), implying that upland soils can be conducive to active methylmercury production. Such level of MeHg in upland soils would be comparable or even higher than those commonly encountered in wetland soils. The methylation potential (i. e., MeHg%), was often thought to be low across terrestrial landscapes due to the unsaturated and oxic nature. However, our results exhibit great variations of MeHg% (50-fold), and significantly correlates with altitude in a positive or negative manner in certain range. I hypothesize that the bioavailability and transformation of mercury in soils result from the equilibrium between the kinetics and thermodynamics of mercury complexation with heterogeneous natural organic matter. Most mercury methylated in anoxic environment settings by microorganism possessing the hgcAB gene, while terrestrial methylation may be due to unknown methylators (e. g., aerobic microbes), and their efficiency may be regulated by distinct factors. This study provides insights into biological and geochemical impacts on methylmercury production in terrestrial landscapes and aims to fully elucidate the mechanism through integrated genomic, transcriptomic, and metabolic studies. This study supports the design of effective strategies to mitigate the environmental impacts of mercury and facilitates better management strategies for forest, agricultural, and animal husbandry land use.

Long-term LDR exposure may induce cognitive impairments: A possible association through targeting gut microbiota-gut-brain axis

Ruixue Huang[a,*]
[a] Department of Occupational and Environmental Health, Central South University, Changsha, Hunan, China

Abstract: Environmental and occupational low-dose radiation (LDR) exposure may be harmful for health but the previous reports regarding effect of LDR on cognition are contradictory. Here we investigated the effect of long-term LDR exposure on cognition. In this study, male Balb/c mice' cognitive functions were tested at 15 weeks after being exposed to 0.5 Gy LDR in 10 fractions at each dose of 0.05 Gy. The results demonstrated that long-term LDR exposure increases escape latency and the time spent in finding exits in mice compared with non LDR exposure. Meanwhile, the inflammation-related proteins including NFκB and p38 also increased. Lipopolysaccharide (LPS) increased and short-chain fatty acid (SCFA) levels decreased following long term LDR exposure. Treatment with microbiota-derived LPS and SCFAs reversed these effects in mice. Furthermore, the gut barrier integrity was damaged in a time-dependent manner with the decreased expression of intestinal epithelial-related biomarkers such as ZO-1 and occludin. Mechanistically, long after exposure to LDR, increased LPS levels may cause cognitive impairment through the regulation of Akt/mTOR signaling in the mouse hippocampus. These findings provide new insight into the clinical applications of LDR and suggest that the gut microbiota-plasma LPS and SCFAs-brain axis may underlie long-term LDR-induced cognition effects.

Hg transformations within organisms: The occurrence and mechanisms

Shouying Li[a], **Huan Zhong**[a,*]
[a] School of Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Mercury (Hg) is a global pollutant showing potent toxicity to living organisms. Organisms are generally considered as Hg "carriers" or "accumulators", absorbing Hg from the ambient environments and then transferring them to humans along food webs. For past decades, Hg transformations, i.e., methylation/demethylation and reduction/oxidization, are believed to mainly occur in ambient environments, such as in the air, water columns, and sediments/soils. It remains unknown whether and to what extent Hg transformations happen within organisms. This critical knowledge gap leads to the failure in liking Hg in the environments and human exposure, as well as an effective strategy to mitigate Hg risk. Here, we reviewed the hidden role of organisms as Hg "transformers": Significant MeHg demethylation and Hg reduction occur within organisms, including rice plants, algae, fish, etc. These processes largely reduce the Hg contents in organisms and the subsequent Hg flux along food webs, mitigating human Hg exposure risks. Importantly, these transformations were induced by neither light nor microbes, the commonly recognized driving forces of Hg transformations in the ambient environments, suggesting the existence of hidden mechanisms of Hg transformations. This study highlights the importance of paying attention to the organism-induced Hg transformations and the potential drivers, which could largely advance our understanding of Hg biogeochemistry and shape the global Hg cycling.

Do wearing masks and preservatives have a combined effect on skin health?

Yu Liu[a,b], Lei Wang[a,*]

[a] The College of Environmental Science and Engineering, Nankai University, Tianjin, China

[b] State Key Laboratory of Environmental and Biological Analysis, Department of Chemistry, Hong Kong Baptist University, Hong Kong, China

Abstract: Chemical exposure and local hypoxia caused by mask-wearing may result in skin physiology changes. The effects of methylparaben (MeP), a commonly used preservative in personal care products, and hypoxia on skin health were investigated by HaCaT cell and ICR mouse experiments. MeP exposure resulted in lipid peroxidation and interfered with cellular glutathione metabolism, while hypoxia treatment disturbed phenylalanine, tyrosine, and tryptophan biosynthesis pathways and energy metabolism to respond to oxidative stress. A hypoxic environment increased the perturbation of MeP on the purine metabolism in HaCaT cells, resulting in increased expression of proinflammatory cytokines. The synergistic effects were further validated in a mouse model with MeP dermal exposure and “mask-wearing” treatment. CAT, PPARG, and MMP2 were identified as possible key gene targets associated with skin health risks posed by MeP and hypoxia. Network toxicity analysis suggested a synergistic effect, indicating the risk of skin inflammation and skin barrier aging.

Occupational exposure to plasticizers in waste recycling: Focus on the size-fractioned particulate-bound phthalates and bisphenols

Ying Guo[a],*, Tingting Xu[a]
[a] College of Environment and Climate, Jinan university, Guangzhou , Guangdong, China

Abstract: Phthalate (PAEs) and bisphenols (BPs) are widely used as plasticizers or additives in a variety of consumer products, and potential human health hazards can occur through inhalation, ingestion, and dermal contact. However, the existing studies on the inhalation exposure assessment of PAEs and BPs take little account of particle size distribution, in spite of particulate-bound pollutants are size dependent. Noting this knowledge gap, we determined the exposure level of size-fractioned particulate-bound PAEs and BPs for workers from waste recycling plants, and the assessment of internal and external exposure were combined to understand occupational health risk comprehensively. Particulate-bound PAEs and BPs mainly concentrated on coarse particles ($Dp > 2.1\mu m$), with a bimodal distribution, and the peak particle size ranged from 9-10 μm to 4.7-5.85 μm. Model calculation revealed that the deposition flux of PAEs in different respiratory regions was follow the sequence of head airways (HA: 167 ± 92.8 ng h^{-1}) > tracheobronchial region (TB: 18.9 ± 9.96 ng h^{-1}) > alveolar region (AR: 9.20 ± 5.22 ng h^{-1}). And the deposition fluxes of BPs in the HA, TB and AR were 28.3-383, 1.67-22.4 and 3.55-48.6 ng h^{-1}, respectively. The daily intake of PAEs and BPs via dust ingestion was the highest among the four external exposure pathways, with a mean value of 96 and 0. 88 ng kg^{-1}-bw day^{-1}, respectively. For internal exposure, the estimated daily intake of PAEs for waste recycling workers were higher than that of many reported data, especially e-waste dismantling workers, while the exposure level of bisphenol tends to be normal. Overall, the potential health risk from inhalation exposure to particulate-bound PAEs and BPs were relatively lower than that to dust and other media, but the unique effect of fine particulate-bound contaminants on the lungs should not be overlooked.

Inhibition, recovery and stabilization in MBR-Anammox process: Enhancing nitrogen removal by biochar supported nano zero-valent iron adoption

Zhenyu Wang[a], Zaoli Gu[a,*], Xuejiang Wang[a]

[a] College of Environmental Science and Engineering, Tongji University, Shanghai, China

Abstract: Anaerobic ammonium oxidation (Anammox) is recognized as a promising option to energy-neutral wastewater treatment, yet difficulties encountered in practice due to its poor stability. This work investigated the effects of biochar supported nano zero-valent iron (nZVI-BC) on nitrogen removal performance of anammox process. Three MBR-anammox reactors were operated for 100 days undergoing adaption, dissolved oxygen inhibition, performance recovery and stabilization periods. The results showed that nZVI-BC adoption could improve the nitrogen removal efficiency by 5.5%-27.3% and 3.1%-20.7% and nitrogen removal rate by 5.4%-28.6% and 3.2%-22.9%, compared with control group and biochar adoption, respectively. Throughout the experimental periods, nZVI-BC was conducive to enrich anammox bacteria and increased the functional genes copies associated with anammox metabolism. Meanwhile, co-occurrence network analysis promulgated that nZVI-BC boosted the robustness and interaction of microbial community. Furthermore, the electrochemical analysis of the extracellular polymeric substance revealed that nZVI-BC adoption augmented the extracellular electron transport process of anammox biomass. Metagenomic sequencing revealed that nZVI-BC reinforced the complete dissimilatory nitrate reduction to ammonium pathway in dominate anammox bacteria Candidatus Brocadia, which could lead to an enhancement of nitrogen removal. The study manifested the possibility of nZVI-BC to improve the anammox robustness and nitrogen removal performance and provided operational guidance for its engineering application.

Reevaluating biostimulation strategies: The impact of humic acid on ofloxacin bioadsorption

Kaiying Chen[a], Qiang Lin[a], Ancheng Luo[a], Chisheng Yu[a], Zhiwei Liang[a,*], Najinwa Hu[a]
[a] College of Environmental and Resource Science, Zhejiang University, Hangzhou, Zhejiang, China

Abstract: The exogenous addition of humic acid (HA) is often seen as a biostimulation strategy to expedite the bioremediation of various pharmaceutical pollutants. Nevertheless, the impact of HA on the bioadsorption of OFL, the main pathway for OFL removal in activated sludge, remains unknown. In this study, the presence of 10 mg/L HA notably decreased the theoretical OFL adsorption capacity from 8.94 to 7.95 mg/g. The inhibitory effect persisted across varying pH and ionic strengths and became more pronounced with increasing HA concentration. The morphological changes on biosolid (BIO) induced by HA indicated that HA was bioadsorbed, which in turn competed with OFL for metal binding sites like Ca and Mg on BIO. Further analysis of the OFL-HA interaction reveals the involvement of hydrogen bonding and electrostatic attraction. The study also demonstrates the bridging role of HA between OFL and BIO through consecutive desorption and re-absorption processes of OFL in the presence of HA. To quantify the direct and indirect adsorption ratios, a new approach was proposed, which determined the mass ratios of direct (OFL:BIO) and indirect bioadsorption (OFL:HA:BIO) as 1:192.27 and 1:26.71:854.71, respectively. These findings suggest that the indirect OFL adsorption through the HA bridge could not compensate for the adverse effects caused by the reduction of metal binding sites. Overall, this study calls for a reassessment of the addition of HA in the antibiotics' bioremediation process. Considering that HA widely coexists with antibiotics in wastewater, the study also provides valuable insights into OFL removal mechanisms in WWTPs.

Aerobic denitrification enhanced by immobilized slow-released iron/activated carbon aquagel treatment of low C/N micropolluted water: Denitrification performance, denitrifying bacterial community co-occurrence, and implications

Haihan Zhang[a,*]

[a] School of Environment and Municipal Engineering, Xi'an University of Architecture and Technology, Xi'an, Shaanxi, China

Abstract: The key limiting factors in the treatment of low C/N micropolluted water bodies are deficient essential electron donors for nitrogen removal processes. An iron/activated carbon aquagel (IACA) was synthesized as a slowly released inorganic electron donor to enhance aerobic denitrification performance in low C/N micropolluted water treatment. The denitrification efficiency in IACA reactors was enhanced by more than 56.72% and the highest of 94.12% was accomplished compared with those of the control reactors. Moreover, the CODMn removal efficiency improved by more than 34.32% in IACA reactors. The Illumina MiSeq sequencing consequence explained that the denitrifying bacteria with facultative denitrification, iron oxidation, and iron reduction function were located in the dominant species niches in the IACA reactors (e.g., *Pseudomonas*, *Leptothrix*, and *Comamonas*). The diversity and richness of the denitrifying bacterial communities were enhanced in the IACA reactors. Network analysis indicated that aerobic denitrifying bacterial consortia in IACA reactors presented a more complicated co-occurrence structure. The IACA reactors presented the potential for long-term denitrification operation. This study affords a pathway to utilize IACA, promoting aerobic denitrification during low C/N micropolluted water body treatment.

Rational design of carbon and spinel-structured nanocomposites toward environmental remediation and green catalysis conversions

Xinyong Li[a,*]
[a] Enviromental Science & Engineering, Dalian University of Technology, Dalian, Liaoning, China

Abstract: Multifunctional nano-structured materials with novel properties, e. g. , magnetism, optics, electricity, and catalysis have received enormous attention from the entire world, which largely depend on their precise tailored structures and chemical compositions. In this talk, various carbon and spinel-structured materials with controlled fabrications and green conversions and solar harvesting and beyond are initially reviewed, the composition and structure of spinels will be briefly introduced and illustrated. Secondly, some of the recent advances in the preparation and characterization of multifunctional nano-structured materials are accordingly summarized, and new strategies are specifically highlighted. The physico-chemical characteristics of multifunctional nano-structured materials such as their interfacial structures, various morphologies and derived defects have been rationally regulated through various approaches, which could incur them with improved catalytic conversion to fine chemicals and energetic utilization as well as conversion shall also be discussed in terms of the tailored surface-interface structures of the afore-mentioned nanocomposite materials.

Application of nanoscale zero-valent iron for soil remediation and safe crop production

Daohui Lin[a,*]

[a] Department of Environmental Science, Zhejiang University, Hangzhou, Zhejiang, China

Abstract: Nanoscale zero-valent iron (nZVI) may antagonize the toxicity of co-existing contaminants to plant, along with the removal of contaminants, which enables the development of nZVI-based phytoremediation technologies. In recent years, we put forward a strategy extracting valuable information from joint nanotoxicity studies as an indicator for the development of nano-enabled bioremediation technologies. We established a new soil remediation strategy using nZVI coupled with safe rice-production in paddy soil contaminated with pentachlorophenol (PCP). The specific role of nZVI-derived root iron plaque formation in the safe production of rice was described, and the synergistic effect of nZVI-treatment and rice cultivation was identified as nZVI-facilitated rhizosphere microbial degradation of PCP. nZVI was also found to interact with alfalfa and synergistically remediate polychlorinated biphenyl-contaminated agricultural soil. An indigenous dehalogenation bacteria was isolated from the agricultural soil, and a synergistic effect of soil organic matter and nZVI was observed on the biodegradation of organochlorines. This paper briefly present these nZVI-bioremediation technologies, with a focus on the interactions among nZVI, biota, and pollutants.

Ecological effects of the antibiotic ciprofloxacin in sub- tropical freshwater mesocosms

Kai-Sheng Yao[a,b], Pei-Liang Zhou[b,c], Lu-Kai Qiao[b,c], Li-Juan Tan[b,c], Fang-Zhou Gao[b,c], Guang-Guo Ying[b,c] and Paul J. Van den Brink[a]

[a] Wageningen University, Aquatic Ecology and Water Quality Management Group, Wageningen, The Netherlands

[b] SCNU Environmental Research Institute, Guangdong Provincial Key Laboratory of Chemical Pollution and Environmental Safety, MOE Key Laboratory of Theoretical Chemistry of Environment, South China Normal University, Guangzhou, Guangdong, China

[c] School of Environment, South China Normal University, Guangzhou, Guangdong, China

Abstract: Antibiotics are widely detected in aquatic ecosystems due to improper use and excretion by humans and animals, which could pose a potential impact on aquatic communities. The main objective of the present study was to assess the ecological effects of the antibiotic ciprofloxacin on the structural (macroinvertebrates, zooplankton, phytoplankton, periphyton and microbes) and functional endpoints of aquatic ecosystems under sub-tropical conditions. Ciprofloxacin was applied at a concentration of 0, 0.5, 5, 50 and 500 μg/L for 21 consecutive days in outdoor mesocosms, followed by a five-week recovery period. At the community level, ciprofloxacin significantly affected the structure of zooplankton, phytoplankton and microbial communities, with calculated NOECs of 0.5, < 0.5 and 0.5 μg/L, respectively. The overall treatment-related effects on the macroinvertebrate community and periphyton biomass could not be demonstrated. The highest sensitivity to ciprofloxacin (NOEC < 0.5 μg/L) was observed for the filamentous cyanobacteria *Cylindrospermopsis* sp., with its abundance significantly decreasing during the exposure period but recovering at the end of the experiment. On the other hand, *Microcystis* sp., *Ankistrodesmus* sp., *Selenastrum* sp. showed the most prominent increase in abundance related to the ciprofloxacin treatments. Furthermore, ciprofloxacin indirectly induced an increase in populations of zooplankton (Cladocera, Copepoda and Rotifera). Significant treatment related effects were found on parameters related to photosynthesis (dissolved oxygen concentration, ecosystem productivity and pH) and parameters related to carbon and nitrogen cycles (dissolved organic carbon and nitrate concentrations). Overall, our study highlights the importance of evaluating the ecological effects of antibiotics (e.g., ciprofloxacin) across multiple trophic levels spanning multiple aquatic communities to fully understand its potential ecological threats in freshwater ecosystems.

Spatiotemporal functional statistics for heterogeneity relationship between artificial planting community and mosquito density in big city of the middle-lower Yangtze plain

Jing Shen[a,*]
[a] College of Ecology and Enviroment, Nanjing Forestry University, Nanjing, Jiangsu, China

Abstract: Green infrastructure(GI) is an important part of the ecological environment, so to search a rationale GI composition structure is important for Regional Sustainable Development and ecology safety. Objective to study methods for surveying of vectors (for example density of mosquito). Based on several periods data of Land use in TM grid type data and principles of ecology management philosophy to regional one health aim. We gave a series of indices in accordance with GI planning character and landscape pattern of landscape ecological theory. We were made up with special attention to the interaction between the human activity and the GI in these indices. From the angle of geography regional analysis, we combine the Hierarchical Bayesian model (HBMMMs) and critical infrastructure systems (CISs) of spatial statistics, we want to try to solve some crucial issues of regional GI system in society community in city site. We pay attention to the plant community. We will study the city of Nanjing, we want to get the data from CDC and we will study the series of areas and get plant community data for model. The application research will include three parts: data set will be build include plant and mosquito indices. This part need theory study; analysis and the investigation Nanjing community plots, we will analyze structure all data sets in the Hierarchical Bayesian model, it also will establish the model between vectors density and community structure.

Extensive reductive dechlorination and anaerobic mineralization of 2,4,6-Trichlorophenol in biocathode constructed with microbial community acclimated by fixed or variable potential

Yanqiang Tang[a], Ying Wang[a], Yan Xu[a,*]

[a] School of Civil Engineering, Southeast University, Nanjing, Jiangsu, China

Abstract: Microbially catalyzed dechlorination of persistent chlorophenols is an important in situ remediation and detoxification route in the environment. However, the low degradation rate and limited dechlorination extent hinder its application. To overcome the obstacles, in this study, new bioelectrochemical systems were established using different microbial community acclimation strategies for the treatment of 2,4,6-trichlorophenol (2,4,6-TCP). The results revealed that the degradation rate of 2,4,6-TCP in the BES acclimated under variable potentials (T-V) reached 0.67 d^{-1}, while that in the BES acclimated at a fixed potential (T-F) was 0.080 d^{-1} and that in the open-circuit control was only 0.038 d^{-1}. Compared to T-F, T-V exhibited much more extensive dechlorination and the products 2,4-dichlorophenol (2,4-DCP), 4-monochlorophenol (4-MCP), 2-monochlorophenol (2-MCP), and phenol did not apparently accumulate. Moreover, the pronounced reduction of TOC, as well as the detection of 4-hydroxybenzoic acid indicated the occurrence of anaerobic mineralization in T-V. The cyclic voltammetry (CV) and differential pulse voltammetry (DPV) results confirmed the presence of electroactive sites in the cathode biofilm of T-V, and the similar oxidation and reduction potential also indicated that both reductive and oxidative reactions were likely to be catalyzed by the same bacterial consortium and the same extracellular electron transport. High-throughput sequencing revealed that more abundant *Mycobacterium* (24.33% in slurry and 19.92% in biofilm) and *Thiobacillus* (2.47% in slurry and 17.85% in biofilm) were in T-V, which are associated with extracellular electron transfer, and Mycobacterium are regarded as chlorophenol degraders. These findings highlight the role of microbial community acclimation on BES and provide insights into the mechanisms of electro-stimulation in conjunction with microbial interrelations.

Size-dependent accumulation and translocation of SiO_2 nanoparticles from roots to shoots in rice seedlings

Wei Pan[a], **Ai-Jun Miao**[a,*]

[a] School of the Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Silica nanoparticles (SiO_2 NPs) are extensively utilized in the agricultural sector for growth regulation, pest control, and as carriers for agrochemicals. However, the bioaccumulation of SiO_2 NPs within plants has received less scrutiny. Given that the uptake and impact of soluble NPs are often influenced by the presence of dissolved ions, this study synthesized SiO_2 NPs in three distinct sizes (20 nm, 50 nm, and 100 nm) using the seed regrowth method. We assessed their stability, with a focus on dissolution rates, and subsequently analyzed their uptake and translocation in *Oryza sativa*. To isolate the effects of SiO_2 NPs, solution pH was carefully controlled to mitigate the impact of dissolved silicon. Our findings indicate that all three SiO_2 NP sizes elevated silicon content in both roots and shoots of rice seedlings, with the 20 nm particles demonstrating the most significant increase in shoot silicon content. To discern the source of silicon in the shoots, whether from particulate SiO_2 or silicate, we conducted parallel experiments with silicate and core-shell structured Au@ SiO_2 NPs. The silicate experiment confirmed that silicon initially dissolved from the SiO_2 NPs was translocated to the shoots. The core-shell Au@ SiO_2 NPs validated the transport of all three SiO_2 NP sizes from roots to shoots, eliminating the necessity for additional imaging to confirm translocation. Interestingly, the 100 nm SiO_2 NPs contributed the most to particulate silicon in the shoots, whereas the 20 nm particles had the highest contribution from initially dissolved silicon to shoot accumulation. Collectively, our study underscores the necessity of accounting for ionic effects when assessing the uptake and biological effects of soluble NPs in plants. It also offers valuable theoretical insights for the development of nanoscale slow-release fertilizers in agricultural applications.

Predicting the adsorption of organic pollutants onto microplastics via GCMC and machine learning

Ya Wang[a,*]

[a] School of Energy and Environmental Engineering, University of Science and Technology Beijing, Beijing, China

Abstract: It is of great significance to study the adsorption of various organic pollutants onto microplastics and establish prediction models for understanding their environmental behaviors and evaluating their ecological risks. In current study, the adsorptions for 54 different organic pollutants onto 12 representative microplastics were simulated with GCMC. The results showed that the top three microplastics with large adsorption capacity were polyethylene (PE), polyoxymethylene (POM) and polyvinyl alcohol (PVA). Electronic structure information was analyzed with density functional theory (DFT) computation. Quantitative structure activity relationship (QSAR) models were developed for predicting the adsorption of organic pollutants onto various microplastics with multiple linear regression and machine learning, respectively. All the models perform well on the goodness of fit, robustness and predictive ability.

Deriving aquatic PNECs of endocrine disruption chemicals by combining species sensitivity weighted distributions (SSWD) and adverse outcome pathway (AOP) networks

Jiawei Zhang[a,b,*]

[a] Institute of Strategic Planning, Chinese Academy of Environmental Planning (CAEP), Beijing, China

[b] School of Environment, Tsinghua University, Beijing, China

Abstract: Endocrine-disrupting chemicals (EDCs), e.g., bisphenols, phthalates, per- and polyfluoroalkyl substances, pose long-term adverse effects on aquatic organisms. The current commonly used ecological risk assessment (ERA) framework mainly focuses on acute and chronic lethal effects of chemicals, rather than reproductive and developmental effects. The mode of toxicity action of EDCs was not fully considered in ERA, which may result in an underestimation of ecological risks. In the study, the species sensitivity weighted distribution (SSWD) models based on adverse outcome pathway (AOP) networks were developed for deriving predicted no-effect concentrations (PNECs) of selected EDCs. Three weighting criteria (intraspecies variation, trophic level abundance, and data quality) and weighted log-normal distribution methods were adopted. This method combined the advantages of both models and provided reliable estimates of PNECs. SSWD models can consider the inter/intraspecies variation and quality of toxicity data of EDCs. AOP network can integrate nontraditional endpoints and muti-biological levels of endocrine disruption effects. For instance, the PNECs of endocrine disruption effects were derived as 8.10 μg/L for BPA, 12.9 μg/L for DBP, and 2.52 μg/L for PFOS, which were more conservative than those derived from the acute toxicity data and were comparable with the values in the literature based on the chronic toxicity data. The long-term effects of EDCs are significant and need to be fully recognized in the ERA. This study provided an ERA framework that can improve the ecological relevance and reduce the uncertainty of PNECs of EDCs.

Environmental behavior of herbicides and arsenic in soil affected by Fenton/Fenton-like reaction

Yanjie Chen[a], **Maojian Gong**[b], **Huashou Li**[a,*]

[a] College of natural resources and environment, south China agricultural university, guangzhou, guangdong, China

[b] Shenzhen Agricultural Science and Technology Promotion Center, shenzhen, guangdong, China

Abstract: Abstract: The Fenton reaction is a widely used advanced oxidation process. It involves the catalysis of H_2O_2 by Fe^{2+} to produce hydroxyl radical (·OH), which is a strongly oxidizing agent. The·OH affects pollutants by direct oxidation or indirectly through the biogeochemical processes of microbial functional bacteria, although the exact interface is not yet fully understood. This process can affect the environmental behavior of chemicals in soil. Glyphosate is one of the most widely used pesticides globally. Large amounts of glyphosate residue can accumulate in the environment, causing adverse effects in organisms. We found that slow-release of H_2O_2 in soil through the application of urea hydrogen peroxide (UHP) can react with Fe^{2+} in a Fenton-like reaction. Among all treatments, the half-life of glyphosate in the mixed application of UHP and ferrous sulphate was the shortest (11.9 d), and its degradation rate was the highest (70.74%), degrading within 28 d. Arsenic (As) is a toxic metalloid, and elevated levels of As in soils are becoming a global problem with potential risks to human health. We investigated the effects of different concentrations of micro-molar H_2O_2 (0, 50 and 100 μM) on changes in soil As and SOM through indoor simulations. The micro-oxidative environment created by the simulated rainwater with 100 μM H_2O_2, as well as its driven Fenton/Fenton-like reaction played important roles in the change in soil As speciation and SOM formation, by (1) driving the conversion of other forms of As to more stable forms of As and reducing the ecological risk of As; and (2) inducing relevant lignocellulose-degrading microbial and driving SOM formation. These findings provide a scientific basis for conducting in situ remediation of herbicide and As contaminated soils in agricultural fields.

Magic golden cudgel with supernatural power: Perfluorooctanoic acid efficient chain reaction degradation in multifunctional iron-sulfur mineral augmentation geobiochemical remediation system

Meng Zhang[a], **Wenbing Wang**[a,*]

[a] School of Environmental and Chemical Engineering, Shanghai University, Shanghai, China

Abstract: Serious contamination of perfluorooctanoic acid (PFOA) has aroused global concern. General biotransformation or iron-based materials did not meet efficient PFOA removal. Here, specific green and low-carbon microorganism-biochar pellets, multi-component and multifunctional iron-sulfur (Fe_xS_y) mineral pellets, and a microbe-Fe_xS_y interaction geobiochemical remediation device were developed to solve this problem. The multi-scale (molecular, interface, and column scales) research method combined with the physical-chemical-biological multi-process reaction model was constructed to explore the PFOA removal and mechanism. Results revealed that the microbe-Fe_xS_y interaction achieved excellent PFOA degradation performance and retention effect, with degradation rate λ (0.213 h^{-1}) increased by 113% than the Fe_xS_y (0.100 h^{-1}) device. The distribution coefficient Kd and kinetic adsorption α increased by 18.54% and 22.61%; the fraction of kinetic sorption increased by 63.83% in the microbe-FexSy device (77%) compared to alone Fe_xS_y (47%) device. High-throughput sequencing showed that microbe-FexSy interaction increased the abundance of bacteria and archaea in the aqueous phase. Delftia and Pseudomonas combined with Fe^{2+} drove an efficient cycle chain reaction for PFOA. Liquid chromatograph mass spectrometer (LC-MS) results and quantitative structure-activity relationship (QSAR) model indicated that intermediates exhibited lower biotoxicity than PFOA. The bioaccumulation factor of intermediates decreased by 40.09%–99.24% than PFOA. Furthermore, the NO_3- further increased the retention effect of the microbe-Fe_xS_y device for PFOA with little reaction rate fluctuation, making it promising for eliminating PFOA contamination, especially in NO_3^- type of groundwater. It provided an efficient technology and device based on microbe-mineral interaction in remediating PFOA-contaminated groundwater.

Ecological risk assessment and ecological security pattern construction in inland river basin

Ranghui Wang[a], **Huizhi Zhang**[a,*]

[a] School of Ecology and Meteorology, Nanjing University of Information Science and Technology, Nanjing, Jiangsu, China

Abstract: Ecological risk and ecological security are closely related, and studying the characteristics and changes of ecological risk is of great significance for building an ESP. Based on the principles of regional differentiation, ecosystem coupling, and ecological complexity, conduct an ecological risk assessment (ERA) of the Tarim River Basin(TRB) in China, analyze the ESP, and reveal the mechanism of ecological stability in the basin. By constructing an ERA index system consisting of four subsystems, e. g., water resource system, land resource system, biological resource system, and environmental system, an evaluation mathematical model is established. The required big data for evaluation is obtained through quantitative remote sensing, actual investigation, public database, laboratory analysis, and other methods. Quantitative data processing methods are used to analyze ecological risks and security characteristics. The ESP of each subsystem and its contribution to the ecological security effect of the basin are different from each other. The various indicators of the water resources subsystem are basically stable and tend to improve, and ESP shows an evolutionary pattern of becoming better while maintaining stability. The coexistence of positive and negative effects of relevant factors in the land resource subsystem, especially the influence of changes in salt alkalization index, suppresses the improvement trend of ESP. The ecological risk index（ERI） values of both the biological resource subsystem and the environmental subsystem significantly decreased, indicating a significant enhancement of ESP. From the perspective of basin landscape pattern, enhancing ecological source areas, dredging ecological corridors, and alleviating ecological resistance surfaces are important ways to curb ecological risks and ensure ecological security. On the basis of revealing the evolution process and laws of ESP, ecological risk control, ecological restoration and management models are proposed to provide support for sustainable development of the basin.

Trends of toxic equivalent contributions from anthropogenic emissions of 11 trace elements in China from 1980 to 2020

Lei Zhang[a,*], **Yunrong Xiao**[a], **Jingmeng Jin**[a]
[a] School of the Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Trace elements, e. g., heavy metals, have potential ecological risks due to their biotoxicity, persistence and bioaccumulation effects. Considerable amounts of incremental trace elements in soil were originated from anthropogenic emissions to the air. In this study, an integrated Dynamic Air Toxics Emissions (DATE) model was developed. Long-term historical emission inventories for 11 trace elements (TEs) in China, including Hg, Cd, As, Pb, Ni, Co, Cu, Cr, V, Zn, and Mn, were established, and trends of their toxic equivalent contributions from 1980 to 2020 were analyzed. The ecological toxicity of each TE was characterized by a dimensionless toxic equivalent (TEQ). The accuracy of emission estimates for key sectors were improved. Four stages with distinct leading drivers were identified. At Stage 1 (1980−1990), the total TEQ emissions almost doubled with the rapid growth of the economy, with Pb accounting for nearly half of the total. Over 70% of the Pb emissions came from liquid fuel combustion. The driver of this trend was suppressed by the reduction of Pb content in leaded gasoline regulated by GB 484–89 at Stage 2 (1991−2000). At this stage, the contribution of Cu and V to the total TEQ emissions both increased rapidly to over 10% in 2000 under the fast growth of coal use. The year 2000 was a pivotal divide for TEQ emission due to the substitution with unleaded gasoline. The Pb emission dropped abruptly in 2001 and initiated Stage 3 (2001−2012). Large increase of the penetration rates of dust and SO_2 control measures at this stage offset the TEQ emission growth driven by coal combustion. At Stage 4 (2013−2020), the ultralow emission retrofits had high removal efficiencies for most TEs. The growing contributions of Cu and V to total TEQ emission were induced by brake wear and denitrification catalysts, respectively.

Recent advances in Hg biogeochemistry in the rice-paddy system

Wenli Tang[a], **Huan Zhong**[a,*]
[a] School of Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Hg biogeochemistry in the rice-paddy system is critical, given that rice is the primary source of MeHg exposure for Asians and infants. Over the past 3 years, we have conducted a series of studies in this field, including the MeHg analysis method, Hg methylation, and MeHg demethylation. We first propose that alkaline extraction (KOH-CH_3OH) is an optimal choice for paddy soils, with negligible MeHg artifacts and consistently high extraction efficiency, while acid extraction, i. e., $CuSO_4$/KBr/H_2SO_4-CH_2Cl_2, is not suitable for paddy soils, given the low extraction efficiency (21.3%−70.8%). For Hg methylation, we report that soil Geobacteraceae could predict MeHg accumulation in rice. This is because the hgcA-containing Geobacteraceae have the highest abundance, their activities are significantly correlated to soil MeHg production, and rice MeHg accumulation is more sensitive to Geobacteraceae activity than Hg input via deposition or irrigation. We also find that soil selenium (Se) could impact Geobacteraceae activity and thus propose an approach to mitigate Hg risk by regulating Geobacteraceae in soils. For MeHg demethylation, we report a light- and microbe-independent pathway in plants. This pathway is mediated by the in vivo generated singlet oxygen, which attacks the C-Hg bound with the aid of thiols, reducing MeHg accumulation in rice by 58%-79% and avoiding an IQ decrement of 0.01–0.51 points/newborn in major rice-consuming countries (equivalent to economic losses of US$30.7–84.2 billion globally). In addition, MeHg photodegradation, a critical natural pathway of MeHg degradation in aquatic systems, is an overlooked process mitigating Hg risks, which reduces MeHg concentrations in water and rice by 82% and 11%, respectively. Without photodegradation, paddy water could be a significant MeHg source for downstream ecosystems, with an annual export of 178–856 kg MeHg. The above findings broadly advance our understanding of Hg global cycling and provide insights into Hg risk mitigation.

Mechanism of synergistic remediation of soil phenanthrene contamination in paddy fields by rice-crab coculture and bioaugmentation with *Pseudomonas* sp.

Nan Sun[a,*]
[a] School of Water Conservancy and Civil Engineering, Northeast Agricultural University, Harbin, Heilongjiang, China

Abstract: Polycyclic aromatic hydrocarbons (PAHs) are persistent and harmful pollutants with high priority concern in agricultural fields. This work constructed a rice-crab coculture and bioaugmentation (RCM) system to remediate phenanthrene (a model PAH) contamination in rice fields. The results showed that RCM had a higher remediation performance of phenanthrene in rice paddy compared with rice cultivation alone, microbial addition alone, and crab-rice coculture, reaching a remediation efficiency of 88.92% in 42 d. The concentration of phenanthrene in the rice plants decreased to 6.58 mg/kg, and its bioconcentration effect was efficiently inhibited in the RCM system. In addition, some low molecular weight organic acids of rice root increased by 12.87%–73.87%, and some amino acids increased by 140%–1150% in RCM. Bioturbation of crabs improves soil aeration structure and microbial migration, and adding Pseudomonas promoted the proliferation of some plant growth-promoting rhizobacteria (PGPRs), which facilitated the degradation of phenanthrene. This coupling rice-crab coculture with bioaugmentation had favorable effects on soil enzyme activity, microbial community structure, and PAH degradation genes in paddy fields, enhancing the removal of and resistance to PAH contamination in paddy fields and providing new strategies for achieving a balance between production and remediation in contaminated paddy fields.

Fine-tuned nano-catalysts for electrochemical CO_2 utilization

Yang Zhou[a], Wenlei Zhu[b,*]
[a] Institute of Advanced Materials, Nanjing University of Posts & Telecommunications, Nanjing, Jiangsu, China
[b] School of the Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: The ever-increasing worldwide consumption of fossil fuels has accelerated the depletion of these finite natural resources and led to overproduction of the greenhouse gas-carbon dioxide. New methods to utilize CO_2 to produce high-value chemical commodities are preferred. Electrochemical methods are suitable for CO_2 reduction reactions (CO_2RR) due to mild reaction conditions and tunable reduction products. However, large overpotentials, low faradaic efficiency, and poor selectivity hinder the advances of the CO_2RR. Advanced synthesis strategies and detailed characterizations have been applied to fully understand the relations between catalysts and CO_2RR products. This paper presents several new strategies to tune the performance of nanoscale catalysts for reducing CO_2 to targeted products.

Reevaluating the role of pollution tolerant protozoa in environmental remediation

Ying Chen[a,*], Weibin Zheng[a], Sen Hou[a], Xiaodan Zheng[a], Aijie Wang[a], Nanqi Ren[a]

[a] State Key Laboratory of Urban Water Resource and Environment, School of Civil and Environmental Engineering, Harbin Institute of Technology (Shenzhen), Shenzhen, Guangdong, China

Abstract: Single-celled eukaryotic microorganisms, notably algae and protozoa, have traditionally been recognized as bioindicators of environmental stress. Protozoa, in particular, have been deemed highly sensitive to environment due to the difficulties of collection, observation, and cultivation, supposedly rendering them less capable of tolerating pollution and participating in bioremediation. However, emerging evidence contradicted this perspective, revealing that many protozoa possess high pollutant tolerance and bioremediation abilities. Besides, some bactivorous protozoa can significantly influence the remediation effectiveness of bacteria. Despite these new findings, research on leveraging protozoa for direct or indirect environmental clean-up remains scant. Since 2017, our targeted efforts to isolate and culture pollution tolerant protozoa from contaminated sites have led to some groundbreaking discoveries. We have been able to provide a soil ciliate as the novel tool for remediation of cadmium and sulfonamides antibiotic contaminations. Based on the full disclosure of their molecular mechanisms, the target proteins responding to cadmium and sulfonamides antibiotics have been identified, expression vectors in vitro have been constructed, and a series of mathematical equations have been established for the evaluation of remediation effects. The discovery of similar mechanisms in more pollution-tolerant protozoa will move forward the significant bioremediation potential of single-celled eukaryotic organisms. Intensive studies into interactions between bactivorous protozoa and bacteria promise to advance new theoretical and technical frameworks for environmental remediation.

Lattice engineered nanoscale Fe^0 for efficient and selective groundwater remediations

Jiang Xu[a,*]

[a] Department of Environmental Science, Zhejiang University, Hangzhou, Zhejiang, China

Abstract: In situ groundwater remediation is in pressing demand for sustainable freshwater supplies. Achieving rapid and highly selective chemical reductions using Fe^0 nanomaterials for groundwater remediation remains challenging. Here, lattice-engineered nFe0 materials with controllable lattice strain and S speciation via a one-step procedure were synthesized to overcome the reactivity–selectivity–stability trade-offs. Chemoselective dehalogenation and hydrogenation at a remarkable activity (up to 956-fold higher than for unmodified Fe^0) outcompete H_2 evolution for >90% electrons from lattice-doped Fe^0, also offering a high stability in air and water. The surface accumulation of heavy metals was tuned into intraparticle sequestration via a boosted Kirkendall-like effect. This talk demonstrates the ability to control the local microenvironment in the Fe^0 crystalline structure via lattice engineering, and the tunable geometric and electronic properties constitute a promising platform for the rational design of metallic nanomaterials with robust performance in efficient and selective groundwater remediation.

The priority of agricultural products to implement virtual water strategy considering production linkage relationship

Lin Yang[a], Xinan Yin[a,*], Zijie Gao[a], Baiheng Yang[a], Yi Tan[a]

[a] State Key Laboratory of Water Environment Simulation, School of Environment, Beijing Normal University, Beijing, China

Abstract: The virtual water strategy proposes that water-scarce regions should reduce the production of water-intensive products. Accordingly, the products with higher water intensity are usually placed higher priority to implement the strategy. However, this priority sorting only considers the water conservation effect of the product itself, while it does not consider the trade-offs between water conservation and economic development at the scale of the whole economic system. To consider the trade-offs effectively, this research proposes a priority determination framework for products to implement the virtual water strategy by considering the production linkage relationship of the whole economic system. In this framework, a computable general equilibrium model is established to explore the impacts of virtual water strategy on water conservation and economic development, and a production reduction priority index (water conservation to GDP loss ratio) is proposed to determine the priority of products to implement the strategy. The agricultural products in the Inner Mongolia province of China are adopted as the study cases. According to previous studies, oil crop was suggested to be given the highest priority to implement the virtual water strategy, while this research showed significant variations in the priority of agricultural products across different sub-modes of the virtual water strategy. Notably, vegetable and coarse cereal should be given the highest priority at given GDP loss under the direct-production-reduction, while potato should be given the highest priority under the indirect-production-reduction. The dual-policy sub-mode exhibited a different hierarchy, with oil crop and corn taking precedence over the other three products.

Optimization method of intelligent rainwater outlets in Southern China

Yi Tan[a], Xinan Yin[a,*], Lin Yang[a], Zijie Gao[a], Baiheng Yang[a]
[a] State Key Laboratory of Water Environment Simulation, School of Environment, Beijing Normal University, Beijing, China

Abstract: In southern cities, a large amount of sewage flows out of stormwater outlet in both rain and non-rain. At present, the indirect control of rainwater outlet is mainly carried out by means of intercepting well, but there are many shortcomings. The rainwater intelligent outlet is a rainwater collection and transport device installed at the outlet of the rainwater drain. It has a water level and water quality sensor, which can dynamically transport high-pollution water to the surrounding sewage network according to the change of water quantity and water quality in the sewage outlet, and discharge low-pollution water into the river and lake, thereby reducing the amount of sewage discharged from the stormwater outlet. The previous design of rainwater intelligent drainage has limitations. By answering the three questions of when to dispatch, how to dispatch and how much to dispatch, this study can realize the high interception amount and low energy consumption of rainwater intelligent outlet, so as to solve the problem of urban water pollution. Finally, the optimization method of intelligent rainwater outlet is proposed, the end of intelligent rainwater outlet is optimized, the intercepting amount of intelligent rainwater outlet is increased, and the operation energy consumption is reduced.

Polystyrene nanoparticles induce biofilm formation in *Pseudomonas aeruginosa*

Mark Bartlam[a,*]

[a] College of Life Sciences, Nankai University, Tianjin, China

Abstract: In recent years, micro/nanoplastics have garnered widespread attention due to their ecological risks. In this study, we investigated the effects of polystyrene nanoparticles (PS-NPs) of different sizes on the growth and biofilm formation of *Pseudomonas aeruginosa* PAO1. The results demonstrated that exposure to certain concentrations of PS-NPs significantly promoted bacterial biofilm formation. Meanwhile, we comprehensively revealed its mechanism whereby PS-NPs induced oxidative stress and altered bacterial membrane permeability by contacting or penetrating bacterial membranes. To counteract the stimulation by PS-NPs and reduce their toxicity, bacteria enhanced biofilm formation by up-regulating the expression of biofilm-related genes, increasing EPS and virulence factors secretion, and enhancing bacterial motility through the participation of the quorum sensing (QS) system. Additionally, we also found that exposure to PS-NPs enhanced bacterial antibiotic resistance, posing a challenge to antimicrobial therapy. Our study reveals the toxic effects of nanoplastics and the defense mechanisms of bacteria, which has important implications for the risk assessment and management of environmental nanoplastics.

Antibiotic resistance genes risks in relation to host pathogenicity and mobility in hospital wastewater treatment process

Chenye Xu[a,*]
[a] College of Environmental Science and Engineering, Donghua University, Shanghai, China

Abstract: Hospital wastewaters (HWWs) serve as vital hotspots in disseminating and propagating the antibiotic resistance genes (ARGs) and antibiotic resistant bacteria (ARB). However, the footprint of ARGs and their host pathogenicity, potential mobility and resistome risks during the HWWs treatment process remain largely unknown. Here, by using metagenomic sequencing and assembly, 817 ARG subtypes conferring resistance to 20 classes of antibiotics were detected in 18 HWW samples from influent to effluent. Genes encoding resistance to multidrug, aminoglycoside and beta_lactam were the most prevalent ARG types, which mirrored the bacterial resistance surveillance in clinics. On-site HWWs treatment could not completely remove the ARGs and chlorine disinfection significantly increased the ARGs abundances to the effluent. Deterministic processes mainly drove the taxonomic assembly and Proteobacteria was most abundant bacterial phylum and dominant host for carrying 15 ARG types. Contig-based analysis further identified 114 pathogenic ARB and the major potential pathogen-host of ARGs (Escherichia coli, Pseudomonas alcaligenes and Pseudomonas aeruginosa) pronounced multiple antibiotic resistance. Contributions of host bacteria and pathogenic ARB changed during wastewater treatment processes. In addition, 7.10%–31.0% ARGs were found to be flanked by mobile genetic elements (MGEs) and generally mediated by transposase (74.1%). Among the 199 MGE subtypes identified, tnpA showed greatest potential for ARGs dissemination and highest co-existence frequency with beta_lactam resistance genes (35.2%). By considering the profile, pathogenic hosts and mobility of ARGs, raw influent was characterized by the highest antibiotic resistome risk index (APRI) followed by final effluent. Chlorine disinfection significantly induced potential pathogenic ARB and mobile ARGs, which aggravated the resistome risk to the receiving environment. This study not only depicted the occurrence patterns but also tackled the ARGs carriage and horizontal gene transfer events, which provided important insights in estimating the resistance risks and supporting the priority clinic setting.

Metagenome sequencing reveals shifts in phage-associated antibiotic resistance genes from influent to effluent in wastewater treatment plants

Zong Li[a], Xinchun Liu[a,*]

[a] College of Resources and Environment, University of Chinese Academy of Sciences, BeiJing, China

Abstract: Antibiotic resistance poses a significant threat to global health, and the microbe-rich activated sludge environment may contribute to the dissemination of antibiotic resistance genes (ARGs). ARGs spread across various bacterial populations via multiple dissemination routes, including horizontal gene transfer mediated by bacteriophages (phages). However, the potential role of phages in spreading ARGs in wastewater treatment systems remains unclear. This study characterized the core resistome, mobile genetic elements (MGEs), and virus-associated ARGs (vir_ARGs) in influents (Inf) and effluents (Eff) samples from nine WWTPs in eastern China. The abundance of ARGs in the Inf samples was higher than that in the Eff samples. A total of 21 core ARGs were identified, accounting for 38.70%–83.70% of the different samples. There was an increase in MGEs associated with phage-related processes from influents to effluents (from 12.68% to 21.10%). These MGEs showed strong correlations in relative abundance and composition with the core ARGs in the Eff samples. Across the Inf and Eff samples, 58 unique vir_ARGs were detected, with the Eff samples exhibiting higher diversity of vir_ARGs than the Inf samples. Statistical analyses indicated a robust relationship between core ARG profile, MGEs associated with phage-related processes, and vir_ARG composition in the Eff samples. Additionally, the co-occurrence of MGEs and ARGs in viral genomes was observed, ranging from 22.73% to 68.75%. This co-occurrence may exacerbate the persistence and spread of ARGs within WWTPs. The findings present new information on the changes in core ARGs, MGEs, and phage-associated ARGs from influents to effluents in WWTPs and provide new insights into the role of phage-associated ARGs in these systems.

Fine particulate matter as a key factor promoting the spread of antibiotics in river network

Tao Zhang[a], **Yuexiang Gao**[a,*]
[a] Basin Center, Nanjing Institute of environmental sciences, Nanjing, Jiangsu, China

Abstract: The extensive use of antibiotics has led to their frequent detection and an increased abundance of antibiotic resistance genes in rivers, posing a grave threat to the environment's health. Particulate matter plays a crucial role as the primary carrier of various pollutants in river transport. Its physicochemical properties and processes of sedimentation and re-suspension can influence the migration and transformation of antibiotics, but the mechanisms of this impact are not yet clear. In this study, the distribution characteristics at the micro-scale of particles in upstream plain river network of Taihu basin and adsorption behaviors of antibiotics in particles matter were studied. The results showed that particles were mainly in the size range of 30 to 150 μm in river network. From the spatial distribution, average particle size and concentrations of antibiotics were both larger in upstream than downstream. Adosorption experiments confirmed that smaller the suspended particle size, the stronger the adsorption capacity for antibiotics. These results indicated that fine particles were the primary carriers of antibiotics and their sorting and transport processes could influence the distribution of antibiotics in water-sediment. This study expanded our understanding of the migration mechanisms of antibiotics in the river networks and will be beneficial for the development of management strategies to control antibiotics dissemination.

Indoor transfer of airborne antibiotic resistance genes in urban and rural homes

Nan Hui[a,*]

[a] Department of Environment and Resources, Shanghai Jiao Tong University, Shanghai, China

Abstract: Over the last few years, the cumulative use of antibiotics in healthcare institutions, as well as the rearing of livestock and poultry, has resulted in the accumulation of antibiotic resistance genes (ARGs). This presents a substantial danger to human health worldwide. The characteristics of airborne ARGs, especially those transferred from outdoors to indoors, remains largely unexplored in neighborhoods, even though a majority of human population spends most of their time there. We investigated airborne ARGs and mobile genetic element (MGE, IntI1), plant communities, and airborne microbiota transferred indoors, as well as respiratory disease (RD) prevalence using a combination of metabarcode sequencing, real-time quantitative PCR and questionnaires in 72 neighborhoods in Shanghai. We hypothesized that (i) urbanization regulates ARGs abundance, (ii) the urbanization effect on ARGs varies seasonally, and (iii) land use types are associated with ARGs abundance. Supporting these hypotheses, during the warm season, the abundance of ARGs in peri-urban areas was higher than in urban areas. The abundance of ARGs was also affected by the surrounding land use and plant communities: an increase in the proportion of gray infrastructure (e. g., residential area) around neighborhoods leads to an increase in some ARGs (mecA, qnrA, ermB and mexD). Additionally, there were variations observed in the relationship between ARGs and bacterial genera in different seasons. Specifically, *Stenotrophomonas* and *Campylobacter* were positively correlated with vanA during warm seasons, whereas *Pseudomonas*, *Bacteroides*, *Treponema* and *Stenotrophomonas* positively correlated with tetX in the cold season. Interstingly, a noteworthy positive correlation was observed between the abundance of vanA and the occurrence of both rhinitis and rhinoconjunctivitis. Taken together, our study underlines the importance of urbanization and season in controlling the indoor transfer of airborne ARGs. Furthermore, we also highlight the augmentation of green–blue infrastructure in urban environments has the potential to mitigate an excess of ARGs.

Reinforcing one health through nano-agriculture: A nano-based solution to combat antibiotic resistance

Feiran Chen[a], **Zhenyu Wang**[a,*]
[a] School of Environment and Ecology, Jiangnan University, Wuxi, Jiangsu, China

Abstract: Antibiotic resistance poses a significant threat to global public health, necessitating innovative approaches to address this pressing issue. Nano-agriculture, an emerging field that leverages nanotechnology in agricultural practices, offers a promising avenue to combat antibiotic resistance while reinforcing the principles of One Health. Here, we explored the potential of nano-based solutions in agriculture for mitigating antibiotic resistance. The precise and localized release of nanomaterials presents opportunities to reduce reliance on conventional antibiotics and can minimize environmental exposure, thereby mitigating the development of resistance in agricultural settings. Considering the transfer of antibiotic resistance genes (ARGs) from environment to human via bacterial hosts, the elimination of ARGs at the gene level is endorsed as a novel strategy to truly reduce ARGs. Nanomaterials serve as optimal non-viral carriers, ensuring both stability and editing capability. Our nano-based CRISPR system, characterized by low toxicity and excellent biocompatibility, achieved efficient elimination of multiple ARGs in soil, offering a fast and precise way to reduce ARG reservoirs. Moreover, nanomaterials capable of regulating reactive oxygen species (ROS), such as nano-CeO_2, possess the potential to inhibit the propagation of ARGs via eliminating ROS and down-regulating expression of genes related to horizontal gene transfer. Unlike existing strategies that focus on the eliminating of ARGs in soil and water systems, nano-CeO_2 can directly target ARGs in plant endosphere by stimulating innate mechanisms while maintaining plant growth. The low estimated daily intake values of Ce and ARGs demonstrate a reduced risk of human exposure, indicating the effective control of nano-CeO_2 in preventing the propagation of ARGs via food chain. Overall, we emphasize the potential of nano-agriculture as a transformative approach to minimize antibiotic resistance. By embracing a One Health perspective, nano-agriculture offers a promising pathway to safeguard public health, enhance food security, and promote environmental sustainability in light of antibiotic resistance.

Deciphering structuring mechanism and health risk of antibiotic resistome from the Qiantang river basin to Hangzhou Bay in the Yangtze River Delta

Xinyu Huang[a], Feng Ju[a,*]
[a] School of Engineering, Westlake University, Hangzhou, Zhejiang, China

Abstract: Environmental and human resistomes constitute complex systems interconnected through bi-directional flows of antibiotic resistance genes (ARGs) as biological contaminants of emerging concerns. The ARGs discharged into estuaries are likely to be transmitted to human pathogens and ultimately dispersed to humans through the water cycle and food chain. Despite increasing reports highlighting global and continental-scale ARG contamination in estuaries, the resistome structure and health risks in heavily impacted brackish water ecosystems are unresolved. This study employs metagenomics-based resistomics and multivariate statistics approaches to elucidate the sediment resistome of the Qiantang estuary and downstream Hangzhou Bay. We identified contrasting dual resistome patterns indicating both river and ocean influences, significantly co-driven by multiple environmental (mainly water pharmaceuticals, nutrients, and heavy metals) and biotic (i.e., vertical and horizontal transfer) factors, suggesting that anthropogenic and tidal disturbances co-shape the sediment resistome. Within Hangzhou Bay, spatial heterogeneity in tidal and land-based discharge leads to significant variations in the resistome structure. Our findings reveal the enrichment of highly transferable and clinically important beta-lactam resistance genes of beta-lactam (LAP-2, CMY-100, and KPC-2) and two synthetic antibiotics (florfenicol-resistant gene floR and sulfonamide-resistant gene sul1) in Hangzhou Bay, indicating a higher health risk of human-influenced mobile ARGs compared with the upstream Qiantang estuary. Notably, clinically relevant ARGs (macrolide-resistant gene macB) hosted by indigenous nitrifying bacteria highlight the alarming invasive of clinical resistomes, but also underscore an unperceived ecological impact of bacterial antibiotic resistance on nitrogen biogeochemical cycles. These results emphasize the crucial role of human activities, such as pollution, in shaping the coastal environmental resistomes structure and associated risks.

Occurrence of antibiotics and antibiotic resistance genes in river sediment in typical e-waste dismantling area: A case study of a river in southern China

Yiwei Li[a], Zelin Ke[a], Bingjie Fang[a], Yeyuan Xiao[a,*]
[a] College of Engineering, Shantou University, Shantou, Guangdong, China

Abstract: The environmental dimensions of antimicrobial resistance (AMR) under One Health are crucial to understanding and addressing this global challenge comprehensively. While AMR primarily occurs in human and animal populations, the environment also plays a significant role in the spread and development of antimicrobial-resistant bacteria. Urban rivers dynamically interfered by anthropogenic activities are considered as a vital reservoir of ARGs. Here, we examined 18 typical antibiotics of 4 categories (Sulfonamides, Macrolides, Fluoroquinolones and Chloramphenicols), five ARGs (sul1, sul2, chl, ermA, qrnB), one integron and microbial communities in sediment from an urban river in Shantou, Guangdong province (China). Sediments were collected at a total of 20 points along the main stream during the dry season, normal water period, and wet season, respectively. The total concentration range of antibiotics in sediments during the dry season, wet season, and normal water period is respectively 580.75–9785.61 ng/kg, 399.77–8474.29 ng/kg, and 716.50–12918.31 ng/kg, with average concentrations of 3202.92 ng/kg, 2644.54 ng/kg, and 5027.50 ng/kg, respectively. The total abundances of five ARGs is 9.65 × 10^3 copies/g to 1.05 × 10^5 copies/g. Proteobacteria, Chloroflexi, Actinobacteria, Bacteroidetes and Acidobacteria were the dominant phyla in the surface sediments of the main stream of Lianjiang River. KEGG prediction showed that among all antimicrobial resistance genes, β-lactam resistance was the highest, followed by vancomycin resistance and peptide resistance. The use of antibiotics will not only select their corresponding resistance genes, but also may play a certain role in the regulation or influence of other antibiotic resistance genes. On the other hand, bacteria containing antimicrobial properties may affect the metabolic degradation of antibiotics.

Soil amoeba-associated viruses are significant vectors of antibiotic resistance genes

Fei Liu[a], **Longfei Shu**[a,*]
[a] School of Environmental Science and Engineering, sun yat-sen university, Guangzhou, Guangdong, China

Abstract: Protists and viruses play pivotal roles in soil ecosystems, yet their direct interactions and implications have remained largely unexplored. In this study, we examined 106 soil amoeba samples through metagenomic approaches, unveiling the role of amoebae as extensive carriers of both prokaryote-associated and eukaryote-associated viruses. Our results revealed that the compositions of viruses were different not only between the amoeba species but also within the same species. These amoeba-virus associations encompassed viruses with known pathogenicity to humans and mammals. While acting as viral reservoirs, the amoebae also harbored a remarkable abundance of antibiotic resistance genes (ARGs). The ARGs hosted by these viruses within amoebae surpassed levels reported in soil environmental contexts. Furthermore, differences in ARG profiles among the amoeba samples suggested a potential link to local soil conditions and amoebae behaviors. Notably, amoeba-associated viruses exhibited unique ARG enrichment patterns, particularly in the prevalence of multidrug resistance genes. Our study exposed a distinct pathway for the cross-species transmission of ARGs facilitated by amoeba viruses through mobile genetic elements (MGEs) in soil environments. This mechanism implies significant risks in the emergence of antibiotic-resistant strains among human and animal pathogens. In summary, our research underscores the dual role of amoebae as carriers of diverse viruses and repositories of ARGs, emphasizing their impact on virus and ARG dynamics in soil ecosystems. These findings shed light on the significance of protists in soil environments and provide insights into monitoring evolving health risks within soils.

GWPD: a multifunctional platform to unravel biological risk factors in global engineered water systems

Shu-Hong Gao[a,*]

[a] School of Civil and Environmental Engineering, Harbin Institute of Technology, Shenzhen, Guangdong, China

Abstract: Engineered water systems such as wastewater treatment plants (WWTPs) are potential reservoirs of various biological risk factors (BRFs), including pathogens, antibiotic resistance genes (ARGs), and virulence factors (VFs). Currently, the BRFs database relevant to engineered water systems on a global scale is lacking. Here, we show the Global Water Pathogen Database (GWPD, http://gwpd. hitsz. edu. cn), an online database that provides the diversity, abundance, and distribution information of BRFs from 1600 metagenome samples obtained from 198 cities in 70 countries on 6 continents. We sorted these samples into six types, including sewer networks, influent, anoxic activated sludge, oxic activated sludge, and effluent of WWTPs, and receiving/natural waters. In total, 490 pathogens, 447 ARGs belonging to 20 ARG classes, and 248 VFs were identified from all collected samples. As a multifunctional database, GWPD provides an interactive visualization of these BRFs in the world map, an information retrieval interface, and an online user-friendly annotation pipeline of BRFs from metagenome sequencing data. GWPD is built based on the web service framework, which can asynchronously manage the annotation and other analytical tasks on the remote computation server. The framework can be easily extended by adding more functional modules and connecting to other data sources (e.g., epidemic databases), thereby supporting risk assessment and control in the context of "One Health".

Microplastic pollution and health effects in karst water

Xubo Gao[a],Ting Tan[a], Chengcheng Li[a], Ling Yi[a], Zhanhui Wu[a], Wenxuan Fu[a], Fengze Yu[a], Yanxin Wang[a]

[a] State Key Laboratory of Biogeology and Environmental Geology & School of Environmental Studies, China University of Geosciences, Wuhan, China

Abstract: About 16.5% of the world's population uses karst water, which is one of the most important water resources for human beings. Karst aquifers are open systems, and microplastics may enteter it easily through karst fissures, windows and cavities. In this study, we found that microplastics in surface water and karst groundwater in the main stream and tributaries of the Yangtze River increasing along the flow direction. The abundance of microplastics in surface water ranged from 3.4 $n \cdot L^{-1}$ to 99 $n \cdot L^{-1}$. While in karst groundwater, it ranged from 6.8 $n \cdot L^{-1}$ to 40.8 $n \cdot L^{-1}$. PP (67.3%) and PET (67.3%) were the main types of microplastics in surface water and groundwater, respectively. It is strongly commented to take actions to protect karst water from microplatic pollution.

Creating a sustainable indoor environment in the post-COVID era

Ji-Xiang Wang[a]
[a] The Hong Kong University of Science and Technology, Hong Kong, China

Abstract: In the post-COVID era, the persistent emergence of new cases and the potential for future pandemics highlight the vulnerability of our healthcare systems to infectious diseases. Lessons from COVID-19, SARS, and MERS are crucial for bolstering defenses against future pathogens, termed "Disease X". COVID-19's predominance of airborne transmission underscores the importance of sustainable indoor environments in reducing cross-infection and controlling outbreaks. This talk focuses on the mechanisms of indoor disease transmission and mitigation strategies, particularly for minimizing contactless and bathroom-related transmissions. By redefining indoor spaces, we aim to align with Sustainable Development Goals 3, 6, and 11, enhancing health, sanitation, and sustainable urbanization. The talk advocates for innovative design and management of indoor environments to prevent future pandemics, using insights from COVID-19 to strengthen our resilience against airborne diseases and promote public health sustainability.

Single cell microbial sequencing: New perspectives in microbial research

Jiale Yu[a]

[a] MobiDrop Co.,Ltd

Abstract: The development of high-throughput sequencing technology has provided powerful tools for microbial research. However, with the deepening understanding of microbiology, traditional omics sequencing techniques are facing increasing challenges, such as (1) how different strains of the same microorganism in complex environmental samples co-evolve, interact, and compete; (2) the patterns and functions of genetic material exchange among microorganisms; (3) whether different individuals of the same microbial community have similar stress responses when facing external environmental pressures. Meanwhile, high-throughput single-cell sequencing based on microfluidic chips has been widely applied in single-cell studies of eukaryotic cells. However, due to issues such as low initial nucleic acid content and difficulties in cell lysis for prokaryotic cells, there has been a lack of widely applicable single-cell microbial sequencing technology. Through targeted development and optimization of microfluidic chips, devices, and biochemical reaction reagents, including the use of multi-step droplet fusion technology to solve the compatibility of single-cell microbial lysis and genome amplification reaction systems, and the use of semi-random primers to complete RNA reverse transcription amplification within cells to solve the problem of inefficient capture of prokaryotic mRNA without polyA tails, we have successfully achieved single-cell microbial genome sequencing of complex samples (such as feces, soil, water, etc.) and single-cell microbial transcriptome sequencing of pure cultured bacterial liquid samples. This breakthrough has led to the discovery of significantly enriched functional strains, plasmids and phages, bringing new research methods and perspectives to microbial studies.

Viral communities locked in high elevation permafrost up to 100 m in depth on the Tibetan Plateau

Qian Wen[a,*]
[a] Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China

Abstract: Permafrost serves as a natural cold reservoir for viral communities. However, little is known about the viromes in deep permafrost soil, as most studies of permafrost were restricted to shallow areas. Here, permafrost soil samples of up to 100m in depth were collected from two sites in the Tuotuo River permafrost area on the Tibetan Plateau. We investigated the viral composition in these permafrost soil samples and analyzed the relationship of viral composition and diversity along with depths. Our study revealed that greater permafrost thickness corresponds to higher diversity within the viral community. Bacteriophages were found to be the dominant viral communities, with "kill the winner" dynamics observed within the Siphoviridae and Myoviridae. The abundance and diversity of viral communities may follow a potential pattern along soil layers and depths, influenced by pH, trace elements, and permafrost thickness. Notably, strong correlations were discovered between the content of inorganic elements, including B, Mg, Cr, Bi, Ti, Na, Ni, and Cu, and the viral composition. Moreover, we discovered highly conserved sequences of giant viruses at the depth of 10 m, 20 m, and 50 m in the permafrost, which play a crucial role in evolutionary processes. These findings provide valuable insights into the viral community patterns from shallow to 100-m-depth in high-elevation permafrost, offering crucial data support for the formulation of strategies for permafrost thaw caused by climate change and anthropogenic activities.

Investigation of comammox activity and abundance of aquatic vascular plants in wetland ecosystem

Qi Xin[a], Lizheng Kui[a,*]

[a] School of Environment, Nanjing University, Nanjing City, Jiangsu, China

Abstract: The emergence of Comammox challenges the traditional understanding of nitrification and alters our perception of it as a rate-limiting step in the nitrogen cycle. Currently, most studies on comammox focus on microorganisms, and research into the contribution of comammox to ammonia nitrogen conversion in natural environments is still in its early stages. In this study, the interaction between comammox and conventional ammonia oxidation in the natural environment was analyzed by measuring the potential rate of comammox in four species of aquatic plants with distinct characteristics, combined with their community distribution characteristics and bacterial abundance. The results revealed that clade A was more abundant in the natural environment than clade B, with clade A. 2 being the dominant subtype. The microbial community structures of four different aquatic plants varied, with a more pronounced difference between rhizosphere and non-rhizosphere samples. In terms of comammox activity, the activity of summer samples (9. 36 ± 5. 13 mg N kg^{-1} day^{-1}) was higher than that of winter samples (7.96 ± 5.39 mg N kg^{-1} day^{-1}), which was consistent with the microbial abundance (summer: $(6.47 \pm 6.01)\times 10^6$ copies g^{-1}; winter: $(3.92 \pm 4.47) \times 10^6$ copies g^{-1}). Combined with traditional ammox analysis, the abundance of comammox was higher than AOB and lower than AOA, and the contribution rate of comammox in non-rhizosphere samples of submerged plants (51.33% ± 6.51%) and in rhizosphere samples of floating plants (52.67% ± 4.51%) in winter was higher than that of traditional ammox. Comammox may be a key ammonia nitrogen removal pathway in the natural environment, with key influencing factors being NH_4^+, pH and DOM (Dissolved Organic Matter).

Impacts of microplastics pollution on lacustrine bacterial community assembly

Mingjia Li[a], Xin Qian[a,*]
[a] School of Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Microplastics (MPs) have garnered a global attention. Lakes serve as significant sinks for MPs, with longer water residence times leading to slow variation in MPs abundance and additional processes such as local fragmentation. Currently, much research focus lies on microbial growth on MPs biofilms, with limited attention paid to the direct impacts of MPs as pollutants on microbial communities in the environment. In this study, the surface water and sediment samples were collected from 20 sites within the Lake Taihu in February and May, representing dry-cold and warm-humid climates, respectively. Results revealed significant effects of MPs abundance, polymer type, and color on Shannon diversity index of the microbial community. Specifically, MPs abundance showed a significant negative correlation with Shannon diversity index in warm sediments, while a significant positive correlation was observed between Shannon diversity index in cold sediments and red polypropylene (PP) MPs. Additionally, color (white), size (<100 μm), shape (film), and polymer type (PP) of MPs were found to have relative importance on dominant bacterial phyla (Proteobacteria, Acidobacteriota, Nitrospirota, etc.), particularly on Nitrospirota, indicating potential impacts of MPs on the microbial nitrogen cycling. Regarding bacterial community assembly, MPs significantly influenced stochastic processes in surface water ($R^2 = 0. 08$, $P < 0.001$), while exhibiting a tendency to influence deterministic processes in sediments ($R^2 = 0. 19$, $P < 0.0001$). Our study provides evidence on the impacts of various MPs factors on processes of microbial community assembly, offering a new perspective for environmental risk assessment of MPs pollution. Moreover, future climate warming may introduce additional uncertainties to these impacts.

Distributions of microbial communities associated with anaerobic oxidation of methane in the sediments of Haima cold seep, South China Sea

Zhishan Huang[a], Lijuan Zhang[a,*]
[a] School of Environment and Engineering, Peking University Shenzhen Graduate School, Shenzhen, Guangdong, China

Abstract: The ocean produces 85–300 Tg of methane annually, and 90% of methane is consumed by anaerobic oxidation of methane (AOM) before being released into the atmosphere. Anaerobic methanotrophic archaea (ANME) are key mediators of the microbial AOM processes, but their crucial role remains largely unexplored in regulating global methane balance and mitigating greenhouse effects. In this study, the microbial diversity was depicted in sediment samples collected from different habitats (non-seepage site, low-seepage site, middle-seepage site and high-seepage site) in the Haima cold seep, South China Sea, with particular interest in the abundance and ecological roles of representative ANME and their syntrophic sulfate-reducing bacteria (SRB). The intensity of methane seepage might distinguish microbial communities in the cold seep sediments. The high-seepage site exhibited significantly different geochemical characteristics, as well as less microbial diversity according to α- and β-diversity analysis. The 16S rRNA gene sequencing further revealed that ANME (ANNME-1/2/3) were the dominant archaea at high-seepage site while *Desulfobacterota* was the dominant bacteria. These groups were rarely found at other sampling sites. In the co-occurrence network analysis, a positive correlation between ANME and SEEP-SRB was discovered, showing that the processes of AOM coupled to sulfate reduction might occur at the high-seepage sites. Phylogenetic analysis revealed that the representative sequences of ANME and SRB found in this study displayed high similarity to those found in other cold seeps. Our study provided new insights into the distribution of microorganisms across different methane seepage regimes in cold seep sediments and provided fundamental reference for further investigation into methane emission and global warming.

Global nitrous oxide emissions from livestock manure during 1890−2020: An IPCC Tier 2 inventory

Lei Zhang[a,*]

[a] Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, China

Abstract: Nitrous oxide (N_2O) emissions from livestock manure contribute significantly to atmospheric N_2O, a powerful greenhouse gas (GHG) and dominant ozone-depleting substance. Here, we estimate global N_2O emissions from livestock manure during 1890−2020 by using the Tier 2 approach of the 2019 Refinement to the 2006 IPCC Guidelines. Global N_2O emissions from livestock manure increased by ~350% from 451 [368−556] Gg N yr^{-1} in 1890 to 2042 [1677−2514] Gg N yr^{-1} in 2020. These emissions contributed ~30% to the global anthropogenic N_2O emissions in the decade 2010−2019. Cattle contributed the most (60%) to the increase, followed by poultry (19%), pigs (15%), and sheep and goats (6%). Regionally, South Asia, Africa, and Latin America dominated the growth in global emissions since the 1990s. We found a substantial impact of livestock productivity, specifically animal body weight and milk yield, on the emission trends. Furthermore, a large spread existed between different methodologies for global N_2O emission estimates from livestock manure, with our estimates 20%−25% lower than those based on the 2006 IPCC Guidelines. This study highlights the need for robust time-variant model parameterization and continuous improvement of emissions factors to enhance the precision of emission inventories. Additionally, urgent mitigation is required, as all available inventories indicate a rapid increase in global N_2O emissions from livestock manure in recent decades.

Co-culture of rice and aquatic animals enhances soil organic carbon: A meta-analysis

Chao Ma[a,*]

[a] Resource and Environment, Anhui Agricultural University, Hefei, Anhui, China

Abstract: Co-culture of rice (*Oryza sativa*) and aquatic animals (CRAAs) is an efficient eco agricultural model and has been widely implemented in many Asia countries. However, its impact on soil organic carbon (SOC) content has not been synthesized and the relative effects of different CRAAs practices on SOC have not been assessed. Our meta-analysis aims to synthesize the effect of diverse CRAAs regimes on SOC content based on results from 205 field experiments. Our results showed that overall, CRAAs significantly increased SOC content by 11. 6% ($P < 0.05$). The highest relative effect on SOC content was found under the rice and amphibian coculture practice ($P < 0.05$). Also, CRAAs caused a significantly higher increase in SOC content in temperate regions (19.1%) than in subtropical (9.7%) and tropical (12.1%) regions ($P < 0.05$). In addition, CRAAs were more effective in enhancing SOC content in paddy soils with low nitrogen content (total nitrogen [TN] ≤ 1.5 g/kg) or alkaline pH. Further, SOC increased more in the CRAAs with Japonica than Indica rice, increasing 17.8% and 6.1% as compared to their respective rice-monoculture controls. Random forest analysis revealed that animal type was the most important factor influencing SOC under CRAAs. These results indicate that CRAAs can significantly enhance SOC, particularly in low-N, alkaline paddy soils. Our findings suggest that CRAAs with appropriate rice and animal varieties can provide unique opportunities for soil C sequestration, while enhancing farmers' profitability.

The oral microbial and its relevance to allergic diseases

Jialu Shi[a], Jin Wang[a,*]
[a] School of public health, Southeast University, Nanjing, Jiangsu, China

Abstract: Allergic diseases (allergic asthma, allergic rhinitis, atopic dermatitis, food allergies, and so on.) have become a major public health problem in developed countries. The etiology of allergic diseases is highly intricate, and the internal development mechanism remains to be fully elucidated. Current belief suggests that it is the combination of individual genetic susceptibility and environmental factors. Most of the microorganisms in the human body are symbiotic or mutualistic, mainly existing in the oral cavity, skin surface, intestine tract, esophagus, lungs, and other parts of the body. The composition and function of these microorganisms are influenced by factors such as birth mode, infant feeding, lifestyle, medication, and host genetics. Presently, oral microbiota has been widely studied in relation to allergies, while the role of dysbiosis in allergic diseases remains unknown. Scientists found that oral microbiota interfaces with the immune system of the human host and has a vital role in allergic diseases. In this review, we provided the change in oral microbiota composition and diversity and discussed the mechanisms by which the oral microbiome regulates allergic diseases. Oral microbiota is a major factor influencing allergic diseases. Significant differences were captured in the characteristic oral microbiota among patients with allergic diseases and healthy individuals. Compared with healthy children, the relative abundance of Streptococcus was lower in asthmatic children. Additionally, oral microbiota may influence the occurrence and development of allergies through immunomodulation, enhancing epithelial barriers, metabolite production, and the oral -gut axis. This paper will contribute to developing targeted interventions and personalized treatment strategies to improve the management and prevention of allergic diseases.

Fabrication of ovalbumin-burdock polysaccharide complexes as interfacial stabilizers for nanostructured lipid carriers: Effects of high-intensity ultrasound treatment

Shanshan Wu[a,*]
[a] School of Public Health, Southeast University, Nanjing, Jiangsu, China

Abstract: Ovalbumin (OVA)-burdock polysaccharide complex emulsiffers were prepared in this work by high-intensity ultrasound (HIU) treatment for nanostructured lipid carriers (NLCs) stabilization. HIU treatment remarkably changed their physicochemical properties and resulted in the cross-linking between these two biopolymers. The diffusion rate of the stabilizers towards oil-water interface and their dilatational elastic modulus increased with increasing ultrasound power at ffrst, reaching a maximum at 400 W cm^{-2}, and decreased thereafter. Therefore, Biopolymers treated with 400 W cm^{-2} energy intensity were most effective in preventing the polymorphic transition of NLCs and degradation of encapsulated curcumin (Cur) because they assembled a compact interfacial layer that blocked the motion of carrier oil. Moreover, they also contributed to a more sustainable Cur release in the simulated gastrointestinal tract. Cur in NLCs presented remarkably higher cellular antioxidant capacity and ROS-scavenging capacity than free Cur, which might arise from the enhanced solubility and chemical stability of the former.

The impact, mechanisms, and novel intervention strategies of environmental microbiota on food allergies in infants and young children

Lan Jiang[a], Jin Wang[a,*]
[a] School of Public Health, Southeast University, Nanjing, Jiangsu, China

Abstract: Food allergies have emerged as a significant health concern worldwide, particularly among infants and young children. Investigating the environmental microbiota's role in the emergence and progression of food allergies is crucial for developing effective prevention and treatment strategies. This study focuses on the influence, mechanisms, and novel interventions regarding how environmental microbiota affect food-allergic responses. Environmental microbial exposure is crucial in early immune development, with a diverse microbial environment being linked to establishing immune tolerance. Lifestyle shifts, such as antibiotic use, high-fat low-fiber diets, cesarean births, and reduced nature interaction, may disturb microbiota diversity and increase food allergy risks. The association between environmental microbiota and food allergies might involve microbiota on the composition and function of the gut microbiome, microbial metabolite on the immune system, and interaction of environmental microbiota components with food antigens. Additionally, direct engagement of microbiota with skin and respiratory mucosa can modulate systemic immunity and allergen susceptibility. New interventional strategies aiming at the environment microbiota demonstrate potential in allergy mitigation. Strategies such as the application of probiotics and prebiotics, diversification of the diet in early infancy, exposure to natural environments, adjustments in diet and lifestyle, and personalized microbial analysis and intervention, have shown potential in modulating immune functions and reducing the risk of sensitization and allergic reactions. In summary, environmental microbiota are pivotal in food allergy development and management in infants and young children. Further research into the complex interactions between environmental microbiota and the immune system is essential for the development of targeted intervention measures to effectively prevent and manage food allergies.

Spatiotemporal distribution, source apportionment, and ecological risk of bisphenol analogues in a highly urbanized river basin

Sheng Zhang[a], **Xin Qian**[a,*]
[a] School of Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Bisphenol analogues (BPs), as one of the endocrine disruptors, have received wide attention due to their adverse impacts on ecosystems. However, the spatiotemporal distribution, source apportionment, and ecological risk of BPs in natural basins are poorly understood. Especially in highly urbanized river basins with anthropogenic activities threaten these critical but ecologically fragile regions. In this study, field investigations of BPs in the waters of the entire Qinhuai River Basin were conducted in June (before the annual flood period) and August (after the annual flood period) 2023. The Qinhuai River, an important primary tributary of the lower Yangtze River, is located in eastern China and the basin is characterized by a high population density and dense urbanization. Thirty-two sites were sampled for six types of BPs known to be ubiquitous in the surface water. The concentration of total BPs (ΣBPs) was significantly higher before than after the flood period: 20.3–472 ng/L (mean = 146 ng/L) and 14.1–105 ng/L (mean = 35.9 ng/L), respectively. BPA was the main contributor to ΣBPs before the flood, and BPB followed by BPA after the flood. ΣBP concentrations were 12%–241% higher downstream than upstream of wastewater treatment plants (WWTPs). The results of a principal component analysis followed by multiple linear regression (PCA-MLR) suggested that untreated wastewater discharge from the WWTPs is an important source of BPs in the basin, with urban rainfall runoff as another potential source after the flood period. An assessment of the ecological risk of BPs showed that BPA and BPS should be given due attention, and overall ecological risk of BPs pose a low risk to local algae but high and medium risks to invertebrates and fish, respectively.

Integration of computational toxicology, toxicogenomics data mining and omics techniques to unveil toxicity pathway

Fei Li[a,*], Huifeng Wu[a], Chenglong Ji[a]
[a] Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai, Shandong, China

Abstract: Growing numbers of synthetic chemicals have potential endocrine-disrupting effects and cause potential ecological and health risks. However, the primary toxicity pathways and mechanisms of endocrine disruption are poorly understood and the existing risk assessment relies heavily on animal testing. Database mining, omics technology and computer simulation can serve as an alternative approach to explore the mechanisms by building adverse outcome pathways (AOPs). The present study took a case of thyroid interference with triphenyl phosphate (TPP) to explain the potential toxic effects at levels from sub-molecules to cells utilizing AOP framework developed by multiple techniques. This study retrieved the data from comparative toxicogenomics database (CTD) and screened out the core gene. Molecular dynamics (MD) analysis was used to explore configuration changes and confirm molecular initiating event (MIE). The transcriptomic analysis was further utilized to supplement the relationships between MIEs and key events (KEs) of AOP. The thyroid hormone receptor beta (THRB) was identified as the core gene at sub-molecular levels. MD analysis found that the configuration changes of C-terminal helix 12 (H12) of thyroid hormone receptor β (TRβ) were discovered as the MIE. The transcriptomic analysis extended the related KE1 at the subcellular level, such as changes in gene expression levels for coding cycle regulation (CCND1), inflammatory response (IL1A and IL6), and cell proliferation and apoptosis (BAD, TP53 and CASP9). Then, the KE2 at cellular levels such as apoptosis, cell cycle control, and cell proliferation were influenced accordingly. As a result, these alterations led to thyroid disorder as adverse outcomes. This study provided an efficient way to facilitate the complement of possible AOP and brought new insights into understanding the toxic mechanism of emerging synthetic chemicals.

Nano polystyrene accelerated the reproductive toxicity induced by the Tris(1,3-dichloro-2-propyl) phosphate via nhr-69/PISD/PE/drp-1-mediated mitochondrial fragmentation in *Caenorhabditis elegans*

Wang Jia[a], Yingchi Shi[a], Ran Liu[a,*]

[a] School of Public Health, Southeast University, Nanjing, Jiangsu, China

Abstract: Tris(1,3-dichloro-2-propyl) phosphate (TDCPP) and nano-polystyrene (NPS) have received concerns due to their frequent detection. However, knowledge of the effects of NPS on the reproductive toxicity of TDCPP are limited. Herein, the effects of NPS (20 nm, 100 μg/L) and TDCPP (1, 10, and 100 μg/L) alone or in combination on the reproductive toxicity in *Caenorhabditis elegans* were explored. The results showed TDCPP could lead to a decrease in brood size, oosperm numbers in uterus, and impair gonadal developmental in N_2. In addition, it also could affect spermatogenesis and formation in him-5 by reducing the brood size, germ cells numbers, sperm cell numbers, sperm size, and sperm activation rate, and increasing sperm malformation rate. The reproductive function did not be affected by NPS. However, combined exposure of NPS and TDCPP resulted in more serious damage to reproduction. The effects of TDCPP and NPS on mitochondria were evaluated by mitochondrial fragment, ROS and mitochondrial membrane potential. It was found TDCPP exposure led to pronounced mitochondrial fragmentation, elevated ROS levels, and decreased mitochondrial membrane potential. Furthermore, co-exposure further exacerbated mitochondrial damage. Non-targeted metabolomics revealed PE was the prominent differential metabolite. The possible molecular mechanisms of mitochondrial damage were identified by observing the effects of TDCPP and NPS exposure on the PE synthesis. The results showed TDCPP exposure led to a decrease in PE and the activity of phosphatidylserine decarboxylase (PISD). Moreover, co-exposure resulted in a further decline in both PISD and PE. Molecular docking results indicated the possibility of binding between the nhr-69 and PISD. The gene expression was analyzed by qPCR, the results demonstrated the expression of the psd-1 and nhr-69 decreased, and drp-1 increased after TDCPP and NPS exposure. In summary, our findings provide important information for revealing the environmental health risks and possible toxic mechanism of TDCPP and NPS.

Beyond mass balance: Development of a distributed watershed-scale model for antibiotics transport and fate

Hui Xie[a,*]

[a] Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, Nanjing, Jiangsu, China

Abstract: Current monitoring studies and multi-media fugacity modeling of antibiotics can reveal their existence forms, distribution characteristics, and pollution levels in different environmental phases. However, the lack of watershed-scale high-precision dynamic process simulation studies limits the systematic understanding of the source-pathway-sink processes and mechanisms of antibiotics. For the first time, a distributed watershed-scale antibiotic transport and fate model was developed. It incorporates three major modules: hydrology, sediment, and antibiotics. By coupling the dynamic interactions across multiple media (atmosphere, soil, water bodies, sediments, etc.) and interfaces (pore water-particulate matter, overlying water-sediment, etc.), the model simulates the antibiotic transport and transformation mechanisms such as sorption/desorption, degradation, transformation, advection, diffusion, settling/resuspension in the terrestrial-aquatic continuum. This study overcomes the difficulties in simulating the non-point source (NPS) process of antibiotics, precisely depicting the transport and fate processes and fluxes of antibiotics. The model was calibrated and validated in a typical agricultural watershed in Lake Chaohu Basin. Results demonstrate that the model can reproduce the dynamics of NPS processes of antibiotics driven by rainfall-runoff events, providing a scientific basis for the comprehensive risk management of antibiotics in watersheds.

Can "risk-sharing" mechanisms help clonal aquatic plants mitigate the stress of nanoplastics?

Hongwei Yu[a], Chengzhi Hu[a], Jiuhui Qu[a,*]
[a] Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, China

Abstract: Most aquatic plants applied to ecological restoration have demonstrated a clonal growth pattern. The risk-spreading strategy plays a crucial role in facilitating clonal plant growth under external environmental stresses via clonal integration. Therefore, this study aimed to investigate the impact of NPs exposure on seedlings of parent plants and connected offspring ramets. A dose response experiment (0.1, 1, and 10 mg/L) showed that the growth of *Eichhornia crassipes* (water hyacinth) was affected by 100 nm polystyrene nanoplastics after 28 days of exposure. Tracer analysis revealed that NPs are accumulated by parent plants and transferred to offspring ramets through stolon. Quantification analysis showed that when the parent plant was exposed to 10 mg/L NPs alone for 28 days, the offspring ramets contained approximately 13±2 μg/g NPs. In the case of connected offspring ramets, leaf and root biomass decreased by 24%–51% and 32%–51%, respectively, when exposed to NP concentrations ranging from 0.1 to 10 mg/L. An imbalance in the antioxidant defense systems, which were unable to cope with the oxidative stress caused by NP concentrations, further damaged various organs. Interference effects of NPs were observed in terms of root activity, metabolism, biofilm composition, and the plant's ability to purify water. However, the risk-spreading strategy employed by parent plants (interconnected offspring ramets) offered some relief from NP-induced stress, as it increased their relative growth rate by 1 to 1.38 times compared to individual plants. These findings provide substantial evidence of the high NP enrichment capacity of *E. crassipes* for ecological remediation. Nevertheless, we must also remain aware of the environmental risk associated with the spread of NPs within the clonal system of *E. crassipes*, and contaminated cloned individuals need to be precisely removed in a timely manner to maintain normal functions.

Comparative study on the resistance of beta-cypermethrin nanoemulsion and conventional emulsion in *Blattella germanica*

Yan Shen[a,*]
[a] School of Public Health, Southeast University, Nanjing, Jiangsu, China

Abstract: This study aimed to compare the resistance rates of Blattella germanica to beta-cypermethrin nanoemulsion and conventional emulsion and establish reference values via biochemical detection for conventional emulsion. We conducted experiments using subcultured Blattella germanica and applied the micro-drop method for treatment. Subsequently, the activity of metabolic enzymes was measured using spectrophotometry. Profile analysis was employed to study the resistance rates of beta-cypermethrin nanoemulsion and beta-cypermethrin emulsion. The regression equation for the relationship between generation and resistance factor in Blattella germanica treated with beta-cypermethrin nanoemulsion was as follows: $y_1 = 0.091x_1 + 0.991$, with an r-value of 0. 990 ($F = 95.184$, $p = 0.01$). Similarly, the regression equation for Blattella germanica treated with emulsion was $y_2 = 0.376x_2 + 1.051$, with an r-value of 0.993 ($F = 141.094$, $p = 0.007$). The comparison of slopes between these two regression equations yielded an F-value of 8.61, indicating a significant difference ($p = 0.001$). Our findings suggest that the resistance factor in Blattella germanica treated with beta-cypermethrin nanoemulsion differs from that treated with beta-cypermethrin emulsion. Specifically, the resistance factor of beta-cypermethrin nanoemulsion increased at a slower rate compared to beta-cypermethrin emulsion.

The destiny of microplastics in one typical petrochemical wastewater treatment plant

Liyan Deng[a,b], Hongbo Xi[a], Changyong Wu[a,*]

[a] Research center of environmental pollution control engineering technology, Chinese Research Academy of Environmental Sciences, Beijing, Chaoyang, China

[b] College of Water Sciences, Beijing Normal University, Beijing, Haidian, China

Abstract: Microplastic (MP) is a type of emerging contaminant that is verified to be threatening to some organisms. Controlling MP emission from the source is preferred for its refractory characteristic. The petrochemical industry is a possible contributor, responsible for the most plastic production, and wastewater is the most possible sink of MP. This study applied the Agilent 8700 Laser infrared imaging spectrometer (LDIR) to detect MPs in one typical petrochemical wastewater treatment plant (PWWTP). It was determined that the abundances of MPs in the influent and effluent of the target PWWTP were as high as 7706 and 608 particles/L. The primary treatment removed most MPs (87.5%) with a final removal efficiency of 92.1%. 23 types of MPs were identified, and Polyethylene (PE), Polypropylene (PP), Silicone resin prevailed in the effluent. All the MPs were smaller than 483.9 μm. All in all, this study preliminarily unveiled the ignorable status of the petrochemical industry in releasing MPs into the water environment for the first time.

Insights into the enzymatic degradation of DNA expedited by typical perfluoroalkyl acids

Chao Qin[a], **Ce-Hui Mo**[b*]

[a] College of Resources and Environmental Sciences, Nanjing Agricultural University, Nanjing, Jiangsu, China

[b] Guangdong Provincial Research Center for Environment Pollution Control and Remediation Materials, College of Life Science and Technology, Jinan University, Guangzhou, Guangdong, China

Abstract: Perfluoroalkyl acids (PFAAs) are considered as the forever chemicals, gaining increasing attention for their hazardous impacts. However, the ecological effects of PFAAs remain unclear. Environmental DNA (eDNA) as the environmental gene pool is often collected for evaluating the ecotoxicological effects of pollutants. In this study, we found that all PFAAs investigated, including perfluorohexanoic acid, perfluorooctanoic acid, perfluorononanoic acid, and perfluorooctane sulfonate, even at low concentrations (0.02 and 0.05 mg/L), expedited the enzymatic degradation of DNA in a nonlinear dose-effect relationship, with DNA degradation fragment sizes being lower than 1000 bp and 200 bp after 15 and 30 min of degradation, respectively. This phenomenon was attributed to the binding interaction between PFAAs and AT bases in DNA via groove binding mode. van der Waals force (especially dispersion force) and hydrogen bonding are the main binding forces. DNA binding with PFAAs led to decreases in base stacking and right-handed helicity, resulting in loose structure of DNA exposed more digestion sites for degrading enzymes and accelerating the enzymatic degradation of DNA. The global ecological risk evaluation results indicated that PFAAs contamination could cause medium and high molecular ecological risk in 497 samples from 11 contamination-hot countries (such as USA, Canada, and China). The findings of this study show new insights into the influence of PFAAs on the environmental fates of biomacromolecules and reveal the hidden molecular ecological effects of PFAAs in the environment.

The sublethal effects of ethiprole on the development, defense mechanisms, and immune pathways of honeybees (*Apis mellifera* L.)

Yueyue Liu[a], **Chen Wang**[a,*]
[a] State Key Laboratory of Environmental Criteria and Risk Assessment, Chinese Research Academy of Environmental Sciences, Beijing, China

Abstract: Ethiprole has been widely used in agriculture, but there have been few studies on the adverse effects of ethiprole on nontarget organisms. This study focused on the mechanism of the sublethal effects of ethiprole on the development, antioxidation mechanisms, detoxification mechanisms and immune-related gene expression of honeybees (*Apis mellifera* L.). Honeybee larvae were found to be more sensitive than pupae to ethiprole. It was found that ethiprole inhibited the pupation and eclosion of bee larvae in a dose-dependent manner, with ethiprole doses of 0.001 mg/L decreasing pupation and eclosion rates to 50.00% ± 8.84% and 20.83% ± 10.62%, respectively. The activities of antioxidative enzymes (superoxide dismutase and catalase) and detoxification factors (glutathione and glutathione S-transferase) were also significantly increased in ethiprole-exposed honeybees, indicating that a sublethal dose of ethiprole also induced oxidative stress in honeybees. In the 0.001 mg/L ethiprole-exposure group, the expression of pathogen recognition-related gene PGRP-4300 was upregulated 11.10 ± 0.45-fold, and that of detoxification-related gene CYP4G11 was upregulated 8.84 ± 0.11-fold, indicating that ethiprole induced an immune reaction in honeybees. To the best our knowledge, this study represents the first demonstration that sublethal concentrations of ethiprole inhibit honeybee development and activate honeybee defense and immune systems.

Alterations of metabolites in follicular fluid associate with perfluorooctanoic acid-induced poor embryo quality

Junting Xu[a], **Qiaoling Wang**[a], **Xiaoming Teng**[a], **Yi Guo**[a,*]
[a] Obstetrics and gynecology hospital, Tongji University, Shanghai, China

Abstract: Perfluoroalkyl and polyfluoroalkyl substances (PFASs) are global pollutants that humans are widely exposed to. We aimed to investigate which specific PFAS have significant adverse effects on embryo quality, and what potential mechanisms are involved. Our study enrolled 378 women undergoing in vitro fertilization (IVF) treatment at the Reproductive Center of Shanghai First Maternity and Infant Hospital from November 2021 to May 2023. Follicular fluid samples were collected during oocyte retrieval and 29 PFAS were measured using ultra-performance liquid chromatography coupled to tandem mass spectrometry. Untargeted metabolomics was performed and causal mediation analysis was used to explore the relationship between metabolites in follicular fluid with PFAS level and embryo quality. Detection frequencies of 15 measured PFAS were higher than 85%, and the one with the highest median concentration was perfluorooctanoic acid (PFOA, 6.54 pg/mL). Bayesian kernel machine regression model showed that overall the PFAS mixture was negatively associated with the high-quality embryo rate and PFOA was the dominant contributor (conditional posterior inclusion probabilities = 0.9698). The poor embryo quality induced by high PFOA level was potentially mediated by the reduction of some organonitrogen compounds in follicular fluid. Higher exposure to PFOA in follicular fluid was adversely correlated with the embryo quality during IVF, which involved the reduction of some organonitrogen compounds and sphingolipids metabolites that was essential for maintaining the normal cellular growth and metabolism.

Effects of *Russula vinosa* Lindblad polysaccharides on the growth status of zebrafish with BPAF-induced neurotoxicity

Bowen Yan[a], Caoxing Huang[a], Qiang Yong[a,*]

[a] Jiangsu Co-Innovation Center of Efficient Processing and Utilization of Forest Resources, Nanjing Forestry University, Nanjing, Jiangsu, China

Abstract: Bisphenol A (BPA), an environmental endocrine disruptor, is one of the most widely used compounds. Owing to its heavy estrogenic-like effects, its use has been banned or strictly restricted in some nations. In recent years, with the ban or restriction of BPA, the production of BPA analogs with structures similar to those of BPA, including bisphenol S (BPS), bisphenol F (BPF), and bisphenol AF (BPAF), has continued to expand. Owing to the rapidly expanding applications of bisphenol analogs, increasing attention has been paid to their toxicity and environmental side-effects, which include neurotoxicity. *Russula vinosa* Lindblad is not only an edible, nutritious mushroom but also contains various bioactive compounds with promising pharmacological applicability. It is rich in proteins, carbohydrates, essential trace elements, amino acids, vitamins, and other functional compounds, among which polysaccharides hold significant importance. Studies have shown that Russula vinosa Lindblad polysaccharides possess a variety of biological activities such as antioxidant, immunomodulatory, anticancer, and anti-inflammatory activities, but the protective effects against nerve damage have not been reported. In this study, we extracted *Russula vinosa* Lindblad polysaccharide (MA-S) using maleic acid and resolved the structure of MA-S by XPS, FTIR, and NMR, secondly, we explored the effects of different concentrations of MA-S on the growth and behavioral profile of zebrafish with BPAF-induced nerve damage. The results showed that MA-S had a molecular weight of 3.62×10^3 g/mol, a glycosyl ratio of Gal:Glu:Man = 0.03:1:0.08, and was mainly composed of six sugar residues. MA-S was able to restore the body weight and length of BPAF-induced damaged zebrafish to normal levels, and 0.5% MA-S significantly promoted the weight gain and length increase of zebrafish. Behavioral experiments revealed that different concentrations of MA-S were able to alleviate the anxiety behaviors of BPAF-induced zebrafish, with 0.1% MA-S being the most effective.

Effect of high-pressure homogenisation of nanolignin on bone metabolism

Wenhui Pei[a], Caoxing Huang[a,*]

[a] Jiangsu Co-Innovation Center of Efficient Processing and Utilization of Forest Resources, Nanjing Forestry University, Nanjing, Jiangsu, China

Abstract: Lignin is a natural macromolecule widely found in plants, and paper wastewater contains a large amount of lignin, which seriously pollutes the environment. The development of high value lignin application is an effective way to eliminate its environmental hazards as waste and achieve sustainable development. It has been reported that pro-inflammatory environment, oxidative stress and other reasons to break the balance, such as rheumatoid arthritis, osteoporosis and other diseases. Therefore, the use of bioactive substances with antioxidant and anti-inflammatory properties for the treatment and prevention of bone-related diseases has received widespread attention. Lignin contains hydroxyl, carboxyl and methoxy groups, which have biological activities such as antioxidant activity and immunomodulation. However, the lack of a sufficient number of functional groups in the lignin structure limits its application. In this study, lignin nanoparticles (KL-Nano) were prepared by high-pressure homogenisation of pristine kraft lignin (KL) with the aim of increasing its functional group content for further application in the field of bone remodelling. The results showed that lignin was able to form structurally homogeneous spherical nanoparticles after 4 and 25 high-pressure homogenisations, and the functional group (alcohol hydroxyl and phenol hydroxyl) content of lignin could be increased by more than 30%. Compared with KL, KL-Nano promotes osteoblast differentiation in inflammatory environments by up-regulating the expression levels of osteoblast-related genes (ALP, Runx2 and Col1a1). Meanwhile, it can down-regulate the expression levels of osteoclast differentiation-related genes (c-Fos, OSCAR, CTSK and TRAP) and inhibit osteoclast differentiation, which makes it more effective in repairing bone defects in inflammatory environment. This excellent result suggests that high pressure homogenisation is a promising technique to enhance the bioactivity of lignin, exploiting the potential of waste for biomedical applications.

Manipulation of radical and electron transfer processes with oxygen vacancies over Cu_2O/Cu heterojunctions for peracetic acid activation

Liying Wu[a], Jun Ma[a,*]
[a] School of Environment, Harbin Institute of Technology, Harbin, Heilongjiang, China

Abstract: Advanced oxidation processes (AOPs) have been widely employed in water purification. Electron transfer processes (ETP) demonstrate higher selectivity and reaction stoichiometric efficiency of oxidants in comparison to radicals-based AOPs. Herein, a novel oxygen vacancies (Vo)-modified heterostructural Cu_2O/Cu was prepared to alleviate the electron transfer barrier by forming continuous electron energy level for the formation of ETP pathway in Peracetic Acid (PAA) activation. After 60 min of reaction, the removal rate of sulfamethoxazole (SMX) was approximately 92.54%. Contributions from the hydroxyl radical (•OH) and ETP pathways were approximately 45.36% and 47.18%, respectively. Vo played a crucial role in regulating the reaction activity and pathway of $Cu_2O/Cu/PAA$ system, with the ETP pathway continuously strengthened as the Vo content increased. The enhancement mechanism of Vo and heterojunctions on ETP pathway was revealed. Firstly, Vo and heterointerfaces acted as electron-rich centers, promoting the formation of continuous electron energy levels and enhancing the efficiency of interfacial electron transfer. Besides, Vo induced the generation of unsaturated metal sites, endowing the Vo-rich heterojunction Cu_2O/Cu with the Lewis acid-base characteristics, enhancing PAA adsorption, forming a unique dual-coordination process, lowering the redox reaction energy barrier. Thus, the decomposition of PAA was facilitated, and a metastable complex was formed accompanying the generation of •OH to reinforce the generation of ETP pathway. The Vo-rich heterojunction $Cu_2O/Cu/PAA$ system, under the synergistic action of the •OH and ETP pathways, exhibited strong resistance to interference and demonstrated universality in the removal of different refractory organics.

Analysis of serum herbicide levels and determinants of exposure in middle-aged and elderly population

Weiya Li[a], **Meian He**[a,*]
[a] School of Public Health, Huazhong University of Science and Technology, Wuhan, Hubei, China

Abstract: Herbicides are widely used in agricultural production. They can enter human bodies by various routes and cause adverse effects. However, there are limited studies evaluating the levels of herbicides in humans, while the determinants of herbicide exposure are inconsistent. We aimed to assessment of serum herbicide levels and their determinants of exposure in middle-aged and elderly population. This study was based on the Dongfeng-Tongji cohort founded in 2008. A total of 2012 subjects were included in this cross-sectional study. The basic information of this population was collected using an epidemiological questionnaire. Serum concentrations of 22 herbicides were measured by GC-MS/MS. Spearman's correlation was used to analyse the correlation between the different herbicides. We performed non-parametric tests to compare the difference between various groups of possible influencing factors. Multivariable regression models were used to analyse the relationship between various influencing factors and serum herbicide concentrations. The mean age of the subjects was 62.8 years, and 44.1% of them were male. Finally, a total of 13 herbicides was included. There was a low-moderate correlation between the various herbicides (r: 0.19–0.83). One-way analysis showed that serum concentrations of oxadiazon, oxyfluorfen, nitrofen, and fluazifop-butyl were higher in subjects aged $\geq$ 60 years than in those aged $<$ 60 years ($P < 0.05$). The serum concentrations of chlorpropham, benfluralin, atrazine, propyzamide, metolachlor, pendimethalin, oxyfluorfen, nitrofen, and fluazifop-butyl were significantly higher in males than in females ($P < 0.05$). Similar results were obtained in multivariate regression analysis. Compared to the population with fruit intake $<$ 5 times/week, serum concentrations of trifluralin, benfluralin, atrazine, propyzamide, metolachlor, pendimethalin, oxadiazon, oxyfluorfen, and fluazifop-butyl were significantly higher in those with fruit intake $\geq$ 5 times/week ($P < 0.05$). Serum herbicide levels in middle-aged and elderly population, may increase with age, and there are gender differences. Dietary habits (e.g., increased frequency of fruit intake) may be a factor affecting herbicide exposure levels.

Gender-specific effect of prenatal OPEs exposure on children neurobehavioral development: A longitudinal study of Shanghai Maternal-Child Pairs Cohort

Liyi Zhang[a,b], Yunhui Zhang[a,b,*]

[a] Key Lab of Health Technology Assessment, National Health Commission of the People's Republic of China, Fudan University, Shanghai, China

[b] Key Laboratory of Public Health Safety, Ministry of Education, School of Public Health, Fudan University, Shanghai, China

Abstract: Organophosphate esters (OPEs) are widely used as flame retardants and plasticizers in various products. Several studies have reported that OPEs may affect neurodevelopment, however, existing epidemiologic research focused on this issue based on a single-point assessment of children neurological behavior. Therefore, this study aimed to evaluate the longitudinal associations of OPEs with children's neurobehavioral development. Based on Shanghai Maternal-Child Pairs Cohort, 508 maternal-child pairs were included in this study. The Strength and Difficulties Questionnaire was used to assess children behavior at 2-year-old and 5-year-old. Seven kinds of OPEs were quantified in maternal serum during pregnancy. OPEs concentrations were adjusted for serum lipid levels and natural logarithm transformed in the subsequent analyses. Generalized estimated equation models (GEE), linear mixed-effect models and multiple linear models were applied to evaluate the longitudinal and cross-sectional associations of OPEs exposure with behavior difficulties risk and scores. The detection rates of 4 OPEs (TBP, TBEP, TDCPP and EHDPP) were over 50% and TBEP exhibited the highest concentration in maternal serum (0.79 ng/g). Among boys, an increase of ln-unit in EHDPP concentration was associated with higher risk of peer problem (RR = 2.39, 95%CI: 1.33, 4.30) and a higher score of peer problem ($\beta = 0.44$, 95%CI: 0.21, 0.67) in longitudinal analyses. In cross-section analyses, EHDPP was significantly associated with increased peer problem scores at 2-year-old and 5-year-old ($\beta_{\text{2-year-old}} = 0.42$, 95%CI: 0.15, 0.69; $\beta_{\text{5-year-old}} = 0.53$, 95%CI: 0.15, 0.91). Among girls, per ln-unit increment of TBEP was related to a higher odds for prosocial behavior problem (RR = 1.86, 95%CI: 1.18, 2.94) in longitudinal analyses and in cross-section analyses at 2-year-old (RR = 2.76, 95%CI: 1.39, 5.50), however, such association at 5-year-old was non-significant. Our results suggested adverse and sex-specific effects of prenatal OPEs exposure on neurobehavioral development in children and these effects could last to the age of 5.

Association of urinary phthalate metabolites with lipid profiles and the mediating role of serum globulin: A panel study in adults

Kun Huang[a], **Xiaomin Zhang**[a,*]
[a] School of Public Health, Huazhong University of Science and Technology, Wuhan, Hubei, China

Abstract: The association of co-exposure to multiple phthalates with blood lipid levels, along with the underlying mechanism, remained unclear. We conducted a panel study involving 119 adults with three repeated visits across three seasons to evaluate associations of phthalate mixture with lipid profiles and the mediation effect of serum globulin. Ten metabolites of phthalates (mPAEs) in urine samples were detected for four consecutive days each season. Linear mixed-effect models, Bayesian kernel machine regression (BKMR), and Bayesian weighted quantile sum (BWQS) regression were utilized to explore the independent and joint associations between mPAEs and lipid profiles. The potential mediating role of serum globulin was explored using mediation analysis. After multiple adjustments, several mPAEs were positively associated with low-density lipoprotein cholesterol (LDL-C) at lag 0 and total cholesterol (TC) at lag 1 ($P\text{-FDR} < 0.\ 05$), and the associations were more prominent in male and abdominal obesity subjects. The BKMR method showed increased LDL-C levels per exposure-mixture quartile increase for ten mPAEs (percentage change [% Change]: 2.45, 95% confidence interval [95% CI]: 0.18, 4.78) and four low-molecular-weight phthalates (% Change: 2.29, 95% CI: 0.51, 4.10), driven by Mono-methyl phthalate (MMP). The higher TC was associated with mPAE mixture (% Change: 1.31, 95% CI: 0.36, 2.27) and high-molecular-weight phthalate mixture (% Change: 1.25, 95% CI: 0.37, 2.14), driven by mono-(2-ethyl-5-carboxypentyl) phthalate and mono-ethyl phthalate. Serum globulin mediated the relationship between MMP and TC, with a mediation proportion of 35.8%. Exposure to mPAEs, individual or in combination, is associated with increased LDL-C and TC levels at lag 0 day and lag 1 day, respectively. Serum globulin may be a potential mediating variable for the increase in TC levels related to mPAE exposure.

Associations of polyfluoroalkyl substances with atherogenic indices in children: A panel study

Biao Zhang[a], Xiaomin Zhang[a,*]
[a] School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, Hubei, China

Abstract: Cardiovascular disease is the leading threat to human health worldwide, with atherosclerosis being the fundamental pathological event. The etiology of atherosclerosis is complex, and there is increasing evidence that per- and polyfluoroalkyl substances (PFASs) may play a role in the risk of atherosclerosis development. However, to date, the existing literature represents somewhat mixed evidence regarding the associations between PFASs and atherosclerosis. Atherosclerosis is a progressive process that begins in childhood. It is critical to evaluate the associations between PFASs and atherosclerosis risk in children. Objectives: To evaluate the associations of PFASs exposure with atherogenic indices in children. Methods: We conducted a panel study with up to 3 visits across 3 seasons in Weinan, Shaanxi Province, China. Total of 142 children aged 4-12 years were available with 381 measurements of 11 plasma PFASs and atherogenic indices (atherosclerosis index (AI) and castelli's risk index I (CRI)). We evaluated the associations of PFASs, either as single compounds or as mixture, with AI and CRI using linear mixed-effects and weighted quantile sum regression (WQS) models. Results: We found that perfluorooctane sulfonate (PFOS) and 6:2 chlorinated polyfluorinated ether sulfonate (6:2 Cl-PFESA) were associated with increased AI and CRI in a dose-response manner, with the top tertiles of TG levels. Each 1-fold increase in PFOS and 6:2 CI-PFESA was associated with increment of 7.82%, 5.31% and 12.73%, 8.22% in AI and CR, respectively (P-FDR < 0.05). WQS regression showed significant associations between PFASs mixture and AI [β (95%CI): 0.15 (0.08, 0.22)] and CRI [β (95%CI): 0.10 (0.05, 0.14)], to which PFOS might be the major contributor. Conclusions: The present study suggested that PFASs exposure was dose-dependently associated with elevated atherogenic indices (AI and CRI) among children, in which PFOS may play important roles.

Association of serum organophosphorus pesticides levels with type 2 diabetes risk and blood glucose changes: A nested case-control study

Yan Yan[a], **Meian He**[a,*]

[a] School of Public Health, Huazhong University of Science and Technology, Wuhan, Hubei, China

Abstract: Organophosphorus pesticides (OPs) are widely used in agricultural field. The associations of OPs exposure with type 2 diabetes (T2D) and glucose metabolism disorders are inconsistent. In addition, most studies focus on agricultural workers and utilize questionnaire information or urine metabolites to assess exposure, especially, prospective epidemiological studies are scarce. Objectives: We investigated the association of serum OPs levels with T2D risk and blood glucose changes over 5 years' follow-up. A nested diabetic case-control study with 1006 pairs subjects based on the Dongfeng-Tongji cohort study were conducted. Serum OPs concentrations were measured by gas chromatography-triple quadrupole mass spectrometry. We used generalized linear models to assess the relationship between single OP and blood glucose changes, and conditional logistic models to assess the odds ratio (ORs) of T2D risk exposure to OPs. Subsequently, the BKMR model and WQS model were used to investigate the joint effects of mixed OPs exposure on blood glucose changes. There were 12 OPs measured with detection rate ≥ 95%, 1 OPs with 84.1%, and 6 serum OPs with detection rate < 60% which were divided into < LOD and ≥ LOD group. The OPs levels were not significantly associated with the risk of T2D. There was a significantly positive correlation between serum Ethion level and changes in blood glucose during 5 years' follow-up. The β values for the second, third, and fourth quartile of blood glucose change compared to the first Ethion quartile were 0.123, 0.290, and 0.261, respectively in the multivariate model. The BKMR model suggested that Ethion played an important role in the blood glucose changes. Ethion contributed to the blood glucose changes during 5 years' follow-up.

Polyparameter linear free energy relationships for partitioning to storage lipids at 25 °C

Zheming Liu[a], Yan Xu[a,*]

[a] Department of Municipal Engineering, School of Civil Engineering, Southeast University, Nanjing, Jiangsu, China

Abstract: Storage lipids, made up of triacylglycerides, are an important compartment for the bioaccumulation of nonionic organic compounds. Reliable models capable of predicting storage lipid–water and storage lipid–air partition coefficients (Kislip/w and Kislip/a) are deemed to be useful. Polyparameter linear free energy relationships (PP-LFERs) are accurate, general, and mechanistically clear models for predicting partition coefficients. About a decade ago, PP-LFERs were calibrated for Kislip/w at physiological temperature of 37 °C (Geisler et al. , Environ. Sci. Technol. 2012, 46, 9519–9524). Nevertheless, to date, a comprehensive collection and sufficiently reliable PP-LFERs for Kislip/w and Kislip/a at the most common standard temperature of 25 °C are still lacking. In this study, experimental-based Kislip/w and Kislip/a values for nearly 300 compounds at 25 °C were extensively collected or converted using related physicochemical quantities (e.g., solubility, activity coefficient) from the literature. Subsequently, universal PP-LFERs were calibrated for Kislip/w and Kislip/a at 25 °C. The PP-LFERs performed well over 10 orders of magnitude, achieving root-mean-square errors of 0.17–0.21 log units for compounds with reliable descriptors. Remarkably, using PP-LFERs calibrated in this and previous studies, low-density polyethylene was confirmed to be a superior analogue for storage lipids in the passive sampling of HOCs, compared to silicone or polyoxymethylene.

Metagenomics insights into the methanogenesis performance and metabolic mechanism of high-solids anaerobic digestion of human feces under gradient domestication

Haipeng Wang[a], Bingfeng Liu[a,*]
[a] School of Environment, Harbin Institute of Technology, Harbin, Heilongjiang, China

Abstract: High-solids anaerobic digestion (HSAD) of low C/N ratio waste was difficult to long-term running and would more likely result in ammonia inhibition. In this study, the reactors with human feces (HF) HSAD were operated in semicontinuous culture with HRT of 20 days for 190 days under mesophilic condition (38 ± 1 °C), granular sludge as inoculum was gradient domesticated by gradually increasing total solid (TS) (8% to 17%). The results showed that the highest tolerated concentration of TS achieved 16% and biogas was stopped producing at TS 17%. Maximum methane production rates of TS and volatile solid (VS) were obtained at TS 11%, 287.08 mL/g TS and 67.67 mL/g VS, respectively. It was worth noted that granular sludge as an inoculum could efficiently remove pathogens (E. coli, 99.80% at TS 11% and Salmonella, 88.98% at TS 12%). High concentrations of HF (TS 13% to 17%) suppressed the growth of dominant methanogens (Methanothrix soehngenii, Methanothrix sp., and Methanothrix harundinacea.) and facilitated the rapid proliferation of acidogenic bacteria (Defluviitoga tunisiensis, Methanoculleus bourgensis, and Tepidanaerobacter acetatoxydans). The absolute abundance of key methanogenesis enzyme-encoding genes (mcr, frh, and fwd) were suddenly increased significantly at TS 12% and 13%. The main types of methanogenesis (acetoclastic at 11% TS, hydrogenotrophic at 12% TS and methylotrophic at 13% TS) would change with the variation of different TS HF. The above studies provide guidance for HF HSAD domestication in practical AD applications and supply an effective disposal method for HF environmental safety issues in rural areas.

Long-term exposure to Microcystin-LR induces gastric toxicity by activating the MAPK signaling pathway

Xueqiong Yao[a,*]
[a] School of Public Health, Hengyang Medical School, University of South China, Hengyang, Hunan, China

Abstract: Microcystin-LR (MC-LR) poses a serious threat to both ecosystems and public health. Previous studies have mainly focused on the hepatotoxicity of MC-LR, whereas its gastric toxicity effects and mechanisms of long-term exposure under low dosage remain unknown. Herein, the gastric tissue from C57BL/6 mice feeding with drinking water contaminated by low-dose MC-LR (including 1, 60, and 120 μg/L) was investigated. The obtained results demonstrated that different concentrations of MC-LR exposure resulted in significant shedding and necrosis of gastric epithelial cells in mice, and a down-regulation of tight junction markers, including ZO-1, Claudin1, and Occludin in the stomach, which might lead to increased permeability of the gastric mucosa. In addition, the proteins expression levels of p-RAF/RAF, p-ERK1/2/ERK1/2, Pink1, Parkin, and LC3-II/LC-3I were increased in 120 μg/L MC-LR exposed group, while the protein expression level of P62 was decreased after exposure to 60 and 120 μg/L MC-LR. Furthermore, we observed an increase in pro-inflammatory factors (IL-6 and TNF-α) and a decrease in anti-inflammatory factors (IL-10) in gastric tissue. The activation of the MAPK signaling pathway and mitophagy might contribute to the development of gastric damage by promoting inflammation. We first reported that long-term low-dose MC-LR exposure activated the MAPK signaling pathway and mitophagy in the gastric tissues of mice, providing new insight into the gastric toxic effects and molecular mechanisms caused by MC-LR, which might be used for the prevention and treatment of gastric diseases. Further studies are needed to elucidate the exact underlying mechanism.

Metagenomic deciphers food waste anaerobic digestion metabolic pathways response to a rapid increase in loading

Zetang Chai[a], Binfeng Liu[a], Haipeng Wang[a,*]
[a] School of Environment, Harbin Institute of Technology, Harbin, Heilongjiang, China

Abstract: The stability and efficiency of Food waste (FW) are easily influenced by the complexity of the substrate. To address the lack of knowledge in food waste high solid anaerobic digestion (FWHSAD) quick started, we implemented a rapid increase in total solid loading in the reactor, from 1% to 13% in 65 days. The result showed that methane production followed four stages: adaptation、development, thriving and failure at TS 2% (216.9±7.14 ml/g VS), TS 3%~8% (370.6±24.03 ml/g VS), TS 9%~12% (458.735±40.5 ml/g VS) and TS 13% (164.59±0.3 ml/g VS), respectively. The failure of reactor at TS 13%was mainly attributed to terrible mass transfer and foaming, rather than the lever of total ammonia (900 mg/L) and volatile fatty acids (VFA)(661.75 mg/L). Meanwhile, the constant accumulation of salt in the system should also be concern. Increasing the total solid loading led to an increase in the abundance of acetate (Mesotoga) and propionate (Propionibacterium) oxidation bacterial and acetotrophic methanogens (Methanothrix). Especially, hydrogenotrophic methanogen (Methanospirillum, Methanobacterium) were enrich to overcome the pressure of loading at TS 13%. Key carbohydrate, amino acid metabolism and methanogenesis enzyme-encoding genes were enrich at TS 12%, indicating the microbial community's resilience to the higher solid loading. This study demonstrates rapidly started of FWHSAD is feasible and provide insights into the microbial mechanisms involved, suggesting promising applications potential.

Ambient temperature causes cardiovascular effects: The controlled temperature study in healthy subjects (CTSHS)

Weihong Qiu[a], Weihong Chen[b,*]

[a] Department of Epidemiology and Health Statistics, School of Public Health, Fujian Medical University, FuZhou, Fujian, China

[b] Department of Epidemiology and Health Statistics, School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, Hubei, China

Abstract: With global warming causing more extreme weather events, researchers have linked non-optimal ambient temperature (NOAT) to adverse cardiovascular outcomes and serum hormones, but the causal relationship remains unclear. In the controlled temperature study, forty-three (20 males, 23 females) healthy non-obese volunteers were recruited. All volunteers were exposed to the middle (18 °C), low (6 °C), and high (30 °C) temperatures successively lasting 12 hours with air pollutants controlled. In each scenario, all volunteers received detailed physical examinations every 2 hours, including body temperature (BT), blood pressure (BP), heart rate (HR), and heart rate variability (HRV). Serum index, containing biomarkers of early myocardial injury [creatine kinase (CK) and creatine kinase-myocardial band (CK-MB)] and HPA and HPT hormones [adrenocorticotropic hormone (ACTH), cortisol, angiotensin II (Ang II), thyroid-stimulating hormone (TSH), and thyroid hormones (T3, T4, FT3, FT4)] were quantified by fully automatic biochemical immune analyzers. Compared with moderate temperature, we found significantly higher BP (SBP, DBP, MAP, and PP), HRV (LF, HF, TP, RMSSD, pNN50), CK-MB, and T4 under low-temperature exposure ($P<0.05$). In contrast, we found significantly higher BT, HR, ACTH, and lower BP (SBP, DBP, and MAP), HRV (LF, HF, RMSSD, pNN50), CK-MB, cortisol, and thyroid hormones (T4, FT3, FT4) under high-temperature exposure ($P<0.05$). Repeated measures correlation analyses revealed that significant correlations between cardiovascular outcomes and HPA and HPT hormones were identified at different temperature strata ($P<0.05$). NOAT exposure alters cardiovascular outcomes, HPA hormones, and HPT hormones. HPA and HPT hormones might be involved in NOAT-related early cardiovascular injury.

Exposure to various pesticides and incidence risk of type 2 diabetes mellitus: Evidence from a case-cohort study and Mendelian randomization analysis

Dandan Wei[a], Jiayu Shi[a], Zhiwei Chen[a], Haoran Xu[a], Yao Guo[a], Chongjian Wang[a], Zhenxing Mao[a,*]

[a] Department of Epidemiology and Biostatistics, Zhengzhou university, Zhengzhou, Henan, China

Abstract: This study aimed to investigate the longitudinal and causal associations between multiple pesticides and the incidence of type 2 diabetes mellitus (T2DM) in the Chinese rural population. Here, we conducted a case-cohort study to investigate the longitudinal and causal associations between pesticides mixture and T2DM, and determine the crucial pesticides highly associated with T2DM in rural China. A total of 925 subjects with normal glucose and 925 subjects with impaired fasting glucose (IFG) were enrolled in this case-cohort study. A total of 51 targeted pesticides were quantified for each participant at baseline. Logistic regression, quantile g-computation, and Bayesian kernel machine regression (BKMR) were used to assess the individual and combined effects of pesticides on IFG and T2DM. Mendelian randomization (MR) analysis was employed to obtain the causal associations between pesticides exposure and T2DM. Effect modification was examined by adding a product term to logistic regression models. After 3-year follow-up, one-unit increment in ln-isofenphos, ln-malathion, and ln-deltamethrin were associated with an increase conversion of IFG to T2DM (FDR-$P<0.05$). One quartile increment in organochlorine pesticides (OCPs), organophosphorus pesticides (OPs), herbicides and pyrethroids mixtures were related to a higher risk of incident T2DM among IFG patients ($P<0.05$). The BKMR results showed a positive trend between exposure to pesticides mixture and T2DM risk. The MR analysis indicated a positive association between exposure to pesticides and T2DM risk ($P<0.05$). No any significant association were found between various pesticides and IFG. In addition, compared to subjects with high levels of PA, those with low levels of PA were related to increased risk of T2DM with the increased levels of isofenphos and deltamethrin among IFG patients. Individual and combined exposure to pesticides increased the progression of T2DM among IFG patients after 3-year follow-up. MR analysis further supported the causal association of pesticides exposure with T2DM risk.

Vitamin D3 suppresses astrocyte activation and ameliorates coal dust-induced mood disorders in mice

Yuanjie Zou[a,b,c], **Min Mu**[a,b,c,*]

[a] Engineering Laboratory of Occupational Health and Safety, Anhui University of Science and Technology, Huainan, Anhui, China

[b] Key Laboratory of Industrial dust deep reduction and occupational health and safety of Anhui Higher Education Institutes, Anhui University of Science and Technology, Huainan, Anhui, China

[c] Key Laboratory of Industrial Dust control and Occupational Health of the Ministry of Education, Anhui University of Science and Technology, Huainan, Anhui, China

Abstract: Pneumoconiosis patients exhibit significantly more anxiety and depression than healthy individuals. However, the mechanism of coal dust-induced anxiety and depression remains unclear. A pneumoconiosis mouse model with anxiety- and depression-like behaviors were established after 28 days of exposure to coal dust. Vitamin D3 treatment (1200 IU/kg/week) was administered intraperitoneally for 3 months starting from the first coal exposure. Tail suspension test (TST), open field test (OFT), and elevated plus-maze (EPM) test were used to assess anxiety- and depression-like behaviors. Theserum concentration of 25(OH)D3 and fibrillary acid protein (GFAP) expression were determined. In addition, the morphology and distribution of GFAP and neurogenic differentiation factor1 expression (NeuroD1) in different cerebral hippocampus were observed. In coal dust-exposed mice, immobility time decreased in OFT and increased in TST, and the frequency of entering the open arm decreased in the EPM compared with the control mice. Coal dust increased hippocampal GFAP expression and astrocyte activation and reduced neurogenic differentiation factor1 expression (NeuroD1). In addition, Vitamin D3 significantly alleviated anxiety- and depressive-like behaviors in TST and EPM test, decreased GFAP expression level, modified hippocampal astrocyte activation pattern, and advanced brain-derived neurotrophic factor (BDNF) distribution and expression in CA1 and CA3 of the hippocampus. Taken together, our results suggest that, by inhibiting the over-activation of astrocytes and increasing BDNF and neuron protection, vitamin D treatment ameliorates coal-dust-induced depressive and anxiety-like behavior, which is the first evidence that vitamin D may be a new approach for treating mood disorders caused by particulate matter.

Short-term effects of exposure to $PM_{2.5}$ and its components on hospital admissions for hypertensive disorders of pregnancy: A multicity case-crossover study in China

Heng He[a,*], Weihong Qiu[a]

[a] Department of Epidemiology and Health Statistics, School of Public Health, Fujian Medical University, Fuzhou, Fujian, China

Abstract: The impact of short-term exposure to fine particulate matter ($PM_{2.5}$) and its components on hospital admissions for hypertensive disorders of pregnancy (HDP) remains unclear. The daily data for HDP hospitalizations and air pollutant concentrations were collected from January 2015 to December 2021 (total of 2557 days) in five cities located in Henan Province, China. A time-stratified case-crossover design with a quasi-Poisson generalized linear model was used to analyze the effects of short-term exposure to $PM_{2.5}$ and its components [organic matter (OM), nitrate ion (NO_3^-), sulfate ion (SO_4^{2-}), ammonium ion (NH_4^+), black carbon (BC)] on the hospital admissions for HDP. Additionally, the modification effects by age, season, and the "Three-Year Action Plan to Win the Blue Sky Defense War" on the above associations were further assessed. A total of 8007 mothers with HDP were gathered. Each 10 μg/m^3 increase (1 μg/m^3 for BC), the strongest relative risks (95% confidence intervals) of hospitalizations for HDP were 1.011 (1.003 to 1.020) for $PM_{2.5}$ in lag01, 1.077 (1.003 to 1.157) for SO_4^{2-} in lag05, 1.032 (1.003 to 1.063) for NO_3^- in lag01, 1.054 (1.006 to 1.105) for NH_4^+ in lag01, 1.062 (1.003 to 1.124) for OM in lag02, and 1.037 (1.001 to 1.075) for BC in lag05, respectively. The effects of exposure to BC (lag07) were stronger in mothers aged $\geqslant 35$ years, and the effects of exposure to OM (lag02) were stronger before implementation of the Action Plan (all P modification < 0.05). Short-term exposure to $PM_{2.5}$ and its components was associated with increased hospitalizations for HDP. This effect was pronounced among mothers aged $\geqslant 35$ years and before the implementation of the Action Plan.

Insights into free and conjugated forms neonicotinoid insecticides in human serum and their association with oxidative stress

Tao Zhang[a,*]

[a] School of Environmental Science and Engineering, Sun-Yat Sen University, Guangzhou, Guangdong, China

Abstract: Following exposure, neonicotinoid insecticides (NEOs) can be metabolized by both Phase I and Phase II reactions catalyzed by human cytochrome P450 enzymes. However, toxicities of parent NEOs and their metabolites are still unclear and little is known about biotransformation rates and pathways of NEOs in humans. In this study, 98 serum samples collected in China were analyzed for free, conjugated and total forms of six parent NEOs (i.e., acetamiprid (ACE), imidacloprid (IMI), clothianidin (CLO), thiacloprid (THD), thiamethoxam (THM) and dinotefuran (DIN)), and four metabolites (i.e., N-desmethyl-acetamiprid (N-dm-ACE), 1-methyl-3-(tetrahydro-3-furylmethyl) (DIN-U), 5-hydroxy-imidacloprid (5-OH-IMI), olefin-imidacloprid (Of-IMI)). NEOs and their metabolites were detected in all serum samples, and the total median concentrations of free, conjugated, and total forms of 10 NEOs were 2.04, 2.01, and 5.12 ng/mL, respectively. Conjugated forms of NEOs accounted for only half (53%) of the total forms of NEOs. Based on the profiles of Phase I and Phase II metabolites of NEOs in serum, it was found that age is a determinant in Phase I metabolism of DIN and Phase II metabolism of IMI. The Phase II metabolites of NEOs are associated with oxidative DNA damage, and the conjugated forms of IMI, DIN and 5-OH-IMI in serum were significantly positively correlated with oxidative stress. Overall, the amount of NEOs present in conjugated forms in human serum was determined to document the existence of considerable proportion of free forms of these insecticides.

Comparative analysis of dissolved oxygen predictions in the Yellow River Basin using different environmental predictors based on machine learning

Lingling Liu[a], Xiaoli Zhao[a,*]
[a] State Key Laboratory of Environmental Criteria and Risk Assessment, Chinese Research Academy of Environmental Sciences, Beijing, China

Abstract: Dissolved oxygen (DO) serves as a crucial water quality indicator reflecting river health. Machine learning (ML) models have gained popularity for water quality prediction; however, their accuracy heavily depends on predictor variables. Predictor availability varies considerably, prompting the inquiry of whether easily accessible catchment attributes, when combined with ML—specifically a random forest (RF) model—can effectively predict river DO dynamics in the Yellow River Basin (YRB). Is there a necessity to collect additional water quality data to improve model performance? To address this, we collected ~11, 500 monthly DO data from 135 monitoring sites in the YRB from 2016 to 2022 and categorized predictor variables into three groups: catchment attributes and meteorology (CAM), water quality parameters (WQPs), and a combination of both (CAM+WQP). The RF models achieved satisfactory performance, with Nash–Sutcliffe efficiency exceeding 0.35 at 68.38%, 61.03%, and 72.06% of sites for CAM, WQP, and CAM+WQP, respectively. CAM alone outperformed WQP alone, with marginal improvement upon including WQP. Nevertheless, all models encountered difficulties with sites showing substantial DO fluctuations, indicating inherent model limitations in reproducing extreme values. Conversely, in heavily human-impacted regions like the Fen River Basin, the addition of WQP notably improved DO prediction accuracy, attributed to the partial reflection of anthropogenic activities through WQP. Despite this, both WQP and CAM+WQP models exhibited diminished performance in highly urbanized areas, implying that WQP inadequately captures human impacts. Further analysis revealed several factors impeding DO predictions, including unbalanced data in high-altitude watersheds, insufficient anthropogenic emission data, and a lack of water transfer information. Our findings underscore the need for additional DO sampling sites in the plateau region of the YRB. Moreover, recognizing the limited enhancement offered by WQP and its spatial extrapolation constraints, acquiring additional data on anthropogenic activity may prove more beneficial in enhancing DO prediction than solely monitoring WQPs.

Metabolomic reveals that nanoplastics exposure-induced cellular toxicity

Chuanli Yang[a], Lin Che[b], Xiaobing Shen[a,*]

[a] Key Laboratory of Environmental Medical Engineering and Education Ministry, School of Public Health, Southeast University, Nanjing, jiangsu, China

[b] Sun Yat-sen University Cancer Center, Sun Yat-sen University, Guangzhou, China

Abstract: Objective: Nanoplastics (NPs) exposure-induced health effects have become a focus in the field of environmental and medical research. NP exposure can induce cellular inflammation and carcinogenesis through mechanisms such as cellular oxidative stress and metabolic dysregulation. However, the metabolic characteristics and toxicity mechanisms of NP exposure-induced cellular toxicity remain unclear. Methods: HEK293T cells were exposed to NPs (0. 05 mg/mL) for 24 hours to establish an in vitro experimental model. Non-targeted metabolomics and bioinformatics analysis were employed to identify changes in cellular metabolites and related toxic metabolic pathways induced by NPs, aiming to identify metabolic biomarkers for monitoring and controlling environmental nanoplastic-induced cellular toxicity. Results: (1) Non-targeted metabolomics analysis detected a total of 1528 small molecule metabolites. (2) Principal component analysis (PCA) and partial least squares discriminant analysis (PLS-DA) revealed significant differences in metabolites between the control group and NPs-exposed group. (3) Compared with the control group, there were 162 differentially abundant metabolites in the NPs-exposed group, including 59 metabolites with decreased such as L-glutamine and phenylalanyl glycine, and 103 metabolites with increased such as 2,3-diphosphoglycerate, phenylalanyl acrylamide, and N-acetyl-D-glucosamine. (4) Functional annotation of differentially abundant metabolites indicated their association with environmental information processing, cancer processes, organismal metabolism, and gene translation. (5) KEGG enrichment analysis revealed that differentially abundant metabolites mainly affected signaling pathways such as ABC transporters, amino acid biosynthesis, cancer central carbon metabolism, and ferroptosis. Conclusion: NPs exposure induces cellular toxicity by altering cellular metabolomic profiles, possibly through pathways involving ABC transporters, amino acid biosynthesis, cancer central carbon metabolism, and ferroptosis. These findings provide insights into metabolic biomarkers and risk prevention and control strategies for evaluating the health effects of nanoplastic exposure.

Long-term investigation of heavy metal variations in mollusks along the Chinese Bohai Sea

Lufeng Chen[a], **Yong Liang**[a], **Jianbo Shi**[b,*]
[a] School of Environment and Health, Jianghan University, Wuhan, Hubei, China
[b] State Key Laboratory of Environmental Chemistry and Ecotoxicology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, China

Abstract: Biomonitoring is an effective way to assess the effects of pollutants on marine ecosystems. As an important fishing region in China, the Chinese Bohai Sea has been contaminated with heavy metals, posing great risks to seafood safety and human health. Herein, the spatiotemporal variations in the concentrations of seven heavy metals (As, Cd, Cr, Cu, Ni, Pb, and Zn) in 11 species of mollusks (658 samples) collected from the Chinese Bohai Sea were studied during 2006–2016. The concentrations of Cr, As, Cd, and Pb in approximately 41%, 100%, 71%, and 18% of the sampled mollusks exceeded the maximum permissible levels in aquatic products set by China, indicating that the mollusks were contaminated with varied concentrations of heavy metals. Except for slight fluctuations, no significant temporal variations were observed during the sampling period, suggesting a relatively stable status of these metals. Cluster analysis showed that oyster had higher bioaccumulation potential for Zn and Cu, whereas Mactra veneriformis, Rapana venosa, Meretrix meretrix, Chlamys farreri, and Mya arenaria had higher bioaccumulation potentials for Cr, As, Ni, Cd, and Pb, respectively. These findings are useful for biomonitoring and developing guidelines for seafood consumption in coastal regions. Significant relationships were observed between heavy metal concentrations in mollusks and socioeconomic indices (gross domestic product, per capita gross domestic product, and population amount), suggesting the effects of anthropogenic activities on heavy metal contamination. Our study established a good model to evaluate the risks of heavy metals and provided a sound scientific basis for controlling seafood safety in coastal regions.

Organochlorine pesticides and polychlorinated biphenyls in sediments of the Lanzhou reach of Yellow River, China: Concentration, spatial variation, sources and risk assessment

Yingqin Wu[a,*], Longmiao Yuan[a]

[a] Key Laboratory of Petroleum Resources Research, Gansu Province, Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou, Gansu, China

Abstract: This study determined the concentrations of organochlorine pesticides (OCPs) and polychlorinated biphenyls (PCBs) in Yellow River sediments from Lanzhou City, Northwestern China. The total concentrations of OCPs and PCBs in the sediment samples ranged from 85.61 to 202.28 ng/g and 3.08 to 32.29 ng/g, respectively. OCPs and PCBs were positively correlated with soil total organic matter (TOC), suggesting that TOC has an important influence on the occurrence and distribution of these contaminants. The data showed that the concentrations of OCPs and PCBs in the eastern Yellow River sediments of Lanzhou were higher than those in the western areas, indicating an obvious trend of increasing contamination levels for OCPs and PCBs downstream in the Yellow River. The composition of hexachlorocyclohexane (HCH) compounds followed this order: β-HCH>δ-HCH>α-HCH>γ-HCH. Among the dichlorodiphenyltrichloroethane (DDT) congeners, it is evident that DDT emerges as the predominant congener. Highly chlorinated compounds, including hexa- and hepta-chlorinated isomers, have a more significant influence on the distribution of PCBs in the study areas. Source identification indicated that HCHs and DDTs are mainly originated from historical residues, new lindane, and dicofol application. Regarding PCBs, the main sources involve a combination of factors, including solid waste incineration and primary commercial products (Kane chlor and Aroclor). According to established sediment quality guidelines, including ERL/ERM and TEC/PEC, it is evident that OCPs and PCBs pose a minimal threat to the sediment environment in our study area. Carcinogenic (ILCR) and non-carcinogenic (HQ) risks associated with PCBs and OCPs contamination in sediments were calculated based on inhalation, ingestion and dermal exposure routes, respectively. The results suggested that the health risks were generally low. This study has advanced our understanding of the distribution and primary sources of POPs in Yellow River sediment, and provided valuable insights to enhance decision-making support for sediment pollution control and monitoring.

Microplastics alter the fates of nitrogen cycling through affecting microbiome in farmland soils

Yuecheng She[a], Zhengkui Li[a,*]
[a] College of the Environment, Nanjing University, Nanjing, Jiangsu, China

Abstract: Microplastics (MPs) are widespread in agroecosystems and profoundly impact soil microbiome and nutrient cycling. However, how MPs regulate soil nitrogen (N) cycling and its pathways remain unclear. Here, the effects of conventional nonbiodegradable and emerging biodegradable MPs on soil N cycling processes, including nitrate reduction (i. e. , denitrification and dissimilatory nitrate reduction to ammonium (DNRA)) and autotrophic ammonium oxidation (i. e. , nitrification, complete ammonium oxidation (comammox), anaerobic ammonium oxidation (anammox), and anaerobic ammonium oxidation coupled to iron reduction (Feammox)) were explored through soil microcosm experiments accompanied with 15N isotope tracer technology and microbiome analysis. Results indicated that nonbiodegradable MPs (including polyethylene (PE), polypropylene (PP)) improved the activities of denitrification but significantly inhibited DNRA, whereas biodegradable MPs (including polylactic acid (PLA) and polybutylene adipate terephthalate (PBAT)) remarkably boosted DNRA pathway with the dominance in nitrate bioreduction (60.7%-76.8%). For autotrophic ammonium oxidation, our work unveiled that exposures of MPs significantly modulated ammonium oxidization pathways with distinct type- and dose-dependent effects. Nitrification remained the main contributor (56.4%-70.7%) to soil ammonium removal, followed by comammox (11.7%-25.6%), anammox (5.0%-20.2%) and Feammox (3.3%-11.6%). Compared to conventional nonbiodegradable MPs (i.e., PE and PP), biodegradable MPs (i.e., PLA and PBAT) exhibited more pronounced impacts on soil nutrient conditions and functional microbes, which collectively induced alterations in soil N cycling. Interestingly, low-dose PLA and PBAT remarkably enhanced the roles of anammox and Feammox in soil ammonium removal, contributing to the mitigation of soil acidification in agroecosystems. This study highlights the diverse responses of N cycling pathways to MPs, further deepening our understanding of how MPs affect biogeochemical cycling and enriching strategies for agricultural management amid increasing MPs pollution.

Weak magnetic fields coupling with biochar-supported nickel/nanoscale zero-valent iron facilitates extensive dechlorination and rapid removal of 2,4,6-Trichlorophenol in aqueous solution

Ying Wang[a], **Yan Xu**[a,*]
[a] School of Civil Engineering, Southeast University, Nanjing, Jiangsu, China

Abstract: The application of nanoscale zero-valent iron (NZVI) on remediating contaminants was limited by its intrinsic passive film. Hence, many efforts were made to improve the NZVI reactivity. In this study, weak magnetic fields (WMF) coupling with nickel/nanoscale zero-valent iron supported by biochar (BC-Ni/NZVI) was successfully synthesized and utilized for highly efficient 2,4,6-Trichlorophenol (2,4,6-TCP) dechlorination in aqueous solution. SEM-EDS analysis revealed the even distribution of Ni/NZVI on the surface of BC. Results showed that BC-Ni/NZVI with Ni doping amount of 0. 6% exhibited the best performance for 2,4,6-TCP removal. With the application of 20 mT of WMF, the removal efficiency of 2,4,6-TCP increased from 80.5% (without WMF) to 93.2% (with WMF) by BC-Ni/NZVI with the material dosage of 0.2 g/L, initial 2,4,6-TCP concentration of 20 mg/L, and initial pH of 3.0. The overall removal of 2,4,6-TCP was well described with the pseudo-first-order kinetics ($R^2>0.9$), and the observed kinetic constant (kobs) is 0.01675 min^{-1}, which increased by 65.7% compared to that without WMF. Furthermore, more extensive dechlorination of 2,4,6-TCP was achieved by BC-Ni/NZVI coupling with 20 mT WMF. The promotion of WMF was mainly attributed to the magnetic field gradient force moved paramagnetic Fe^{2+} to the direction at the BC-Ni/NZVI surface perpendicular to the external applied field, which could break down the passive film and localized corrosion. The hydrogen gas generated from the corrosion of Fe^0 is adsorbed by the loaded Ni and catalyzed the production of proton hydrogen. These findings provide insights into BC-Ni/NZVI coupling with WMF as an alternative engineering carbon based NZVI material for treating chlorinated phenols.

Characterization of an antimony-resistant fungus Sarocladium kiliense ZJ-1 and its potential as an antimony bio-remediator

Qianhui Gong[a], Xiaolu Lu[a,*], Chang Qing[a], Xiuyang Xie[a]
[a] School Of Environmental Studies, China University of Geoscience (Wuhan), Wuhan, Hubei, China

Abstract: Antimony (Sb) is a toxic metalloid widely distributed in the natural environments. Microorganisms, especially fungi, could serve as ideal biomaterials for bioremediation of Sb-polluted soils and waters. In this study, we isolated an antimony-resistant fungus, Sarocladium kiliense ZJ-1, from a slag sample collected in Xikuangshan Sb mine in China. ZJ-1 showed an extremely high resistance to Sb, with a MIC level of >175 mM for arsenite [Sb(III)] and 40 mM for arsenate [Sb(V)]. Whole genomic analysis identified multiple Sb (III)- and/or As(III)- resistant genes on ZJ-1's genome, which may partially explain its hyper-resistance to Sb. The potential of ZJ-1 in removing Sb from Sb(III) or Sb(V) solutions was also quantified. The average biosorption capacity of ZJ-1 for Sb (III) and Sb(V) is 635.14 mg/g and 149.65 mg/g, respectively, in Sb aqueous solutions with an initial concen tration of 2000 mg/L (16.43 mM). Besides, almost 99% of Sb(III) in the growing system was removed with an initial concentration of 500 mg/L (4.11 mM). Furthermore, Fourier transformation infrared spectroscopy (FT-IR) and X-ray photoelectron spectroscopy (XPS) were used to probe the Sb adsorption mechanism on ZJ-1, and -OH, -NH_2, -COOH, C-O and C-O-C were found to be the main surface functional groups of ZJ-1 cells to adsorb Sb.

Flood prediction of Dahuofang Reservoir based on machine learning

Zeqi Li[a], Jing Zhang[a,*], Bin Yan[a]

[a] College of Water Conservancy, Shenyang Agricultural University, Shenyang, Liaoning, China

Abstract: The flood of Dahuofang Reservoir is mainly caused by the runoff after the rainstorm in the basin. In the basin, many rainfall stations and hydrological stations provide relevant data. Due to the large number of rainfall stations and hydrologic stations, their importance to flood is different. In the construction of the model, simply inputting all data will lead to the problem of inputting non characteristic data, which will lead to the decline of model accuracy. In this paper, the grey correlation analysis is adopted to calculate the grey correlation of the stations in the basin, and the stations with the highest correlation are chosen out. After optimization and combination, the gamma test method is used to optimize the analysis data, and KNN algorithm is used to help find the adjacent points in the gamma test and select the optimal data combination. A two-layer LSTM neural network rainfall flood model is established and different models are compared. The results show that the LSTM model built after data processing can well predict the flood process and prevent over fitting. The research result plays an important role in flood prevention and disaster control.

Resilience assessment and optimisation logic of urban neighbourhood disaster bearing bodies based on extreme weather： A case study of Shijingshan district, Beijing, China

Shurui Yin[a], Jing Li[a,*]
[a] College of Architecture and Art, North China University of Technology, Beijing, China

Abstract: High-density cities have high development intensity and high population density, and are more seriously affected by extreme weather. How to improve the safety and resilience of high-density cities has become an important issue in urban construction. Since the 14th Five-Year Plan period, Beijing has carried out a lot of work on the construction of resilient cities, and the "237" heavy rainstorm in 2023 has made it realise that assessing the resilience of the city's disaster-bearing body is of great significance to the improvement of the city's disaster prevention construction. Compared with the macro nature of traditional data in urban resilience assessment, the text data based on street interviews can better reflect the problems of urban neighbourhood resilience from the micro perspective. This paper collects disaster prevention data and nine street interview samples from Shijingshan District, Beijing, through multiple interviews with relevant departments, and quantitatively analyses flood-prone points, accessibility to evacuation sites, accessibility to public green spaces, and accessibility to healthcare facilities from the supply and demand side of urban resilience through spatial quantification with GIS, and qualitatively analyses street interview samples through Nvivo software. At the same time, the qualitative analysis of street interview samples is carried out by Nvivo software, so as to study the vulnerability of urban neighborhoods in terms of macro and micro perspectives, and to reveal the problems and bottlenecks of "decoupling" of China's neighbourhood emergency management system in the context of extreme weather, which is conducive to the exploration of the resilient neighborhoods in terms of the law of disaster-bearing. The "DS3" decision-making model is constructed to apply resilience to the logic of neighbourhood governance, and optimization strategies are proposed in terms of planning layout, spatial integration and institutional management, which will provide effective reference for the future resilience construction at the neighbourhood level.

In-situ degradation of phenol using CuMgFe-LDO catalyst and assessment of its service life in the persulfate activation process

Jing Wei[a,*], Yun Chen[a]

[a] Key Laboratory of Soil Environment Management and Pollution Control, Nanjing Institute of Environmental Sciences, MEE, Nannjing, Jiangsu, China

Abstract: Layered double oxides (LDOs) have been proven effective and reusable materials in removing phenols. However, the service life of LDOs in an application remains unclear. This study optimized the properties of CuMgFe-LDO and assessed its service life for in-situ groundwater remediation. Phenol degradation in CuMgFe-LDO-activated persulfate (PS) system with various groundwater matrix was analyzed. Results showed improved phenol degradation with increasing Cu content and calcination temperature in LDO production, with a decrease in degradation beyond a certain level of Cu. Phenol removal was slightly influenced by fulvic acid and sodium humate below 20.0 mg/L but strongly affected by 1.0 mmol/L of SO_4^{2-} and HCO_3^-. A high TOC removal of 80% in all three recycled tests was found within 30 minutes, with intermediate products identified as benzoquinone, fumaric/maleic acid, and finally, oxalic and acetic acid. The CuMgFe-LDO showed demonstrated exemplary performance in a continuously flowing phenol and PS solution column, with a long service life of 12 days and low copper leaching (1.8 mg/L) at pH 6.55. This study supports the potential of the CuMgFe-LDO-activated PS system for remediating groundwater contaminated with phenolic compounds and mitigating acidification from PS use.

A Bayesian network-GIS probabilistic model for addressing human disturbance risk to ecological conservation redline areas

Jing Liu [a], **Xiaojuan Xu**[a], **Kun Zhang**[a,*]

[a] Ecological Conservation and Restoration Department, Nanjing Institute of Environmental Science, Ministry of Ecology and Environment, Nanjing, Jiangsu, China

Abstract: Population growth and associated ecological space occupation are posing great risks to regional ecological security and social stability. In China, “Ecological Conservation Redline” (ECR) that prohibited urbanization and industrial construction has been proposed as a national policy to resolve spatial mismatches and management contradictions. However, unfriendly human disturbance activities (e.g., cultivation, mining, and infrastructure construction) still exist within the ECR, posing a great threat to ecological stability and safety. In this article, a Bayesian network (BN)-GIS probabilistic model is proposed to spatially and quantitatively address the human disturbance risk to the ECR at the regional scale. The Bayesian models integrate multiple human activities, ecological receptors of the ECR, and their exposure relationships for calculating the human disturbance risk. The case learning method geographic information systems (GIS) is then introduced to train BN models based on the spatial attribute of variables to evaluate the spatial distribution and correlation of risks. This approach was applied to the human disturbance risk assessment for the ECR that was delineated in 2018 in Jiangsu Province, China. The results indicated that most of the ECRs were at a low or medium human disturbance risk level, while some drinking water sources and forest parks in Lianyungang City possessed the highest risk. The sensitivity analysis result showed the ECR vulnerability, especially for cropland, that contributed most to the human disturbance risk. This spatially probabilistic method can not only enhance model’s prediction precision, but also help decision-makers to determine how to establish priorities for policy design and conservation interventions. Overall, it presents a foundation for later ECR adjustments as well as for human disturbance risk supervision and management at the regional scale.

Optimization for bioformatics identification of antibiotic resistance genes in metagenomic data

Haobin Yao[a,*]

[a] Computer Science, University of Electronic Technology, Zhongshan Institute, Zhongshan, Guangdong, China

Abstract: Antibiotic Resistance is a contemporary global threat to human health. With the rapid thread of resistant pathogens, antibiotic resistance genes (ARGs) have been detected in all kinds of environments, from municipal wastewater plants to Tibet's high mountains. Fortunately, Metagenomic sequencing together with bioinformatics methods provides an effective way to identify and monitor environmental ARGs. Nowadays, the most widely used ARG database for bioinformatics analysis is the Comprehensive Antibiotic Resistance Database (ARG). The current ARG identification algorithm adopted by CARD is based on pair-wise alignment with a pre-trained score cutoff. Researchers have proposed alternative schemes to determine whether a query gene is sufficiently similar to a reference gene to be within the same ARG family. This paper will simulate the ARG evolution models according to studies in the dissemination of ARGs, and then compare the effectiveness and precision of different ARG identification methods.

Non-antibiotic pharmaceuticals exhibit antibacterial activity and enhance bacterial evolution towards antibiotic resistance

Yue Wang[a], Hui Jia[a], Yun Wu[a], Jinda Wang[b], Jianhua Guo[c], Jie Wang[a,*]
[a] School of Environmental Science and Engineering, Tiangong University, Tianjin, China
[b] School of Energy and Environmental Engineering, Hebei University of Technology, Tianjin, China
[c] Australian Centre for Water and Environmental Biotechnology, The University of Queensland, Brisbane, Queensland, Australia

Abstract: Non-antibiotic pharmaceuticals are widely used to treat human diseases and can also ubiquitously detected as emerging contaminants in the environment, thus co-existing with various environmental bacteria. Several non-antibiotic pharmaceuticals have been proven to trigger mutation and promote horizontal transfer of antibiotic resistance genes between bacteria. However, it is still unclear whether non-antibiotic pharmaceuticals have antibiotic-like antimicrobial activity against environmental bacteria under One Health Perspective. In this study, we aim to investigate antimicrobial effects of four typical non-antibiotic pharmaceuticals (gemfibrozil, ibuprofen, propranolol and sertraline) against environmental bacteria and the evolution of bacterial antibiotic resistance when challenged with these pharmaceuticals. Surprisingly, all four pharmaceuticals exhibit antibacterial activity through a mechanism similar to antibiotics. They can increase reactive oxygen species production and enhancing membrane permeability up to 2.7- and 2.4-fold, respectively. The expressions of sodA, sodB and recA genes related to reactive oxygen species detoxification and SOS response were up-regulated. We also found that these pharmaceuticals can up-regulate the expression of the efflux pump gene tolC with 2.5-fold to promote the evolution of bacterial antibiotic resistance. This study provides insights into the role of non-antibiotic pharmaceuticals in the emergence of antibiotic resistance, and highlights negative effects of non-antibiotic pharmaceuticals on environmental bacteria.

Integrating global microbiome data into antibiotic resistance assessment in large rivers

Fang-Zhou Gao[a], Tong Zhang[b], Guang-Guo Ying[a,*]
[a] School of Environment, South China Normal University, Guangzhou, Guangdong, China
[b] Department of Civil Engineering, The University of Hong Kong, Hong Kong, China

Abstract: Rivers are important in spreading antimicrobial resistance (AMR). Assessing AMR risk in large rivers is challenged by large spatial scale and numerous contamination sources. Integrating river resistome data into a global framework may help addressing this difficulty. Here, we conducted an omics-based assessment of AMR in a large river (i. e. the Pearl River in China) with global microbiome data. Results showed that antibiotic resistome in river water and sediment was more diversified than that in other rivers, with contamination levels in some river reaches higher than global baselines. Discharge of WWTP effluent and landfill waste drove AMR prevalence in the river, and the resistome level was highly associated with human and animal sources. Detection of 54 risk rank I ARGs and emerging mobilizable mcr and tet(X) highlighted AMR risk in the river reaches with high human population density and livestock pollution. Florfenicol-resistant floR therein deserved priority concerns due to its high detection frequency, dissimilar phylogenetic distance, mobilizable potential, and presence in multiple pathogens. Co-sharing of ARGs across taxonomic ranks implied their transfer potentials in the community. By comparing with global genomic data, we found that *Burkholderiaceae*, *Enterobacteriaceae*, *Moraxellaceae* and *Pseudomonadaceae* were important potential ARG-carrying bacteria in the river, and WHO priority carbapenem-resistant *Enterobacteriaceae*, *A. baumannii* and *P. aeruginosa* should be included in future surveillance. Collectively, the findings from this study provide an omics-benchmarked assessment strategy for public risk associated with AMR in large rivers.

Behaviors of antibiotic resistance genes (ARGs) and metal resistance genes (MRGs) during the pilot-scale biophysical drying treatment of sewage sludge: Reduction of ARGs and enrichment of MRGs

Sai Xu[a,*]

[a] School of Environmental and Biological Engineering, Nanjing University of Science and Technology, Nanjing, Jiangsu, China

Abstract: Biophysical drying (BPD) is one of the best alternatives for reducing the moisture content from sewage sludge by utilizing biological heat from aerobic reactions. However, the fate of emerging pollutants during BPD process is largely unknown. The fates of antibiotic resistance genes (ARGs) and metal resistance genes (MRGs) were investigated during a pilot-scale BPD treatment of sewage sludge by metagenomic sequencing. The total abundance of ARGs decreased from 1.78 ± 0.13 copies/16S rRNA to 0.55 ± 0.01 copies/16S rRNA and meanwhile, the total abundance of MRGs increased from 3.81 ± 0.01 copies/16S rRNA to 6.30 ± 0.02 copies/16S rRNA. The reduction of ARGs fitted the first-order kinetic model ($p < 0.01$). Microbial community analysis showed that the abundance of potential pathogens was also decreased during BPD process. On the contrary, the abundances of most MRG subtypes (78.3%) were enriched during BPD process with up to 122-fold change. This study demonstrated that BPD treatment was an effectively way to reduce the moisture content of sewage sludge and meanwhile, remove the ARGs and potential pathogens. The reduction of ARGs followed the first-order kinetic model and the temperature and moisture were the main factors influencing the pattern of ARGs. On the contrary, an increasing tendency for the abundance of MRGs during BPD process was observed with up to 122-fold change. These results imply that the potential of risks for the end product of BPD treatment of sewage sludge need to be considered due to the enrichment of MRGs.

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