Investigating the presence of environmental rare earth elements in activated sludge systems

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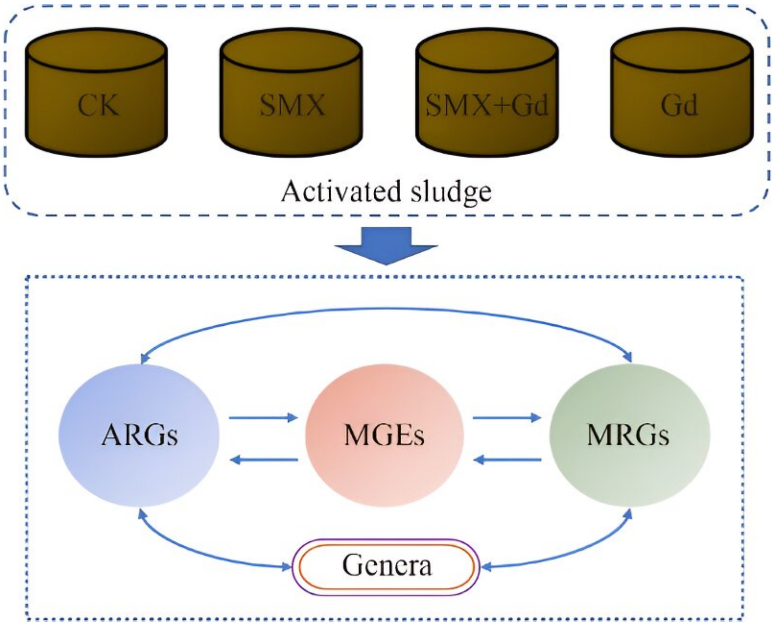

Credit: *Frontiers of Environmental Science & Engineering* (2023). DOI: 10.1007/s11783-023-1754-5

The pandemic has triggered a major increase in the use of medical facilities and drugs, which has exacerbated pollution in wastewater biochemical treatment systems. Pollution from environmental rare earth elements (REE) has increased due to the widespread use of REE in medical applications.

Gadolinium (Gd) is commonly used in contrast agents and is released as a monomer that is toxic to organisms. Studies have shown the presence of Gd in both the influent and effluent of wastewater treatment plants (WWTPs). In addition, different types of antibiotics were detected in WWTPs, with some antibiotic concentrations being detected at mg/L levels.

The accumulation of antibiotics in WWTPs is detrimental to microorganisms and negatively impacts the performance of WWTPs. Therefore, the combined pollution of REE and antibiotics in wastewater cannot be ignored, especially in the context of the COVID-19 pandemic. Notably, due to the increased risk of bacterial infections, medical institutions need more sulfamethoxazole (SMX) to treat infected patients in the pandemic.

Magnetic resonance imaging (MRI) enables visualization of pulmonary structures and assessment of COVID-19-related lung damage, inflammation, and complications like thrombosis and myocarditis. Gd is a key component of contrast agent in MRI, and the increased demand for MRI detection leads to an increase in the use of Gd. Therefore, Gd and SMX have been extensively used during this pandemic. However, the impact of co-occurring Gd and SMX in wastewater on bacterial resistance in WWTPs remains unclear.

Long-term use of antibiotics in medical, agricultural, animal husbandry, and aquaculture industries eventually leads to the dissemination of antibiotic resistance genes (ARGs).

ARGs pose a serious threat to human health and environmental safety. Therefore, many researchers have studied the effects of antibiotics on ARGs in wastewater treatment systems. Studies have shown that a 55%–81% decrease in the concentration of antibiotics resulted in a 13-order of magnitude decrease in the relative abundance of ARGs in activated sludge systems.

Furthermore, scientists have noted that heavy metals drive the co-selection of ARGs and heavy metal resistance genes (MRGs). Studies have reported an increased relative abundance of ARGs and MRGs in heavy metal-polluted environments, and high concentrations of metals could promote multi-metal and multi-antibiotic resistance.

Moreover, studies have investigated the co-selection of ARGs and MRGs under combined pollution of antibiotics and heavy metals. However, only a few reports have investigated the effects of Gd on ARGs and MRGs, and the succession and transmission characteristics of resistance genes under combined Gd and antibiotics exposure remain unclear.

Quantitative polymerase chain reaction (qPCR) and 16S rRNA gene high-throughput sequencing can quantify some known ARGs and MRGs, but the mobility of ARGs and the correlation with host bacteria are unelucidated.

In addition, 16S rRNA sequencing is limited by microbial isolation and culture, and cannot detect or describe the diversity and function of complex microbial communities. As a more advanced sequencing technology, metagenomics enables the assessment of uncultured microbial genes, which greatly expands the applications of microbial resources. Moreover, metagenomic sequencing can also be used for the in-depth study of genes and functions.

Researchers have used metagenomics to explore ARGs, MRGs and host bacteria in an aquatic environment, demonstrating the broad-spectrum diversity of bacteria in water and the related resistance genes. Some researchers have used metagenomics to explore the selection process of antibiotic resistance in WWTPs. However, few studies have focused on core genomes and the interaction between ARGs and MRGs in WWTPs.

In addition, previous reports revealed the impact of antibiotics and heavy metals on ARGs and MRGs in an aquaculture environment and discussed the interaction between ARGs, MRGs, and bacteria.

Nevertheless, these studies mostly ignored the interaction between ARGs, MRGs, and mobile genetic elements (MGEs), which play essential roles in the proliferation and transmission of resistance genes. The work of Professor Kangping Cui's team fills this gap.

In a new study, the research team investigated the co-occurrence of Gd and SMX in wastewater pollution by applying metagenomics to analyze the mechanisms of changes in ARGs, MRGs, MGEs, and genera in an activated sludge system. Details of the study have been published in *Frontiers of Environmental Science & Engineering*.

This study offers an in-depth and new understanding of the mechanisms underlying the changes and interactions between ARGs and MRGs in activated sludge, providing technical support for the removal of ARGs and MRGs in WWTPs. To help reach the overarching aim, the following specific goals were set by the rfesearch team:

1. To explore the dynamic change in characteristics of ARGs, MRGs, and MGEs, and identify the core genome
2. To evaluate the joint effect of Gd and SMX on ARGs, MRGs, MGEs, and abundant genera
3. To reveal the interactions and shifts in ARGs, MRGs, and MGEs

The effects of SMX and Gd(III) on ARGs and MRGs were studied by metagenomic sequencing in an activated sludge system. The findings demonstrated that single SMX alone and co-occurrence of SMX and Gd(III) resulted in an increase in the abundance of ARGs, while most

MRGs decreased in abundance.

Furthermore, the co-occurrence of SMX and Gd(III) significantly promoted the HGT of ARGs and MRGs. Gd(III) alone caused a decrease in ARGs and MRGs, whereas the abundance of Hg MRGs was increased. Compared to core MRGs, core ARGs exert a greater negative effect in the presence of Gd or SMX alone.

Streptomyces, Pseudomonas, and Thauera were abundant under SMX exposure and may be potential hosts for ARGs and MRGs. The bacterial community was sensitive to single Gd(III) stress. Moreover, the correlations among ARGs, MRGs, MGEs, and the bacterial community were discussed in this study, suggesting a positive relationship between internal ARGs and MGEs, while positive and negative relations were found in MRGs. Moreover, most ARGs and MRGs were closely related to MGEs.

More information: Xinrui Yuan et al, Response of antibiotic and heavy metal resistance genes to the co-occurrence of gadolinium and sulfamethoxazole in activated sludge systems, *Frontiers of Environmental Science & Engineering* (2023). DOI: 10.1007/s11783-023-1754-5

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