

Press release

For immediate release

HKU Hydrogeologists Identify Fermentation as Key Pathway for Ammonium Production Beneath the Pearl River Delta

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Figure 1: Artist's impression of ammonium accumulation beneath the Pearl River Delta. The illustration shows terrestrial, transitional and marine depositional zones, where microbial fermentation is the likely dominant ammonium-producing pathway. The illustration was created based on the study's findings and is not drawn to scale.

A study led by Professor Jimmy Jiujiu JIAO from the Department of Earth and Planetary Sciences at The University of Hong Kong (HKU) and Professor Meng LI from Shenzhen University has identified microbial fermentation as the likely main pathway for ammonium production in sediments beneath the Pearl River Delta, helping to explain the region's exceptionally high natural groundwater ammonium levels.

The Pearl River Delta hosts the highest naturally occurring groundwater ammonium concentrations reported globally, making affected groundwater unsuitable for drinking without treatment. Previous studies linked this accumulation to nitrogen-rich organic matter in fine-grained sediments and restricted groundwater circulation, but the responsible microbial pathways and organisms remained unclear.

By analysing sediment samples across the delta, the team identified the major microbial processes involved and showed how sediment depth, age and salinity shape microbial communities and ammonium-producing pathways. The findings were recently published in the journal *Nature Communications*.

Fermentation Identified as the Main Pathway for Ammonium Production

The researchers combined geochemical and metagenomic analyses of 36 sediment samples collected from three boreholes spanning different depths. The samples covered approximately 13,000 years of geological history and represented terrestrial-dominated, transitional and marine-dominated depositional environments.

By analysing microbial genetic material preserved in the sediments, the team reconstructed 770 representative metagenome-assembled genomes (MAGs), providing detailed insights into the microorganisms present and their

potential metabolic functions. Microbial communities and ammonium-related metabolic potential varied significantly along the land–sea gradient. Bacteria showed greater metabolic flexibility across different sediment conditions, which may help explain these shifts, while archaea tended to retain more conserved functional traits.

The team found that fermentation-related genes were the most abundant across all three depositional zones, suggesting that fermentation is likely the primary microbial pathway for ammonium production. The abundance of these genes declined with sediment depth and age as readily degradable organic matter became depleted, leaving fewer substrates for microbial fermentation and ammonium production. This accumulation was particularly pronounced in the marine-dominated zone, where fine-grained, organic-rich sediments promote microbial production while restricting groundwater flow, trapping ammonium over thousands of years.

Beyond fermentation, other microbial nitrogen-processing pathways also varied across the land–sea gradient. Nitrogen occurs in several chemical forms, and in some microbial pathways, nitrate is first reduced to nitrite, which can be converted into ammonium. In the terrestrial-dominated zone, genes associated with the first step—nitrate reduction—were the second most abundant. In the more saline transitional and marine-dominated zones, genes associated with the second step—the direct conversion of nitrite into ammonium—became more prominent. These differences suggest that salinity and the availability of nitrate and nitrite influence how ammonium is produced in different depositional environments.

Among the bacteria identified, the marine-associated genus *Brevirhabdus* emerged as a potentially important contributor to ammonium cycling. Likely a legacy of past marine depositional conditions, it carries genes involved in fermentation and the conversion of nitrite into ammonium, suggesting that ancient depositional environments may continue to shape present-day groundwater chemistry.

Professor Jimmy Jiao said, “Our findings move beyond the general understanding that buried organic matter is the source of ammonium. We have identified the microbial pathways and organisms that are likely responsible for producing it and shown how these processes vary across sediments formed under different environmental conditions.”

Implications for Groundwater Management

By linking depositional history, hydrogeochemistry and microbial function, the study provides a framework for understanding ammonium accumulation in delta regions worldwide. The findings may help identify vulnerable areas and improve groundwater assessment, monitoring and treatment planning in densely populated delta regions.

Dr Meiqing LU, first author of the paper, completed her doctoral training under Professor Jimmy Jiao at HKU before joining Professor Meng Li’s group at Shenzhen University as a postdoctoral researcher. Professor Jiao and Professor Li are the co-corresponding authors of the study. The research also involved scientists from the Southern University of Science and Technology, The Hong Kong University of Science and Technology, and East China Normal University.

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For details of the research, please refer to the paper “Microbial Drivers of Ammonium Accumulation in Holocene Sediments of the Pearl River Delta”, published in *Nature Communications*: <https://doi.org/10.1038/s41467-026-72058-8>

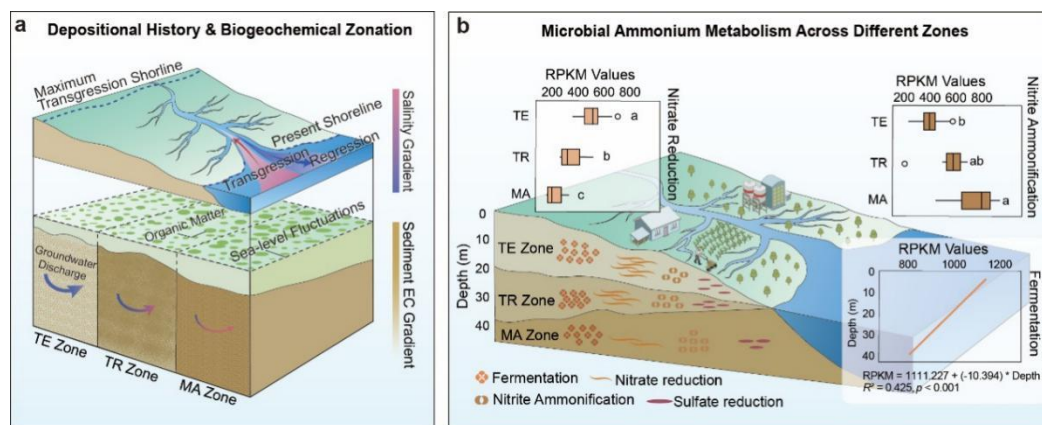


Figure 2: Conceptual model of historical depositional processes, biogeochemical zonation, and microbial ammonium metabolism. Image credit: Adapted from Lu *et al.*, *Nature Communications* (2026).

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