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Photolytic quorum quenching effects on the microbial communities and functional gene expressions in membrane bioreactors

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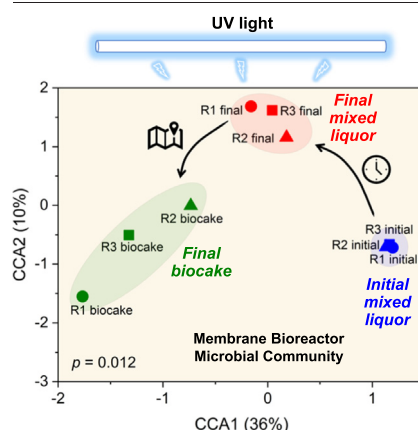
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HIGHLIGHTS

- Photolytic quorum quenching effects on microbial ecology are explored.
- Continuous UV photolysis mitigates bio-fouling in membrane bioreactors.
- Microbial community structures are highly influenced by spatiotemporal factors.
- *Sphingomonadaceae* and *Xanthomonadaceae* become more abundant with UV irradiation
- Monooxygenase and hydroxylase enzyme-related genes increase with longer UV exposures.

GRAPHICAL ABSTRACT



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ABSTRACT

Photolytic quorum quenching by ultraviolet A (UVA) irradiation is an effective strategy for controlling membrane bioreactor (MBR) biofouling; however, its effects on MBR microbial communities and functional genes have not yet been explored. Here, we report on the effects of the UVA irradiation, which mitigates membrane biofouling, on the microbial community structures, alpha and beta diversities, and functional gene expressions in the MBR mixed liquor and biocake (membrane fouling layer) for the first time. The results show that the microbial communities become less diversified when alternating UVA is applied to the MBRs. The changes in the community structure are highly influenced by spatiotemporal factors, such as microbial habitats (mixed liquor and biocake) and reactor operation time, although UVA irradiation also has some impacts on the community. The relative abundance of the *Sphingomonadaceae* family, which can decompose the furan ring of autoinducer-2 (AI-2) signal molecules, becomes greater with continuous UVA irradiation. *Xanthomonadaceae*, which produces biofilm-degrading enzymes, is also more abundant with UVA photolysis than without it. Copies of monooxygenase and hydroxylase enzyme-related genes increase in the MBR

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