Microbial defluorination of TFA, PFOA, and HFPO-DA by a native microbial consortium under anoxic conditions

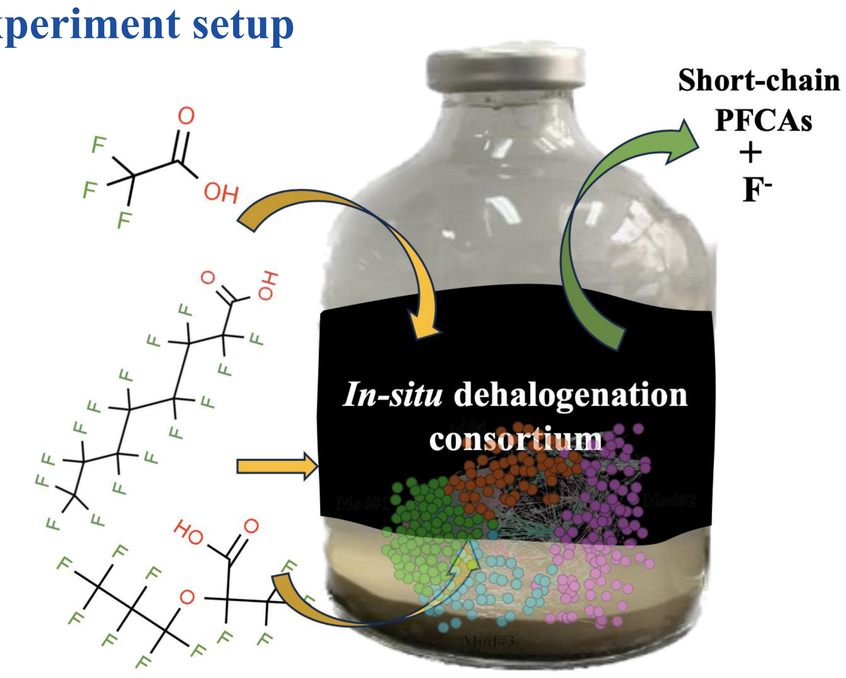
Zhiwen Tang[a, b], Timothy M. Vogel[c], Qing Wang[a], Changlong Wei[a], Mukhtiar Ali[a, b], Xin Song[a, b*]

[a] Institute of Soil Science, Chinese Academy of Sciences; [b] University of Chinese Academy of Sciences, Beijing 100049, China

[c] Ecologie Microbienne, Université Claude Bernard Lyon 1, Ecologie Microbienne, F-69622, Villeurbanne, France

Motivation: There is a lack of knowledge regarding the fate of PFASs in the environment and whether the organohalide enriched consortium *in-situ* have the defluorination ability is still unclear. Therefore, the aim of this study was to explore the biodegradability of three typical perfluorinated compounds, TFA, PFOA, and HFPO-DA by a native microbial community from a PFAS-chlorinated solvent sites after long-term exposure. The associated response of the microbial community was also examined.

Experiment setup



Treatment	Note
Blank	Without PFAS
Sterilized	Autoclaved
Biodegradation	TFA
	PFOA
	HFPO-DA

Results

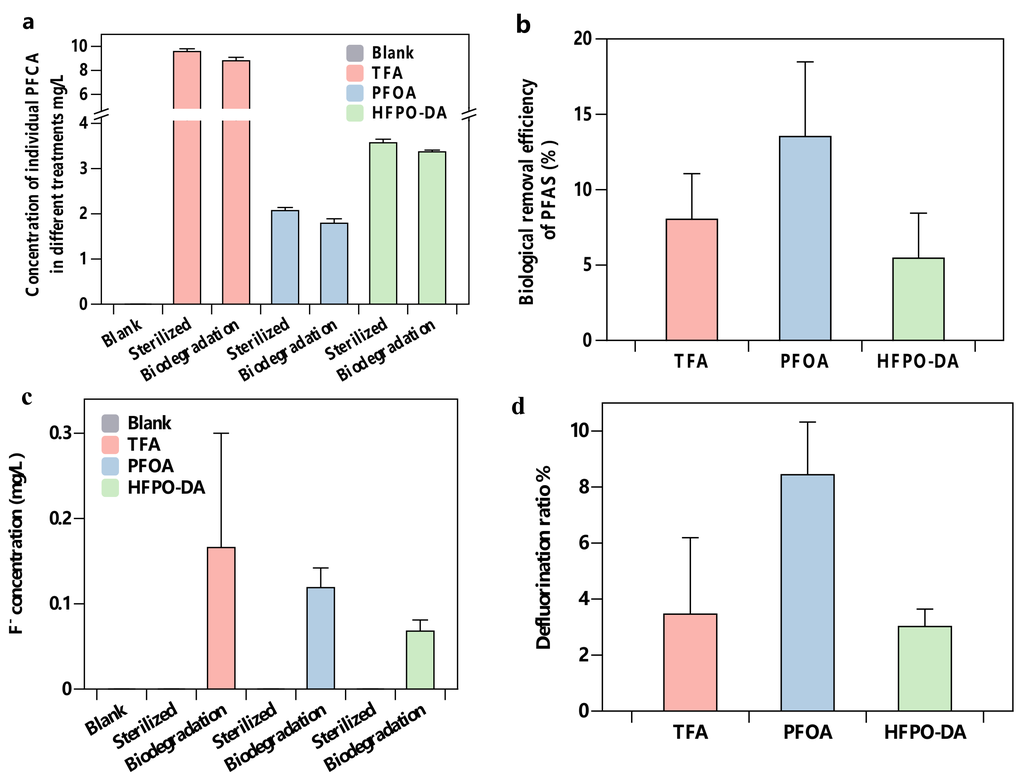


Fig. 1 The biological removal (a, b) and defluorination (c, d) efficiency of TFA, PFOA and HFPO-DA groups after 10 months incubation.

The observed biological removal efficiency and microbial defluorination ratios were 8.03 (± 3.03)% and 3.46 (± 2.73) %, 13.52 (± 4.96)% and 8.44 (± 1.88)%, 5.45 (± 2.99) % and 3.02 (± 0.62)% for TFA, PFOA and HFPO-DA, respectively, after 10-month incubation.

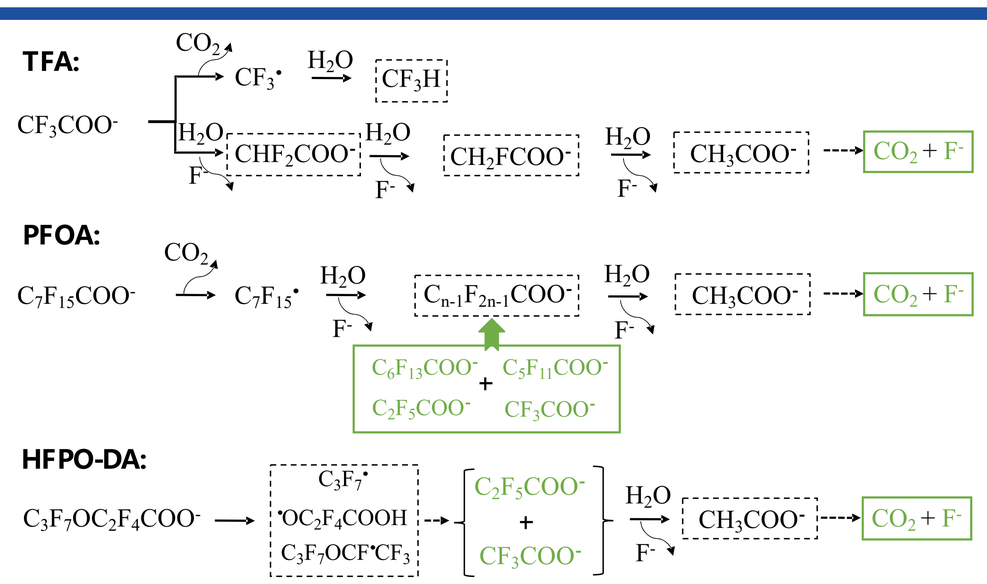


Fig. 2 Proposed biodegradation pathways for TFA, PFOA, and HFPO-DA based on the intermediates identified in this study and previous studies. Note: the green color labelled chemicals have been detected as intermediate products in the current study and the chemicals in the box with dashed lines are potential intermediates based on previous studies.

Decarboxylation, hydrolytic elimination and H/F exchange might be the main pathways to achieve defluorination of selected PFASs.

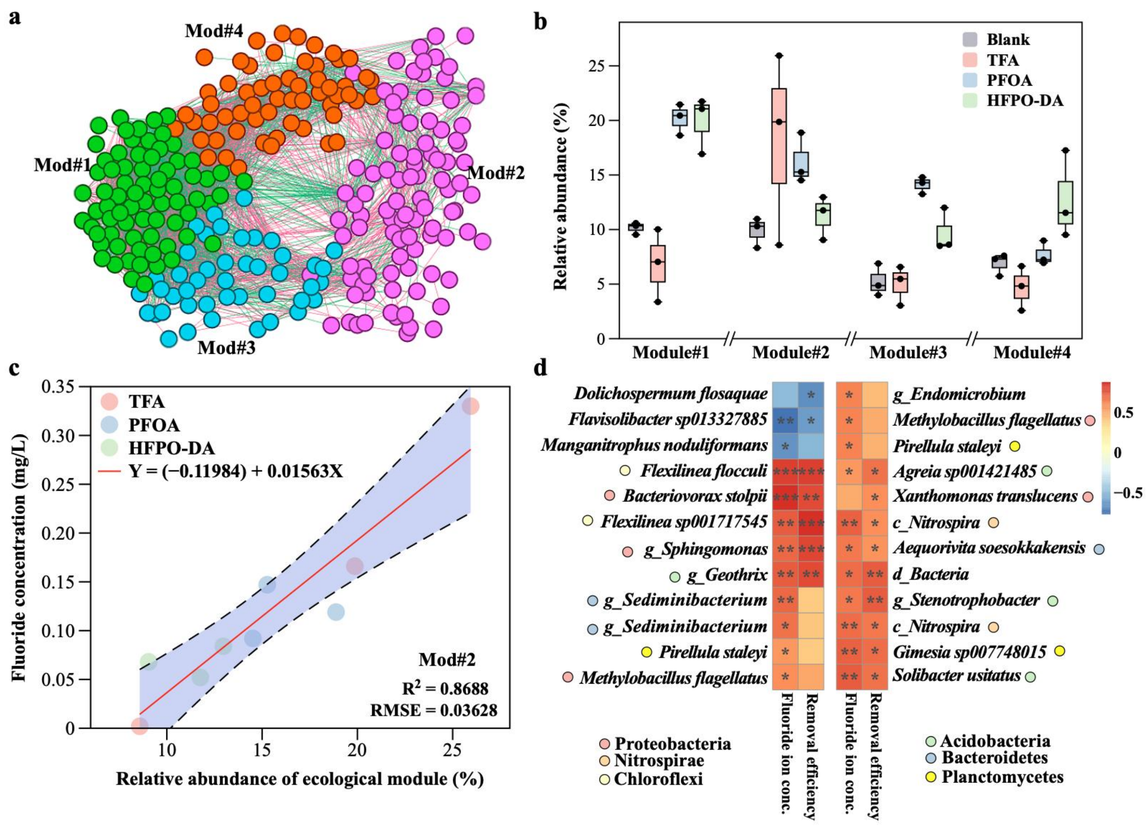


Fig. 3 Microbial co-occurrence network analysis and potential defluorination microbes. Network diagram with nodes colored according to the four ecological clusters, Module#1-4 (a), the relative abundance of the four modules in the different treatments (b), the linear relationship between F^- concentration and the relative abundance of ecological Module#2 in selected groups (c), the relationships between species of Module#2 and the generation of F^-, as well as the removal efficiency of TFA, PFOA and HFPO-DA (d).

Microbes potentially contributing to the removal of TFA, PFOA and HFPO-DA were grouped into four ecological modules ($r > 0.6$ and p-value < 0.05) .Only the relative abundance of Module #2 is positively correlated to the generation of F^- , and some of them, such as *Flexilinea flocculi*, *Bacteriovorax stolpii*, and g_*Sphingomonas*, are positively correlated with the defluorination ratios.

Conclusions

The generation of F^- and intermediate short-chain PFCAs, such as PFHpA and PFHxA, were the key lines of evidence for the selected PFASs biodegradation. Moreover, some low abundance species, such as *Flexilinea flocculi*, *Bacteriovorax stolpii*, and g_*Sphingomonas*, are positively correlated with the defluorination ratios and might participate in the biodefluorination processes through their potential collaborative functions.

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