
Proteomic Insights into Fungal-Mediated PFAS Precursor Biotransformation

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Glenn Nurwono, Junyoung O. Park, James Wohlschlegel, Shaily Mahendra

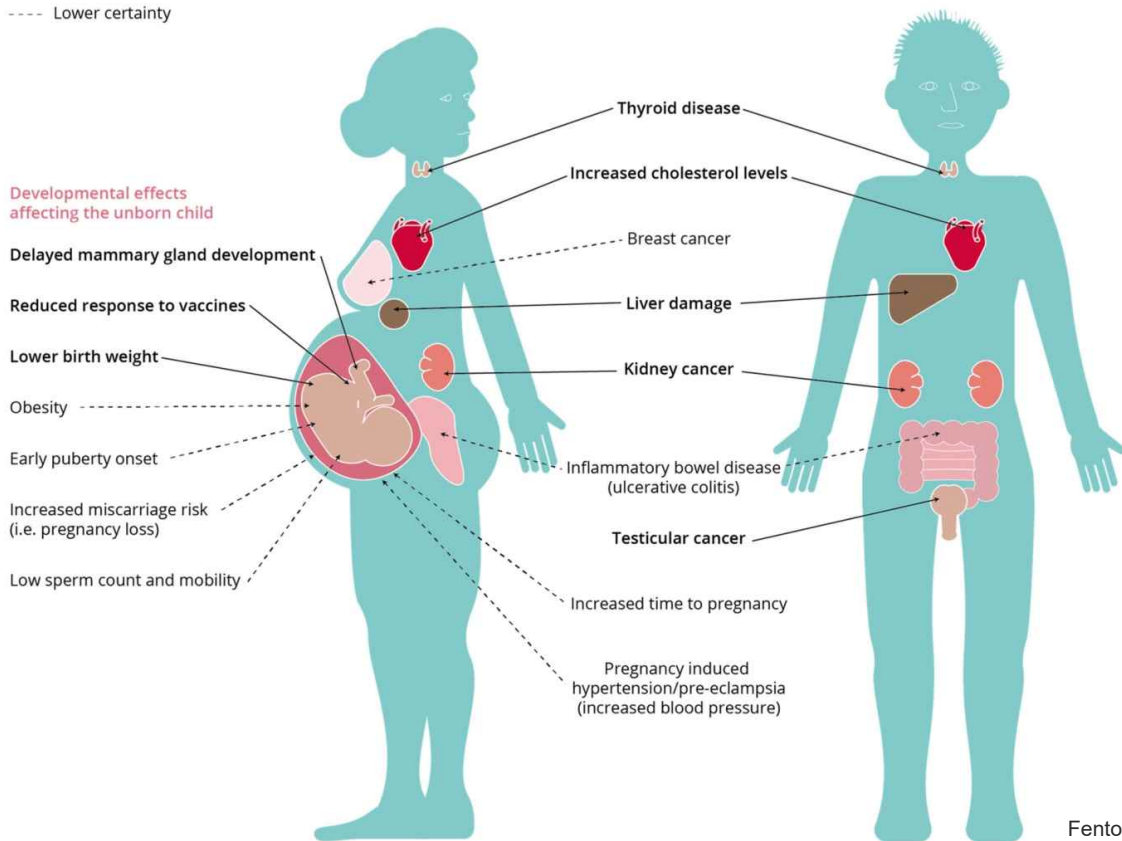
Per- and Polyfluoroalkyl Substances (PFASs) are Everywhere



PFASs are Environmentally Persistent and Have Toxic Health Effects

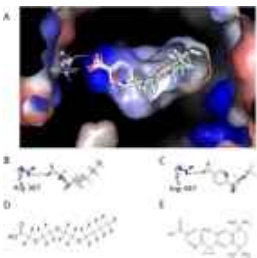
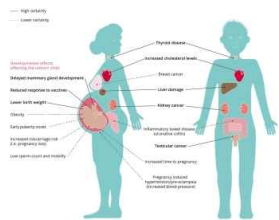
— High certainty

- - - Lower certainty



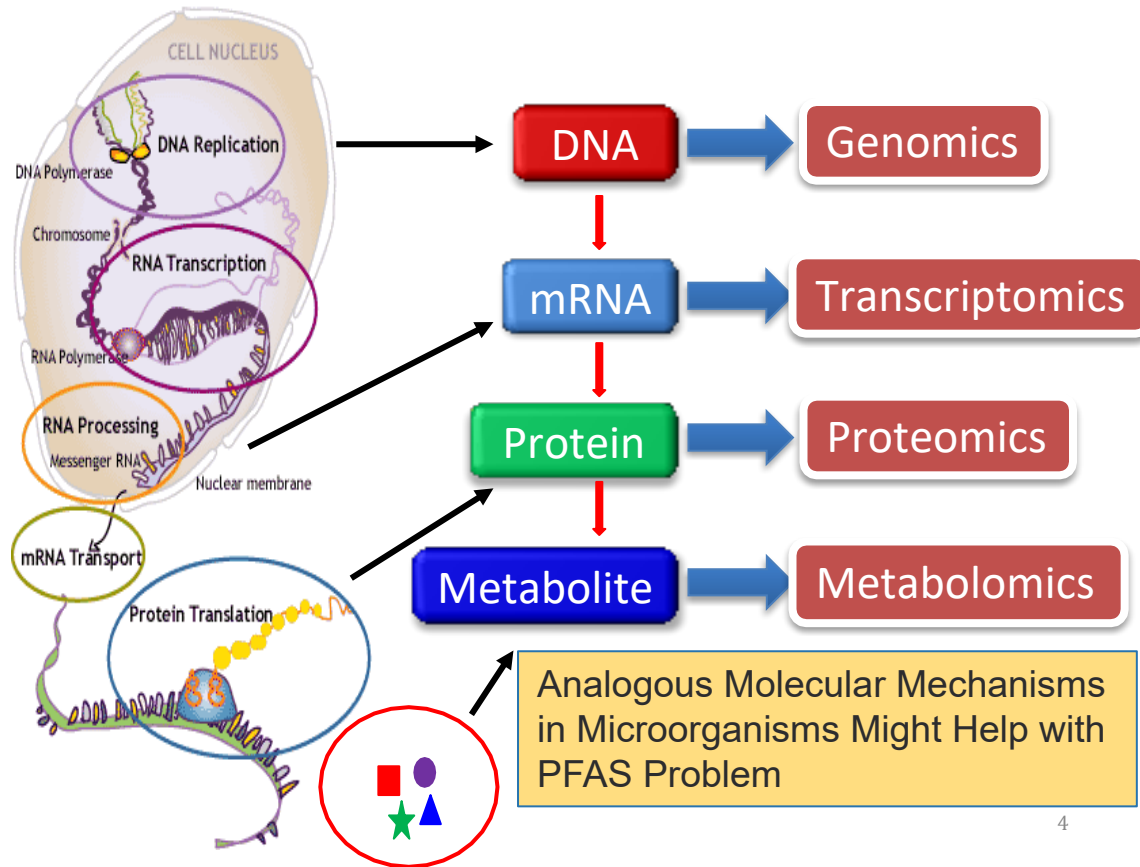
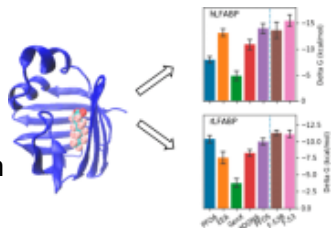
Molecular Toxicology of PFASs is Characterized by Differential Gene & Protein Expression

Per- and Polyfluoroalkyl Substance Toxicity and Human Health Review: Current State of Knowledge and Strategies for Informing Future Research (Fenton et al., ET&C 2021)



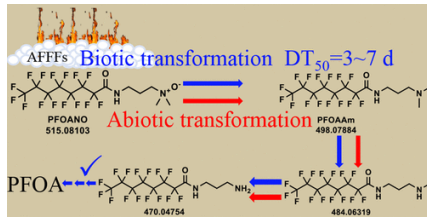
Bioactivity profiling of per- and polyfluoroalkyl substances (PFAS) identifies potential toxicity pathways related to molecular structure (Houck et al., Toxicol 2021)

Predicting Relative Protein Affinity of Novel Per- and Polyfluoroalkyl Substances (PFASs) by An Efficient Molecular Dynamics Approach (Cheng and Ng., ES&T 2018)



Biotransformation of PFASs by Bacteria

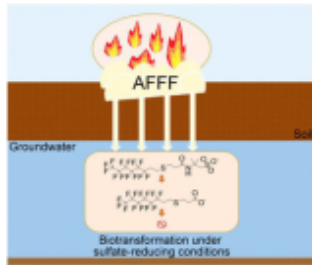
Fast Generation of Perfluoroalkyl Acids from Polyfluoroalkyl Amine Oxides in Aerobic Soils (Chen et al., ES&TL 2020)



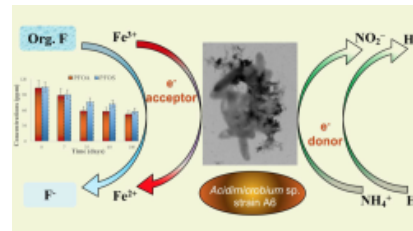
Microbial cleavage of C–F bonds in two C6 per- and polyfluorinated compounds via reductive defluorination (Yu et al., ES&T, 2020)



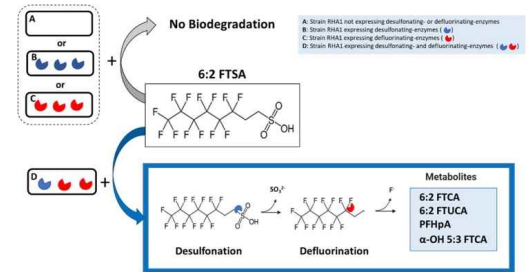
Biodegradation of 6:2 FtTAoS (75% removal) from AFFF contaminated soil in sulfate reducing conditions (Yi and Alvarez-Cohen et al., ES&TL, 2018)



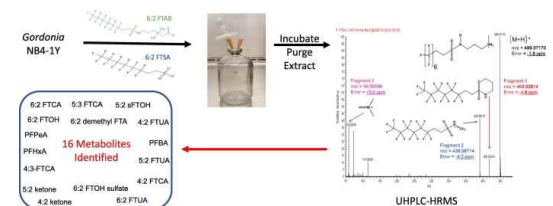
Enrichment cultures of *Acidimicrobium* sp. strain A6 (A6) removed 60% PFOA and PFOS in 100 days (Huang and Jaffe, ES&T, 2019)



Desulfonation and defluorination of 6:2 fluorotelomer sulfonic acid (6:2 FTSA) by *Rhodococcus jostii* RHA1 (Yang et al., JHM, 2022)

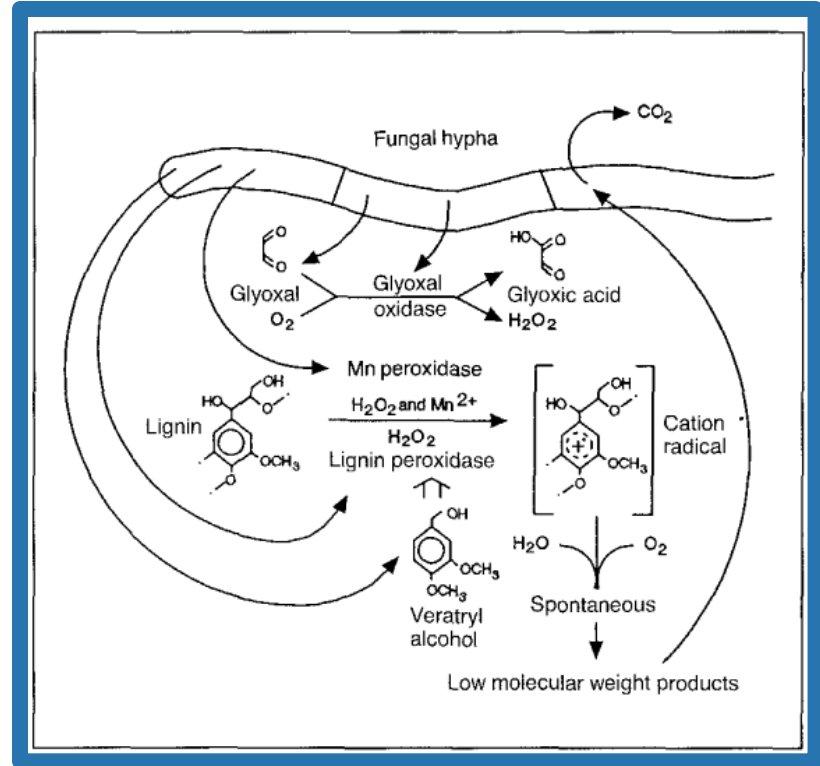


Rapidly metabolization of 6:2 FTAB (70.4%) & 6:2 FTSA (99.9%) by *Gordonia* sp. NB4-1Y (Shaw et al., Sci. Total Environ., 2019)



Fungi are Strong Biotransformers!

Fungal enzymes such as extracellular oxidoreductases and peroxidases may be involved in the biodegradation of large organic molecules.

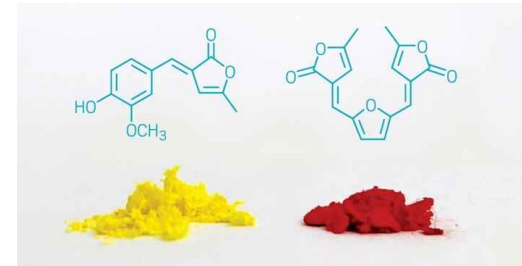


Fungi Degrade a Variety of Organic Toxicants

- Fungi have an edge in remediation:
 - extracellular enzymes
 - non-specific degradation
 - extensive surface area
 - require cheap nutrients



Pesticides; NIEHS



Synthetic Dyes; Mark Mascal. C&EN (2019)

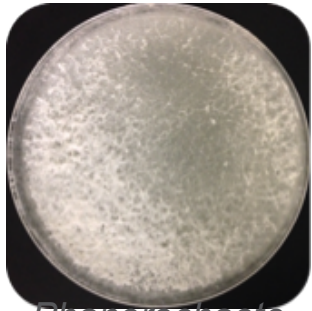


Crude Oil; Fox News



Munitions; ch.ic.ac.uk

Fungal Biotransformation of 6:2 FTOH



*Phanerochaete
chrysosporium*
(PC)



Grow spores in liquid medium
(~5-7 days w/ blending)



Blend and
resuspend in
fresh medium



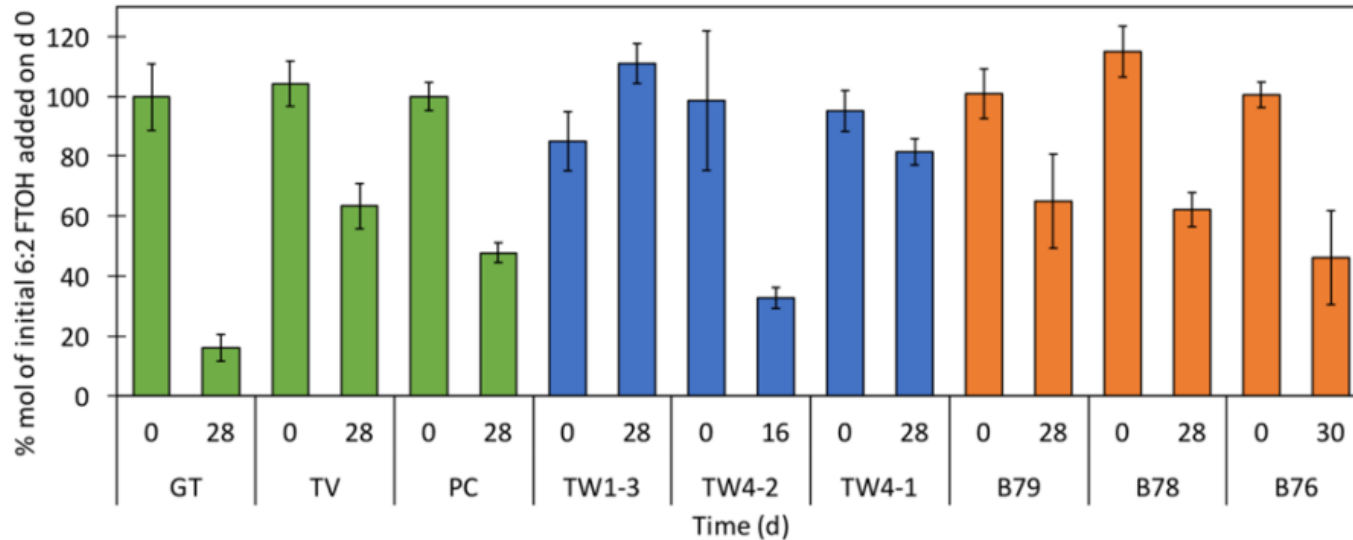
Expose to 3 mg/L
6:2 FTOH for 28
days



Measure 6:2 FTOH, metabolites, qPCR
(LC/MS/MS & high-resolution mass spec)

Fungi Biotransform 6:2 FTOH

A – Transformation of 6:2 FTOH



Key takeaways

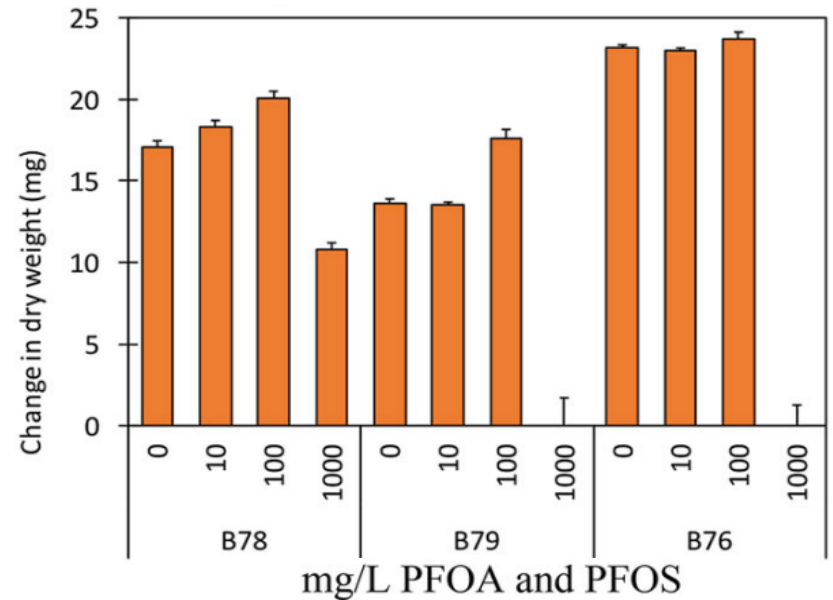
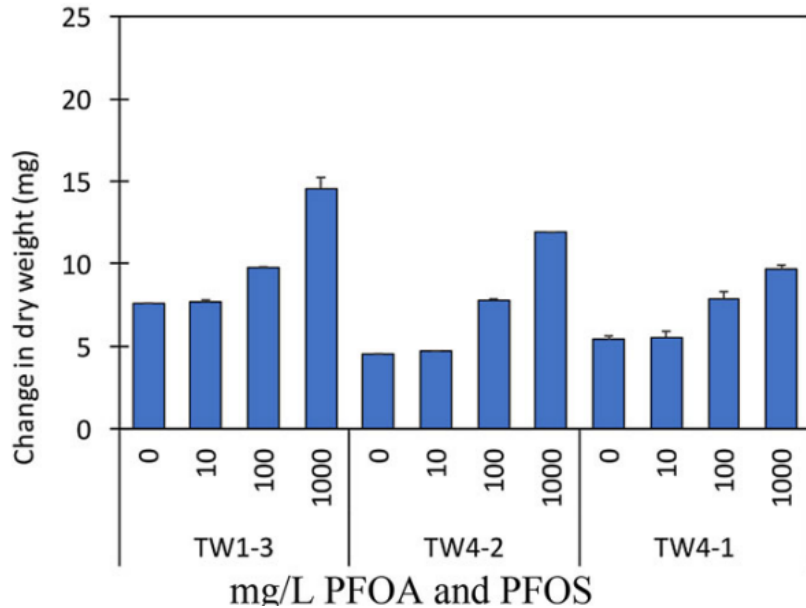
- 3 characterized fungi and 6 fungal isolates exposed to 6:2 FTOH
- 30-day experiment
- Distinct % mol reduction of 6:2 FTOH observed

Gloeophyllum trabeum (GT)

Trametes versicolor (TV)

Phanerochaete chrysosporium (PC)

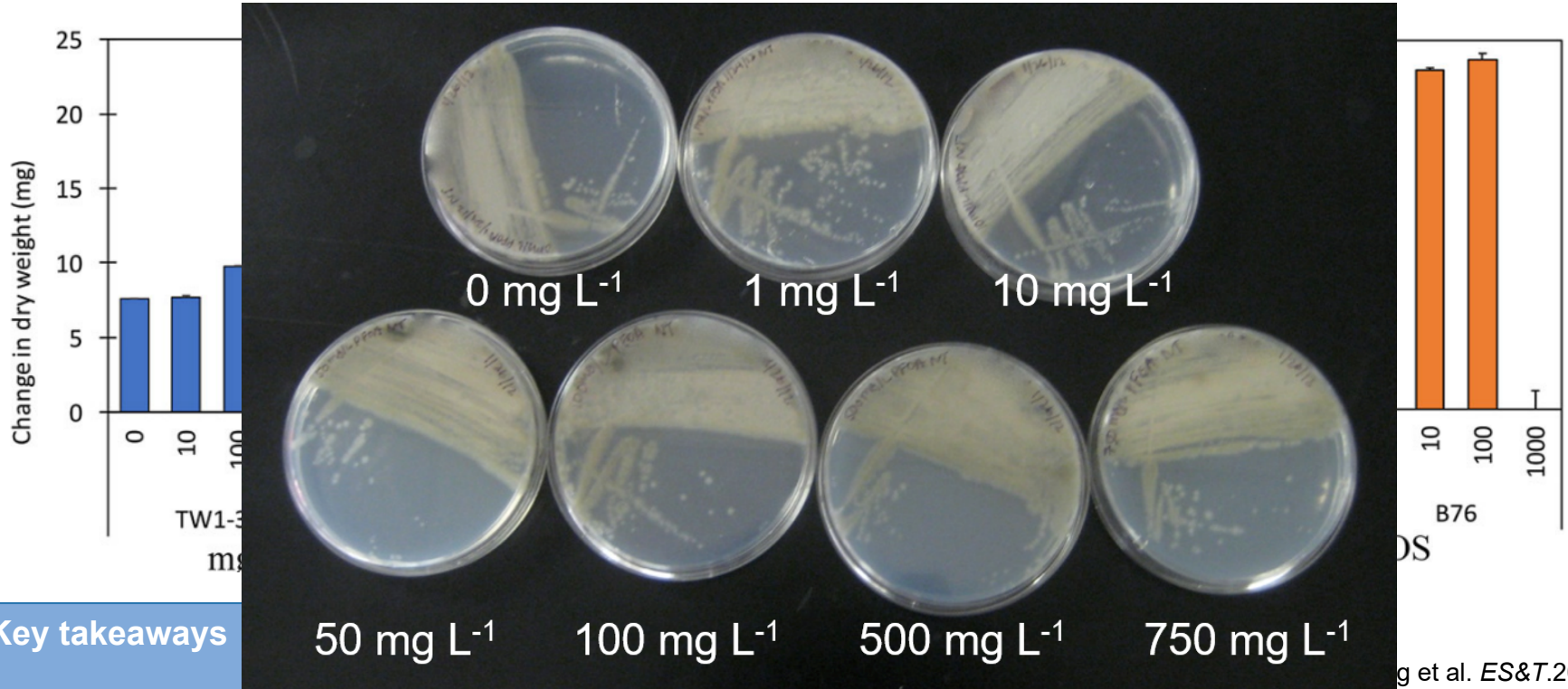
PFASs do not Inhibit Fungal Growth



Key takeaways

- 6 fungal isolates exposed to 0-1000 mg/L of PFOA & PFOS
- Growth uninhibited except for isolates B79 and B76 at 1000 mg/L

PFASs do not Inhibit Fungal Growth

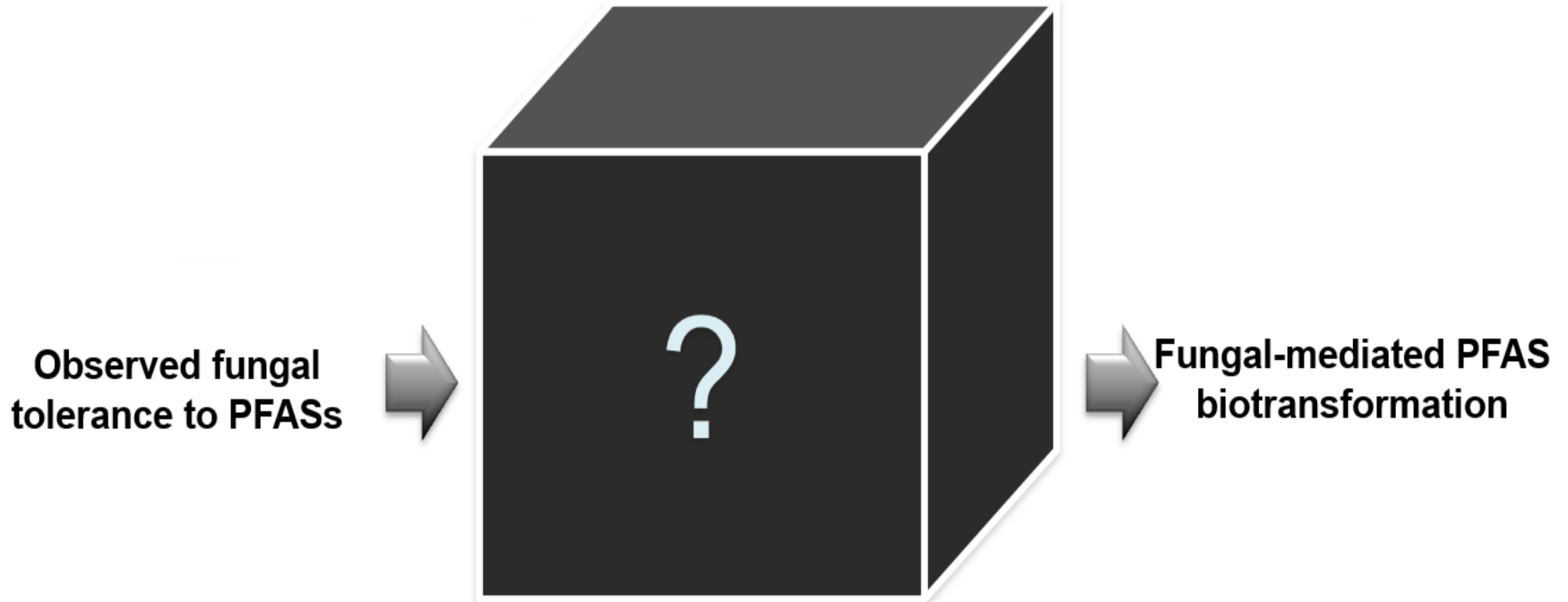


Key takeaways

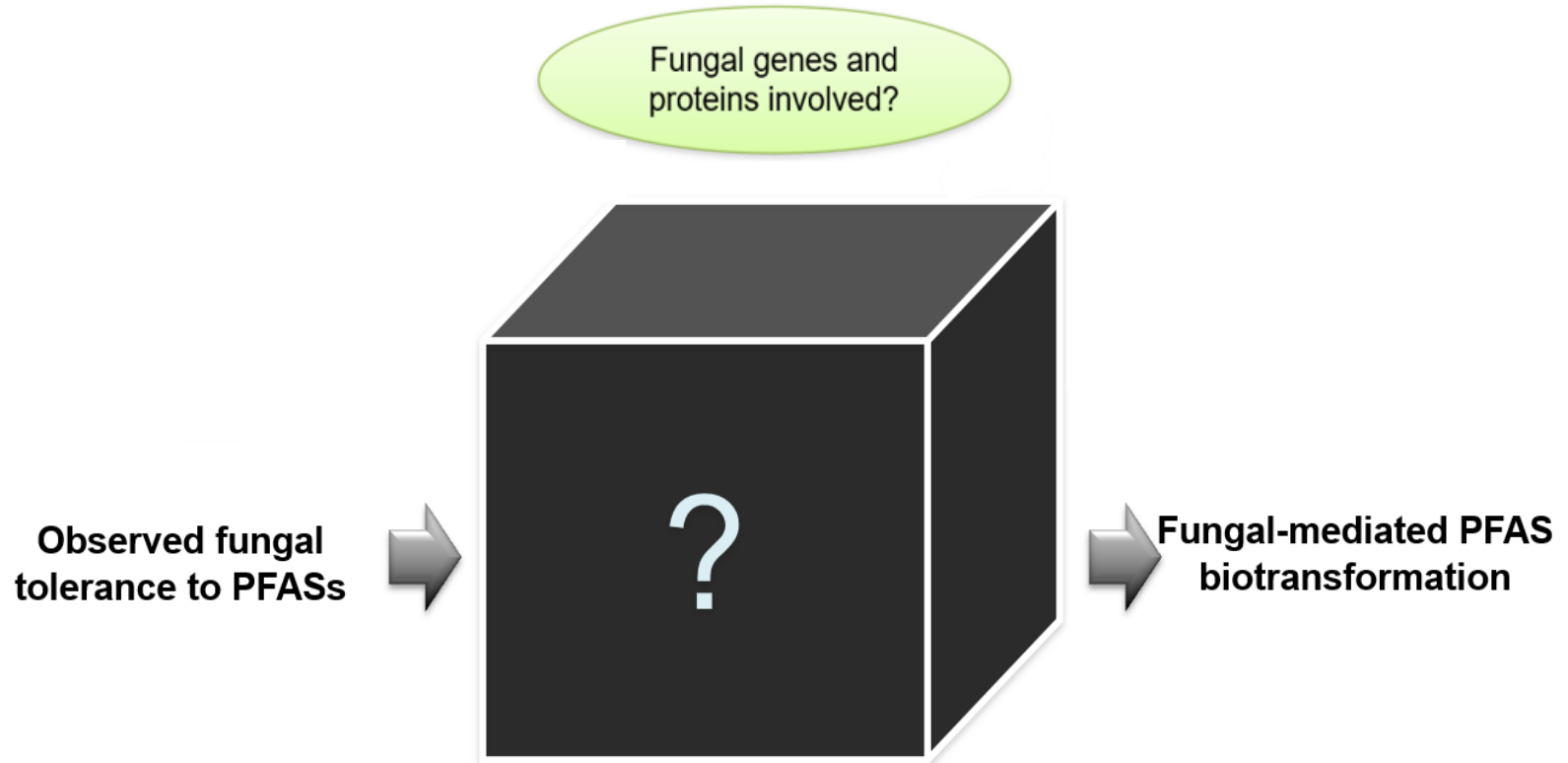
- 6 fungal isolates exposed to 0-1000 mg/L of PFOA & PFOS
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g et al. *ES&T*.2014
Merino et al. *Remediation*. 2018

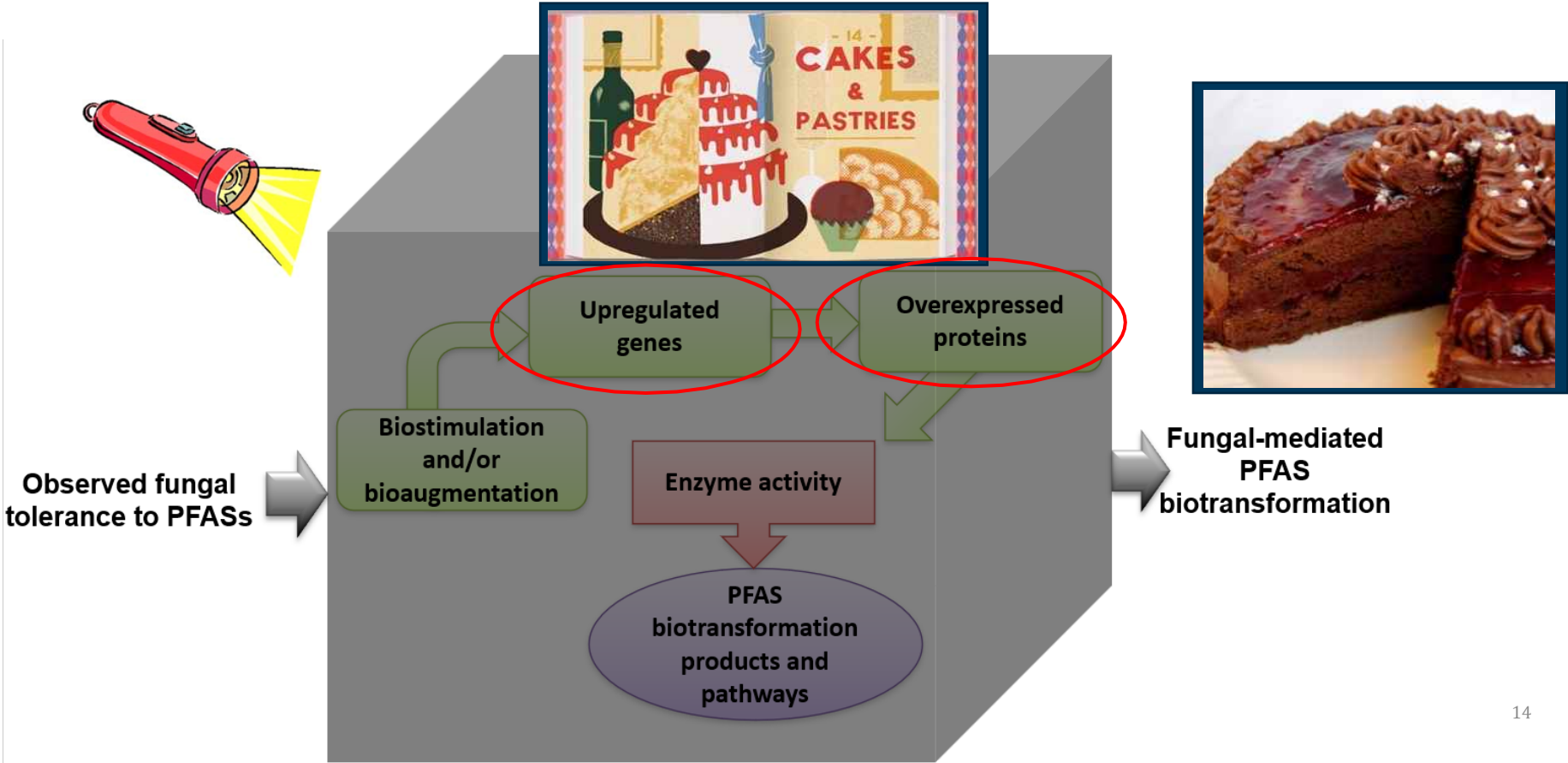
PFAS Biotransformation: A Black Box



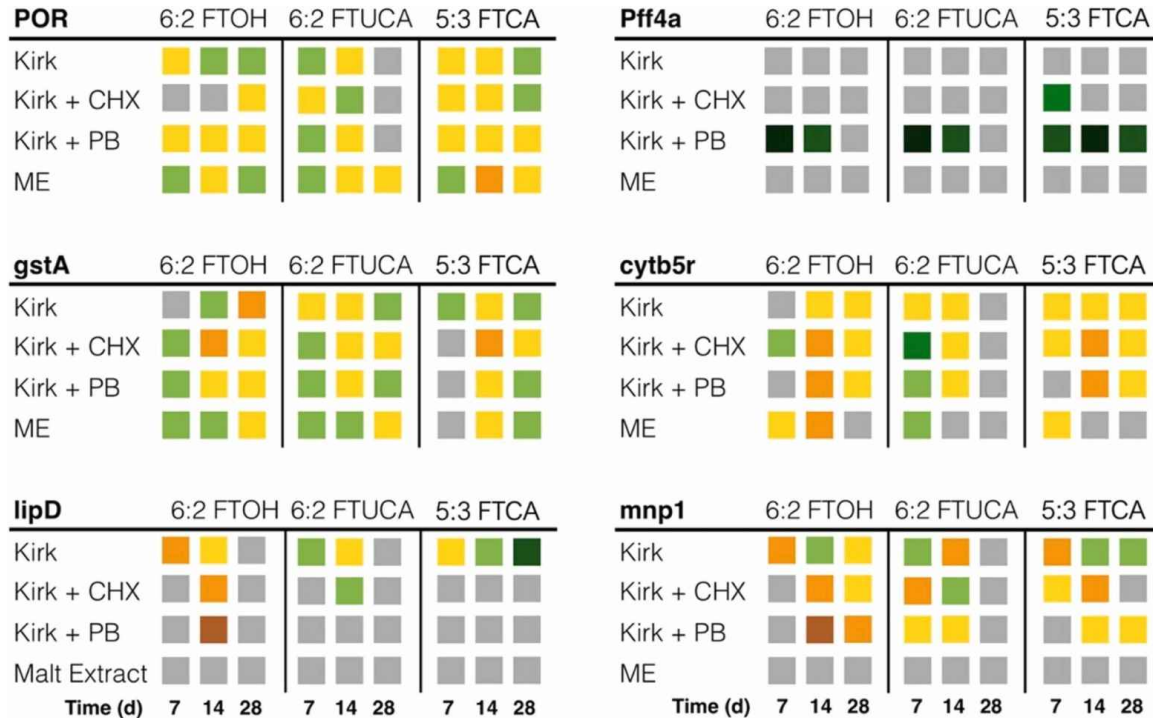
PFAS Biotransformation: Identifying the Unknowns



Tweak Recipe for Improved PFAS Biotransformation

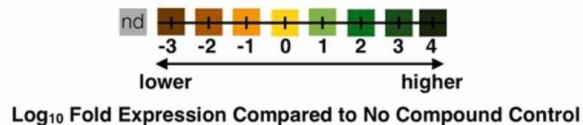


Key *P. chrysosporium* Genes Differentially Expressed in Different Media

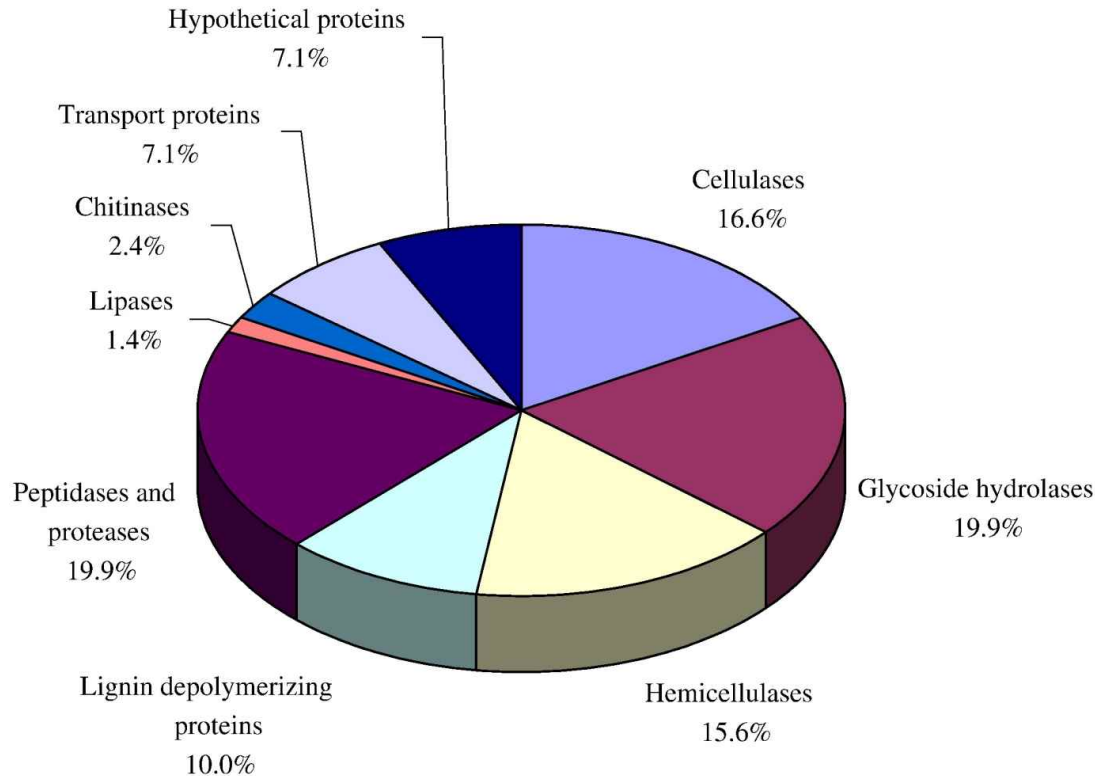


Key takeaways

- Genes for manganese (*mnp1*) and lignin (*lipD*) peroxidase, were differentially expressed according to media formulations
- Prolonged induction and activity of LiP and MnP for 5:3 FTCA-dosed cultures → LiP and MnP either played roles in 5:3 FTCA biotransformation or were positively affected by 5:3 FTCA and 5:3 FTCA metabolites



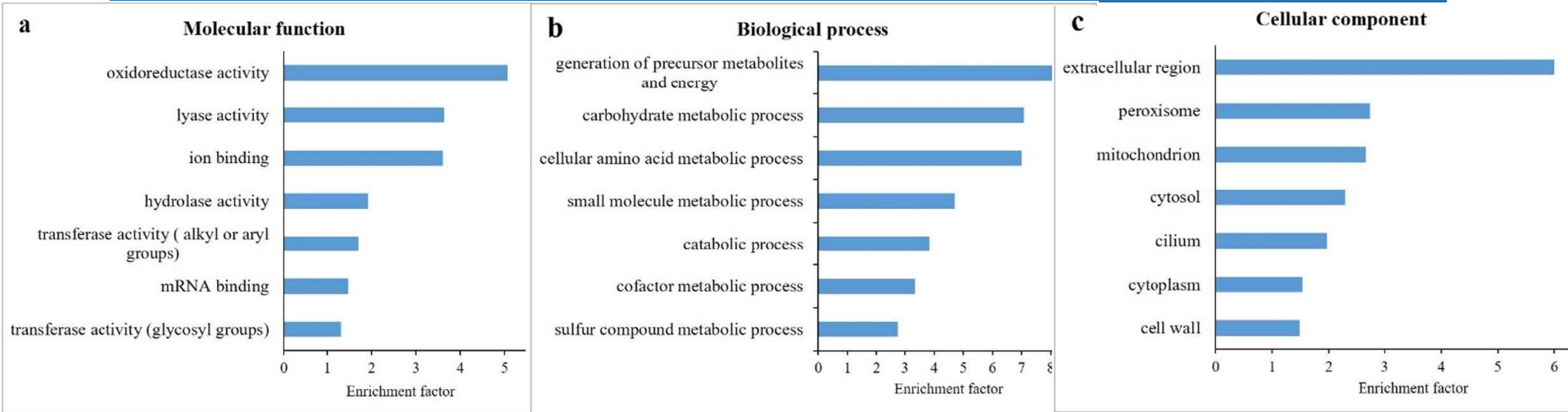
Reported *Phanerochaete chrysosporium* protein profiles



Key takeaways

- Quantitative proteomic analysis of lignocellulolytic enzymes within *Phanerochaete chrysosporium* in the presence of different lignocellulosic biomass

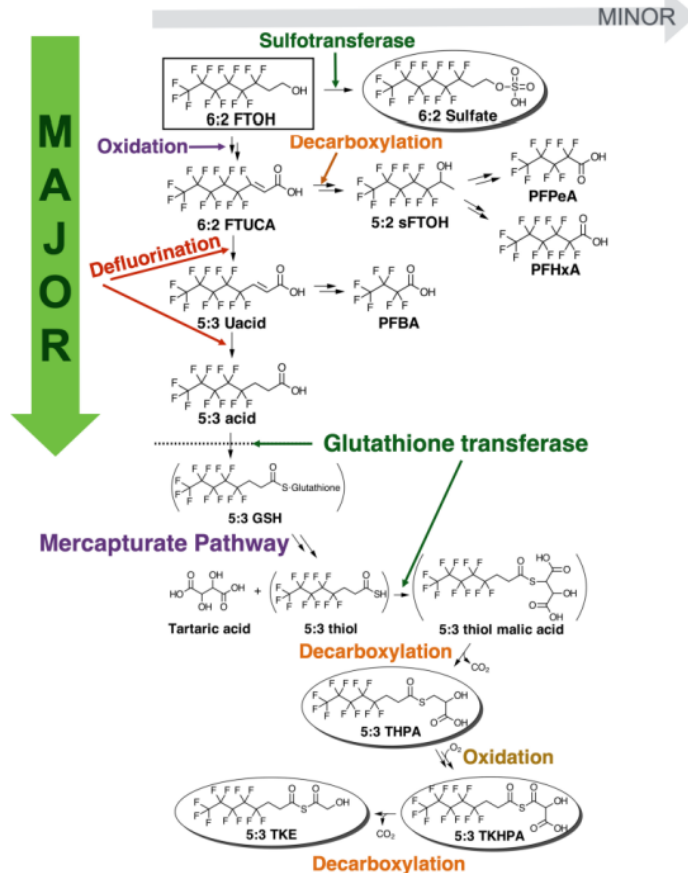
Reported *Phanerochaete chrysosporium* protein profile



Key takeaways

- Functional annotation of differentially expressed proteins in *Phanerochaete chrysosporium* exposed to environmental stressor tetrabromobisphenol A (TBBPA)
- Extracellularly secreted oxidoreductases are involved in precursor metabolism of TBBPA

6:2 FTOH biotransformation pathway in *P. chrysosporium*

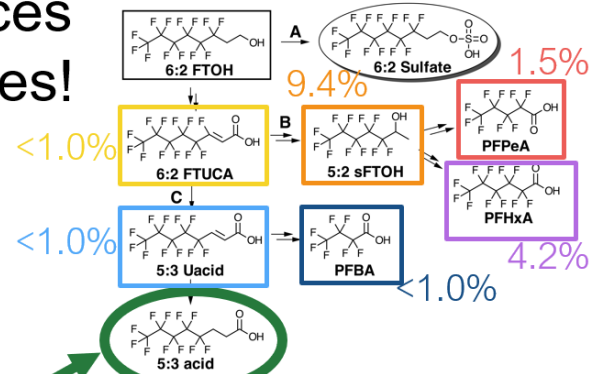


Key takeaways

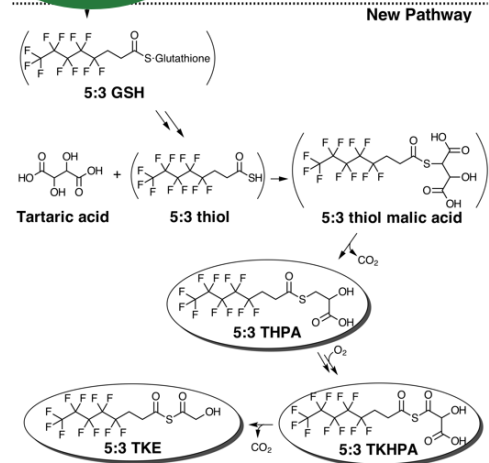
- Minor pathway forms 6:2 Sulfate
- Major pathway leads to defluorination and the formation of 5:3 TKE (5:3 polyfluorothiolketoethanol)
- Minor pathway of fungi is the major pathway of bacteria in PFAS degradation, often resulting in terminal PFAAs
- 2 key enzymes involved in the biotransformation pathway identified

6:2 FTOH biotransformation pathway in *P. chrysosporium*

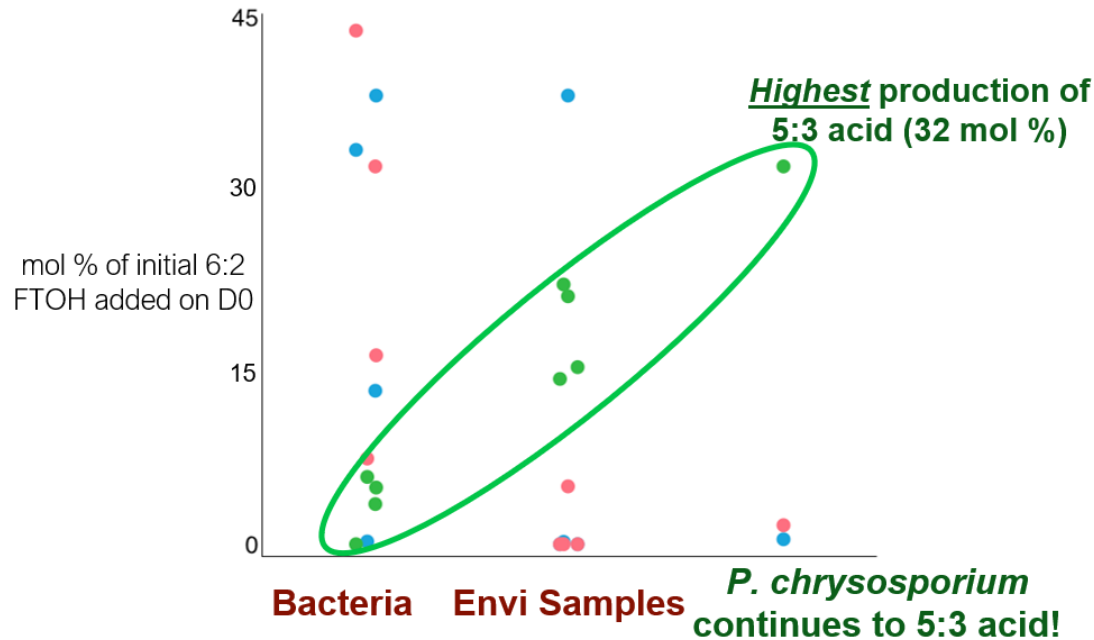
P. chrysosporium produces **less perfluorocarboxylates!**



MORE 5:3 acid production!
 32.2–43.1%



6:2 FTOH biotransformation pathway in *P. chrysosporium*

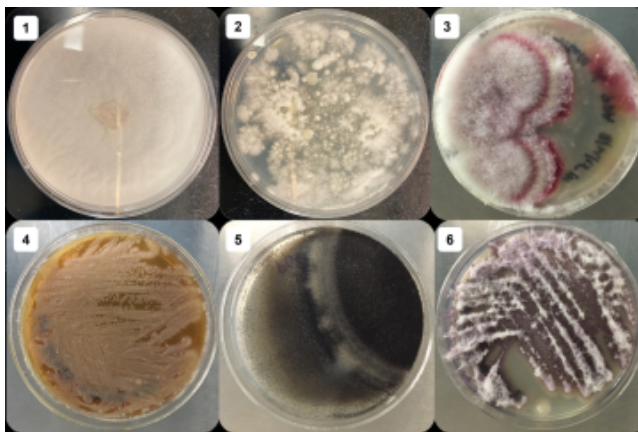


- 6:2 FTUCA
- 6:2 FTCA
- 5:3 acid

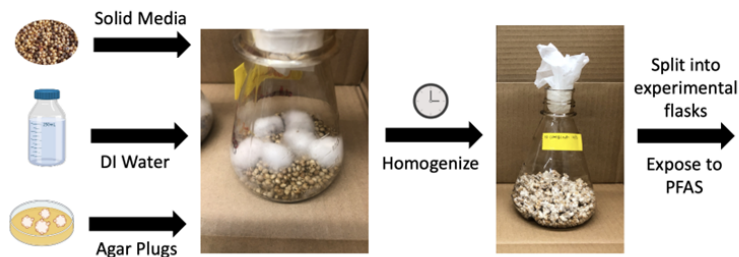
Key takeaways

- 5:3 FTCA yields for fungi compared with environmental consortia and bacteria – fungi achieve highest yield at ~32%
- In the biotransformation of 6:2 FTOH, bacteria quickly oxidize 6:2 FTOH to 6:2 FTUCA or 6:2 FTCA in less than 3 days and fungi produce higher 5:3 FTCA yields

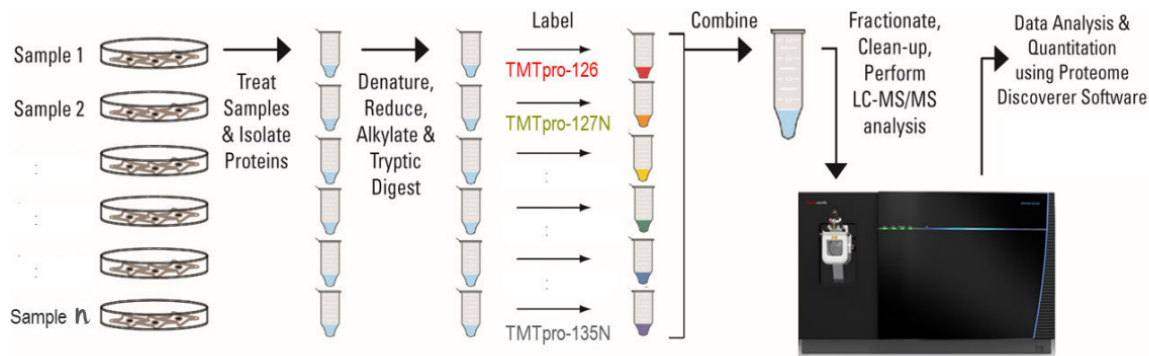
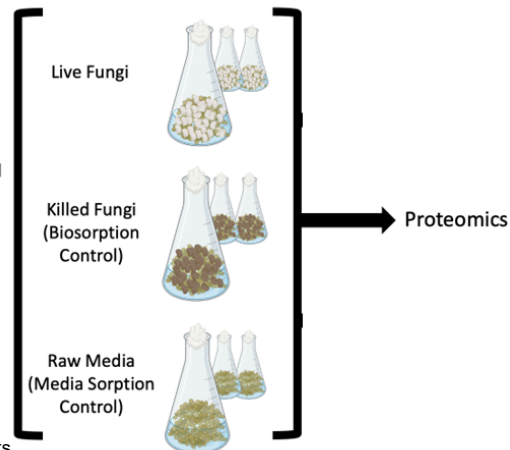
Proteomics Analysis after Fungal Exposure to 6:2 FTS



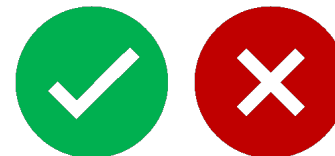
Six fungal isolates being characterized for PFAS biotransformation



Sample preparation for Proteomics experiments

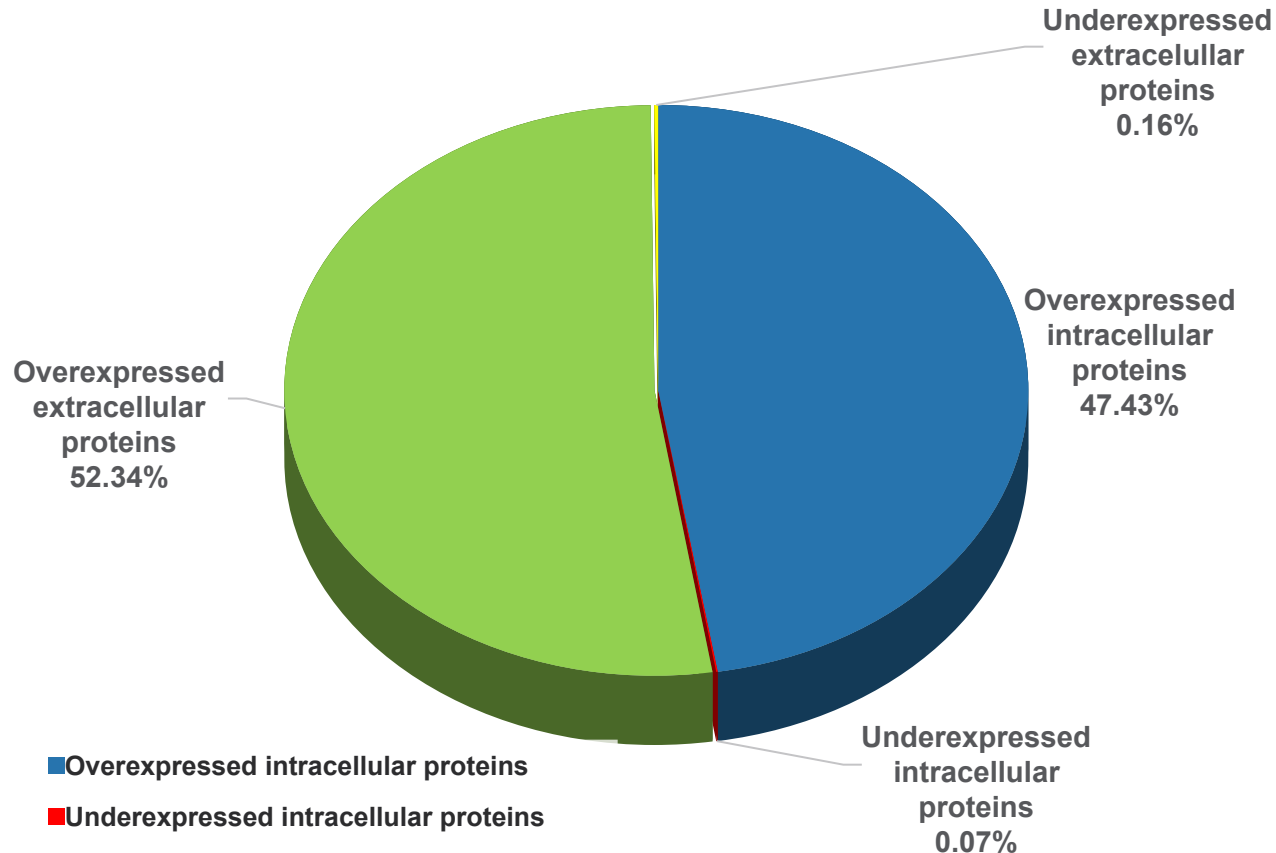


Proteomics pipeline (ThermoFisher Scientific)

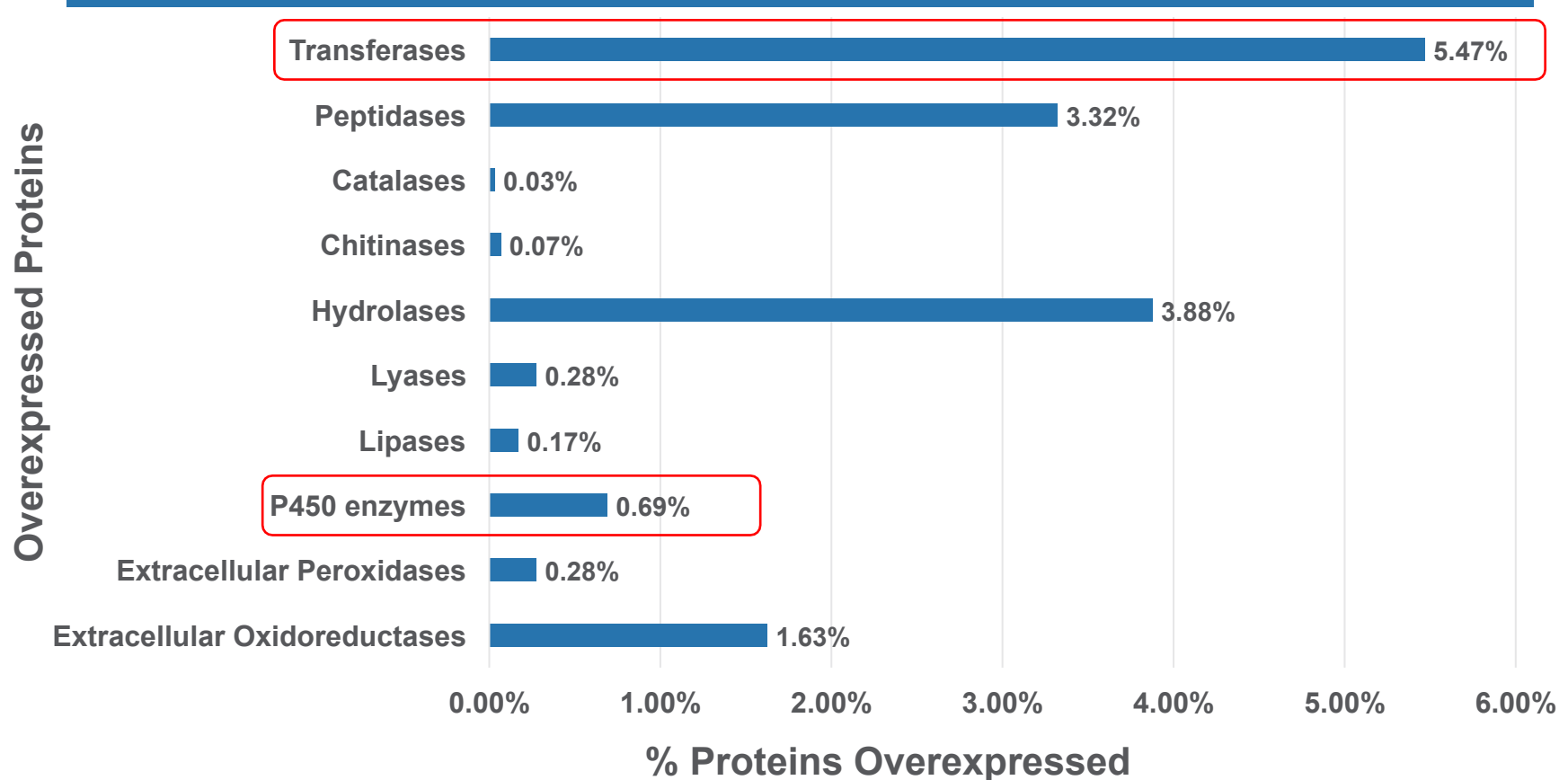


6:2 Fluorotelomer sulfonate (6:2 FTS)

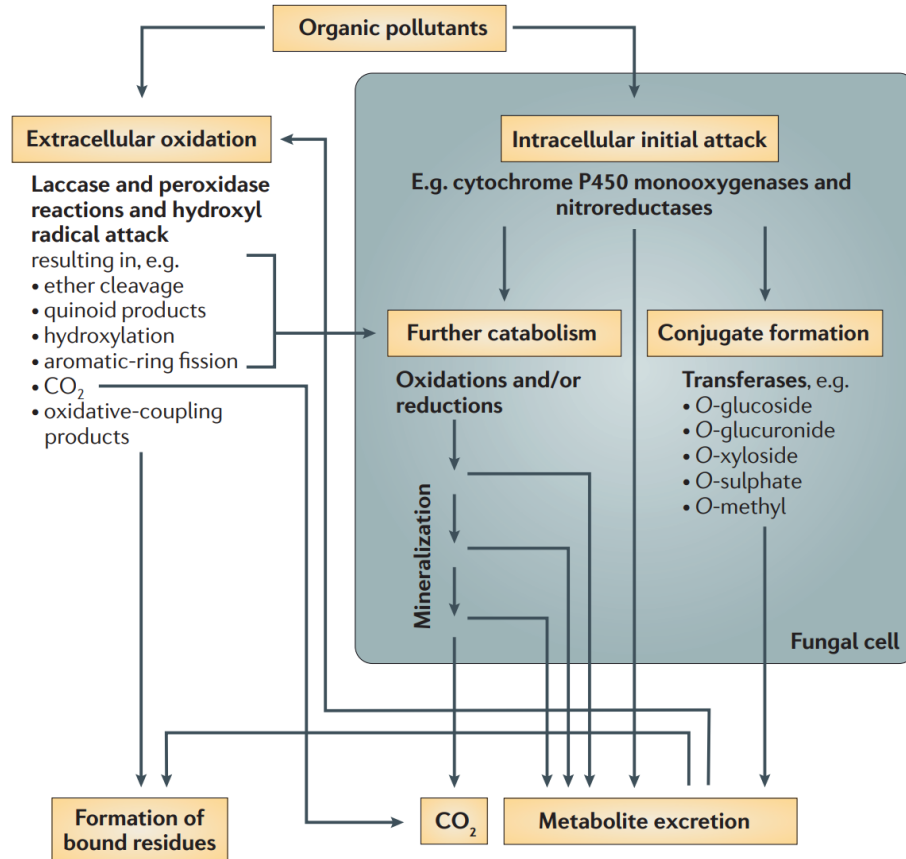
Approximately 50% Extra- and Intracellular Fungal Enzymes are Overexpressed upon Exposure to 6:2 FTS



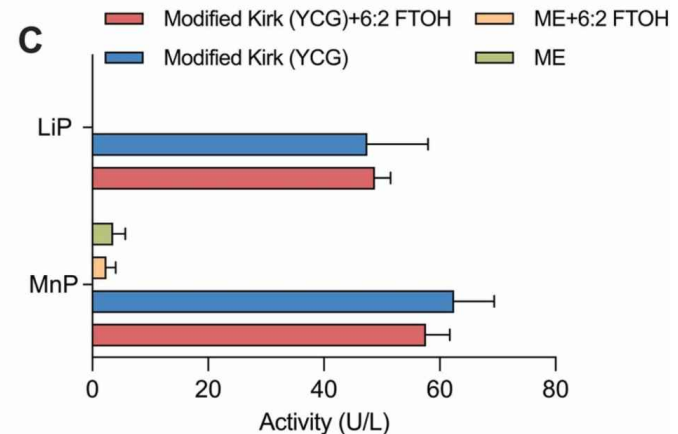
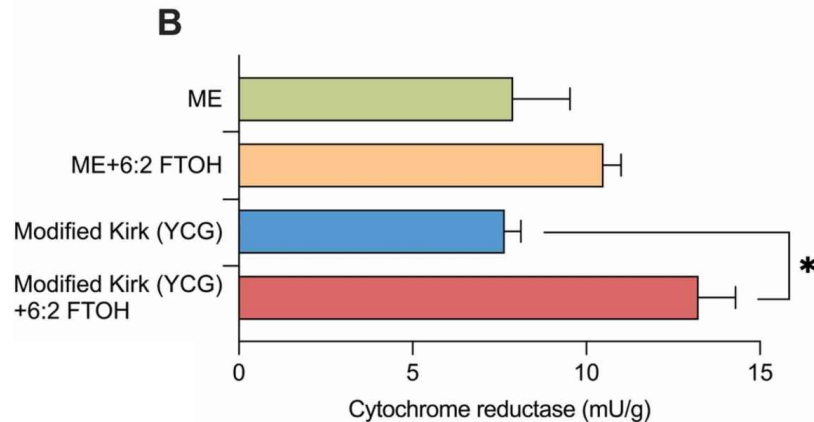
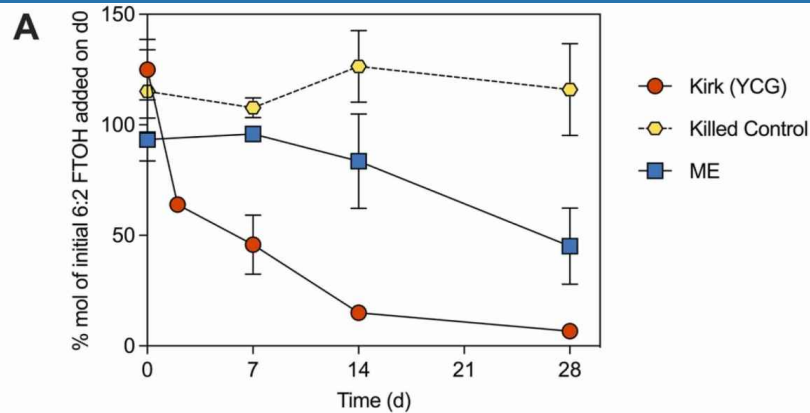
Percentage of Key Fungal Enzymes Overexpressed in the presence of 6:2 FTS



Key Fungal Enzymes Associated with Organic Pollutant Transformation



Key Fungal Enzymes are Associated with 6:2 FTOH Degradation under Different Nutrient Conditions



Key Takeaways

1. Fungal proteomic profile is influenced by biogeochemical conditions as well as PFAS exposure.
2. Approximately 50% of extra- and intracellular fungal proteins are overexpressed within 1 week of exposure to 6:2 FTS.
3. Key fungal enzyme groups potentially involved in PFAS biotransformation pathways include (EC1) oxidoreductases, (EC2) transferases, (EC4) lyases, (EC3) hydrolases and peptidases.
4. Both constitutive and inducible enzymes likely catalyze various steps of PFAS biotransformation mediated by fungi.
5. Identification of specific nutrients required for enzyme induction will inform biostimulation strategies to enhance fungal-mediated PFAS biotransformation for *in situ* and *ex situ* treatment.

Acknowledgements



National Philanthropic Trust

