



Characterizing Molecular Drivers of PFAS Uptake and Distribution

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The Ng Lab at Pitt

PFAS Toxicokinetics and Toxicodynamics



- Physiologically based toxicokinetic models that incorporate protein binding.
- Predict tissue distribution, biological half-life.
- In silico and in vitro toxicity.





- Proteins and phospholipids.
- Sorbent development.
- Transporter impacts on toxicokinetics.
- Enzymatic degradation
- PFAS simulations and force fields.

Human Exposure via Food



- PFAS in seafood and packaged foods.
- Pesticides, POPs, veterinary drugs in seafood.
- PBDEs in farmed salmon.

Regional PFAS Contamination



- McKeesport AFFF drinking water spill
- Regional industrial activity (e.g. ethane cracker plant).
- Regional soil-air contamination (e.g. East Palestine derailment).

Observations for PFAS suggest importance of specific interactions



Substantial differences across species and sex.



perfluorooctanoic acid (PFOA)



octanoic acid



Fatty acid carriers in the body: Serum albumin and liver fatty acid binding protein.

Organic anion transport proteins and polypeptides in the liver, kidneys, ... others?

Nigam et al. 2015 Physiol Rev

Simple lipid partitioning doesn't predict PFAS behavior



By incorporating key binding proteins (serum albumin, fatty acid binding proteins) models are better able to predict bioconcentration potential.

Ng & Hungerbuehler 2013 ES&T

Tissue-specific patterns suggest further interactions

 Not only proteins but phospholipids also shown to contribute.



Key needs to advance understanding:

Build tissue-specific descriptions including key phases: proteins, phospholipids.



Build in dynamics: proteins, transporters.

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Understanding the dynamics of physiological changes, protein expression, and PFAS in wildlife

Jacqueline Bangma a,* , T.C. Guillette a , Paige A. Bommarito b , Carla Ng c,d , Jessica L. Reiner e , Andrew B. Lindstrom f , Mark J. Strynar g



Build multi-species and multi-PFAS frameworks.









In Silico Framework



 $K_{Tissue-Fluid} = K_{PL}f_{PL} + K_{SL}f_{SL} + K_{SP}f_{SP} + K_{FP}f_{FP}$

In Vitro Evaluation



Equilibrium dialysis for protein-PFAS interactions and SSLM assay (Transil assay) for PFAS-phospholipid interactions.





 $K_{Tissue-Fluid} = K_{PL}f_{PL} + K_{SL}f_{SL} + K_{SP}f_{SP} + K_{FP}f_{FP}$

SP, structural protein FP, functional protein SL, storage lipid PL, phospholipid Protein and Phospholipid Binding: Strong, Complementary



- No strong correlation between membrane (K_{MLW}) and protein(K_A for HSA) binding.
- Suggests different mechanisms and influence of chain length/structural features at play.
- This is good news! These are complementary, not redundant data.



"Other" Lipids and Proteins: Storage and Structural

Phase		Estimation Method	Value for PFOA (log10K)
Storage Lipids	Dow	Apparent log Kow, Xiang et al., "Measuring Log Kow Coefficients of Neutral Species of Perfluoroalkyl Carboxylic Acids Using Reversed-Phase High- Performance Liquid Chromatography."	-2.42
Structural Proteins	Dpw	PP-LFERs method from Henneberger, Goss, and Endo, "Partitioning of Organic Ions to Muscle Protein."	-0.36



Drivers of PFAS-tissue Distribution for PFOA



Phospholipids and binding proteins, as expected, contribute most to distribution.

Structural proteins are "neutral". Storage lipids do not contribute.

Binding proteins in other tissues remains incompletely studied.

Future needs: from PFOA to other PFAS

- Other functional Proteins
 - L-FABP, α2u-globulin... others?
- Membrane transporters
 - Oat1, Oat3, Oatp1a1, Ntcp, Ost α/β ...
- These additional data can inform tissue partition coefficients:
 - D_{OW} , D_{MLW} , D_{PW} , K_{PW} (specific binding)



Next: understanding key differences across species, ecosystems



Sequence Alignment to Predict Across Species Susceptibility

What is SeqAPASS?

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS), is a fast, online screening tool that allows researchers and regulators to extrapolate toxicity information across species. For some species, such as humans, mice, rats, and zebrafish, the EPA has a large amount of data regarding their toxicological susceptibility to various chemicals. However, the toxicity data for numerous other plants and animals is very limited.



Dr. Carlie Lalone, US EPA, Duluth



Dr. Jon Doering, now faculty at LSU

Which model organism for which purpose? Which protein? Which PFAS?

Understanding key differences



Observations on key differences



Which model organism for which purpose? Which protein? Which PFAS?

- Humans most sensitive species for LFABP binding for many PFAS.
- Chicken, zebrafish, rainbow trout LFABP show similar affinity.
- Japanese medaka and fathead minnow proteins predicted to bind have lower affinity for most PFAS.
- **BUT**: all based on a single protein, and a static picture.

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Environmental Toxicology

From Protein Sequence to Structure: The Next Frontier in Cross-Species Extrapolation for Chemical Safety Evaluations



Evidence of structural conservation to inform SeqAPASS predictions

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Finally: important to consider dynamics

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PFAS Exposure Pathways for Humans and Wildlife: A Synthesis of Current Knowledge and Key Gaps in Understanding

Amila O. De Silva,^a James M. Armitage,^b Thomas A. Bruton,^c Clifton Dassuncao,^d Wendy Heiger-Bernays,^e Xindi C. Hu,^f Anna Kärrman,^g Barry Kelly,^h Carla Ng,ⁱ Anna Robuck,^j Mei Sun,^k Thomas F. Webster,^e and Elsie M. Sunderland^{i,*}



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Understanding the dynamics of physiological changes, protein expression, and PFAS in wildlife

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How do PFAS influence proteins, and how do proteins influence PFAS?

Inter-individual differences

• the role of *dynamic kidney function*



Renal reabsorption is understood to contribute to the long half-life of PFOA in humans and to the sex differences observed between male and female rats.

But many more transporters and many more PFAS exist than have been tested.

And protein expression is dynamic. \rightarrow *Reverse causation vs. causation*.



Shan Niu, Ducatman, Sanders and Ng, in preparation



Inter-individual differences

• the role of *dynamic kidney function*



Niu, Ducatman, Sanders and Ng, in preparation

Tracking Regional PFAS Contamination



17 Months after the fire drinking water samples were down to background levels. Project has turned to investigating environmental impacts of hydrant flushing.

Can We Engineer Enzymes for PFAS Destruction?



The defluorination pathway of fluoroacetate by FAcD, one of the few known natural defluorination pathways with an identified enzyme.



His

Left: CH₃(CH₂)₂(CF₂)₃CF₃ from MD with parameters autogenerated by GAFF2 forcefield, quantum mechanical results at the MP2/6-31G* level, and MD with an optimized torsion angle parameter. *Right:* The difference in torsion angle energy barriers for each structure.(*Träg and Zahn 2019*)



Representation of $C_4F_9SO_3^-$ electrostatic potential mapping by an additive forcefield (left) and polar forcefield (middle) compared to quantum mechanical on the B3LYP/6-311+G** level





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