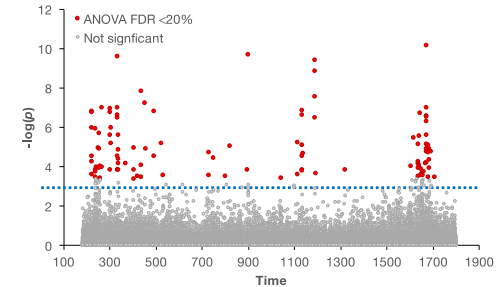


# The exposome and health



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 @exposome  
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# The exposome: a Wild idea

## Editorial

### **Complementing the Genome with an “Exposome”: The Outstanding Challenge of Environmental Exposure Measurement in Molecular Epidemiology**

Christopher Paul Wild

Molecular Epidemiology Unit, Centre for Epidemiology and Biostatistics, Leeds Institute of Genetics, Health and Therapeutics, Faculty of Medicine and Health, University of Leeds, Leeds, United Kingdom

Defined the “*Exposome*” as all exposures from conception onwards, including those from lifestyle, diet and the environment.

### **The Nature of Nurture: Refining the Definition of the Exposome**

Gary W. Miller<sup>1</sup> and Dean P. Jones

Rollins School of Public Health, School of Medicine, Emory University, Atlanta, Georgia 30322

The cumulative measure of environmental influences and corresponding biological responses throughout the lifespan



A systematic, unbiased, and omic-scale examination of external factors contributing to disease or health status\*

\*avoid candidate gene search faults

# A strategy for exposomics

The exposome is vast. We need a suite of tools to capture the breadth of external factors that influence health: satellite imaging, wearable devices, sensors, sentinel animals, computational approaches, and analysis of biological samples.

The approach that we have taken is to use high-resolution mass spectrometry (HRMS) to extract as much data as possible out of human blood samples.

HRMS on plasma/serum provides an excellent initial scan of the exposome, capturing hundreds of exogenous chemicals/features, as well as the biological state of the individual. It can be conducted on biobanked samples, leveraging the large longitudinal studies supported by other mechanisms.

# A strategy for exposomics

The exposome is vast. We need a suite of tools to capture the breadth of external factors that influence health: satellite imaging, wearable devices, sensors, sentinel animals, computational approaches, and analysis of biological samples.

The approach that we ~~could take~~ ~~have taken~~ is to use high-resolution mass spectrometry (HRMS) to extract as much data as possible out of ~~human~~ blood samples.

Dog/Cat/Goldfish

HRMS on plasma/serum provides an excellent initial scan of the exposome, capturing hundreds of exogenous chemicals/features, as well as the biological state of the individual. It can be conducted on biobanked samples, leveraging the large longitudinal studies supported by other mechanisms.

# External factors → internal biological signals

## Ecosystems

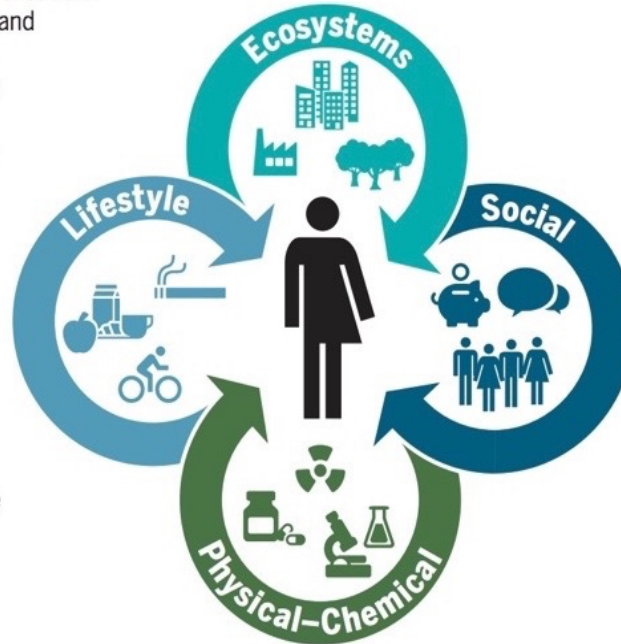
Food outlets, alcohol outlets  
Built environment and  
urban land uses  
Population density  
Walkability  
Green/blue space

## Lifestyle

Physical activity  
Sleep behavior  
Diet  
Drug use  
Smoking  
Alcohol use

## Social

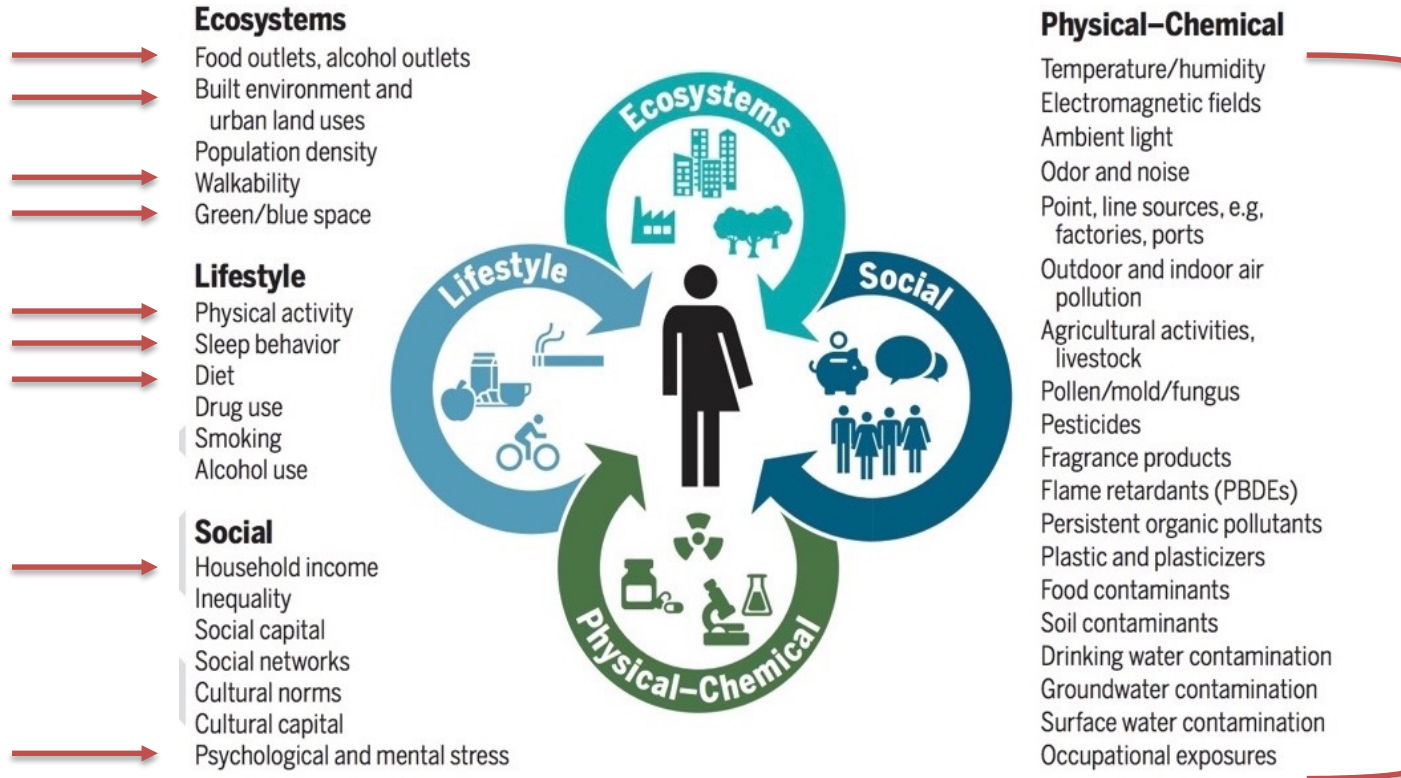
Household income  
Inequality  
Social capital  
Social networks  
Cultural norms  
Cultural capital  
Psychological and mental stress



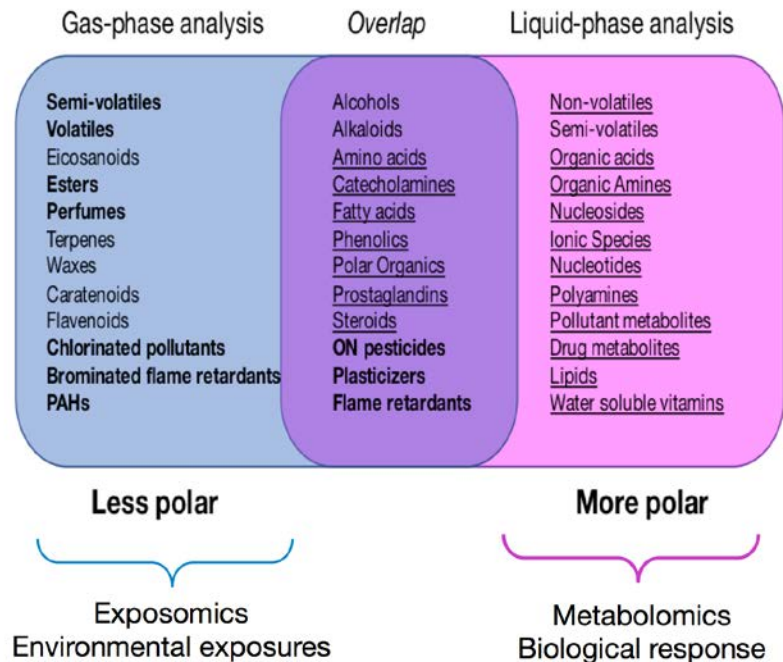
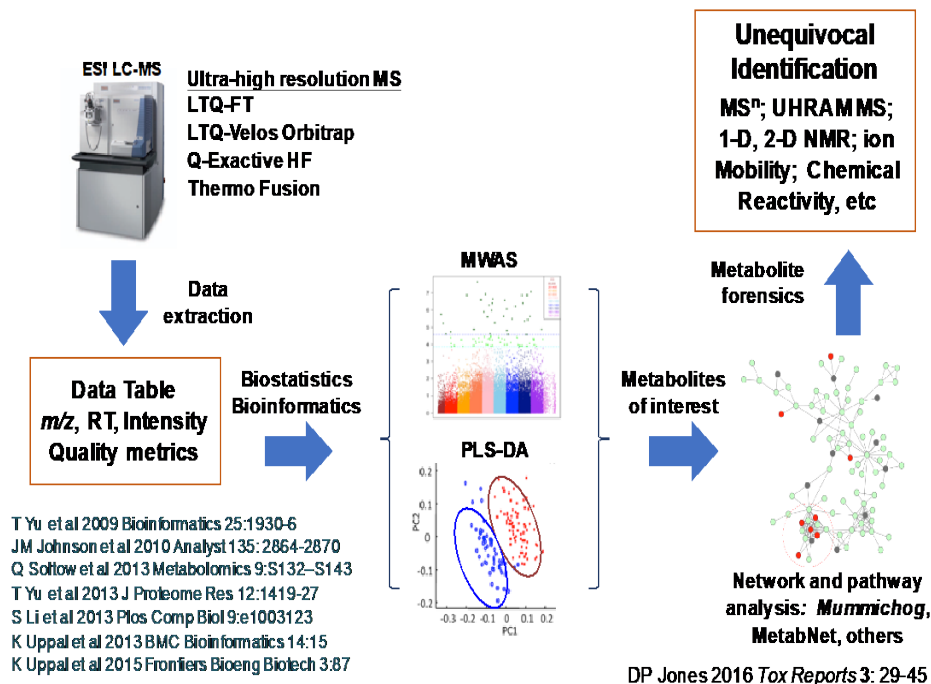
## Physical-Chemical

Temperature/humidity  
Electromagnetic fields  
Ambient light  
Odor and noise  
Point, line sources, e.g.,  
factories, ports  
Outdoor and indoor air  
pollution  
Agricultural activities,  
livestock  
Pollen/mold/fungus  
Pesticides  
Fragrance products  
Flame retardants (PBDEs)  
Persistent organic pollutants  
Plastic and plasticizers  
Food contaminants  
Soil contaminants  
Drinking water contamination  
Groundwater contamination  
Surface water contamination  
Occupational exposures

# External factors → internal biological signals



# LC and GC based high resolution mass spectrometry to detect exogenous chemicals and endogenous metabolites



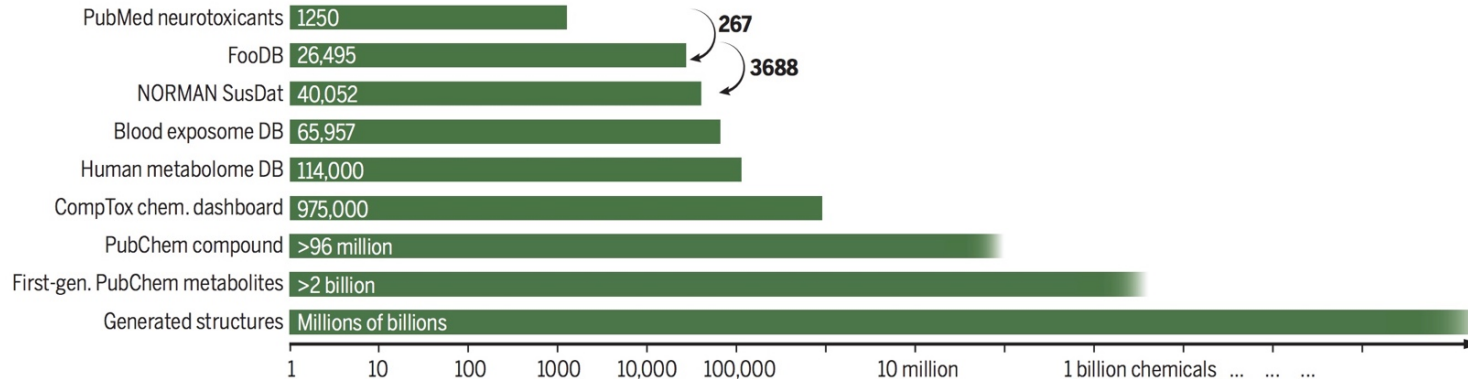
Walker, Miller, Jones

Because authentic standards are rarely available for xenobiotics and their metabolites, identification relies heavily on accurate mass and RT matching with databases

#### Typical HRMS sample

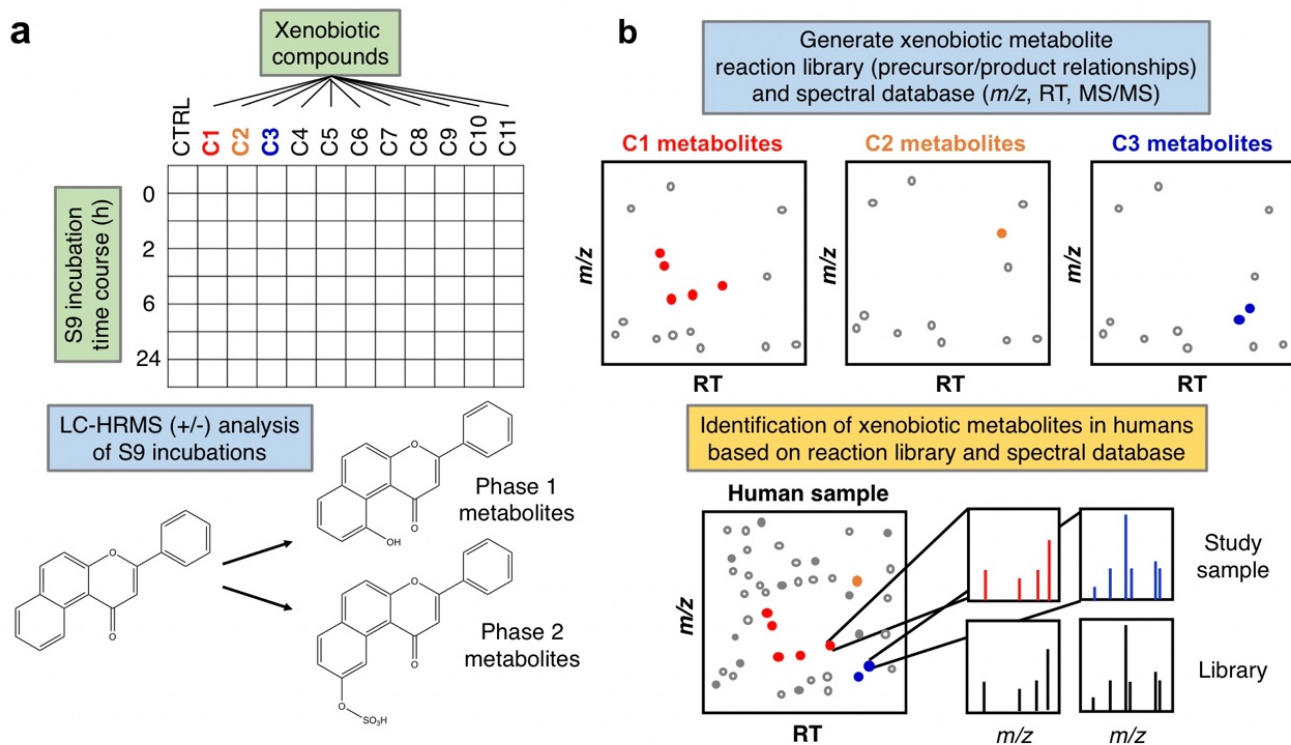


#### Selected exposomics, chemical data sources

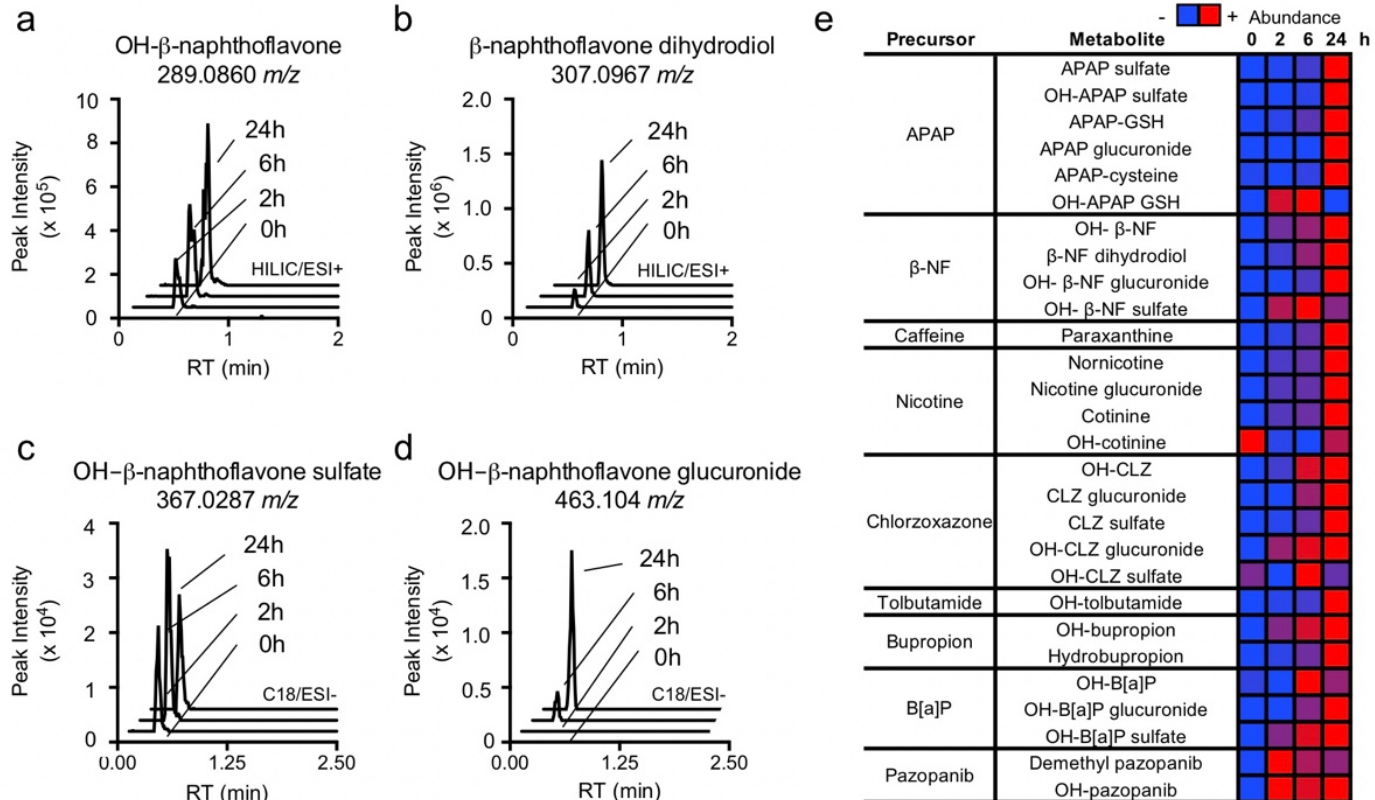


**Fig. 2. Chemical complexity of HRMS and the exposome.** Top: Known versus unknown features in a typical HRMS measurement [data from (7)]. Bottom: Selected data sources relevant to the chemical exposome (10–14, 19). Arrows show the overlap of potential neurotoxicants in FooDB (<http://foodb.ca/>) and FooDB components in NORMAN SusDat ([www.norman-network.com/nds/susdat/](http://www.norman-network.com/nds/susdat/)) (prioritized chemicals of environmental interest).

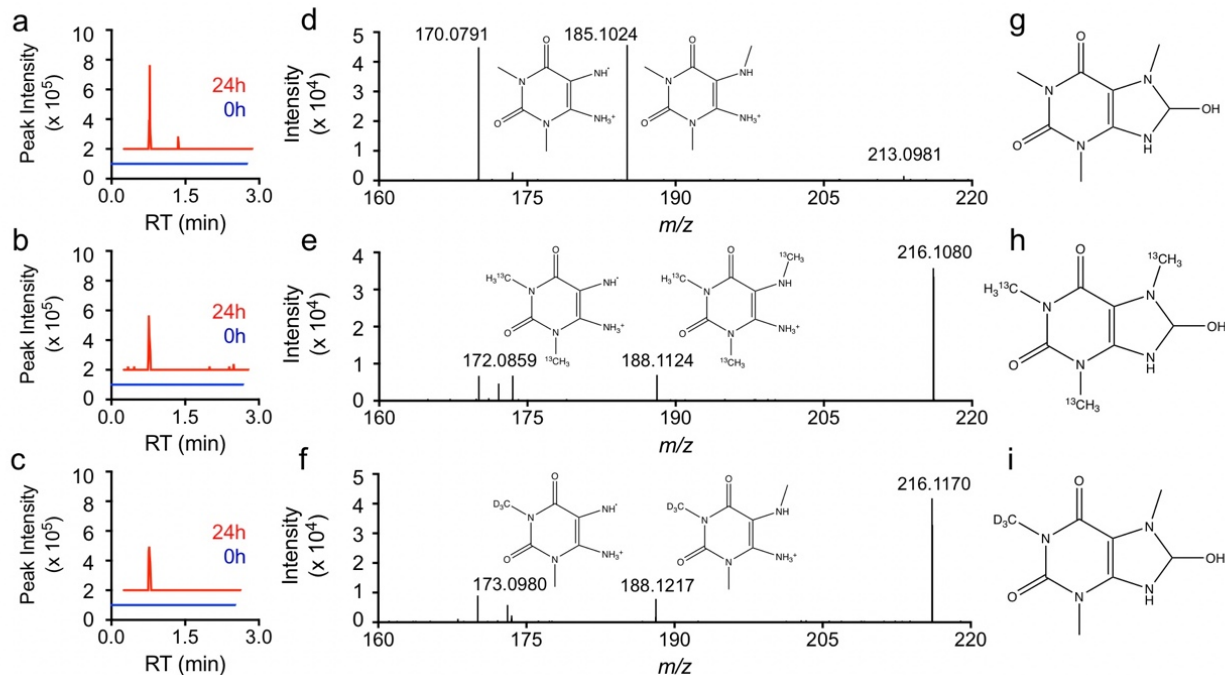
# Large-scale xenobiotic metabolite identification for exposomics



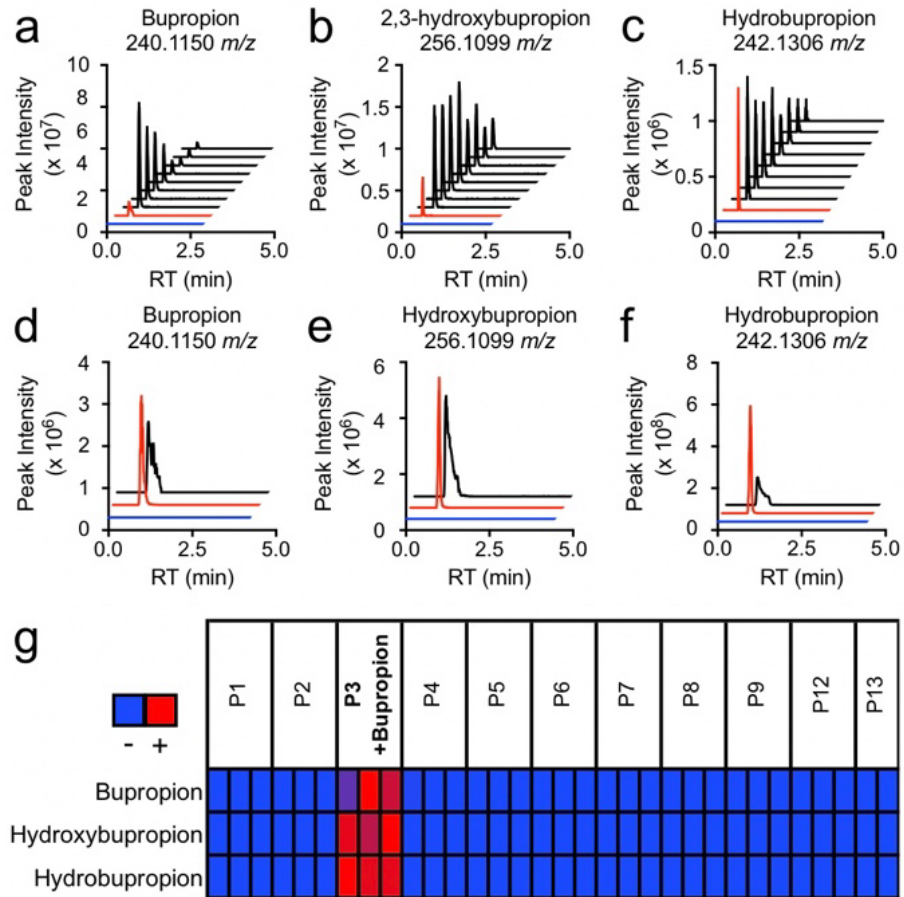
# Human liver S9 enzymes generate phase I and II xenobiotic metabolites in a time-dependent manner



# Stable isotope-assisted unexpected metabolite identification



# Identification of documented xenobiotic exposure



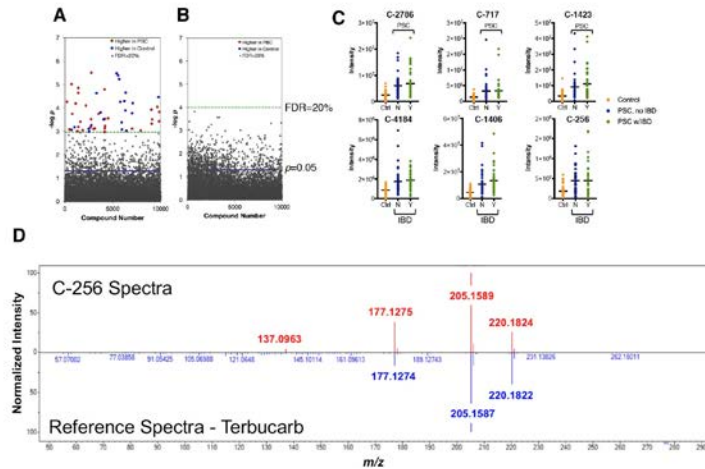
Liu et al., Nature Communications, 2021

# Mayo Clinic, Emory, Columbia

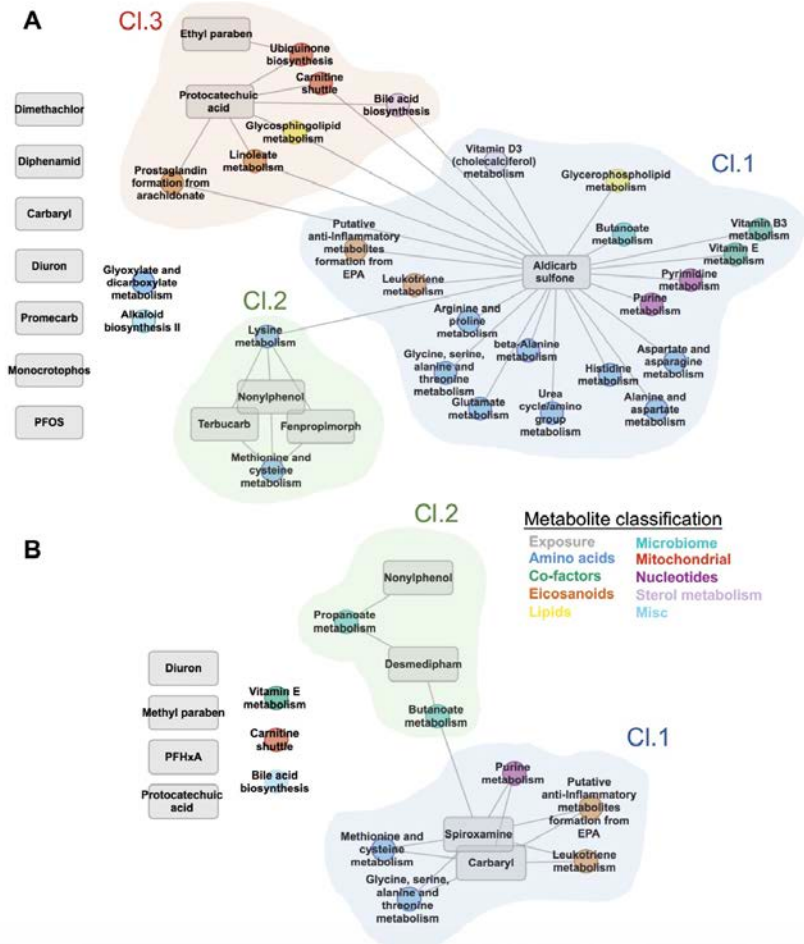
## Primary sclerosing cholangitis

### EWAS x MWAS

\*high incidence of liver cancer

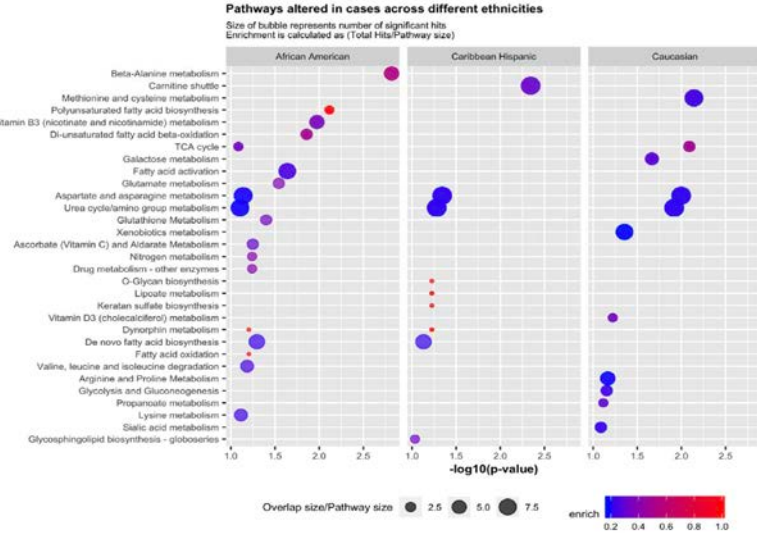
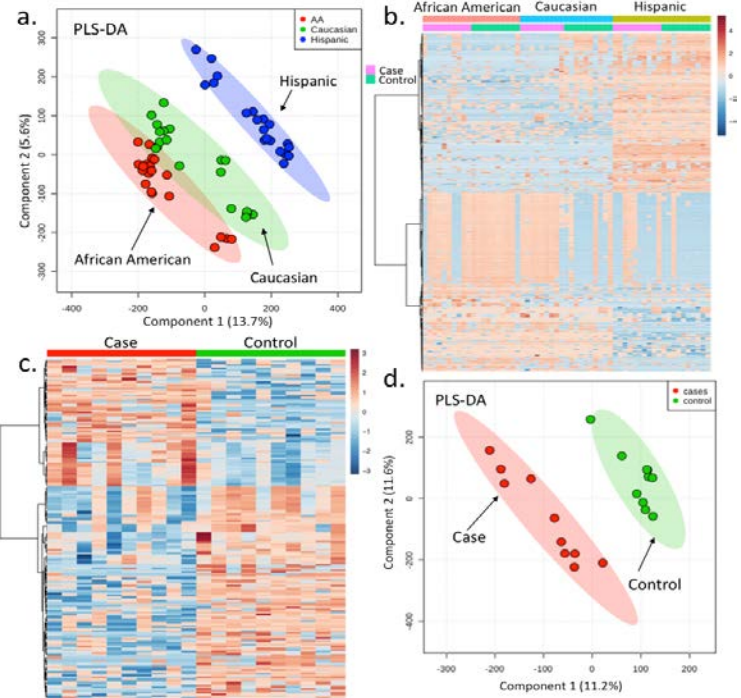


Exogenous chemicals vs. endogenous metabolites



Walker et al., Hepatology Communications, Nov, 2021

# Alzheimer's disease and WHICAP



N=160

Vardarajan, Kalia, et al.  
Alzheimer's Dementia, 2020  
Richard Mayeux, PI

| Table 2. Number of blood samples | SA1      |             | SA 2a        | All Aims    |
|----------------------------------|----------|-------------|--------------|-------------|
|                                  | Controls | Incident AD | Prevalent AD | Metabolomes |
| 2 +                              | 724      | 247         | 375          | 3,692       |
| 3 (or more) ++                   | 760      | 529         | 260          | 4,647       |
| Totals                           | 1484     | 776         | 635          | 8,339       |

# EFIGA Genetic epidemiology of Alzheimer's disease in Caribbean Hispanics

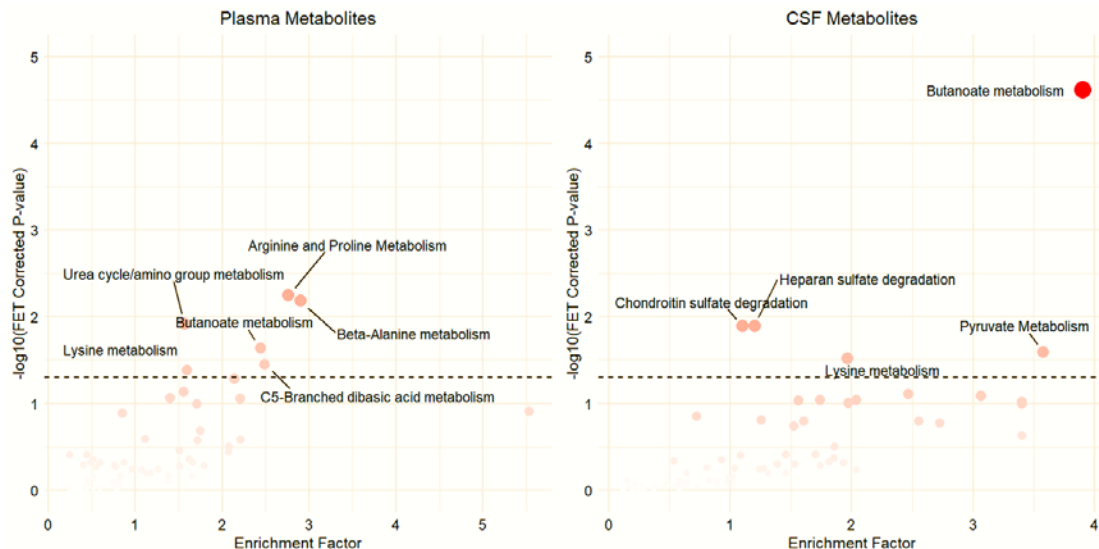
AD biomarkers: NfL, AB40, AB42,  
total-Tau, pTau181, pTau 217

CSF and plasma

LC-HRMS is completed  
data analysis in process

GC-HRMS pending

84 control, 33 AD (will increase 4x)



Based on observation that Caribbean Hispanics in Northern Manhattan have increased risk of AD, Richard Mayeux started EFIGA. Located in the Dominican Republic, EFIGA follows participants over time with cognitive testing, blood and CSF samples.

# Exposomics of cognitive decline

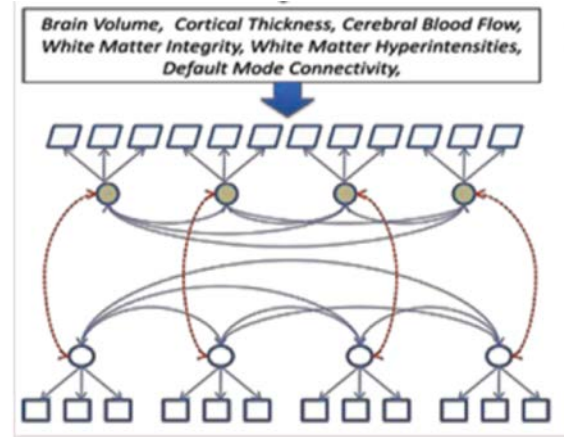
12 cognitive tasks that assess:

- episodic memory
- fluid reasoning ability
- perceptual speed
- vocabulary

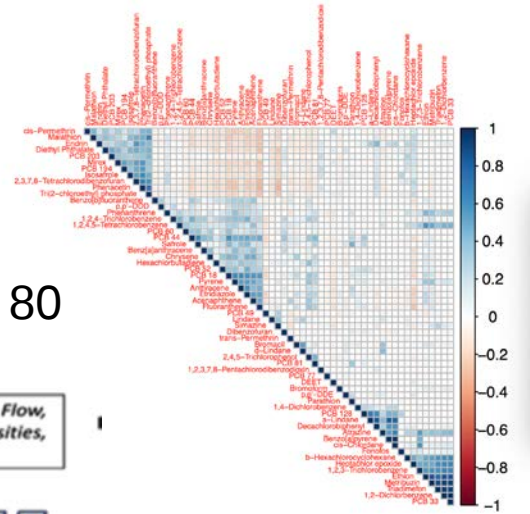
fMRI imaging during tasks  
plasma collected at  
baseline and 5-yr follow up

IQ tests administered

Yaakov Stern, PI -20/group  
Ages 20, 30, 40, 50, 60, 70, 80



LC-HRMS-untargeted (Kalia, Miller-Columbia)  
GC-HRMS-targeted(80)/untargeted (Manz, Pennell-Brown)



# Alzheimer's disease (93), Mild cognitive impairment (50), controls (59) APOE genotype, CSF (AB42, pTau)

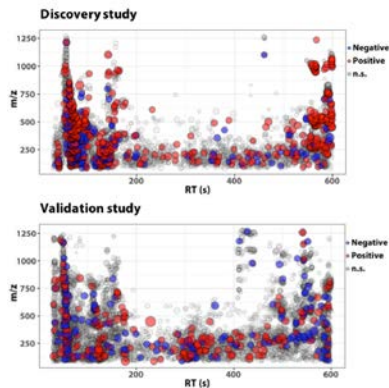
Table 4. Putative compound identification of plasma features from MWAS.

| <i>m/z</i> | RT  | Change in AD | Putative compound(s)                                                                                                 | Predicted adduct    | ID level <sup>a</sup> | Notes                           |
|------------|-----|--------------|----------------------------------------------------------------------------------------------------------------------|---------------------|-----------------------|---------------------------------|
| 129.0661   | 89  | Higher       | Glutamine (2 ppm)                                                                                                    | -H <sub>2</sub> O+H | 1                     | --                              |
| 231.1205   | 211 | Higher       | 5S,6S-epoxy-15R-hydroxy-ETE (+Na, 0 ppm)                                                                             | --                  | 3                     | --                              |
| 246.9550   | 127 | Higher       | Numerous database matches                                                                                            | -H <sub>2</sub> O+H | --                    | Contains halogen (Cl and/or Br) |
| 334.1410   | 86  | Lower        | Piperettine (1 <b>Hydroxylated metabolite of DDE</b> )                                                               |                     |                       | --                              |
| 349.1515   | 80  | Lower        | Piperine (1 ppm)                                                                                                     | +ACN+Na             | 4                     | --                              |
| 386.8946   | 61  | Higher       | 1,1-Dichloro-2-(dihydroxy-4'-chlorophenyl)-2-(4'-chlorophenyl)ethylene (9 ppm)                                       | +K                  | 2                     | Contains halogen (Cl and/or Br) |
| 662.0933   | 158 | Higher       | GDP-D-mannuronate (+ACN+H [M+1], 0 ppm); Chaetocin (-2H <sub>2</sub> O+H [M+1], 8 ppm); Blighinone (+H [M+1], 9 ppm) | [M+1] isotope       | 4                     | --                              |
| 663.4524   | 36  | Higher       | Lipid A-disaccharide-1-P (+2H, 2 ppm); Aluminium dodecanoate (+K, 2 ppm)                                             | --                  | 4                     | --                              |

<sup>a</sup>ID level indicates annotation confidence: 1, *m/z* and retention time confirmed with MS<sup>2</sup>; 2: Multiple/isotopes present; 3: *m/z* matched single adduct mass within 10 ppm mass error, 4: *m/z* matched adduct mass of multiple isobaric species, probable identifications listed.

\*Adduct of rivastigmine strongest feature associated with AD

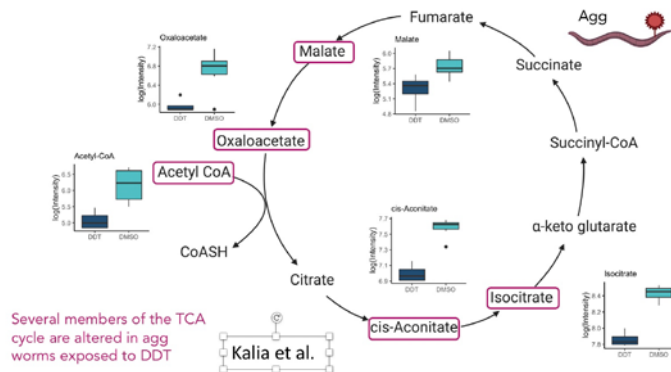
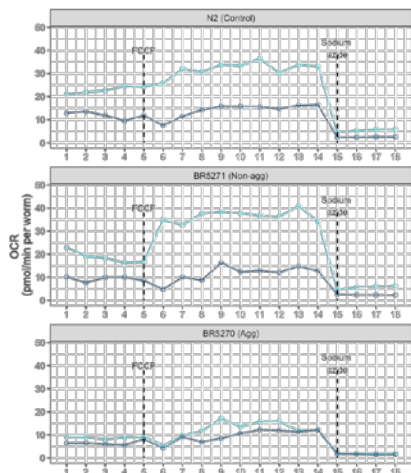
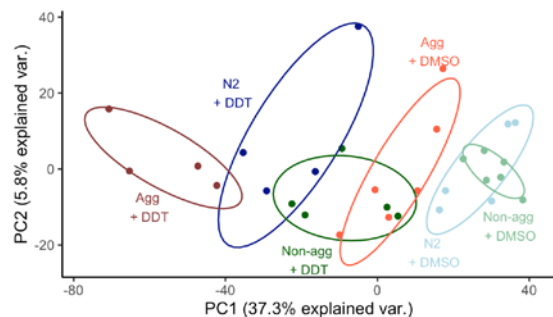
Niedzwiecki, Walker, Howell, Watts, Jones, Miller, Hu preliminary data



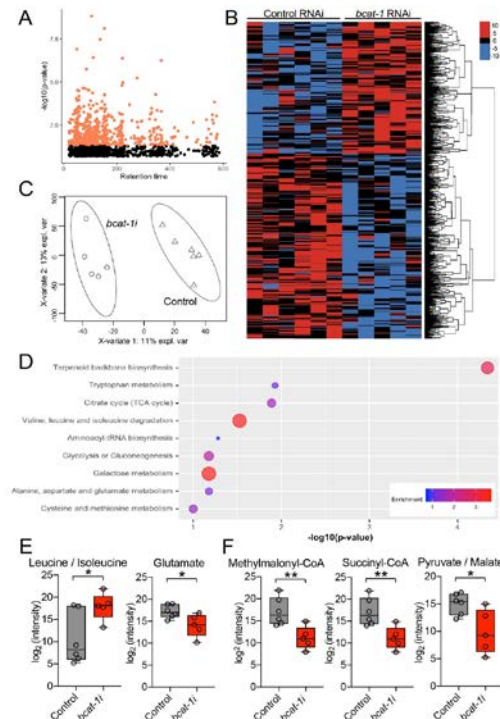


# DDT, p-Tau, and metabolites in Alzheimer's

The metabolomic/  
exposomic analysis  
works in *C. elegans*



Kalia et al., posted on bioRxiv



Mor et al., PNAS, 2020

# Cross-species analysis

## Worms and plasma

| Annotation                           | <i>C. elegans</i>     | Human plasma            |
|--------------------------------------|-----------------------|-------------------------|
| Lipoamide                            | Lower<br>(p = 0.027)  | Negative<br>(p = 0.035) |
| Diethylthiophosphoric acid           | Lower<br>(p = 0.044)  | Negative<br>(p = 0.015) |
| 11, 12-dihydroxy eicosatrienoic acid | Higher<br>(p = 0.029) | Positive<br>(p = 0.01)  |
| N-acetyl-lysine                      | Lower<br>(p = 0.042)  | Negative<br>(p = 0.033) |
| Cystine                              | Lower<br>(p = 0.01)   | Negative<br>(p = 0.032) |

## Worms and CSF

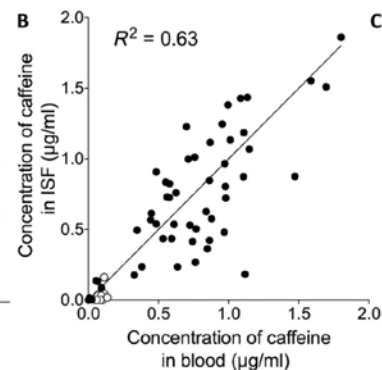
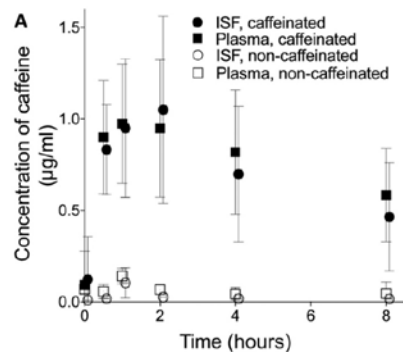
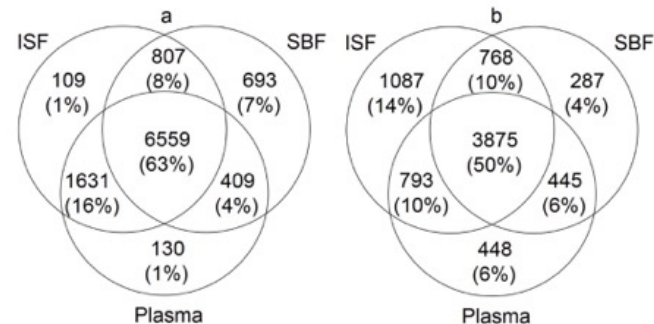
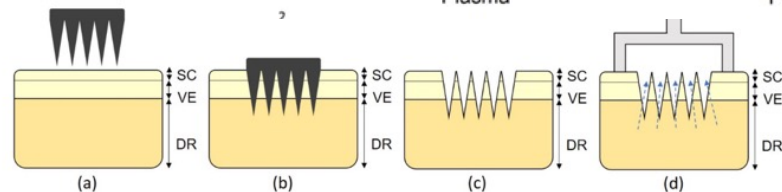
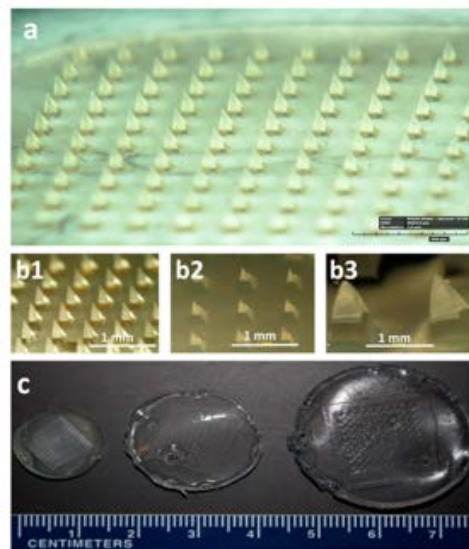
| Annotation                  | <i>C. elegans</i>      | Human CSF               |
|-----------------------------|------------------------|-------------------------|
| Tyrosine                    | Lower<br>(p = 0.046)   | Negative<br>(p = 0.039) |
| Carnitine                   | Lower<br>(p = 0.0001)  | Negative<br>(p = 0.048) |
| Cystine                     | Lower<br>(p = 0.011)   | Negative<br>(p = 0.031) |
| N,N-dimethylaniline-N-oxide | Lower<br>(p = 0.00002) | Negative<br>(p = 0.042) |

If we can perform this analysis between humans and *C. elegans*, an organism with only 959 cells in its entire body, the comparison from humans to dogs is undoubtedly feasible.

## INTERSTITIAL FLUID

## Sampling interstitial fluid from human skin using a microneedle patch

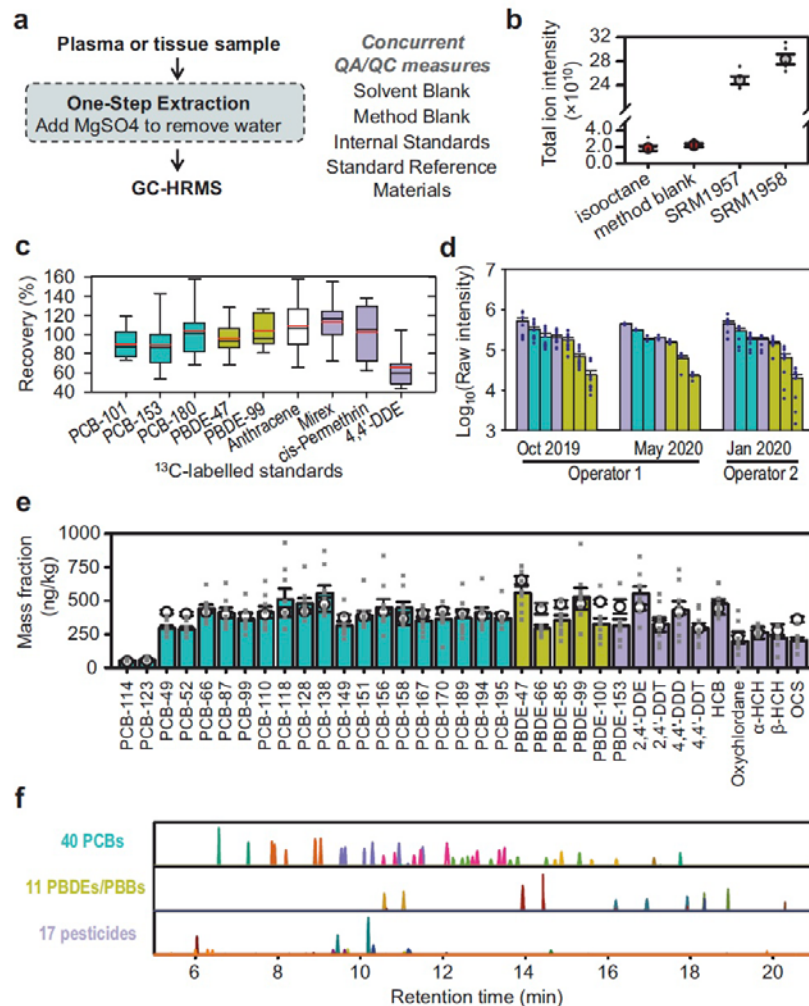
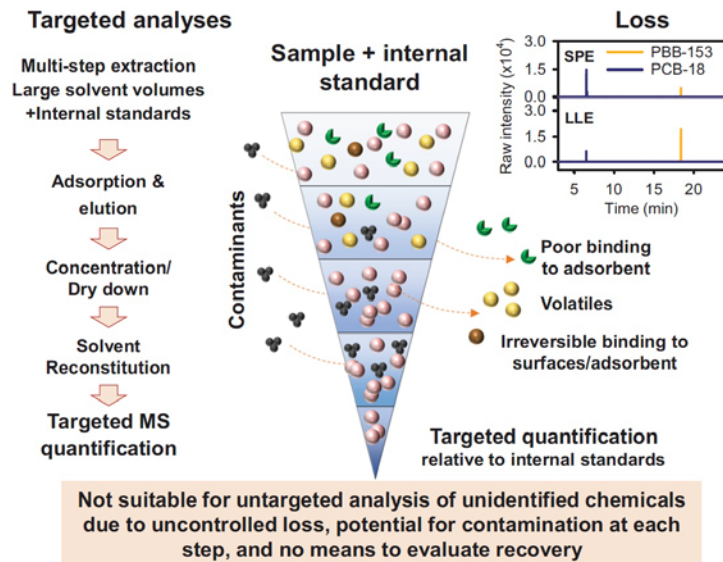
Pradnya P. Samant<sup>1</sup>, Megan M. Niedzwiecki<sup>2,3</sup>, Nicholas Raviele<sup>1</sup>, Vilinh Tran<sup>4</sup>, Juan Mena-Lapaix<sup>1</sup>, Douglas I. Walker<sup>2,3,4</sup>, Eric I. Felner<sup>5</sup>, Dean P. Jones<sup>4</sup>, Gary W. Miller<sup>2,6</sup>, Mark R. Prausnitz<sup>1\*</sup>



**C**

| PK parameter                | Plasma        | ISF           |
|-----------------------------|---------------|---------------|
| $C_{max}$ (µg/ml)           | 1.06 (0.31)   | 1.03 (0.42)   |
| $t_{max}$ (hours)           | 1 (0.61)      | 1 (0.61)      |
| $AUC_{(0-8h)}$ (µg/ml-hour) | 0.084 (0.031) | 0.148 (0.116) |
| $t_{1/2}$ (hours)           | 9.4 (3.9)     | 7.5 (5.0)     |
| CL (liter/hour)             | 4.1 (2.9)     | 4.7 (2.8)     |

# A scalable workflow to characterize the human exposome-Hu et al., Nature Communications 2021



Express liquid extraction to LC-HRMS

# Toward Capturing the Exposome: Exposure Biomarker Variability and Coexposure Patterns in the Shared Environment

Ming Kei Chung,<sup>†</sup> Kurunthachalam Kannan,<sup>‡</sup> Germaine M. Louis,<sup>§</sup> and Chirag J. Patel<sup>\*,†</sup>

“Shared household explained 43% and 41% of the total variance for PFASs and blood metals, but less than 20% for the remaining 11 EDC classes.”

“Our findings suggest that individual, rather than shared environment, could be a major factor influencing the covariation of the exposome.”

\*N.B. couples do not share their environments in the first 20-30 years of life. Need to pay attention to developmental windows/life stages.

# The exposome in companion animals

Exposomics is gaining acceptance within the U.S. biomedical research community. We must continue to innovate and demonstrate to be able to analyze biobanks like NIH All of Us, UK Biobank. NCI Cohort Consortium.

The approaches I have described have been used in a variety of animals: mice, rats, drosophila, zebrafish, *C. elegans*, and dogs.

There are essentially no technical limitations. HRMS-based exposomics and metabolomics can be performed on blood samples from any species. The question is what are we trying to learn? Are we trying to identify hundreds of environmental compounds in companion animals? Are we trying to discover links to disrupted global metabolism? Are we looking for specific contaminants?

# The exposome in companion animals

I favor untargeted HRMS due to its relative lack of streetlamp bias, but that is merely my opinion. Targeted approaches have greater sensitivity and greater confidence in identification, but they require that you know what you are looking to measure. But then you must ask yourself:

# The exposome in companion animals

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- 1) Do you know what you are looking for?

# The exposome in companion animals

I favor untargeted HRMS due to its relative lack of streetlamp bias, but that is merely my opinion. Targeted approaches have greater sensitivity and greater confidence in identification, but they require that you know what you are looking to measure. But then you must ask yourself:

- 1) Do you know what you are looking for?
- 2) Do you really know that you know what you are looking for?

# Acknowledgements

- Miller Lab (Columbia)
- Jones Lab (Emory)
- Walker Lab (Mt. Sinai)
- Pennell Lab (Brown)
- Lazaridis Group (Mayo)
- Pollitt Lab (Yale)
- Irving CTSA Biomarkers Lab (Columbia)
- Mayeux team (Columbia)
- Stern team (Columbia)
- Schymanski team (Luxembourg)
- Klanova team (Czech Republic)
- Barouki team (France)
- Vermeulen team (Netherlands)
- NIEHS, NIA, NIDDK

COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK



Precision medicine and the exposome  
December 17, 2021



**Exposome: a new field, a new journal**

Gary W. Miller \*

Department of Environmental Health Sciences, Mailman School of Public Health, Columbia University, New York, NY, USA

\*To whom correspondence should be addressed. Email: gary.miller@columbia.edu

I would like to suggest that there is need for an 'exposome' to match the genome....

Christopher Wild<sup>1</sup>

Essentially, once one subtracts the genetic component from the phenotypic manifestations, one is left with E. We have incredible clinical, cellular, and molecular characterization of the phenotype (P) and the extraordinary advances in genomics and genet-

*Exposome*, 2021, osab001

DOI: 10.1093/exposome/osab001

Advance Access Publication Date: 16 March 2021

Editorial

Published by  
Oxford University Press