Associations between Halogenated Flame Retardants Exposure and Childhood Gut Microbiome Multi-omics Profiles in a Canadian Cohort

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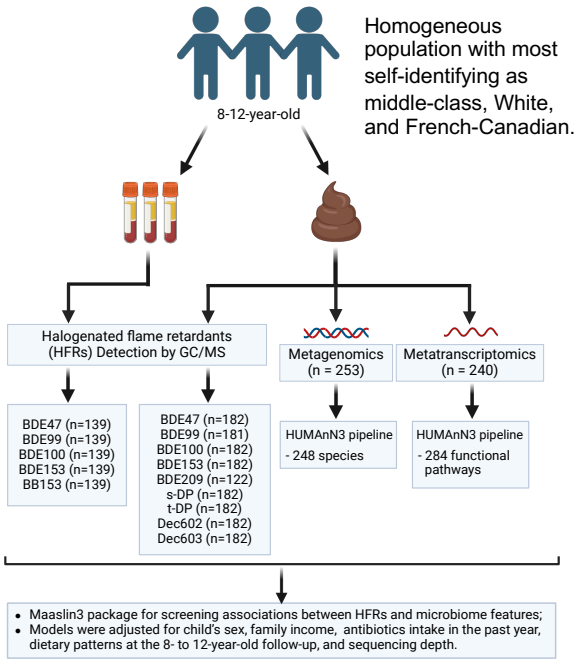
Background & Objective

- Imbalance in the childhood gut microbiota has been linked to long-term adverse health outcomes, including metabolic disorders, infections, and autoimmune diseases. Early-life exposure to halogenated flame retardants (HFRs) may alter the gut microbiota, but this association remains unexplored.
- This study examined the associations of HFRs in plasma and stool with gut microbiome and transcriptome profiles in children aged 8-12 years from a birth cohort in Sherbrooke, Quebec, Canada.

Methods



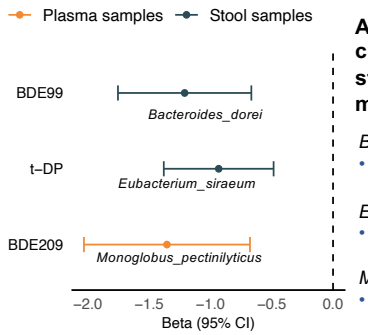
Study population

Characteristics	Distributions
Sex (%)	
Male	106 (44.5)
Female	132 (63.5)
Family income {1,000$ (mean (SD))}	104.2 (71.4)
Parents' education level (%)	
College and University	151 (63.4)
Vocantional Training or Secondary school	85 (35.7)
Other	2 (0.9)
Food Frequency Questionnaire Class (%)	
Class 1	37 (15.5)
Class 2	86 (36.1)
Class 3	115 (48.4)
Metagenomic sequencing depth[a] (mean (SD))	34.7 (27.0)
Metatranscriptomic sequencing depth[a] (mean (SD))	33.26 (31.4)

[a]The unit for sequencing depth is million reads

HFRs	Detection (%)	Mean ± SD (ng/g)
Plasma		
BDE47	83.7	10.04 ± 19.77
BDE99	53.5	3.53 ± 12.17
BDE100	80.2	4.64 ± 8.33
BDE153	95.9	1.22 ± 6.93
BB153	44.7	6.02 ± 7.23
Stool		
BDE47	78.6	3.57 ± 6.60
BDE99	53.4	0.23 ± 0.03
BDE100	71.3	0.09 ± 0.15
BDE153	83.9	0.06 ± 0.09
BDE209	95.4	154 ± 711
s-DP	77.6	0.04 ± 0.14
t-DP	91.7	0.35 ± 2.84
Dec602	35.9	0.006 ± 0.001
Dec603	37.5	0.003 ± 0.005

HFRs ~ microbiome species



Associations between childhood plasma and stool HFRs and gut microbial species

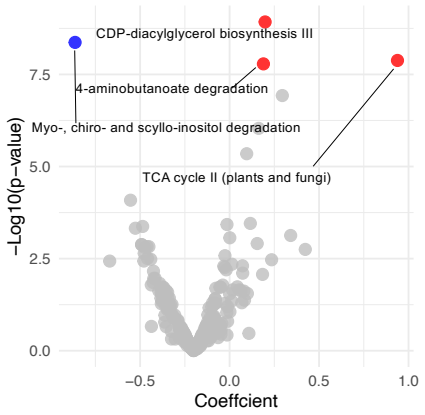
Bacteroides_dorei
- Carbohydrate metabolism

Eubacterium_siraeum
- Short-chain fatty acid (SCFA) producing

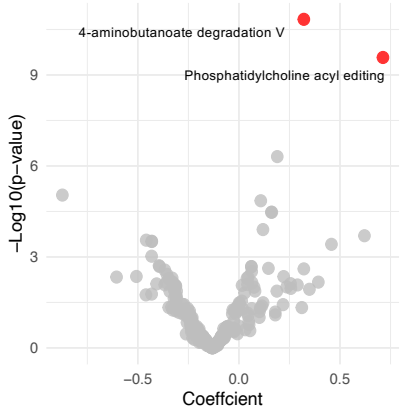
Monoglobus_pectinilyticus
- SCFA producing

HFRs ~ microbiome functional pathways

Associations between childhood plasma and stool HFRs and gut microbial transcriptomic functional pathways: six pathways are associated with stool HFRs, while no significant associations were observed between plasma HFRs and functional pathways.



Exposure: BDE153 (stool)



Exposure: t-DP (stool)

4-aminobutanoate degradation;
- Associated with γ-aminobutyric acid (GABA) degradation

CDP-diacylglycerol biosynthesis III
- Phospholipid synthesis, cell membrane integrity, gut barrier.

Myo-, chiro- and scyllo-inositol degradation
- Enhances lipid absorption and obesity

TCA cycle II (plants and fungi)
- Regulating energy metabolism

Phosphatidylcholine acyl editing
- Phosphatidylcholine (PC) metabolism, associated with gut barrier function.

Conclusions

In children from the GESTE cohort, both plasma and stool HFRs exposure were associated with alterations of gut microbiome, with stronger associations observed for stool HFRs.

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