



Organic Stable Isotope Analysis with GC-qMS for PBDEs in a molecular view

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PBDEs:Brominated Flame Retardant & Persistent Organic Pollutants

Table 5

Concentrations of eight PBDE congeners (BDE28, BDE47, BDE99, BDE100, BDE153, BDE154, BDE183, BDE209) in serum samples from the general population in China (ng/g lipid wt).

Types of sites	Electronic-waste recycling sites		Production area	Cities		
	Luqiao (Taizhou)	Wenling (Taizhou)	South coastal area of Laizhou Bay	Tianjin	Hongkong	
Sampling year	2006	2006	2007	2006	2008	
Sample size (n)	27	23	156	115	51 (female)	60 (male)
BDE28	2.3	31.28	29.2	0.38		
BDE47	5.76	44.72	21.4	1.19	2.57	2.59
BDE99	1.96	7.90	23.4	0.95	0.11	0.06
BDE100	0.88	4.12	14.8	0.25	0.06	0.06
BDE153	14.6	26.12	32.5	0.48	0.67	0.63
BDE154	0.96	2.30	41.8	0.15	0.06	0.05
BDE183	3.92	7.26	46.9	0.59	0.30	0.27
BDE209	87.20	210.48	403	36.4	1.32	1.03
\sum_PBDEs	117.58	334.18	613	40.39	5.74 ^a	5.25ª
Reference	Zhao et al. (2010)	Zhao et al. (2010)	Jin et al. (2009)	Zhu et al. (2009)	Qin et al. (2011a,b)	

 $^{^{}a}\sum_{10}$ PBDEs: Sum of BDE47, 85, 99, 100, 119, 153, 154, 183, 184, 209.

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- Sources of high concentration BDE-47 in Environmental samples
 - Release from e-waste
 - Debromination from high brominated PBDEs

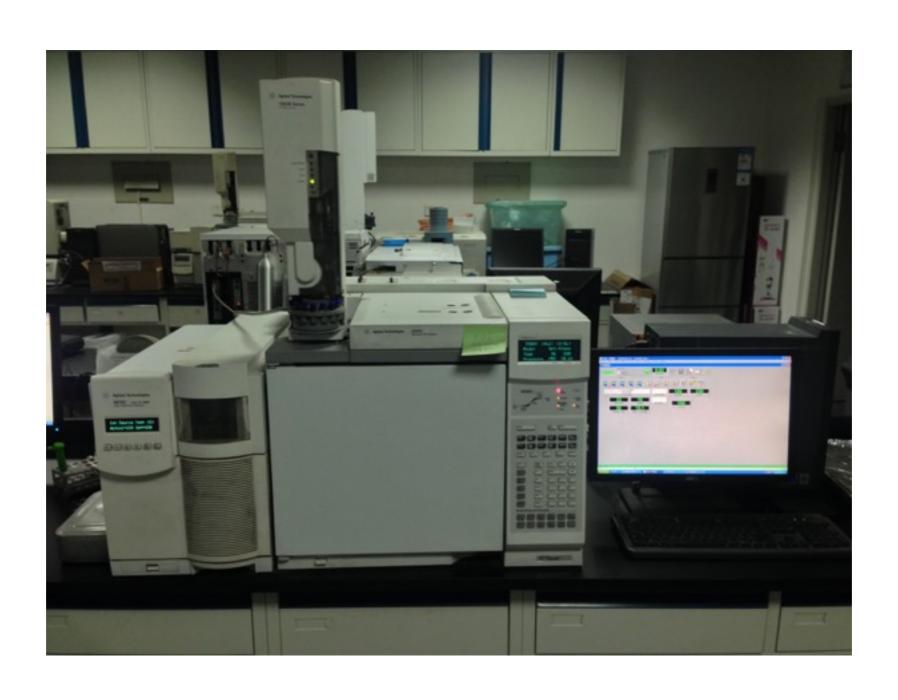
$$Br_m$$
----- Br_n

ISOTOPE

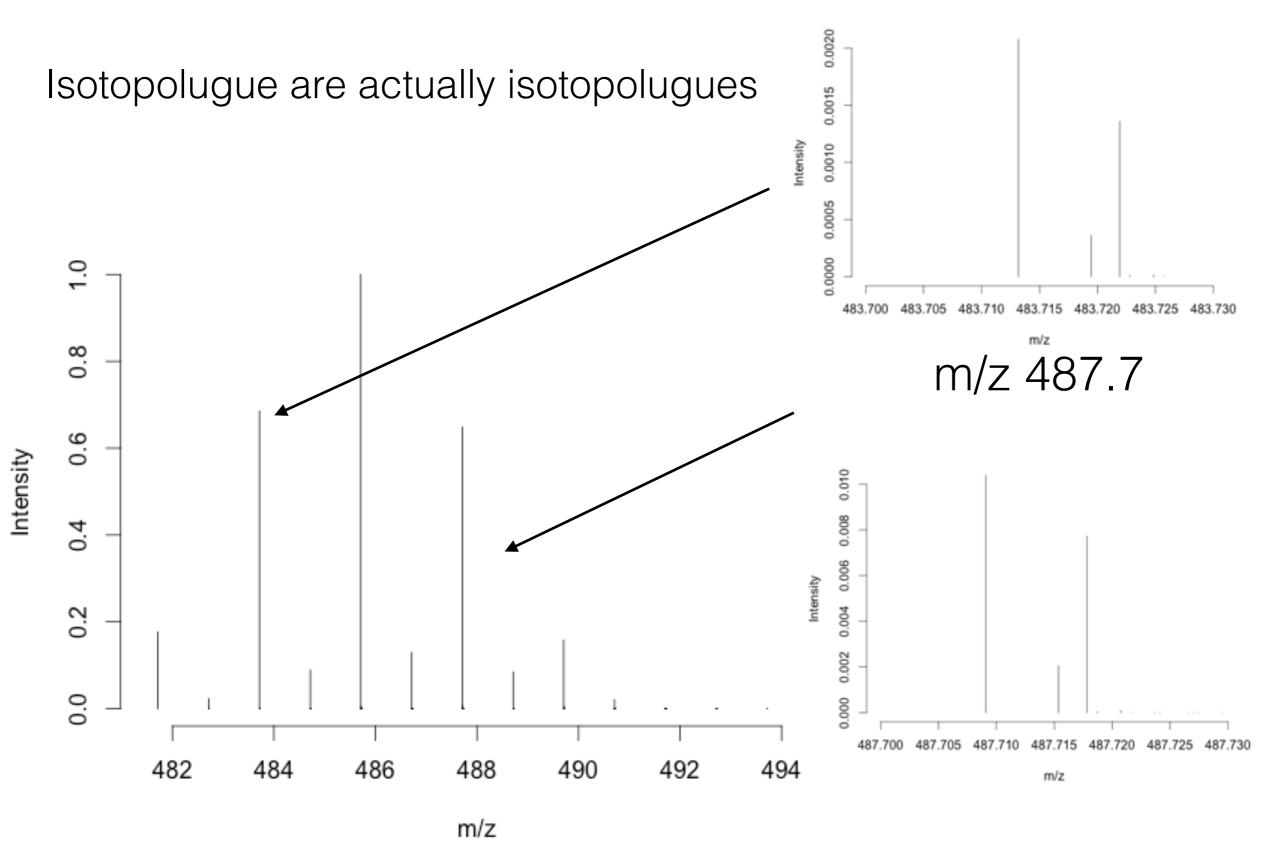
We need another method to get the sources of PBDEs



Why molecular?



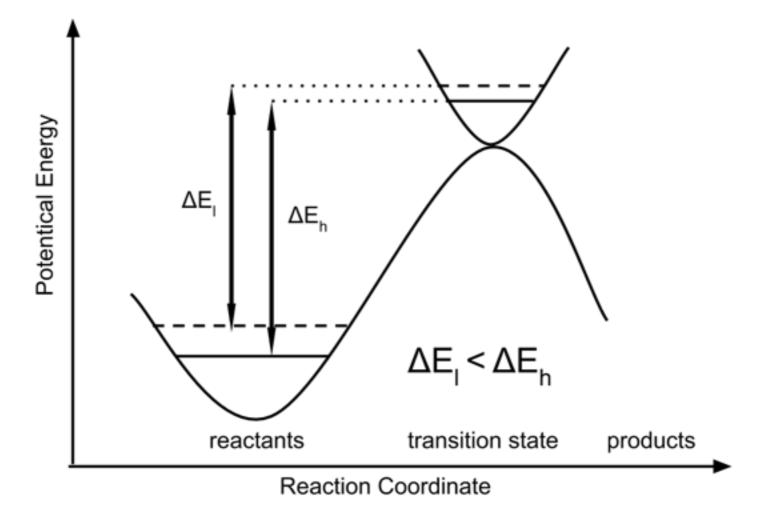
m/z 483.7



Molecular Isotope Ratio

$$Molecular\ isotope\ ratio(R_m) = \frac{Isotopologues_L}{Isotopologues_H}$$

$$\delta_m = \left(\frac{R_m}{R_{ms}} - 1\right) \times 1000\%$$



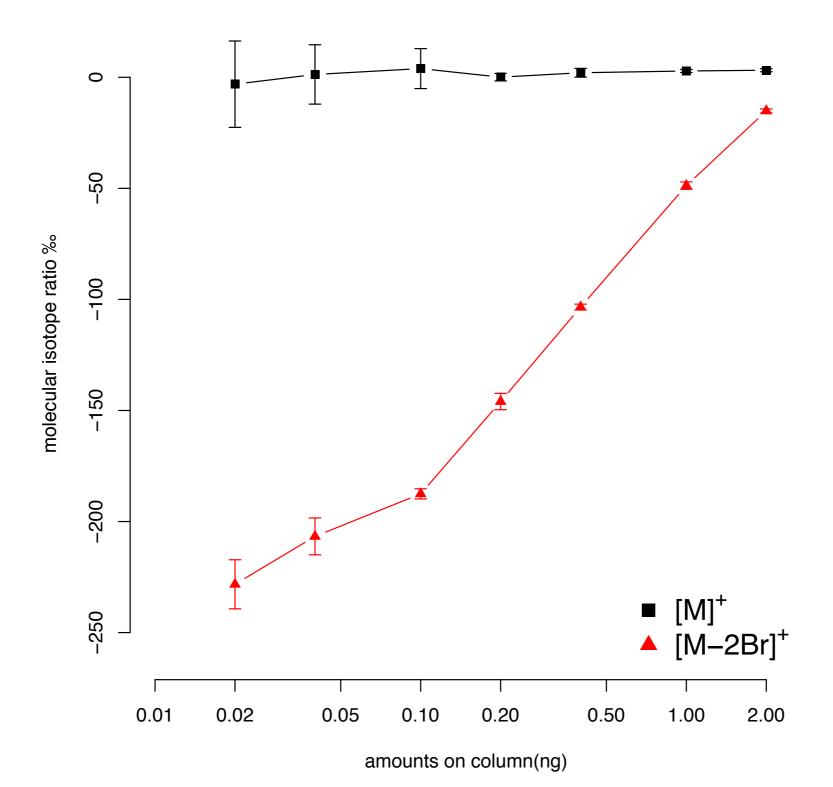
Which pair?

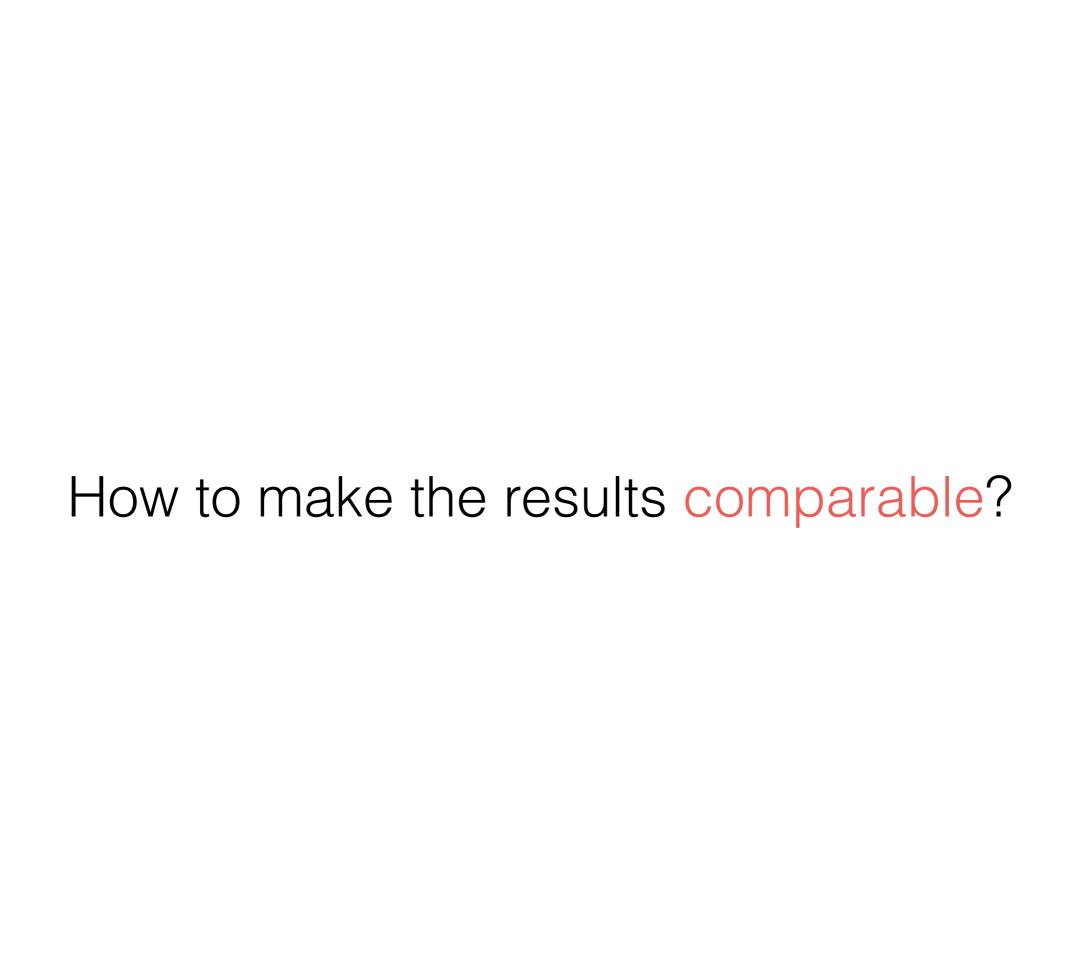
$$R_m = \frac{IsotopolguesA_L}{IsotopolguesA_H} = \frac{IsotopolguesB_L}{IsotopolguesB_H} = \frac{\alpha \cdot IsotopolguesA_L + \beta \cdot IsotopolguesB_L}{\alpha \cdot IsotopolguesA_H + \beta \cdot IsotopolguesB_H}$$



m/z

Which pair?





General web app

https://yufree.shinyapps.io/MIRtools/

Molecule Isotop Ratio(MIR)





This app is developed for molecular isotope studies.

Usage

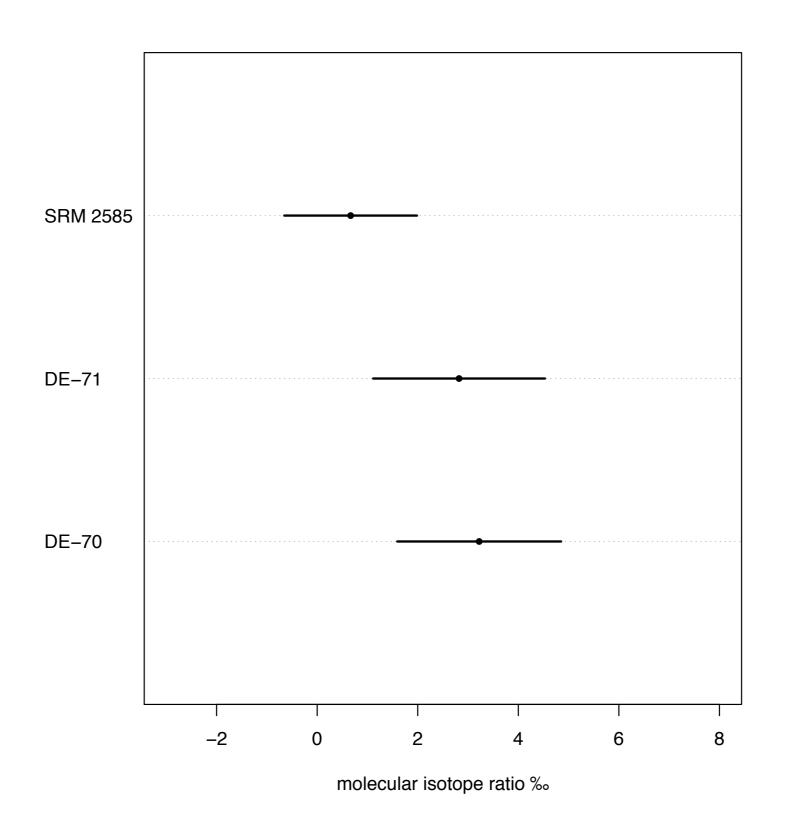
Input the molecular formula and the peak width of isotopologues on your mass spectrum in the side bar. Then in the 'Peaks' tab, you might find the selected peaks for that mulecular and a caculated ratio of selected peaks on your mass spectrum. The defalt molecular is BDE-47

You may upload your data of certain isotopologues in csv format to get the molecular isotope ratio for your experiment in tab 'Molecule Isotop Ratio'. The first column would be time and second column responses. The 'SKIP' means you can skip certain header lines and row numbers means the lines for that isotopolgues. When both of the light and heavy isotopolgues were in the same file, such parameters will help you to seperate them apart.

RT start and RT end mean the scale of your retention time which included the peaks for light and heavy isotopologues.

Points in the moving average smooth box, numbers of points for regression, threshold value for start/stop peaks and points

BDE-47 in SRM



Summary

- GC-qMS could be used to get molecular isotope ratio
- In-source fractionation phenomena for fragmental ions
- BDE-47 in SRM has different MIR compared with technical product DE-70

Thank you for your attention!

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