

First insight into human extrahepatic metabolism of flame retardants

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24 **Abstract**

25 2-ethylhexyl-2,3,4,5-tetrabromobenzoate (EH-TBB) and a mixture of EH-TBB, Bis(2-
26 ethylhexyl)tetrabromophthalate (BEH-TEBP) and Triphenyl phosphate (TPhP), prepared in
27 a ratio similar to the Firemaster-550™ (FM550) flame retardant formulation, were exposed
28 to human skin subcellular fractions (S9) to evaluate their dermal *in vitro* metabolism for
29 the first time. After 60 mins of incubation, tetrabromobenzoic acid (TBBA) and diphenyl
30 phosphate (DPhP) were identified as the major metabolites of EH-TBB and TPhP,
31 respectively using UPLC-Q-Exactive Orbitrap™-MS analysis. Dermal biotransformation of
32 EH-TBB and TPhP was catalyzed by skin carboxylesterases rather than CYP450 enzymes,
33 while no stable metabolites could be identified for BEH-TEBP. Metabolite formation rates
34 of EH-TBB as individual compound and as a component of FM550 fitted the Michaelis-
35 Menten model, while no steady state could be reached for TPhP under experimental
36 conditions. Estimated maximum metabolic rate (V_{max}) for TBBA formation upon exposure
37 to FM550 was lower than V_{max} for EH-TBB (1.08 and 15.2 pmol min⁻¹ mg protein⁻¹,
38 respectively). This indicates dermal metabolism would contribute less to the clearance of
39 EH-TBB body burden than hepatic metabolism ($V_{max} = 644$ pmol min⁻¹ mg protein⁻¹).
40 Implications for human exposure include EH-TBB accumulation in skin tissue and human
41 exposure to dermal metabolic products, which may have different toxicokinetic and
42 toxicodynamic parameters than parent flame retardants.

43

44 **Keywords:** *Flame retardants; Firemaster 550; EH-TBB; dermal metabolism; human exposure.*

45

46 Introduction

47 2-ethylhexyl-2,3,4,5-tetrabromobenzoate (EH-TBB) is an additive flame retardant
48 produced by Chemtura™ Corporation. It is available in 2 commercial mixtures: Firemaster
49 550™ (FM550) and Firemaster BZ-54™ (FMBZ-54). In FM550, EH-TBB is mixed with bis(2-
50 ethylhexyl) tetrabromophthalate (BEH-TEBP), triphenyl phosphate (TPhP) and assorted
51 isopropyl triphenylphosphate (ITP) isomers in the ratio: 36% EH-TBB, 14% BEH-TEBP,
52 18% TPhP and 32% ITPs by weight (Belcher et al., 2014). As additive FRs, EH-TBB and the
53 other components of FM550 may leach out from treated consumer goods and contaminate
54 the environment. They have been detected globally in various environmental matrices
55 including indoor dust,(Carignan et al., 2013; Tao et al., 2016; Hammel et al., 2017) indoor
56 air,(Cequier et al., 2014; Tao et al., 2016) outdoor air,(Ma et al., 2012) chicken eggs,(Zheng
57 et al., 2016) aquatic biota (Strid et al., 2013) and foodstuffs (Xu et al., 2015).

58 Similar to other emerging FRs, the environmental occurrence of EH-TBB and FM550
59 components is expected to be mainly in indoor dust. Residential dust in the UK contained
60 median concentrations of EH-TBB and BEH-TEBP at 4 - 23 (median = 5.8) and 80 - 3187
61 (median = 320) ng/g, respectively (Al-Omran and Harrad, 2016). In the U.S.A., house dust
62 samples from California collected in 2011 showed higher levels of FM550 components than
63 those collected in 2006. Specifically, concentration ranges of EH-TBB and BEH-TEBP in
64 2011 were 45-5900 (median = 100) and <2-3800 (median = 260) ng/g, while those in 2006
65 were 4-740 (median = 48) and 36-1900 (median = 140), respectively (Dodson et al., 2012).
66 Extremely high concentrations of EH-TBB and BEH-TEBP were reported in dust from an
67 American gymnasium ranging from 20,800 to 85,600 (median = 28,900) ng/g for EH-TBB
68 and 17,300 to 44,900 (median = 30,000) ng/g for BEH-TEBP (Carignan et al., 2013). This is

69 of concern due to the potential toxicity of FM550 components to humans and wildlife. Both
70 EH-TBB and BEH-TEBP expressed *in vitro* antiestrogenic and antiandrogenic effects in the
71 yeast estrogen screen and yeast androgen screen assays (reflected in inhibition of β -
72 galactosidase production by the assays), as well as increased oestrogen production in the
73 human H295R steroidogenesis assays (Saunders et al., 2013). By use of primary porcine
74 testicular cells, Mankidy et al. also investigated the effects of EH-TBB and BEH-TEBP on
75 steroidogenesis via different mechanisms; EH-TBB induced the production of cortisol and
76 aldosterone while BEH-TEBP promoted sex hormones synthesis (Mankidy et al., 2014).
77 FM550-administered rats showed many negative health effects e.g. advanced female
78 puberty, weight gain, altered exploratory behaviours and hepatic carboxylesterases activity
79 (Patisaul et al., 2013). FM550 (mainly driven by the TPhP component) was found to bind to
80 human peroxisome proliferator-activated receptor γ (PPAR γ 1) and subsequently induced
81 PPAR γ 1 transcription activity. The same study also reported adipogenesis induction in
82 primary mouse bone marrow cultures by FM550 and TPhP (Pillai et al., 2014).

83 Accidental indoor dust ingestion is reported as a major exposure pathway of humans to
84 EH-TBB, BEH-TBP and TPhP (Besis et al., 2017; Tao et al., 2017). However, the significance
85 of dermal absorption as a pathway of human exposure to halogenated flame retardants via
86 contact with contaminated dust or flame retarded consumer products has been recently
87 highlighted (Abdallah et al., 2016; Frederiksen et al., 2016; Abdallah and Harrad, 2018;
88 Frederiksen et al., 2018). This is of particular relevance to EH-TBB and FM550, which are
89 widely used to flame proof upholstered furniture including childcare products (e.g. car
90 seats and nap mats) (Hammel et al., 2017; Stubbings et al., 2018). A recent study by our
91 research group revealed dermal uptake of some brominated FRs via contact with

92 upholstered furniture may even exceed exposure via dust ingestion or dietary exposure
93 (Abdallah and Harrad, 2018). Frederiksen et al. reported on the dermal uptake of EH-TBB,
94 BEH-TEBP and TPhP using a human skin *ex vivo* model. Based on the mass balance exercise,
95 dermal biotransformation was suggested for all 3 flame retardants based on their ester
96 chemical structure (Frederiksen et al., 2016; Frederiksen et al., 2018). This is supported by
97 Hopf et al. who found that diethyl hexyl phthalate is completely hydrolysed to monoethyl
98 hexyl phthalate by freshly excised human skin, such that only the metabolites penetrate
99 through the skin to reach systemic circulation (Hopf et al., 2014). While it is reasonable to
100 hypothesize that dermal exposure to EH-TBB and FM550 components via contact with
101 furniture may be substantial, very little is known about human dermal metabolism of these
102 flame retardants. While the hepatic metabolism of these FRs has been studied using various
103 *in vitro* techniques,(Roberts et al., 2012; Van den Eede et al., 2013) the products and role of
104 extrahepatic dermal metabolism of FRs remains largely unknown. Consequently,
105 understanding of the skin biotransformation pathways, rates and products of the esterified
106 flame retardants EH-TBB, BEH-TEBP and TPhP is important for comprehensive risk
107 assessment of these chemicals. Against this backdrop, the current study aims to provide the
108 first insights into the dermal biotransformation of EH-TBB, BEH-TEBP and TPhP using *in*
109 *vitro* human skin S9 fractions. Specific objectives include: (a) dermal metabolite
110 identification; (b) metabolic rate estimation for EH-TBB as a single compound (FMBZ-54)
111 and in a mixture with BEH-TEBP and TPhP (FM550); and (c) an evaluation of the
112 implications of dermal metabolism for human dermal exposure to the studied flame
113 retardants.

114 **Materials and Methods**

115 *Chemicals and Standards*

116 All solvents and reagents used in this study were purchased from Fisher Scientific
117 (Loughborough, UK) and were of HPLC grade or higher. 2-Ethylhexyl-2,3,4,5-
118 tetrabromobenzoate (EH-TBB) and bis(2-ethylhexyl) tetrabromophthalate (BEH-TEBP)
119 for dosing solutions (purity >95%) were obtained as neat standards from AccuStandard,
120 Inc. (New Haven, CT, USA). High-resolution Orbitrap-MS scan of the neat standards
121 revealed no brominated impurities/degradation products. Moreover, no effects on the
122 metabolic activity of the human skin enzymes were observed upon exposure to the EH-TBB
123 and BEH-TEBP standard solutions. High purity standards of EH-TBB, BEH-TEBP, triphenyl
124 phosphate (TPhP), 2-ethylhexyl-2,3,4,5-tetrabromo[¹³C₆]benzoate (¹³C-EH-TBB), bis(2-
125 ethylhexyl-d₁₇)-tetrabromo[¹³C₆]phthalate (¹³C-BEH-TEBP), tetrabromobenzoic acid
126 (TBBA), ¹³C-labelled tetrabromobenzoic acid (¹³C-TBBA) and α-1,2,5,6,9,10-
127 hexabromo[¹³C₁₂]cyclododecane] (¹³C-α-HBCDD) were purchased from Wellington
128 Laboratories (Guelph, ON, Canada). Triphenyl phosphate-d₁₅ (TPhP-d₁₅) and diphenyl
129 phosphate (DPhP) were purchased from Sigma Aldrich (Dorset, UK). RapidStart™ NADPH
130 regenerating system was purchased from XenoTech (Kansas, KS, USA), William's E medium
131 was obtained from Thermo Fisher Scientific (Paisley, UK). Human skin S9 fractions (HS-S9)
132 was purchased from Biopredic International (Saint Grégoire, France), comprising a pooled
133 sample prepared from the abdominal skin of 3 white female donors after plastic surgery
134 (age range 33-46 years – *further details are provided in the supporting information*).
135 Individual EH-TBB dosing solutions were prepared by dissolving EH-TBB in dimethyl
136 sulfoxide (DMSO). Firemaster 550™ (FM550)-equivalent mixtures were prepared by

137 dissolving EH-TBB, BEH-TEBP and TPhP in the ratio 53:20.5:26.5 by weight in DMSO,
138 similar to the reported ratio for the technical FM550 mixture (Belcher et al., 2014).
139 Isopropyl triphenylphosphate isomers (ITP) of sufficient high purity were not available to
140 our lab at the time of conducting this study; hence these were not included in the FM550
141 dosing solutions applied in the current study. FM550 solutions were prepared such that
142 each dosing level contained concentrations of EH-TBB similar to those in the individual EH-
143 TBB dosing solutions.

144 *In vitro Incubation Experiments*

145 Pre-incubations were performed at different HS-S9 concentrations and different times.
146 After optimization of the reaction parameters, the following exposure protocol was
147 applied: 0.11 mg of HS-S9, William's E medium and 10 μ L of EH-TBB/FM550 dosing
148 solutions (final concentration 10 μ M of EH-TBB) were pre-incubated for 5 minutes at 37°C.
149 NADPH regenerating system (final concentration: 2.0 mM nicotinamide adenine
150 dinucleotide phosphate, 10.0 mM glucose-6-phosphate and 2 units/mL glucose-6-
151 phosphate dehydrogenase) was added to make a final volume of 1 mL. The samples were
152 then incubated at 37 °C, 5% CO₂ and 98% relative humidity for 60 min. At the end of the
153 incubation, 1 mL of ice-cold ethyl acetate was added to stop the reaction prior to sample
154 extraction.

155 *Sample extraction*

156 Incubated EH-TBB samples were spiked with 20 ng each of ¹³C-EH-TBB and ¹³C-TBBA
157 while FM550 samples were spiked with 20 ng each of ¹³C-EH-TBB, ¹³C-TBBA, ¹³C-BEH-
158 TEBP and TPhP-D₁₅ as internal (surrogate) standards. Spiked samples were mixed with 3
159 mL of ethyl acetate by vortexing for 60 s, followed by ultrasonication for 5 min and

160 centrifuged at 4000 g for 5 min. The organic layer was collected and the extraction
161 procedure was repeated twice. The combined extracts were evaporated to dryness under a
162 gentle stream of nitrogen then reconstituted in 100 μ L of methanol containing 20 ng of ^{13}C -
163 α -HBCDD as a recovery determination (syringe) standard for QA/QC purposes.

164 *Instrumental analysis*

165 Samples were analyzed on a UPLC-Orbitrap-HRMS platform (Thermo Fisher Scientific,
166 Bremen, Germany) composed of a Dionex Ultimate 3000 liquid chromatograph composed
167 of a HPG-3400RS dual pump, a TCC-3000 column oven and a WPS-3000 auto sampler,
168 coupled to a Q-Exactive Plus Orbitrap mass spectrometer. Chromatographic separation was
169 performed on an Accucore RP-MS column (100 x 2.1 mm, 2.6 μm) with water (mobile
170 phase A) and methanol (mobile phase B). A gradient programme at 400 $\mu\text{L}/\text{min}$ flow rate
171 was applied as follows: start at 20% B; increase to 100% B over 9 min, held for 3 min; then
172 decrease to 20% B over 0.1 min; maintained constant for a total run time of 15 min. The
173 mobile phase composition and gradient were selected based on the polarity and solubility
174 of the target compounds and their reported metabolites. Methanol is used as the organic
175 phase because none of the target compounds or their reported metabolites (e.g.
176 monohydroxy or dihydroxy metabolites) are freely water soluble (Roberts et al., 2012; Van
177 den Eede et al., 2013). Orbitrap-MS data from both electrospray ionization (ESI) and
178 atmospheric pressure chemical ionization (APCI) modes was acquired for each sample.
179 Negative APCI was used for determination of EH-TBB, ^{13}C -EH-TBB, BEH-TEBP, ^{13}C -BEH-
180 TEBP and screening for potential metabolites. The more universal, softer ESI mode was
181 used in positive/negative alternative switching mode for screening and identification of the
182 produced metabolites, as well as determination of TPhP and TPhP- d_{15} . The optimized

183 Orbitrap-MS parameters for the analysis of EH-TBB, FM550 and their potential metabolites
184 are provided in Table SI-1.

185 Compound Discoverer 2.0 software (Thermo Fisher Scientific, Bremen, Germany) was used
186 to detect potential metabolites and elucidate their chemical formulae, while quantification
187 of target FRs was performed using Quan Browser 3.0 (Thermo Fisher Scientific, Bremen,
188 Germany).

189 *QA/QC*

190 Metabolic activity of phases I enzymes including NADPH-cytochrome C reductase, carboxyl
191 esterase and FMO3 were measured using guidelines and specific kits provided by Biopredic
192 International and showed normal activities of all enzymes after HS-S9 thawing.

193 Quality assurance samples comprising William's E medium spiked with EH-TBB and
194 FM550 mixture at all dosing levels were analyzed, with recoveries of dosing chemicals
195 falling between 80 to 115% of the theoretical dosing concentrations. Internal standard
196 recoveries in all HS-S9 incubation experiments ranged from 65-115%.

197 In all incubation experiments, a solvent blank comprising William's E medium was
198 performed and analysed alongside the sample batch. No parent compounds or metabolites
199 were found in solvent blanks with the exception of TPhP at negligible levels (< 1% of the
200 lowest dosing level). Therefore, no blank correction was needed. Additionally, no
201 metabolites were found in the non-enzymatic (all experimental components except HS-S9)
202 and heat-inactivated (HS-S9 inactivated by heating at 70 °C for 30 min) controls run in
203 parallel to each sample batch.

204 *Biotransformation kinetic modelling*

205 The metabolite formation rate and substrate concentration of the studied chemicals were
206 fitted to different biotransformation kinetic models (Northrop, 1983; Lipscomb and Poet,
207 2008) by nonlinear regression analysis using the SigmaPlot Enzyme Kinetics Module v.1.1
208 (Systat Software Inc., Richmond, CA) to determine the enzyme kinetic model that best
209 describe the formation rates of the metabolites. The models used were the Michaelis-
210 Menten equation (Equation 1), the Hill equation (Equation 2), and the substrate-inhibition
211 kinetic equation (Equation 3) :

212
$$v = \frac{V_{\max} \times [S]}{K_m + [S]} \quad (\text{Equation 1})$$

213
$$v = \frac{V_{\max} \times [S]^n}{K' + [S]^n} \quad (\text{Equation 2})$$

214
$$v = \frac{V_{\max}}{1 + \frac{K_m}{[S]} + \frac{[S]}{K_i}} \quad (\text{Equation 3})$$

215 where v is initial velocity of the reaction, Vmax is the maximum metabolic rate, [S] is the
216 substrate concentration, Km is the Michaelis-Menten constant, K' is the Hill dissociation
217 constant, n is the Hill coefficient and Ki is the inhibitory dissociation constant. Selection of
218 the best fitted model was determined by statistical criteria to evaluate the goodness of the
219 fit. The two statistical criteria used were Akaike Information Criterion corrected for small
220 sample size (AICc) and the standard deviation of the residuals (Sy.x). The model with the
221 lowest values for AICc and for the standard deviation of the residuals was considered to be
222 the model that best fit the data. When the formation rate of a primary metabolite is best
223 described by the Michaelis-Menten model (Equation 1), the part of the *in vitro* intrinsic
224 clearance (Cl_{int,M}) due to the formation of that metabolite can be calculated as follows:

225
$$CL_{\text{int,M}} = \frac{v}{[S]} = \frac{V_{\max}}{K_m + [S]} \quad (\text{Equation 4})$$

226 If the levels of the substrate of interest in human blood are negligible compared to the
227 apparent Km value associated with the formation of the metabolite, then $(K_m + [S]) \approx K_m$
228 therefore Equation 4 can be written as follows (Lipscomb and Poet, 2008):

$$229 \quad CL_{int} = \frac{v}{[S]} = \frac{V_{max}}{K_m} \quad (\text{Equation 5})$$

230 The total Clint value of the substrate of interest can then be calculated as the sum of the
231 Clint of each of its primary metabolites.

232 The intrinsic *in vitro* clearance of a xenobiotic by an organ on kilogram human body weight
233 (CL_{int-organ}) basis can be scale up by the following equation:

$$234 \quad CL_{int-organ} = CL_{int} \times p \times w \quad (\text{Equation 6})$$

235 Where p is the amount of protein per gram of an organ and w is the average weight of that
236 organ per kilogram body weight.

237 The blood flow of an organ per kilogram body weight (kg b.w) Q_h was taken into account
238 for extrapolation of *in vitro* clearance to *in vivo* clearance (CL_h) as follows (Lipscomb and
239 Poet, 2008):

$$240 \quad CL_{organ} = \frac{Q_h \times CL_{int-organ}}{CL_{int-organ} + Q_h} \quad (\text{Equation 7})$$

241

242 **Results and Discussion**

243 *Dermal metabolic profiles of EH-TBB and FM550*

244 Due to the chemical structure of EH-TBB, BEH-TEBP and TPhP (Figure SI-1), we
245 hypothesized that their metabolism by HS-S9 would be catalysed by carboxyesterases
246 and/or cytochrome P450 enzymes. Full scan mode with either APCI or alternate switching
247 positive/negative ESI ionization were used to screen for EH-TBB and FM550 dermal

248 metabolites. No potential metabolites were found in (+)ESI or (-)APCI mode. For EH-TBB
249 samples, in (-)ESI mode there was one potential metabolite with the ion mass of 436.66814
250 and the proposed ion formula $[C_7HBr_4O_2]^-$. By comparing with the authentic standard, this
251 was confirmed as the $[M-H]^-$ molecular ion for TBBA (Figure 1). This is in agreement with
252 the results of Roberts et al., who reported TBBA as the only *in vitro* metabolite of EH-TBB
253 by human and rat liver microsomes (Roberts et al., 2012).

254 Following exposure of HS-S9 to FM550 mixture components, TBBA was also identified as
255 the sole metabolite of EH-TBB. In addition, another potential metabolite with the ion mass
256 of 249.03204 was detected in (-)ESI mode. The proposed chemical structure for this ion
257 was $[C_{12}H_{10}O_4P]^-$. In order to elucidate the chemical structure of this compound, a MS/MS
258 experiment was carried out in (-)ESI-SIM-MS² mode. A combination of low, medium and
259 high collision energies were applied stepwise to achieve a diverse range of fragmentation
260 ions. Specific Orbitrap-MS parameters for this experiment are provided in Table SI-2. The
261 ion $m/z = 249.03204$ was fragmented mainly into three ions: 154.98895, 93.03284 and
262 78.95728. The proposed chemical formula for these fragments were: $[C_6H_4O_4P]^-$, $[C_6H_5O]^-$
263 and $[PO_3]^-$, respectively (Figure 2). Based on the proposed parent ion formula and the MS²
264 fragmentation data, this metabolite was identified as diphenyl phosphate (DPhP), assigned
265 as a primary metabolite of TPhP. Metabolite identity was further confirmed via comparison
266 and augmentation with an authentic chemical standard of DPhP. Previous studies have
267 reported that *in vitro* metabolism of TPhP by human liver microsomes or chicken embryo
268 hepatocytes formed DPhP, hydroxylated TPhP (OH-TPhP) and dihydroxylated TPhP
269 ($(OH)_2$ -TPhP) (Van den Eede et al., 2013; Su et al., 2014). *In vivo* metabolism of TPhP in fish
270 produced DPhP, OH-TPhP, $(OH)_2$ -TPhP and monophenyl phosphate among which DPhP

271 was the major metabolite (Wang et al., 2016). However, DPhP was detected as the sole
272 metabolite of TPhP by HS-S9 in the present study.

273 By comparison of the *in vitro* human dermal (this study) and hepatic metabolic profiles of
274 EH-TBB and TPhP,(Roberts et al., 2012; Van den Eede et al., 2013) it was obvious that the
275 oxidative metabolites could not be identified in the HS-S9 experiments under the current
276 experimental conditions. Proteomic profiling of the metabolic activity of dermal HS-S9
277 fractions show that both CYP450 and carboxylesterases are active, albeit at much lower
278 levels than in the liver cells (Oesch et al., 2018). Moreover, the reported levels of CYP450
279 enzymes in human skin were at least 300 fold lower than that in human liver. In contrast,
280 the relative level of carboxylesterase 1 (CES1) in human skin and liver was 0.62 with no
281 significant level difference ($P = 0.21$) (van Eijl et al., 2012). Such low level of CYP450
282 enzymes and similar level of CES1 in the skin in comparison with liver might explain why
283 no oxidative metabolites were observed in the present study. To test this hypothesis, we
284 performed NADPH-independent (i.e. without NADPH cofactor) *in vitro* incubation of EH-
285 TBB and FM550 with HS-S9 under the same conditions. The absence of NADPH did not
286 result in significant changes in the formation rates of TBBA, DPhP or depletion rates of the
287 parent compounds ($P > 0.05$). These results reveal differences from hepatic metabolism as
288 dermal carboxylesterases seem to be the major metabolizing enzymes of the target FRs in
289 human skin. This does not eliminate the possibility of oxidative metabolite formation upon
290 dermal contact under real-life situations (i.e. upon exposure to larger doses) but if formed,
291 they are likely to be at lower rates and concentrations than de-esterified metabolites.

292 Finally, no stable metabolites of BEH-TEBP were identified in HS-S9 exposed to FM550
293 mixture at any of the studied concentrations (0.3 – 4.5 μM – Table SI-2), despite the high

294 sensitivity and selectivity of the Orbitrap-MS platform applied in this study. This is in
295 agreement with the results of Roberts et al. who did not detect any metabolites for BEH-
296 TEBP in human and rat hepatic subcellular fractions. Interestingly, mono(2-ethylhexyl)
297 tetrabromophthalate, was only detected in purified hepatic porcine carboxylesterase,
298 although at a very slow formation rate of $1.08 \text{ pmol min}^{-1} \text{ mg protein}^{-1}$ (Roberts et al.,
299 2012). This may reflect inter-species variation in the biotransformation of this flame
300 retardant and warrants further studies to elucidate the hepatic and extrahepatic metabolic
301 profiles of BEH-TEBP in human.

302 *Biotransformation kinetics of EH-TBB and FM 550 by HS-S9*

303 In a previous communication, our research group reported the hepatic metabolic rates of
304 the brominated FR, 1,2-dibromo-4-(1,2 dibromoethyl) cyclohexane (TBECH), were largely
305 dependent on whether the metabolizing enzymes were challenged with a single compound
306 or a mixture of components (Nguyen et al., 2017). Therefore, a series of incubation
307 experiments of HS-S9 with different concentrations of EH-TBB and FM550 components
308 (Table SI-3) were performed. With these experiments, we aimed to investigate whether the
309 metabolic rate will be different upon challenging the HS-S9 with a multi-component
310 mixture representing FM550 (i.e. mimicking real-life situation) compared to exposure to a
311 single flame retardant (EH-TBB). The concentrations of TBBA and DPhP were quantified
312 using isotope dilution series method with ^{13}C -TBBA and d_{15} -TPhP as internal (surrogate)
313 standards. The results from kinetic modelling in SigmaPlot® software revealed the
314 formation of TBBA in both pure EH-TBB and FM550 mixture experiments was best fitted
315 by the Michaelis-Menten model (Figure 3). The model-derived kinetic parameters for the
316 formation of TBBA are presented in Table 1. Estimated maximum metabolic rate (V_{max}) for

317 the formation of TBBA upon exposure to FM550 mixture was significantly lower ($p < 0.05$)
318 than V_{\max} upon exposure to individual EH-TBB (1.80 and 15.2 $\text{pmol min}^{-1} \text{mg protein}^{-1}$,
319 respectively). However, in both cases, V_{\max} was substantially less than that reported
320 previously for EH-TBB metabolism by human liver microsomes (644 $\text{pmol min}^{-1} \text{mg}$
321 protein^{-1}) (Roberts et al., 2012). The estimated Michaelis constant (K_m) for FM550 is lower
322 than K_m for EH-TBB metabolism by HS-S9 (Table 1). Such significant decreases in both K_m
323 and V_{\max} suggest that the rate of metabolite formation (TBBA) from FM550 by HS-S9 has
324 potentially been influenced by competitive substrate inhibition. The competitive inhibitors
325 could be BEH-TEBP and/or TPhP in the FM550 dosing solutions.

326 The formation rate of DPhP (primary metabolite of TPhP) did not fit any of the assessed
327 enzyme kinetic models (Michaelis-Menten, Hill or substrate-inhibition). Indeed, it did not
328 show any signs of reaching a plateau to indicate a steady state was reached. Another series
329 of incubation experiments with higher doses of FM550 were carried out at equivalent TPhP
330 concentrations of 16.8, 25 and 33.6 μM . Close to linearity increment of DPhP formation rate
331 was still observed and steady state conditions could not be achieved. This observation is in
332 agreement with a previous study on TPhP biotransformation in human serum, where the
333 formation rate of DPhP did not reach a plateau even at concentrations up to 100 μM of
334 TPhP (Van den Eede et al., 2016). The lack of fit to the investigated kinetic models
335 precluded the estimation of metabolic kinetic parameters for TPhP under the applied
336 experimental conditions.

337 *In vitro – in vivo extrapolation for dermal clearance of EH-TBB*

338 As the formation rates of TBBA were best described by the Michaelis-Menten model, the
339 model was applied to estimate *in vivo* dermal clearance of EH-TBB assuming average adult

340 bodyweight of 70 kg. We then compared our results for dermal clearance to those reported
341 previously by Roberts et al. for human hepatic clearance of EH-TBB (Roberts et al., 2012).
342 The following parameters were applied: 24.84 mg protein/g skin for HS-S9 (calculated as
343 total of microsomes and cytosol),(Jewell et al., 2007) 37 g skin/kg bodyweight, 52.5 mg
344 protein/g liver for HLM, 25.7 g liver/kg bodyweight, $Q_h = 20.7$ mL/min/kg bodyweight and
345 $Q_{skin} = 4.37$ mL/min/kg bodyweight (Manevski et al., 2015). Our model calculations
346 estimated *in vivo* dermal clearance of individual EH-TBB and EH-TBB in FM-550 to be 0.48
347 and 0.92 mL/min/kg bodyweight, respectively (Table 2). These rates were much smaller
348 than the skin blood flow (4.37 mL/min/kg bodyweight), suggesting EH-TBB is not readily
349 cleared by dermal metabolism and is likely to accumulate in the skin tissue. Indeed, the
350 extraction ratios (defined as the ratio between the *in vivo* clearance of a xenobiotic to the
351 blood flow for a specific organ)(Manevski et al., 2015) of EH-TBB by human skin were only
352 11% and 21% for individual and mixture exposures, respectively. This is also in agreement
353 with the results of Frederiksen et al. (2016) who reported the accumulation of EH-TBB in
354 the skin using a human *ex vivo* dermal model. In contrast, human liver showed higher EH-
355 TBB extraction ratio up to 80% with *in vivo* hepatic clearance of 16.4 mL/min/kg
356 bodyweight (Table 2). These results suggested that dermal metabolism contributed
357 marginally to the clearance of internal EH-TBB body burden in comparison with liver
358 metabolism.

359 *Study limitations*

360 It is important to note that due to limited availability, the skin HS-S9 applied in this study
361 was pooled from the abdominal skin of 3 white female donors (age range 33-46 years). The
362 dermal metabolic activity may vary widely depending on age, race, gender and skin

363 location (Oesch et al., 2018). Additionally, our *in vitro* – *in vivo* metabolic clearance
364 calculations were based on the assumption that the unbound fraction of chemical pollutant
365 to blood proteins equals 1, meaning all EH-TBB in the blood was free and available for
366 metabolism. This can cause overestimation of the estimated xenobiotic clearance.
367 Furthermore, TBBA was treated as the only primary metabolite of EH-TBB. While our
368 experimental measurements support this assumption, it is possible that other metabolites
369 (e.g. oxidative or debrominated metabolites) may be formed under real conditions of
370 prolonged skin contact with high concentration of EH-TBB (e.g. sleeping on a flame
371 retarded mattress). The potential formation of other primary metabolites under different
372 conditions may also influence the estimated metabolic rates for EH-TBB in the current
373 study.

374 *Implications for human exposure*

375 Even though the outer most layer of skin (*stratum corneum*) serves as a barrier to prevent
376 unwanted chemicals from entering the human body, recent studies have confirmed the
377 dermal uptake of several lipophilic pollutants such as hexabromocyclododecanes
378 (HBCDDs), tetrabromobisphenol-A (TBBPA), organophosphate flame retardants or novel
379 brominated flame retardants via contact with skin (Abdallah et al., 2015; Abdallah et al.,
380 2016; Frederiksen et al., 2016; Knudsen et al., 2017). Frederiksen et al. reported roughly
381 10% dermal absorption and 0.1 - 0.2% penetration of several FRs including EH-TBB
382 following a single dose (of several hundred nanograms) application to *ex vivo* human skin
383 for 72 h (Frederiksen et al., 2016). Higher dermal uptake at 20% with 0.2% penetration of
384 administered ¹⁴C-labelled EH-TBB to *in vitro* human skin after 24 h exposure was also
385 reported (Knudsen et al., 2016). Nevertheless, it is proven that EH-TBB as well as other

386 organic FRs can penetrate the skin barrier and be “trapped” within the skin tissue until
387 reaching the blood circulation (i.e. become bioavailable). In such an event, skin metabolism
388 may play an important role in the clearance of the trapped dose within the skin tissue, yet it
389 may also help create a concentration gradient through the different layers of the skin tissue
390 to facilitate further uptake of the parent FR. Moreover, the slow *in vitro* clearance rates in
391 the skin could translate into slow EH-TBB *in vivo* percutaneous metabolism and
392 subsequently result in inefficient removal of EH-TBB from the skin. This partially explains
393 the reported accumulation of EH-TBB in the skin tissue prior to reaching the systemic
394 circulation (Knudsen et al., 2016). In addition, very little is known about the toxicokinetics
395 and toxicodynamics of the dermal biotransformation products (i.e. TBBA and DPhP). This is
396 of concern as these metabolites may lead to potential adverse health effects similar to that
397 reported previously for PBDE metabolites (Saquib et al., 2018). Therefore, further studies
398 on dermal uptake and metabolism of emerging flame retardants are required to fully
399 understand both the toxicological and exposure implications of dermal biotransformation
400 of these hazardous chemicals.

401

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409

410 **Supporting information**

411 Details of analytical method parameters and metabolite identification workflow are
412 provided as supporting information.

413

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550 **Tables**

551 Table 1: Kinetic parameters derived from Michaelis-Menten model for the formation of
 552 TBBA following incubation of HS-S9 with pure EH-TBB and FM550 mixture in the present
 553 study compared to the reported parameters for EH-TBB incubation with human liver
 554 microsomes (HLM).(Roberts et al., 2012)
 555

Substrate	Model	K_m (μM) \pm standard deviation	V_{max} (pmol/min/mg protein) \pm standard deviation
EH-TBB	HS-S9	4.57 \pm 1.2	15.2 \pm 5
FM550	HS-S9	0.84 \pm 0.19	1.80 \pm 0.05
EH-TBB	HLM	11.1 \pm 3.9	644 \pm 144

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559 Table 2: Estimated *in vitro* and *in vivo* clearance of EH-TBB by human skin (the current
 560 study) compared to those reported in human liver (Roberts et al., 2012).
 561

Chemical	Organ	$CL_{\text{int-organ}}$ (<i>in vitro</i> , mL/min/kg b.w)	CL_{organ} (<i>in vivo</i> , mL/min/kg b.w)
EH-TBB	Skin	0.54	0.48
EH-TBB in FM550	Skin	1.18	0.92
EH-TBB	Liver	78.3	16.4

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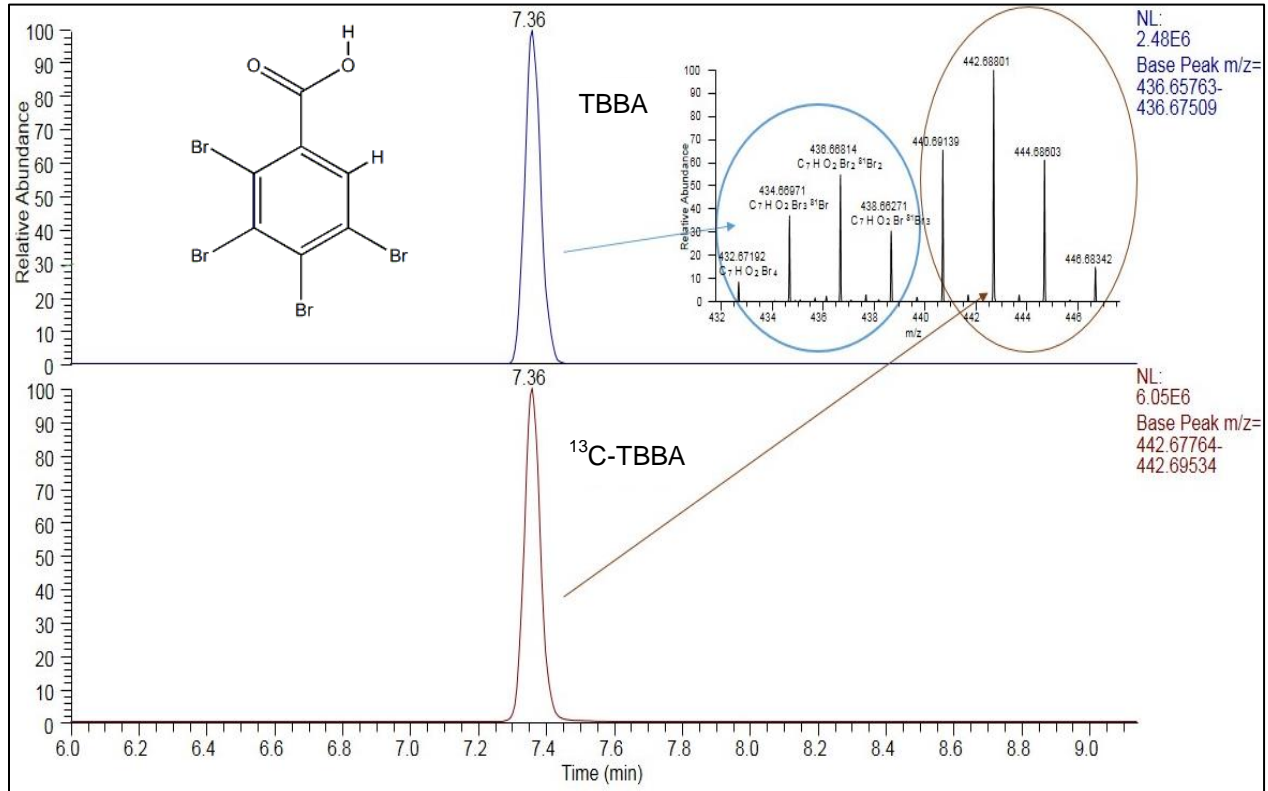
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569 **Figures**

570 Figure 1: TBBA detected as the sole metabolite of EH-TBB in Human Skin S9 fraction (HS-
571 S9) exposed to 10 μ M of EH-TBB. 13 C-TBBA is the isotope-labelled form used for identity
572 confirmation and quantification of TBBA.
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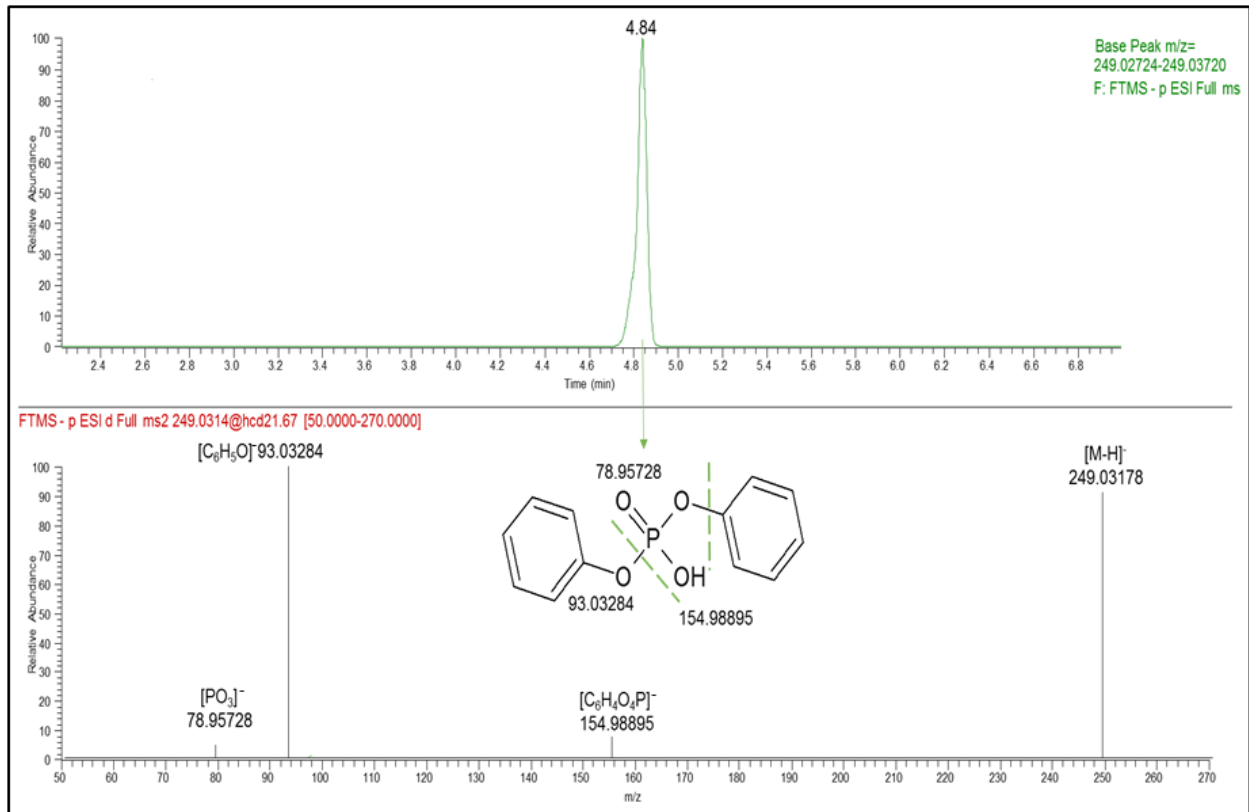
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584 Figure 2: (-)ESI-MS/MS² spectrum of the ion 249.03204 by UPLC-Orbitrap HRMS



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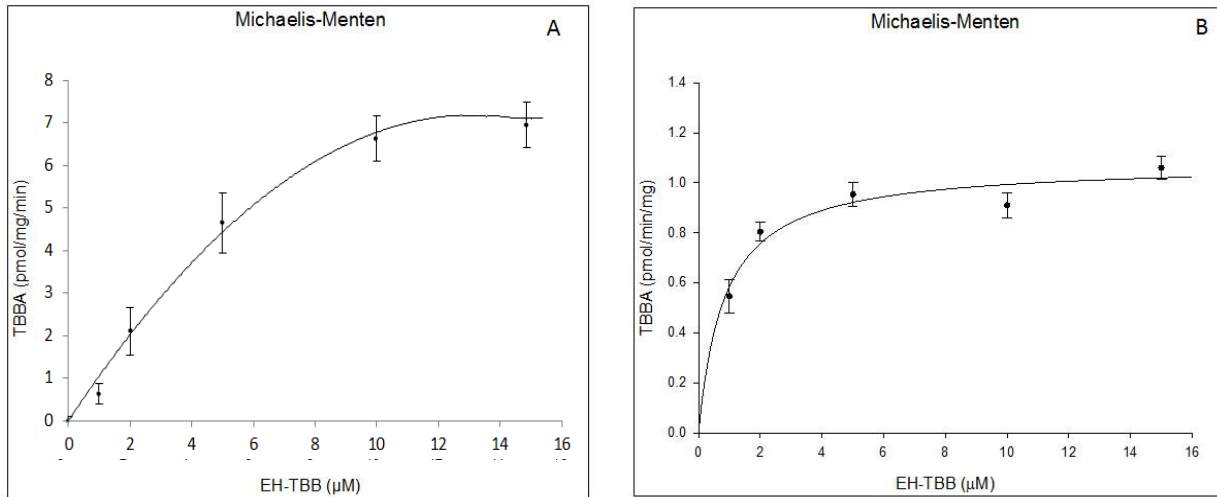
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597 Figure 3: Kinetics of TBBA formation in EH-TBB (A) and FM550 mixture (B) incubation
598 experiments with HS-S9 using the Michaelis-Menten model. Error bars represent 1
599 standard deviation (n=3).
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