

Exposure to pollutants altered glucocorticoid signaling and clock gene expression in female mice. Evidence of tissue- and sex-specificity

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27 Abstract

Environmental pollutants suspected of disrupting the endocrine system are considered 28 29 etiologic factors in the epidemic of metabolic disorders. As regulation of energy metabolism relies on the integrated action of a large number of hormones, we hypothesized that certain 30 chemicals could trigger changes in glucocorticoid signaling. To this end, we exposed 31 32 C57Bl6/J female and male mice between 5 and 20 weeks of age to a mixture of 2,3,7,8tetrachlorodibenzo-p-dioxin (20 pg/kg body weight/day [bw/d]), polychlorobiphenyl 153 (200 33 ng/kg bw/d), di-[2-ethylhexyl]-phthalate (500µg/kg bw/d) and bisphenol A (40µg/kg bw/d). 34 In female mice fed a standard diet (ST), we observed a decrease in plasma levels of leptin as 35 well as a reduced expression of corticoid receptors Nr3c1 and Nr3c2, of leptin and of various 36 canonical genes related to the circadian clock machinery in visceral (VAT) but not 37 subcutaneous (SAT) adipose tissue. However, Nr3c1 and Nr3c2 mRNA levels did not change 38 in high-fat-fed females exposed to pollutants. In ST-fed males, pollutants caused the same 39 40 decrease of Nr3c1 mRNA levels in VAT observed in ST-fed females but levels of Nr3c2 and other clock-related genes found to be down-regulated in female VAT were enhanced in male 41 SAT and not affected in male VAT. The expression of corticoid receptors was not affected in 42 the livers of both sexes in response to pollutants. In summary, exposure to a mixture of 43 pollutants at doses lower than the no-observed adverse effect levels (NoAELs) resulted in sex-44 45 dependent glucocorticoid signaling disturbances and clock-related gene expression modifications in the adipose tissue of ST-fed mice. 46

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50	Key w	ords: Pollutant mixture; mouse; Adipose tissue; Glucocorticoid signaling; Clock-
51	related	genes
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53	Highli	ghts
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55	-	A mixture of low-dosed pollutants trigger metabolic changes in exposed mice
56	-	In females, pollutants affect glucocorticoid signaling in VAT and leptin synthesis
57	-	Mode of action may involve alteration of clock-related genes in female VAT
58	-	Glucocorticoid signaling was not affected in the female or male liver

59 - In males, pollutants mainly affect the signaling of glucocorticoids in SAT

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1. Introduction

Metabolic-related diseases, such as diabetes and obesity, are prominent public health 61 challenges of the 21st century. In the last decades, prevalence of these chronic diseases 62 reached epidemic proportions worldwide. Metabolic diseases have multifactorial causes. 63 Genetic predisposition, high calorie intake, poor physical activity and also environmental 64 pollutants are among the etiological factors identified. The capacity of some pollutants to 65 interfere with hormonal action, also known as endocrine disruptors has been well documented 66 67 (Carpenter, 2008, Diamanti-Kandarakis et al., 2009, Thayer et al., 2012, Ibrahim et al., 2011, Ruzzin et al., 2010, Alonso-Magdalena et al., 2011, Heindel and Blumberg, 2019, Le 68 Magueresse-Battistoni et al., 2015). Endocrine disruptors have been shown to target the 69 estrogen, androgen, thyroid, and steroidogenesis pathways and others (e.g., through binding to 70 estrogen-related receptor, peroxisome proliferator-activated receptor, xenobiotic receptors) 71 (Diamanti-Kandarakis et al., 2009, Reif et al., 2010, Delfosse et al., 2015), depending on the 72 73 repertoire of co-expressed nuclear receptors and hormonal environment (Casals-Casas and Desvergne, 2011, Le Magueresse-Battistoni et al., 2017). Therefore, chemicals targeting 74 energy homeostasis could have extensive metabolic implications. Indeed, energy homeostasis 75 76 is a complex process orchestrated by multiple hormones adjusting energy intake to energy 77 expenditure including sex hormones (Mauvais-Jarvis et al., 2013) and glucocorticoids (Vegiopoulos and Herzig, 2007). 78

Over the course of a lifetime, humans are exposed to a plethora of chemicals that can interact
in vivo by modifying each other's effect. In addition, some chemicals such as bisphenol A
(BPA) were shown to cause adverse effects in experimental studies (Vandenberg et al., 2012,
Angle et al., 2013) even at doses lower than those considered to be safe in humans (Koch and
Calafat, 2009, Schafer and Kegley, 2002). Therefore, the cocktail effect resulting from
exposure to complex mixtures makes it difficult to predict the health consequences (Le

Magueresse-Battistoni et al., 2018b, Kortenkamp, 2008, Heindel et al., 2017b). Interestingly, 85 86 we have recently implemented a model in which mice were exposed through diet to a mixture of pollutants made of BPA, di-[2-ethylhexyl]-phthalate (DEHP), polychlorinated biphenyl 87 (PCB) 153 and 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD). These chemicals are part of a 88 large group of archetypal endocrine disruptors present in food (Casals-Casas and Desvergne, 89 90 2011, Heindel et al., 2017a, Vandenberg et al., 2012) with different characteristics regarding 91 half-lives, endocrine disrupting activities and activation of nuclear receptors/transcription factors (Le Magueresse-Battistoni et al., 2018a). 92

BPA is probably the most emblematic chemical since humans are almost continuously 93 exposed to it, with estimated daily doses of 0.4 to 5 μ/kg body weight (Vandenberg et al., 94 95 2012). BPA has large industrialized applications, particularly in plastics and resins, and its global production exceeds millions of tons per year (Vandenberg et al., 2007). Initially 96 described as pro-estrogenic because of its binding to estrogen receptors (ERs), the modes of 97 98 action of BPA may involve non-estrogenic receptors including the peroxisome proliferator activator receptor (PPAR)y, the glucocorticoid receptor (GR) or the thyroid receptor, all 99 intricately linked to metabolic health and body weight (Le Magueresse-Battistoni et al., 100 101 2018a, Zoeller et al., 2005, Casals-Casas and Desvergne, 2011). Disruptive effects on glucose 102 and lipid metabolism or insulin resistance may also result from mechanisms linked to hormonal metabolism, oxidative stress, inflammation, mitochondrial dysfunction and 103 104 epigenetic changes (Vandenberg et al., 2012, Vom Saal et al., 2012, Ma et al., 2019, Nadal et al., 2017). Phthalates are other short-lived chemicals that are used primarily to soften plastics. 105 106 They are of great concerns for human health with an average exposure of 0.5 to 25 μ/kg body 107 weight per day for DEHP (Vandenberg et al., 2012). As with BPA, the diet is the main source 108 of contamination and results from the chemical leaching of food and drink containers and 109 packaging (Koch and Calafat, 2009, Vandenberg et al., 2007). Experimental studies have

shown that DEHP exposure can cause adverse effects on energy balance and glucose

111 homeostasis through binding to PPARs (Feige et al., 2007). Phthalates can also bind to

112 xenobiotic receptors but not to androgen receptors although they exert anti-androgenic effects

113 (Schug et al., 2011, Casals-Casas and Desvergne, 2011, Le Magueresse-Battistoni et al.,

114 2017).

115 Dioxins and polychlorinated biphenyls (PCBs) are lipophilic and belong to the group of persistent organic pollutants (POP). Epidemiological and experimental studies demonstrated 116 117 that exposure to POPs could lead to detrimental metabolic effects including obesity and type 2 diabetes (Wahlang et al., 2013, La Merrill et al., 2013, Gauthier et al., 2014, Ibrahim et al., 118 119 2011, van Esterik et al., 2015). Dioxins result from incomplete combustion, which occurs 120 during industrial processes, forest fires or volcanic eruptions. PCBs had a large number of industrial applications because of their low-flammability and high-thermal conductivity 121 properties. Today, the production of PCBs is banned and industrial emissions of dioxins are 122 limited. However, they still contaminate food by bio-amplification in the food chain and are 123 concentrated in fatty foods due to their low degradability (Guo et al., 2019). It was reported 124 that average daily exposure to TCDD (the most toxic dioxin congener that includes the 125 126 coplanar PCBs) was below the tolerable daily intake (TDI) dose but it was up to 80 ng/kg 127 body weight per day for non-coplanar PCBs thus exceeding the toxicological reference values for certain groups of consumers (Baars et al., 2004, EFSA, 2005). Interestingly, PCB153 a 128 129 non-coplanar PCB is considered as a marker for the total PCB exposure (Hagmar et al., 2006). TCDD and co-planar PCBs can bind to the aryl hydrocarbon receptor (AHR) (Barouki et al., 130 131 2012, Bock, 2019, Van den Berg et al., 1998) while non-coplanar PCBs cannot bind to AHR although they can interact with its signaling mechanisms. They may as well activate the 132 pregnane X receptor (PXR) and the constitutive androstane receptor (CAR) (Chen and Liu, 133 134 2019). Dioxins and PCBs can also interact with the estrogen and thyroid signaling pathways,

respectively (Diamanti-Kandarakis et al., 2009, Casals-Casas and Desvergne, 2011, Pavek,
2016).

Using the exposure model to a mixture of BPA, DEHP, PCB153 and TCDD, we previously 137 138 demonstrated that the metabolic adverse impact in mice was strongly sex-dependent altering estrogen signaling in the liver of exposed females and hepatic cholesterol metabolism in 139 140 males (Naville et al., 2013). In addition, the mixture of pollutants affected other metabolic 141 tissues including the adipose tissues and involved other nuclear receptors than the estrogen 142 and xenobiotic receptors (Julien et al., 2018, Julien et al., 2019, Naville et al., 2015, Naville et al., 2019). The purpose of the current study was to address the implication of glucocorticoid 143 144 signaling in mediating the effects of the pollutants in female mice. We also looked for sexual dimorphism benefiting from male samples taken in a previous study (Naville et al., 2019). 145 Glucocorticoids (GC) are steroid hormones with strong anti-inflammatory properties. They 146 147 are produced by the adrenal glands under the negative feed-back involving the hypothalamicpituitary-adrenal (HPA) axis. They exert vital roles on behavior, immunity and metabolism 148 149 through binding to corticoid receptors in target cells including the liver and adipocytes (Vegiopoulos and Herzig, 2007). Recent reports highlighted that xenobiotics could bind to 150 GR (Gulliver, 2017), and that BPA and phthalates had a weak GR agonist activity in 151 152 adipocytes (Gulliver, 2017, Le Magueresse-Battistoni et al., 2017, Casals-Casas and Desvergne, 2011, Sargis et al., 2010). 153

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2. Materials and Methods

156 2.1.Animals, diet and experimental design

All procedures were performed with the approval of the Regional Committee of Ethics for
Animal Experiments. Four-week (wk) old C57Bl/6J female and male mice (Envigo; Gannat,

France) were randomly housed two per polypropylene cage at 21°C with normal light/dark 159 160 cycle and free access to water and standard chow diet (from Genestil, Royaucourt, France) for a one- week acclimatization period. Mice were next randomly assigned to four different 161 groups (n=7-8 / group). Two groups were fed a standard diet (ST; 10% Fat and 35.6% 162 maltodextrin) and two groups were fed a high-fat high-sucrose diet (HF; 39.4% Fat and 163 16.6% maltodextrin +16.6% sucrose, Envigo). The STp and HFp groups correspond to the ST 164 or HF diet, containing respectively a mixture of 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD, 165 CAS N° 1746-01-6 from LGC Promochem, Molschein, France), polychlorinated biphenyl 166 (PCB) 153 (CAS N° 35065-27-1), bisphenol A (BPA, CAS N° 80-05-7) and di-[2-167 168 ethylhexyl]-phthalate (DEHP, CAS N°117-81-7) (all three from Sigma-Aldrich). The STO and HF0 groups correspond to the ST or HF diet containing the vehicle, only. To prepare the 169 170 contaminated food, stock solutions of pollutants dissolved in DMSO were diluted in corn oil 171 and they were mixed into diet (316 µl DMSO in 60 ml corn oil/kg diet) using a foodprocessor to ensure good distribution in the food. Specifically, mice were exposed to 20 pg 172 173 TCDD /kg bw/day, 200 ng PCB153/kg bw/day, 500µg DEHP/kg bw/day and 40µg BPA/kg bw/day (Supplementary Table 1). These doses were at least 10 times lower than the NoAEL 174 (No-observed Adverse Effect Level) dose for each pollutant when taken individually (DEHP, 175 176 BPA) or representative congener (TCDD, PCB153) (Beausoleil et al., 2018, van Leeuwen et al., 2000, WHO, 2003). To ensure that animals ingested the correct amount of polluted 177 food/kg bw/day and were fed ad libitum, the calculations of intake of pollutants in the diet 178 179 were based on 1 g of contaminated food /17 g of body weight / day, and pollutant-free food was provided to the animals at libitum. Food was given on Mondays, Wednesdays and 180 Fridays. Body weight was recorded weekly and the amount of polluted food distributed was 181 adjusted, accordingly over a 15 weeks period. It should be noted that the male samples used in 182 the present study have previously been analyzed for lipid metabolism in the liver and jejunum, 183

and adipogenesis and inflammation of the fat pads (Naville et al., 2019), but notglucocorticoid signaling.

186 2.2.Tissue collection and blood and plasma analyses

187 Before sampling, mice were fasted six-hour and weighed. Blood was collected by retro-orbital

188 sampling and mice were euthanized by cervical dislocation. Adipose tissues and liver were

189 quickly removed, weighed, frozen in liquid nitrogen and stored at -80°C. Blood glucose

190 concentrations (Accucheck Performa glucometer; Roche Diabetes Care France, Meylan), and

191 plasma levels of insulin and corticosterone (Mouse Ultrasensitive ELISA, Eurobio,

192 Courtaboeuf, France), leptin and adiponectin (ELISA kits from Crystal Chem Europe,

193 Zaandam, Netherlands), triglycerides (Biolabo, Maizy, France) and free fatty acids, total

194 cholesterol and cholesteryl esters (all kits from Sigma-Aldrich) were measured.

195 2.3. RNA extraction and real-time PCR analyses

196 Total RNA was extracted from subcutaneous (SAT) and visceral (VAT) adipose tissue using

197 TRI Reagent (Applied Biosystems, Courtaboeuf, France). RNA integrity was determined with

the Agilent 2100 Bioanalyzer and RNA 6000 Nano Kit (Agilent Technologies, Massy,

199 France). Samples were reverse-transcribed using the Prime Script RT Reagent kit (Takara

Bio Europe SAS, Saint-Germain-en-Laye, France). We performed real time PCR using a set

of specific primers specifically designed to encompass an intron (Supplemental Table 2). Data

were normalized using Tbp encoding TATA-Box Binding Protein as described for adipose

tissues and beta-glucuronidase (Gusb) for liver samples (Naville et al., 2011, Naville et al.,

204 2019).

205 2.4.Western blotting analyses

Proteins prepared from adipose tissues were separated by SDS-10% polyacrylamide gel 206 207 electrophoresis and transferred to a polyvinylidene difluoride membrane. Immunoblotting was performed as previously described (Naville et al., 2013, Longin et al., 2001) using a rabbit 208 209 polyclonal anti-glucocorticoid receptor (dilution 1/5000, Ab3580; Abcam France) or β-Actin (dilution1/10,000, A5060, Sigma). Blots were revealed using Luminata Classico Western 210 211 HRP substrate (Millipore, Molsheim, France), detected using the ChemiDoc XRS+ imaging 212 system (Biorad), and analyzed with Image Lab software (Bio-Rad). Data were normalized relative to β -Actin. 213

214 2.5.Statistical analyses

Results are presented as means \pm S.E.M. Graphpad Prism 8.01 software was used for statistical analyses. The overall impact of the pollutant exposure and of the diet was determined using the two-way Anova analysis followed by the Bonferroni's multiple comparisons post-hoc test to determine significant differences between relevant groups. In experiments only assessing the impact of pollutant exposure, differences were tested using the non-parametric Mann-Whitney test. Differences between means were considered significant at *p*-value < 0.05.

222 **3. Results**

3.1. Metabolic phenotyping of female mice

We explored the metabolic alterations of female mice in response to pollutant exposure including the analysis of the systemic levels of corticosterone. No changes in body weight, blood glucose, plasma insulin and corticosterone levels and no dyslipidemia were observed between control and pollutant-exposed mice. As expected, female mice fed a HF diet showed enhanced body weight, blood glucose, plasma insulin levels, and dyslipidemia as compared to ST-fed mice. Plasma corticosterone levels were in the control range (Fig. 1).

- 3.2. Expression of various nuclear receptor/transcription factors and of 11 β -
- hydroxysteroid dehydrogenase1 (11 β HSD1) in the visceral adipose tissues of female mice fed a ST or a HF diet and exposed to the mixture of pollutants

Adipose tissues express several nuclear receptor/transcription factors that pollutants can bind 233 to initiate downstream activation signals among which the estrogen receptors, the aryl 234 235 hydrocarbon receptor (AhR) but also the glucocorticoid (GR) and the mineralocorticoid (MR) receptors (Swedenborg et al., 2009, Lee et al., 2018). In addition to analyzing these receptors 236 237 by RT-qPCR, we also studied *Hsd11b1* which encodes the 11β-hydroxysteroid dehydrogenase1 (11\betaHSD1). Indeed in the adipose tissue, 11\betaHSD1 catalyzes the conversion 238 239 of the inactive cortisone into the active corticosterone thus locally regulating availability of 240 GCs (Sandeep and Walker, 2001). Two-way Anova analysis indicated that the "Pollutant" factor had significant effects on all the genes studied, excepted for Esr1 and Gper1 encoding 241 ERα and GPR30, respectively. The "Diet" factor had significant effects on all the genes 242 243 studied, but not on Nr3c2 encoding MR. A trend was observed for Esr1 (Fig. 2, insert). Post *Hoc* analysis determined that pollutant exposure significantly down-regulated *Nr3c1* encoding 244 GR, *Nr3c2*, *Hsd11b1* and *Esr2* (encoding ERβ) in ST-fed but not in HF-fed nutritional 245 conditions. A trend was observed for Ahr (Fig. 2A). Western-blotting analysis of VAT 246 proteins confirmed decreased protein levels of GR in females exposed to the mixture of 247 pollutants (Fig. 2B). 248

3.3. Expression of various nuclear receptor/transcription factors and of 11βHSD1 in
the subcutaneous adipose tissue of female mice fed a ST or a HF diet and exposed to the
mixture of pollutants

252 Contrary to the results observed in VAT, exposure to pollutants in SAT did not affect the
253 levels of expression of the glucocorticoid and estrogen receptors, of 11βHSD1 and of AHR

(Fig. 3). In addition, the mRNA levels of *Nr3c1* and *Nr3c2* remained constant in the SAT of
females fed a HF diet (Fig. 3). Two-way Anova analysis indicated that the "Diet" factor had
significant effects on *Hsd11b1* and the estrogen receptors, and a trend was observed for *Ahr*(Fig. 3, insert). Specifically, as in VAT (Fig. 2), the expression levels of *Hsd11b1* and the
estrogen receptors *Esr1* and *Esr2* were significantly decreased and the mRNA levels of *Gper1*were significantly increased in the SAT (Fig. 3).

260 3.4. Low-dosed pollutant exposure targeted leptin gene expression in females

To decipher mechanisms underlying changes in glucocorticoid signaling observed in the 261 262 adipose tissues of standard-fed females, plasma leptin was measured. Indeed, leptin is an adipokine involved in satiety mechanisms which gene is regulated by glucocorticoids (Zhang 263 and Chua, 2017). We observed significant changes in leptin plasma levels (- 55%; p < 0.05) 264 265 together with a small but significant increase in food intake (Fig. 4), despite no changes in the 266 weight of SAT and VAT (Fig. 1). Gene expression analysis showed a significant reduction in Lep mRNA levels in VAT but not in SAT. Adiponectin is another hormone produced by 267 adipocytes. Exposure to pollutants had no effects on adiponectin levels measured in plasma 268 or on the mRNA levels of the adipose tissue depots (Fig. 4). To determine if other markers of 269 270 adipogenesis displayed altered expression following pollutant exposure, we quantified the mRNA of Nr1c3 encoding PPARy and other target genes including Fabp4 encoding fatty acid 271 272 binding protein 4 (FABP4) and *Cidec* encoding fat protein specific 27 (FSP27). Expression mRNA levels were similar to controls in both adipose tissues (Supplementary Fig. 1). We also 273 274 quantified inflammatory cytokines in VAT and SAT. Pollutants did not affect *Tnfa*, *Ccl2*, Ccl5, and Illb mRNA levels in SAT and VAT (Supplementary Fig.2). 275

3.5. Pollutant exposure caused changes in the expression levels of glucocorticoid-induced
genes including circadian clock genes in the adipose tissues

278	It is well demontrated that leptin displays a circadian cycling pattern (Fu et al., 2005) and that
279	adrenalectomy results in changes in leptin secretion (Yilmaz et al., 2002) and in circadian
280	gene expression in VAT (Sotak et al., 2016). Therefore, we quantified a glucocorticoid- and
281	clock controlled gene namely Tsc22d3 encoding the glucocorticoid induced leucine zipper
282	(GILZ) protein (Ayyar et al., 2015) and also various core clock genes including Clock, Arntl,
283	Per1, Per2 and Nr1d1 encoding CLOCK, BMAL1, PER proteins and NR1D1, respectively
284	(Reppert and Weaver, 2002). Quantification of these genes by RT-qPCR revealed a
285	significant down-regulation of <i>Per1</i> and <i>Per2</i> and a trend for <i>Tsc22d3</i> (<i>p</i> =0.07) in VAT but
286	not in SAT from pollutant-exposed females. Clock and Arntl mRNA levels remained in the
287	control range (Fig. 5A-B).
288	3.6 Analysis of the response to pollutant mixture in male mice
289	To determine if changes in glucocorticoid signaling also occurred in males in response to the

pollutant mixture in ST-fed conditions, we screened all the genes investigated in females,
including *Nr3c1*, *Nr3c2*, *Hsd11b1* as well as *Tsc22d3*, *Clock*, *Arntl*, *Per1*, *Per2* and *Nr1d1* in
the VAT and the SAT of males fed a standard diet and exposed to the mixture of pollutants. In
the VAT of ST-fed males, we observed a significant decrease of *Nr3c1* mRNA levels and of *Arntl* while in the SAT, several genes were significantly up-regulated including *Nr3c2*, *Tsc22d3*, *Per1*, *Per2* and *Nr1d1* (Fig. 6). Finally, plasma corticosterone levels, food intake,
and expression of *Lep* and *Adipoq* were analyzed in males (Fig. 7). Plasma corticosterone

levels did not change. Contrary to females, food intake and *Lep* mRNA levels did not change
in males but *Adipoq* mRNA levels were enhanced in the SAT (Fig. 7). The mRNA levels of *Nr3c1*, *Nr3c2* and *Hsd11b1* were not affected by exposure to pollutants in the liver, in both
sexes (Supplementary Fig. 3).

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4. Discussion

303 Glucocorticoids exert a strong effect on lipid metabolism via binding to the steroid receptor GR in the adipose tissues and the liver (Lee et al., 2018, Woods et al., 2015) in which 304 11βHSD1 has predominantly reductase activities allowing local amplification of 305 glucocorticoid action in the absence of changes in plasma corticosterone levels (Lee and 306 307 Fried, 2014). Although weakly expressed, MR mediates as well metabolic effects related to glucocorticoid binding rather than aldosterone binding in liver and ATs (Kuhn and Lombes, 308 309 2013). Based on findings presented herein showing coordinated and reduced expression of Nr3c1, Nr3c2 and Hsd11b1 mRNA levels and decreased GR protein level in VAT of females 310 311 fed a standard diet; we concluded that pollutant exposure caused a defect in glucocorticoid signaling. Importantly, these effects exhibited tissue-specificity because they were not 312 observed in female SAT or in liver of both sexes. They also exhibited sex-specificity. Indeed, 313 while the levels of Nr3c1 were down-regulated in VAT as shown in ST-females, the levels of 314 315 Hsd11b1 did not change in VAT and the levels of Nr3c2 were up-regulated in the SAT of STmales exposed to pollutants, unlike females. 316

The origin of the sex-dimorphism probably stems from differences in sexual steroids, 317 318 estrogens and androgens. It is well described that manifestation of metabolic syndrome caused by GC excess depend on interactions between glucocorticoids and sex hormones (Alemany, 319 320 2012, Quinn et al., 2014). For example, a high-fat feeding resulted in enhanced corticosterone 321 plasma levels in males (not shown) but not in females (the present study). Origin of the sex-322 dimorphism could as well stem from cross-interactions of AHR, glucocorticoids and estrogen signaling as reviewed (Mauvais-Jarvis, 2018, Swedenborg et al., 2009, Casals-Casas and 323 324 Desvergne, 2011, Leblanc et al., 2019), raising the hypothesis that a mixture of pollutants 325 could locally contribute to the alteration of GC signaling in females without impacting corticosterone plasma levels. Consistently, we detected mRNA changes in Ahr and Esr2 in the 326

VAT of pollutant-exposed ST-females in addition to the decreased expression of the 327 328 glucocorticoid receptors. These effects were restricted to the VAT in pollutant-exposed females and distinct from those observed in males [(present study and (Naville et al., 2019)], 329 330 suggesting that changes in GC but also in estrogen and AHR signaling in response to exposure to the mixture of pollutants may cause the overall metabolic changes in females, 331 332 described in the present study. Certain effects caused by pollutant exposure overlapped those 333 described following a high-fat feeding as previously reported (Labaronne et al., 2017). It included decreased of Nr3c1, Hsd11b1, AhR mRNA levels but also of the estrogen receptor 334 Esr2 (a trend was observed for Esr1) and enhanced expression of Gper1. This may explain 335 336 why exposure to pollutants did not cause changes in the VAT of females fed a high-fat diet. Noteworthy, Gper1 increased in SAT and VAT in both females (present study) and males 337 (Naville et al., 2019) in response to a high-fat diet indicating that this estrogen receptor was 338 339 not regulated in a sex-dependent way.

340 Glucocorticoids regulate almost every aspect of adipose tissue biology metabolism including adipogenesis, adipocyte metabolism, inflammation and adipokine production 341 preferentially targeting visceral adipose tissue as exemplified in Cushing's syndrome with the 342 development of visceral obesity at the expense of the subcutaneous adipose tissue (Lee and 343 344 Fried, 2014). Importantly, the pollutant-induced effects described herein in female mice occurred in the absence of changes in the weight of SAT and VAT excluding impact of 345 346 pollutant exposure on adipogenesis. Accordingly, adipogenic markers remained in the control range. To validate glucocorticoid-signaling disturbances in pollutant-exposed females, we 347 348 analyzed the mRNA levels of one primary GR target gene presenting glucocorticoid response elements (GREs) in the promoter, Tsc22d3 encoding GILZ for glucocorticoid induced leucine 349 zipper (Ayroldi and Riccardi, 2009). Tsc22d3 mRNA levels decreased in VAT (a trend) but 350 351 no changes were observed in SAT in females, thus suggesting pollutants interfered with

glucocorticoid signaling in VAT, only. In addition, as pollutants may have pro-inflammatory 352 353 actions (Naville et al., 2015, Kim et al., 2012, Pardo et al., 2018, Rebourcet et al., 2010), we measured mRNA levels of several cytokines in VAT (and SAT) but they remained in the 354 control range. Eventually, we demonstrated that leptin plasma levels and Lep mRNA levels 355 significantly decreased in VAT of the pollutant-exposed females (not in SAT) while 356 357 adiponectin plasma levels and Adipoq mRNA levels in VAT and SAT remained in the control 358 range. Interestingly, males exposed to the mixture of pollutants exhibited enhanced mRNA 359 levels of several adipogenic markers including Adipoq in SAT but not in VAT and no changes in Lep mRNA levels or leptin plasma levels [the present study and (Naville et al., 2019)], 360 361 again highlighting sex-differences in the response to pollutant-exposure in metabolicallyactive tissues. Further studies will aim at understanding the coordinated regulation of Nr3c2 362 and Tsc22d3 mRNA levels in the SAT of exposed males together with the enhanced 363 364 expression of several adipogenic markers including Nr1c3, Fabp4 and Cidec described elsewhere (Naville et al., 2019). 365

Leptin level was the only significant metabolic phenotype difference measured in 366 females in response to exposure to the mixture of pollutants. Leptin is an adipokine that exerts 367 satiety effects and reduced leptin fits with enhanced food intake as we observed in females but 368 369 not in males. Leptin is expressed as a function of adipose tissue mass and is more expressed in females than in males (Zhang and Chua, 2017); thus, reduced leptin levels in basal conditions 370 371 of feeding without gain of weight despite enhanced food intake could indicate enhanced energy expenditure and thermogenesis. Since we did not measure these parameters in the 372 373 present study, validation of the hypothesis will await further studies. A second hypothesis to explain the reduction of glucocorticoid signaling and leptin expression in females exposed to 374 pollutants could be a possible dysregulated peripheral clock in VAT. There are several clues 375 376 in the literature to support this hypothesis. Glucocorticoids are secreted in circadian cycles to

coordinate the circadian rhythm with energy balance and leptin synthesis (So et al., 2009).
Adrenalectomy diversely affected peripheral circadian clocks including GILZ expression in
the adipose tissue (Sotak et al., 2016) and led to decreased serum leptin (Yilmaz et al., 2002).
The powerful GR agonist, dexamethasone led to the disappearance of clock gene rhythmicity
in adipose tissues (Gomez-Abellan et al., 2012).

The circadian clock regulates metabolism and energy homeostasis in peripheral tissues 382 including the adipose tissues and synchronization with the master clock in the hypothalamic 383 384 suprachiasmatic nuclei (SCN) would be in part orchestrated by glucocorticoids to keep in step diurnal functions with the environmental cycles of light and nutrition (Dickmeis, 2009, 385 Balsalobre et al., 2000). Circadian rhythms are generated by feedback loops in core clock 386 387 gene expression (Reinke and Asher, 2019). Among core clock components investigated, we demonstrated herein significant reduction of Perl and Per2 mRNA levels in VAT but not in 388 SAT in response to pollutant exposure in females, and no effect on *Clock* and *Arntl*. 389 390 Interestingly, both Perl and Per2 mRNA levels enhanced in the SAT (not in VAT) of males exposed to the mixture of pollutants. These findings are consistent with the presence of GRE 391 elements in the promoters of Perl and Per2 genes (Koyanagi et al., 2006, So et al., 2009). 392 393 They also validate changes in GC signaling in the VAT of exposed females and in the SAT of 394 exposed males. Overall, these findings pointed that several peripheral circadian clock-related genes were diversely affected by exposure to a mixture of pollutants in a sex- and tissue-395 396 dependent way (at least at the mRNA level in the ATs) extending previous reports (Labaronne et al., 2017) (Shen et al., 2019, Kopp et al., 2017). Further studies are needed to explore why 397 398 VAT in females and SAT in males were differentially regulated in response to the mixture of pollutants in a context of standard diet feeding, and why SAT in females was not affected. It 399 400 may explain the mild metabolic phenotype described in females (the present study). Indeed, 401 circadian metabolic disturbances may be early events and exposure to pollutants greater than

402 15 weeks could have resulted in more harmful phenotypes than what was described herein.403 This hypothesis merits further attention.

Consistent with the definition that endocrine disruptors may influence any hormonal action to 404 mediate their disruptive effects, we also identified that the mixture of pollutants targeted 405 11βHSD1 in addition to corticoid receptors. These findings extend previous reports that 406 407 endocrine disrupters can affect enzymes involved in hormone metabolism including the steroidogenic acute regulatory protein (STAR) (Guyot et al., 2004), the estrogen 408 sulfotransferase (SULT1E1) (Naville et al., 2013), aromatase and others (Beausoleil et al., 409 2018) (Zoeller et al., 2012, Nadal et al., 2017). Noteworthy, pollutants used in the mixture 410 were incorporated at a dose lower than their no-observed adverse effect level (NoAEL) and 411 just above their tolerable daily intake (TDI) dose. The TDI is supposedly the dose without 412 adverse effect in humans and it is derived from the NoAELs determined through experimental 413 studies applying corrective factors to take into account inter- and intra-species variations 414 415 (Dorne, 2010) of 100 to 1000 (Supp. Table 1). Therefore, this study gave further evidences that the risk assessment procedure which is based on NoAELS for single chemicals may not 416 be protective enough. In addition, comparison of metabolic disturbances elicited by the 417 mixture versus pollutants individually will allow determining if the observed effect resulted 418 419 from the action of one or several pollutants or from a cocktail effect.

420

421 **5.** Conclusions

We here demonstrated that exposure to a mixture of low-dosed pollutants caused reduced
expression of glucocorticoid receptors in the visceral but not in the subcutaneous adipose
tissue or in the liver in female mice and that it was associated with decreased plasma levels of
leptin and reduced expression of *Lep* and of various canonical genes related to the circadian

- 426 clock machinery in visceral adipose tissue. Inasmuch as lowering glucocorticoid signaling
- 427 following adrenalectomy prevents physiological oscillations of circadian genes and impact
- 428 adipokine secretion (Sotak et al., 2016, Yilmaz et al., 2002), our data fuel the hypothesis that
- 429 a mixture of low-dosed chemicals may alter clock genes resulting in metabolic effects at least
- 430 in the visceral adipose tissue in female mice.

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437

438 **Declaration of competing interest**

439 The authors declare that there are no conflicts of interest.

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700 FIGURE LEGENDS

Figure 1: Metabolic phenotyping of female mice fed a standard (ST) or a high-fat (HF) diet
and exposed to pollutants (grey columns) or not (dark columns). Results are expressed as
means±SEM of n=7-8 female mice/group. Statistical analysis was performed using a two-way
Anova analysis to determine the overall effect of the pollutant mixture and the diet. ns: not
significant;*, p<0.05; **p<0.01; ***p<0.001.

706 Figure 2 : Effect of the mixture of pollutants and of the high-fat high-sucrose (HF) diet on the expression of genes encoding GR and MR, 11βHSD1, AHR and estrogen receptors in female 707 708 VAT (A). Values are means \pm SEM with n=7-8. Data were analyzed using two-way Anova as presented in the insert followed by Post hoc analysis between relevant groups; ns: not 709 significant; *p<0.05; ** p<0.01; ***p<0.001; ST : standard diet. (B) Western-blotting 710 711 analysis of the effect of pollutant exposure on GR protein expression in female VAT. Values 712 are means \pm SEM with n = 6. ST0: standard diet not containing the mixture of pollutants; STp : standard diet containing the mixture of pollutants. 713

Figure 3 : Effect of the mixture of pollutants and of the high-fat high-sucrose (HF) diet on the expression of genes encoding GR, MR, 11 β HSD1, AHR and estrogen receptors in the SAT of female mice. Values are means ± SEM with n=7-8. Data were analyzed using two-way Anova as presented in the insert; ns: not significant; ** *p*<0.01 ; ****p*<0.001. ST : standard diet.

718 **Figure 4** : Effect of the mixture of pollutants on plasma leptin and adiponectin levels, food

719 intake (A) and on the expression of *Lep* and *Adipoq* in female VAT (B) and SAT (C). Values

are means \pm SEM with n = 7-8 except for food intake (n = 4 because mice were 2 per cage).

*p>0.05; ** p<0.01. ST0 : standard diet not containing the mixture of pollutants ; STp :

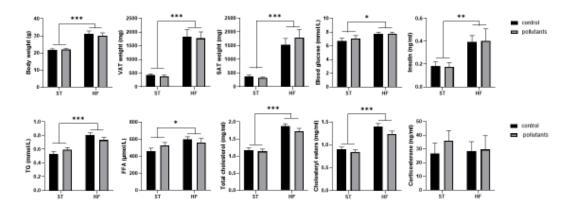
standard diet containing the mixture of pollutants.

723	Figure 5 : I	Effect of the	mixture of	pollutants	on the e	xpression	of Tsc.	2 <i>2d3</i> ar	d the	circadian
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- genes Clock, Arntl, Per1, Per2 and Nr1d1 in female VAT (A) and SAT (B). Values are
- means \pm SEM with n=7-8. **p*>0.05 ; ** *p*<0.01. ST0 : standard diet not containing the
- mixture of pollutants ; STp : standard diet containing the mixture of pollutants.
- 727 **Figure 6**: Effect of the mixture of pollutants on the expression of *Nr3c1*, *Nr3c2*, *Hsd11b1*,
- 728 Tsc22d3, Clock, Arntl, Per1, Per2 and Nr1d1 in the VAT (A) and SAT (B) of male mice fed a
- standard-diet. Values are means \pm SEM with n=8. **p*>0.05 ; ** *p*<0.01 ; *** *p*<0.001. ST0 :
- standard diet not containing the mixture of pollutants ; STp : standard diet containing the
- 731 mixture of pollutants.
- 732 **Figure 7** : Effect of the mixture of pollutants on food intake and corticosterone plasma levels
- (A), and on the expression of *Lep* and *Adipoq* in male VAT (B) and SAT (C). Values are
- means \pm SEM with n=8 (n=4 for food intake). **p*>0.05 ; ** *p*<0.01. ST0 : standard diet not
- containing the mixture of pollutants ; STp : standard diet containing the mixture of pollutants.

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Figure 1



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Figure 2

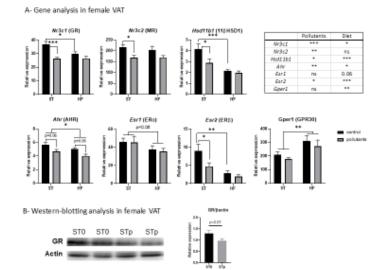


Figure 3

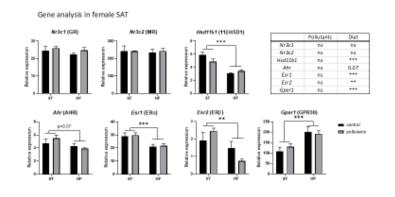
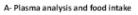


Figure 4



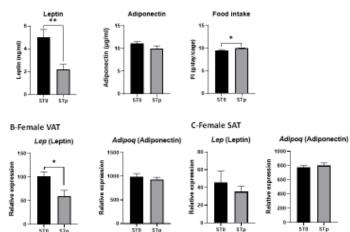
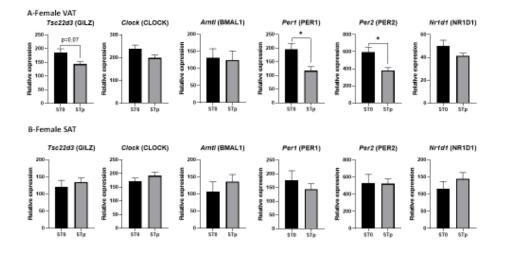
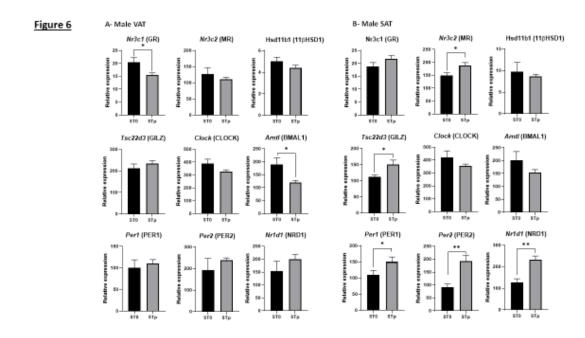
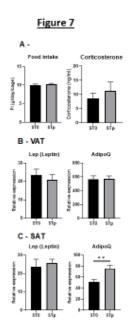


Figure 5







746 Supplementary File

Supplementary Table 1: References doses of the pollutants present in the mixture and doses

used in the diets (all per kg and per day) (From Naville et al., 2019).

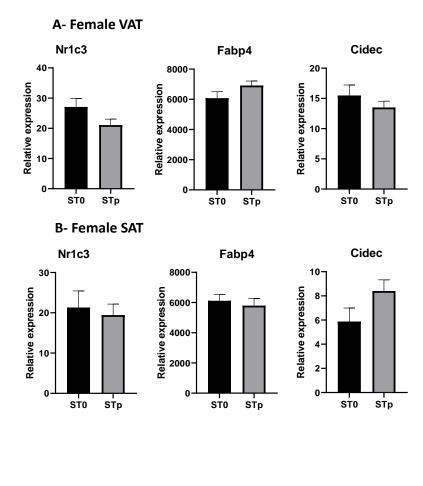
Pollutants in the mixture	PCB153	BPA	TCDD	751 DE持₽2	
NOAEL	40µg	5mg	2 ng	5m ⁷⁵³	
TDI	20ng	4µg	1-4pg	50 µ75 4	
doses used	200ng	40µg	20pg	500p/g5	

Supplementary Table 2: List of the primers used in RT-qPCR

		sequences: 5'->3'					
gene	reference	sense	antisense				
Adipoq	NM_009605	AGGCCGTGATGGCAGAGATG	CTTCTCCAGGTTCTCCTTTCCTGC				
Ahr	NM_013464.4	TCA-TCT-GGT-TTC-CTG-GCA-ATG-AAT	ATA-AGC-TGC-CCT-TTG-GCA-TC				
Arntl	NM_007489	CTGCCTGGAAGGAAGTTACA	AAGGTCCACAGGATTTGACT				
Ccl2	NM_011333	TGG-AGC-ATC-CAC-GTG-TTG-GC	ACT-ACA-GCT-TCT-TTG-GGA-CA				
Ccl5	NM_013653	TCAAGGAGTATTTCTACACCAG	TGGCACACACTTGGCGGTTC				
Cidec	NM_178373;NM_001301295	TGG-CAC-AAT-CGT-GGA-GAC-AG	AGA-GGG-TTG-CCT-TCA-CGT-TC				
Clock	NM_007715,NM_001289826,N M_001305222	ACAGCAGCTTCCTTCAGTTC	TGCTCTGTTGTAGTGGAAAG				
Esr1	NM_000125;NM_001122740;N M_001122741;NM_001122742	TGT-TTG-CTC-CTA-ACT-TGC-TC	CCT-TCT-CTT-CCA-GAG-ACT-TC				
Esr2	NM_207707; NM_010157	CTCTTCCCAGCAGCAGTCAGTC	AGCATCTCCAGCAGCAGGT				
Fabp4	NM_024406	CAG-AAG-TGG-GAT-GGA-AAG-TCG	CGA-CTG-ACT-ATT-GTA-GTG-TTT-GA				
Gper1	NM_029771	AGC-TGA-TCA-GAT-CTA-GGG-AG	GTC-CTG-GGA-GCC-TGT-TAG-TC				
Gusb	NM_010368	CTT-CAT-GAC-GAA-CCA-GTC-AC	GCA-ATC-CTC-CAG-TAT-CTC-TC				
Hsd11b1	NM_181755, NM_005525,NM_001206741	TTGCCCATGCTGAAGCAGAGC	CTGTTTCTGTGTCTATGAGGC				
ll1b	NM_008361	ACT-GTT-CCT-GAA-CTC-AAC-TG	CTT-GTT-GAT-GTG-CTG-CTG-CG				
Lep	NM_008493	CACCAGGATCAATGACATTTC	TGCCAGTGTCTGGTCCATCTTG				
Nr1c3	NM_001127330,NM_011146	TCT-CTC-CGT-AAT-GGA-AGA-CC	GCA-TTA-TGA-GAC-ATC-CCC-AC				
Nr1d1	NM_021724	GGGAGGTGGTAGAGTTTGCC	CCAGGGAGTTGAGCTTCTCG				
Nr3c1	NM_008173	ACACCTGGATGACCAAATGACC	GCAGGGTAGAGTCATTCTCTGC				
Nr3c2	NM_001083906	CCAAGTGTCCCAACAGTTCT	CATCTTCCATCACTTCCTGT				
Per1	NM_0011065; NM_001159367	TGAGCCAGAGGCCAGATTG	TGTATGGCTGCTCTGACTG				
Per2	NM_011066	ATCTCCAGGCGGTGTTGAAG	TGCCTTTCTCCTCACTCTCG				
Tbp	NM_013684	TGG-TGT-GCA-CAG-GAG-CCA-AG	TTC-ACA-TCA-CAG-CTC-CCC-AC				
Tnfa	NM_013693	CCA-GAC-CCT-CAC-ACT-CAG-ATC	CAC-TTG-GTG-GTT-TGC-TAC-GAC				
Tsc22d3	NM 001077364,NM 010286	AACAAGATTGAGCAGGCCAT	TGGAACTTTTCCAGTTGCTC				

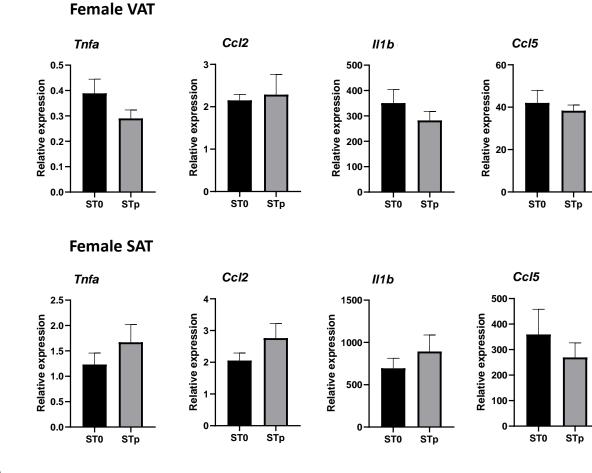
Supplementary Figure 1: Effect of the mixture of pollutants on the expression of Nr1c3, *Fabp4* and *Cidec* in female VAT (A) and in female SAT (B). Values are means \pm SEM with n=7-8. ST0: standard diet not containing the mixture of pollutants; STp: standard diet containing the mixture of pollutants.





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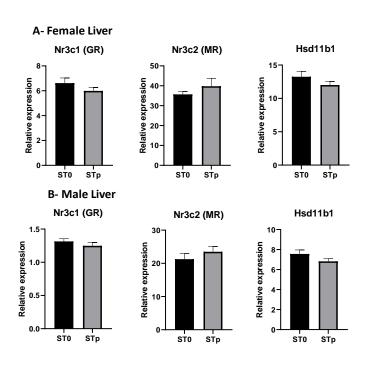
Supplementary Figure 2: Effect of the mixture of pollutants on the expression of *Tnfa*, *Ccl2*, *Il1β* and *Ccl5* in female VAT and in female SAT. Values are means \pm SEM with n=7-8. ST0: standard diet not containing the mixture of pollutants; STp: standard diet containing the mixture of pollutants.



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Supplementary Figure 3: Effect of the mixture of pollutants on the expression of Nr3c1, *Nr3c2* and *Hsd11b1* in female liver (A) and male liver (B). Values are means \pm SEM with n=7-8. ST0: standard diet not containing the mixture of pollutants; STp: standard diet containing the mixture of pollutants.

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