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Nanomolar levels of PAHs in extracts from urban air induce MAPK signaling in HepG2 cells.

Jarvis, Ian WH; Bergvall, Christoffer; Morales, D.A.; Kummrow, F; Umbuzeiro, GA; Westerholm, Roger; Stenius, Ulla; Dreij, Kristian

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4	Jarvis IWH ^a , Bergvall C ^b , Morales DA ^c , Kummrow F ^d , Umbuzeiro GA ^c , Westerholm R ^b ,
5	Stenius U ^a and Dreij K ^a *
6	
7	^a Institute of Environmental Medicine, Karolinska Institutet, Box 210, SE-171 77 Stockholm,
8	Sweden.
9	^b Department of Analytical Chemistry, Stockholm University, Svante Arrhenius väg 16, SE-
10	106 91 Stockholm, Sweden.
11	^c Faculty of Technology, State University of Campinas (UNICAMP), Limeira, SP, 13484-332,
12	Brazil.
13	^d Institute of Environmental, Chemical and Pharmaceutical Sciences, Federal University of
14	São Paulo (UNIFESP), Diadema, SP, 09972-270, Brazil.
15	
16	*Corresponding Author
17	Kristian Dreij, PhD
18	Address: Institute of Environmental Medicine, Karolinska Institutet, Box 210, SE-171 77
19	Stockholm, Sweden. Email: Kristian.Dreij@ki.se Tel: +46 8 524 87566
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21	Running Title
22	Environmental PAH mixtures activate MAPK signaling
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24	Abbreviations

- AP-1, activator protein 1; BP, benzo[*a*]pyrene; ERK, extracellular regulated kinase; JNK, cJun N-terminal kinase; MAPK, mitogen-activated protein kinase; MEK4, MAPK kinase 4;
 PAH, polycyclic aromatic hydrocarbon; PM, particulate matter; TEF, toxic equivalency
 factor; TNF, tumor necrosis factor;

30 Abstract

Polycyclic aromatic hydrocarbons (PAHs) are common environmental pollutants that occur 31 naturally in complex mixtures. Many of the adverse health effects of PAHs including cancer 32 are linked to the activation of intracellular stress response signaling. This study has 33 investigated intracellular MAPK signaling in response to PAHs in extracts from urban air 34 collected in Stockholm, Sweden and Limeira, Brazil, in comparison to BP in HepG2 cells. 35 Nanomolar concentrations of PAHs in the extracts induced activation of MEK4 signaling with 36 down-stream increased gene expression of several important stress response mediators. 37 Involvement of the MEK4/JNK pathway was confirmed using siRNA and an inhibitor of JNK 38 signaling resulting in significantly reduced MAPK signaling transactivated by the AP-1 39 transcription factors ATF2 and cJun. ATF2 was also identified as a sensitive stress responsive 40 protein with activation observed at extract concentrations equivalent to 0.1 nM BP. We show 41 42 that exposure to low levels of environmental PAH mixtures more strongly activates these signaling pathways compared to BP alone suggesting effects due to interactions. Taken 43 44 together, this is the first study showing the involvement of MEK4/JNK/AP-1 pathway in regulating the intracellular stress response after exposure to nanomolar levels of PAHs in 45 environmental mixtures. 46

47

48 Key Words

49 PAHs, Air particulate matter, Complex mixtures, Benzo[*a*]pyrene, MAPK

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51 **1. Introduction**

52 Human exposure to environmental pollutants in air particulate matter (PM) has been 53 identified to cause a number of adverse health effects including cancer and various 54 cardiovascular and respiratory diseases [1, 2]. One important group of environmental

pollutants that are associated with PM and play an important role in the reported detrimental 55 health effects are the polycyclic aromatic hydrocarbons (PAHs) [3]. PAHs are ubiquitous 56 environmental pollutants that are naturally present as mixtures and are formed during 57 combustion of carbon-containing fuels. Both individual and mixtures of PAHs are classified 58 as carcinogens or probable carcinogens by the International Agency for Research on Cancer 59 [4]. Recent data from us and others have suggested synergistic effects due to interactions 60 between PAHs in complex mixtures on the genotoxic and carcinogenic properties of PAHs [5-61 8], though conversely, strong antagonistic effects have also been observed in human cells, 62 probably resulting from competitive inhibition of metabolizing enzymes [9-11]. However, the 63 64 role of interactions between PAHs in complex mixtures in relation to the adverse health effects of PAHs is poorly understood [12]. 65

The activator protein-1 (AP-1) transcription factor is a dimeric complex comprising 66 67 members of the ATF, FOS, JUN and MAF protein families that has functions in many areas of cellular homeostasis [13, 14]. In response to cellular stress stimuli AP-1 proteins are 68 activated by the mitogen-activated protein kinase (MAPK) family of proteins, including c-Jun 69 N-terminal kinase (JNK), p38 and extracellular signal-regulated kinase (ERK) [15, 16]. The 70 protein MAPK kinase 4 (MEK4/MKK4) specifically activates JNK and p38 [17] and has been 71 72 identified as an important metastasis suppressor in several organs [18] and a possible target for small molecule inhibition in therapy for tumor necrosis factor alpha (TNF) mediated 73 diseases [19]. The present study focuses on activation of MAPK signaling in response to 74 environmental mixtures of PAHs compared to single benzo[a]pyrene (BP) exposure in 75 76 human-derived hepatoma (HepG2) cells. It has previously been shown that in vitro exposure to BP leads to activation of MAPK signaling associated with apoptotic cell death via p53 [20, 77 21]. However, the role of MAPK signaling in the stress response after exposure to nanomolar 78 concentrations of PAHs in air PM remains unclear. 79

Using PAH-containing air PM extracts from Stockholm, Sweden and Limeira, Brazil 80 at nanomolar concentrations we studied the time-dependent activation of MAPK signaling 81 and downstream gene expression in HepG2 cells. Our results show that nanomolar 82 concentrations of PAH extracts more strongly activate MAPK signaling and proteins of the 83 AP-1 transcription factor than BP alone suggesting effects due to interactions and that this 84 activation is mediated via MEK4 and JNK. Furthermore, the transactivation of cellular stress 85 mediators including interleukin 8 in response to PAH extract was shown to be mediated 86 through a MAPK. To the authors knowledge this is the first study to demonstrate activation of 87 MEK4/JNK/AP-1 with downstream increased gene expression in the cellular stress response 88 89 after exposure to nanomolar levels of PAHs found in air PM.

- 90
- 91 **2. Materials and Methods**
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93 2.1. Reagents and antibodies

Unless otherwise stated all chemicals, including BP, were of analytical grade and obtained 94 from Sigma Aldrich (Stockholm, Sweden). Detailed information on manufacturer and purity 95 of the standards and solvents used for PAH analysis have been published previously [22, 23]. 96 Gibco (Invitrogen, Paisley, UK) supplied all cell culture reagents. Cell Signaling Technology 97 (Beverly, MA) provided the following antibodies: phospho-ATF2 Thr71, phospho-cJun 98 Ser63, JNK, phospho-JNK Thr183/Tyr185, MEK4, phospho-MEK4 Thr261. Santa Cruz 99 Biotechnology (Santa Cruz, CA, USA) provided the Cdk2, phospho-Erk Tyr204 and 100 phospho-p38 Thr180/Tyr182 antibodies, secondary anti-rabbit, anti-mouse 101 and siRNA against MEK4 and control siRNA-A. Calbiochem (Gibbstown, NJ, USA) provided the JNK 102 103 inhibitor VIII.

105 2.2. Air sampling, sample preparation and PAH analysis

Air PM was collected at two sites: the campus of Stockholm University, Stockholm, Sweden 106 and the campus of the Faculty Technology at UNICAMP, Limeira, Brazil. At both collection 107 sites total PM was collected. The air PM sample from Stockholm was collected at roof-top 108 level on a Teflon-coated glass fiber filter (Ø149 mm, Pallflex Inc., Putnam, CT, USA) with an 109 average flow rate of 509 l min⁻¹ for 170 h. The total PM concentration for this sample was not 110 determined, but PM concentration from other similar urban sites in Stockholm during the 111 same season ranged from $10.4 - 19.4 \ \mu g/m^3$ (unpublished data). The air PM sample from 112 Limeira was collected at street level on a glass-fiber filter (254×233 mm, 0.33 mm pore size, 113 Energética Ind. Com. LTDA, Rio de Janeiro, RJ, Brazil) using a high-volume sampler 114 (Energética Ind. Com. LTDA, Rio de Janeiro, RJ, Brazil) operated at an average flow rate of 115 1130 l min⁻¹ for 24 h. The total PM concentration in the Limeira sample was 95.8 μ g/m³ [24]. 116 117 Extraction was performed using an ASE 200 accelerated solvent extraction system (Dionex Corporation, Sunnyvale, CA, USA). Toluene was used as an extraction solvent at 200 °C and 118 119 3000 psi for five consecutive 30 min static extraction cycles as described previously [6]. PAH 120 content in the extracts was determined by HPLC-GC/MS as described previously [6, 22].

121

122 **2.3.** Cell culture and exposure

Human-derived hepatocellular carcinoma cells (HepG2) were obtained from the American Type Culture Collection (Rockville, MD, USA). The motivation for the use of this cell line in this study is the metabolic competence for PAHs [25] and a previously demonstrated response to low levels of PAHs (in mixtures) extracted from environmental samples by ourselves and others [5-7]. HepG2 cells were cultured in minimal essential medium supplemented with 10 % fetal bovine serum, sodium pyruvate (1 mM), non-essential amino acids (0.1 mM), penicillin (100 units/ml) and streptomycin (0.1 mg/ml) and maintained at 37 °C in 5 % CO₂. Prior to exposure cells were seeded at 3×10^5 cells/ml in 6-well plates and cultured for 72 h unless otherwise stated. Cells were exposed to solvent control (0.1 % DMSO), BP, or PAH extracts for up to 24 h.

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134 2.4. RNA interference

Transfection of cells was performed using Lipofectamine 2000 reagent (Invitrogen, Paisley, UK). Briefly, cells were seeded into 35 mm culture dishes and after 24 h transfected with 50 nM siRNA. siRNA sequences are shown in Supplementary Table 1. After 48 h of incubation cells were exposed to PAHs or solvent control, and then harvested for Western blot analysis.

139

140 **2.5. Western blotting**

Western blotting was performed as described previously [6]. Briefly, whole cell lysates were 141 142 subjected to standard SDS-PAGE and separated proteins transferred to a PVDF membrane (Bio-Rad, Hercules, CA, USA) by wet electro-blotting. Non-specific antibody binding was 143 144 reduced by incubating membranes in 5 % non-fat dry milk. Signals were detected using enhanced chemiluminescence (Amersham GE Healthcare Bio-Sciences AB, Uppsala, 145 Sweden). Experiments were performed at least in triplicate and analyzed separately. 146 Densitometric analysis was performed using ImageJ software version 1.45s (National Institute 147 of Health, USA). 148

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150 2.6. RNA purification and real-time RT-PCR

Total RNA was prepared using the RNeasy Mini Kit (Qiagen, Hilden, Germany) and 1 µg used to generate cDNA with the High Capacity cDNA Reverse Transcription kit (Applied Biosystems, Foster City, CA, USA) according to protocol. Subsequently, quantification of gene expression was performed in duplicates using Maxima[™] SYBR® Green qPCR Master Mix (Fermentas, St. Leon-Rot, Germany) with detection on an Applied Biosystems 7500 Real-Time PCR System. The reaction cycles used were 95 °C for 2 min, and then 40 cycles at 95 °C for 15 s and 60 °C for 1 min followed by melt curve analysis using GAPDH as housekeeping gene. Primer sequences are shown in Supplementary Table 1. Relative gene expression quantification was analyzed with the mathematical model described in [26].

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161 **2.7. Statistical analysis**

162 All data presented are means \pm SE. One-way ANOVA with Bonferroni's t-test correction was 163 used to determine statistical significance (p < 0.05).

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165 **3. Results and discussion**

166

167 **3.1. Analysis of PAH content in air PM extracts**

The PAH content in the two air PM extracts was determined using our recently developed 168 169 methodology that is capable of quantifying 42 unique PAHs of between 3 and 6 rings [6, 24] 170 (Supplementary Table 2). PAHs at the LIMEIRA sampling site mainly result from heavy traffic (including cars and trucks), industrial emissions and biomass burning, whereas those at 171 the STHLM site can mainly be attributed to heavy traffic emissions. The results showed that 172 173 the air PM extract from Limeira (LIMEIRA) had approximately 3-fold higher total PAH content than the extract from Stockholm (STHLM) (10169.2 and 3392.6 pg/m³, respectively), 174 in agreement with recent data [24]. The level of BP was approximately 5-fold higher in the 175 LIMEIRA sample (807 pg/m^3) compared to the STHLM sample (160 pg/m^3). The level of the 176 highly potent dibenzo [a, l] pyrene was approximately 9-fold higher in the LIMEIRA sample 177 (9.07 pg/m^3) compared to the STHLM sample (1.05 pg/m^3) . 178

In order to compare the cellular response to the two PAH extracts and with BP alone, 179 the extracts were prepared in DMSO to contain a concentration equivalent of 1 μ M BP (BP_{eq}) 180 (actual 0.91 and 1.10 µM for STHLM and LIMEIRA respectively, Supplementary Table 2). 181 Cells were exposed to the PAH extracts with a final concentration of 1 nM BP_{eq}, and hence, 182 cells were also exposed to 1 nM BP alone for comparative purposes. The final total PAH 183 concentration the cells were exposed to was 21.6 and 14.4 nM for the STHLM and LIMEIRA 184 185 extracts respectively. When assessing human exposure to PAHs in ambient air BP is often used as a surrogate indicator [27, 28] and thus, normalizing the PAH extracts to a set 186 concentration of BP allows us to evaluate how well the BP content can predict the observed 187 effects. Neither the Stockholm [6] nor the Limeira extract (data not shown) demonstrated 188 cytotoxicity in the HepG2 cell line. 189

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191 **3.2.** Nanomolar levels of PAH extracts activate JNK signaling

Activation of DNA damage signaling in cells after exposure to nanomolar concentrations of 192 the STHLM extract has been demonstrated previously [6]. To identify regulatory pathways 193 involved in different cellular responses including inflammation, apoptosis and cell cycle 194 control, we assessed activation of MAPK proteins that have previously been shown to be 195 activated in response to PAHs [29-32]. The results showed a significant increase in levels of 196 phosphorylated JNK (pJNK) whilst no significant effect was observed on total JNK protein or 197 on phosphorylation of Erk (pERK) or p38 (pp38) (Figure 1). Phosphorylation of JNK in 198 response to the two PAH extracts followed different kinetics with the STHLM extract 199 200 inducing a persistent increase in activation throughout the 12 hours whereas the LIMEIRA extract induced the highest levels of pJNK after 3 h which decreased thereafter. It is probable 201 202 that this difference in trends is a result of different extract composition though further

investigation is required to confirm this. Both extracts induced a stronger activation of JNKthan exposure to 1 nM BP alone (Figure 1).

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Figure 1. Nanomolar concentrations of PAH extracts activate JNK signaling. Cells were exposed to the PAH extracts (1 nM BP_{eq}) or 1 nM BP alone. Total and phosphorylated levels of the indicated proteins were determined by Western blot at 3, 6 and 12 h. Cdk2 was used as a loading control. Densitometric analysis is shown to the right. *p<0.05 compared with DMSO control levels.

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3.3. AP-1 transcription factors are activated in response to nanomolar levels of PAH extracts

215 ATF2 and cJun are important proteins that form part of AP-1 and that are activated downstream of JNK [33, 34]. In agreement with the increased levels of pJNK, we observed 216 increased phosphorylation of ATF2 and cJun (Figure 2A). Levels of phosphorylated ATF2 217 (pATF2) showed a significant increase in response to both BPeq extracts, with the STHLM 218 extract inducing higher and more sustained levels of pATF2 than the LIMEIRA extract, 219 displaying >8-fold higher levels than control up to 12 h post-exposure. Levels of 220 phosphorylated cJun (pcJun) displayed the same pattern as pATF2 with the highest levels in 221 response to the STHLM extract (Figure 2A). Similar to the effect on pJNK, both extracts 222

induced higher levels of phosphorylation of ATF2 and cJun compared to 1 nM BP alone 223 (Figure 2A). As shown in Figure 2B, significant increase in level of pATF2 could be detected 224 in response to the STHLM extract at BP_{eq} concentrations down to 0.1 nM (1.8-fold, p = 0.03, 225 226 total PAH concentration = 2.2 nM). These results suggest that pATF2 could be a sensitive biological marker for activation of MAPK signaling in response to PAHs. ATM-mediated 227 activation of ATF2 by phosphorylation at Ser490/498 is implicated in the DNA damage 228 response [35] and the possible role of ATF2 connecting MAPK and DNA damage signaling 229 in response to PAHs is interesting. 230

The results presented here show clear differences in the observed responses between 231 the PAH extracts. The signaling was also in general much stronger in response to the PAH 232 extracts compared to BP alone, similar to what we have reported earlier for DNA damage 233 signaling [6]. Since the total PAH content was quite similar for the 1 nM BP_{eq} STHLM and 234 LIMEIRA extracts this implies that the observed differences more likely are due to sample 235 composition. An explanation for this observation could be that there are different PAHs 236 237 present in the STHLM extract that are more potent MAPK inducers than BP. Alternatively, substituted PAHs such as nitro-PAHs, which are known to induce stress signaling [36], might 238 also contribute to the effects of the extracts. In addition, non-PAH compounds could affect the 239 response of the extracts. The level of polychlorinated biphenyls were approximately 0.5 % of 240 the PAH level (pg/m^3) in the STHLM extract (unpublished data) and thus are predicted to 241 have minimal effects. Other polychlorinated compounds such as dibenzo-dioxins and furans 242 may also contribute to the overall effect of the extracts [37, 38]. Metals are also known to be 243 present in environmental air PM, and although the levels of metals in our extracts is unknown, 244 we speculate that due to the sampling and processing methods the levels are likely to be low 245 [11]. 246



Figure 2. AP-1 transcription factors are activated in response to nanomolar levels of PAH extracts. Cells were exposed to the PAH extracts (1 nM BP_{eq}) or 1 nM BP alone. Total and phosphorylated levels of the indicated proteins were determined by Western blot at 3, 6 and 12 h (A). Cells were exposed to decreasing concentrations of the STHLM extract and level of pATF2 was assessed at 12 h (B). Cdk2 was used as a loading control. Densitometric analysis is shown below. *p<0.05 compared with DMSO control levels.

256 3.4. Activation of JNK/AP-1 signaling is mediated through MEK4

MEK4 has previously been shown to be involved in regulating pro-apoptotic signaling in human 293T and HeLa cells and rat F258 cells in response to BP treatment, albeit at higher concentrations than used here, leading to downstream caspase activation [39, 40]. However, it has not been established if MEK4 is activated in response to levels of PAHs found in urban air. The results showed significantly increased levels of phosphorylated MEK4 (pMEK4) after exposure to both extracts and 1 nM BP, though highest levels were observed after 12 h exposure to the STHLM extract (4.5-fold, p = 0.028, Figure 3A). No changes were observed on levels of total MEK4. These results clearly show that MEK4 is activated in response to nanomolar levels of PAHs in mixtures and that the levels are higher compared to BP alone.

To determine if JNK/AP-1 activation was dependent on activation of MEK4 HepG2 266 cells were exposed to the STHLM extract for 12 hours following pre-treatment with siRNA 267 against MEK4 (Figure 3B). Based on the effects in the time-response experiments shown in 268 269 Figure 3A, only exposure to the STHLM extract was investigated with siRNA. Transfecting the cells with siRNA against MEK4 significantly reduced the levels of total MEK4 protein 270 resulting in significantly reduced signaling through JNK, ATF2 and cJun (Figure 3B). No 271 effect was observed with control siRNA confirming that the observed response resulted from 272 interference of MEK4 and was not a by-product of the transfection procedure. Taken together, 273 274 these data show that activation of JNK/AP-1 signaling in response to environmental PAH 275 extracts results from activation of the upstream MAPK kinase MEK4. To our knowledge this 276 is the first time MEK4 is identified as a mediator of stress signaling in response to 277 concentrations of PAHs found in urban air.



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Figure 3. MEK4 mediates signaling through MAPK leading to activation of AP-1 279 transcription factors. Cells were exposed to the PAH extracts (1 nM BPeq) or 1 nM BP alone 280 and total and phosphorylated levels of MEk4 were determined by Western blot at 3, 6 and 12 281 282 h (A). Cells transfected with either mock siRNA or siRNA against MEK4 were exposed to the STHLM extract (1 nM BPea) for 12 h and effects on phosphorylation status of JNK, ATF2 283 and cJun were assessed by Western blot (B). Cdk2 was used as a loading control. 284 Densitometric analysis is shown to the right. *p<0.05 compared with DMSO control levels. 285 [#]p<0.05 compared with STHLM treatment. 286

288 3.5. JNK mediates transactivation of cellular stress mediators through AP-1

To confirm the role of activation of JNK signaling in activation of AP-1 proteins in response to PAH extracts, HepG2 cells were pre-treated for 1 h with a JNK inhibitor (JNKi, 20 μ M) [41] followed by exposure to the STHLM extract for 12 h (Figure 4). Significantly reduced levels of both pATF2 and pcJun were observed confirming the involvement of JNK in activation of ATF2 and cJun in this study. JNK and cJun have previously been reported to be mediators of cellular stress responses to PAHs [42, 43]. However, this is the first time that activation of ATF2 can be linked to cellular stress signaling in response to PAHs.

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Figure 4. Activation of AP-1 transcription factors is mediated through JNK. Cells pretreated
for 1 h with JNKi (20 μM in DMSO) were exposed to the STHLM extract (1 nM BP_{eq}) for 12
h and effects on phosphorylation status of ATF2 and cJun was assessed by Western blot.
Densitometric analysis is shown below. *p<0.05 compared with DMSO control levels.
#p<0.05 compared with STHLM treatment.

To investigate if activation of MAPK signaling in response to nanomolar levels of 304 PAH extracts would result in induction of cellular stress mediators, effects on expression of 305 MAPK regulated genes were examined by qRT-PCR (Figure 5). The results showed 306 significant effects on the mRNA levels of tumor necrosis factor alpha (TNF), interleukin 8 307 (IL-8), tumor necrosis factor receptor superfamily member 6 (TNFR6 or FAS) and, epidermal 308 growth factor receptor (EGFR). Expression levels of TNF and IL-8 displayed the strongest 309 response with 13.3- and 5.7-fold up-regulation at 12 h, respectively. These genes are 310 transactivated via MAPK signaling and involved in stimulating inflammation, proliferation or 311 apoptosis and have all been shown to be play important roles in regulation of human diseases 312 such as cancer (reviewed in [13, 14]. Moreover, in the presence of JNKi, mRNA levels of 313 TNF, IL-8 and FAS were significantly reduced 12 h post treatment to the level of the DMSO 314 control. Although the mRNA levels of EGFR were reduced in response to blocked JNK 315 316 signaling 24 h post treatment, no significant effects were observed. These results confirm the 317 involvement of MAPK signaling in transactivation of cellular stress mediators in response to 318 nanomolar levels of PAH mixtures.



Figure 5. Induction of gene expression of stress response mediators is mediated through a MEK4/JNK/AP-1 signaling pathway. Cells were exposed to the STHLM extract (1 nM BP_{eq}) for 12 h with or without JNKi pretreatment and effects on gene expression were determined by qRT-PCR. *p<0.05 compared with DMSO control levels. $^{\#}p$ <0.05 compared with STHLM treatment.

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326 **3.6.** Comparison with toxic equivalency factors

In order to compare the extracts with BP they were prepared to have a final exposure concentration equivalent to 1 nM BP. An alternative approach is to derive BP equivalent concentrations using toxic equivalency factor (TEF) scales. Using previously published TEF values [44] we calculated BP_{TEQ} concentrations of 1.74 and 1.46 for the STHLM and LIMEIRA samples. Data for fold difference for pATF2, pcJun, pJNK and pMEK4 are given in Supplementary Table 3 and are presented as fold differences compared to BP. As can be

seen, the fold differences for pATF2 are higher than predicted based on BP_{TEO} concentrations 333 334 of the PAH extracts, emphasizing pATF2 as a sensitive biological marker for activation of MAPK signaling following PAH exposure. An explanation for this observation is that there 335 336 could be different PAHs present in the extracts that are more potent inducers of the stress response than BP. Fold differences were similar to what would be predicted for pcJun, pJNK 337 338 and pMEK4 based on BP_{TEO} concentrations. However, it should be noted that there are a 339 number of important considerations and requirements that make the TEF-based approach insufficient for mixture assessment as discussed recently [12]. 340

341

342 4. Conclusion

Here we report that nanomolar concentrations of environmental PAH mixtures, extracted 343 from urban air PM collected in Stockholm, Sweden and Limeira, Brazil, induce a time-344 345 dependent activation of MAPK signaling in HepG2 cells. We show that exposure to low levels of PAH extracts more strongly activates signaling pathways compared to BP alone 346 347 suggesting possible effects from interactions. Exposure to the PAH extracts induces activation of MEK4 signaling with down-stream increased expression of several important stress 348 response mediators. Abrogation of the MEK4-JNK pathway using siRNA and a specific 349 inhibitor against JNK significantly reduces the transactivation mediated through AP-1 350 transcription factors ATF2 and cJun. This is the first study showing activation of 351 MEK4/JNK/AP-1 pathway in in response to nanomolar levels of PAHs in environmental 352 353 mixtures.

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364

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490 Nanomolar levels of PAHs in extracts from urban air induce 491 MAPK signaling in HepG2 cells

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493 Jarvis IWH^a, Bergvall C^b, Morales DA^c, Kummrow F^d, Umbuzeiro GA^c, Westerholm R^b, 494 Stenius U^a and Dreij K^a*

495

^aInstitute of Environmental Medicine, Karolinska Institutet, Box 210, SE-171 77 Stockholm,
Sweden.

- ^bDepartment of Analytical Chemistry, Stockholm University, Svante Arrhenius väg 16, SE-
- 499 106 91 Stockholm, Sweden.
- ^cFaculty of Technology, State University of Campinas (UNICAMP), Limeira, SP, 13484-332,
 Brazil.
- ^dInstitute of Environmental, Chemical and Pharmaceutical Sciences, Federal University of
- 503 São Paulo (UNIFESP), Diadema, SP, 09972-270, Brazil.

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505 *Corresponding Author

- 506 Kristian Dreij, PhD
- 507 Address: Institute of Environmental Medicine, Karolinska Institutet, Box 210, SE-171 77
- 508 Stockholm, Sweden. Email: <u>Kristian.Dreij@ki.se</u> Tel: +46 8 524 87566

509

- 510 **Running Title**
- 511 Environmental PAH mixtures activate MAPK signaling

512

513 Abbreviations

- AP-1, activator protein 1; BP, benzo[*a*]pyrene; ERK, extracellular regulated kinase; JNK, cJun N-terminal kinase; MAPK, mitogen-activated protein kinase; MEK4, MAPK kinase 4;
 PAH, polycyclic aromatic hydrocarbon; PM, particulate matter; TEF, toxic equivalency
 factor; TNF, tumor necrosis factor;

519 Abstract

Polycyclic aromatic hydrocarbons (PAHs) are common environmental pollutants that occur 520 naturally in complex mixtures. Many of the adverse health effects of PAHs including cancer 521 are linked to the activation of intracellular stress response signaling. This study has 522 investigated intracellular MAPK signaling in response to PAHs in extracts from urban air 523 collected in Stockholm, Sweden and Limeira, Brazil, in comparison to BP in HepG2 cells. 524 Nanomolar concentrations of PAHs in the extracts induced activation of MEK4 signaling with 525 down-stream increased gene expression of several important stress response mediators. 526 Involvement of the MEK4/JNK pathway was confirmed using siRNA and an inhibitor of JNK 527 signaling resulting in significantly reduced MAPK signaling transactivated by the AP-1 528 transcription factors ATF2 and cJun. ATF2 was also identified as a sensitive stress responsive 529 protein with activation observed at extract concentrations equivalent to 0.1 nM BP. We show 530 531 that exposure to low levels of environmental PAH mixtures more strongly activates these signaling pathways compared to BP alone suggesting effects due to interactions. Taken 532 533 together, this is the first study showing the involvement of MEK4/JNK/AP-1 pathway in regulating the intracellular stress response after exposure to nanomolar levels of PAHs in 534 environmental mixtures. 535

536

537 Key Words

538 PAHs, Air particulate matter, Complex mixtures, Benzo[*a*]pyrene, MAPK

539

540 **1. Introduction**

Human exposure to environmental pollutants in air particulate matter (PM) has been identified to cause a number of adverse health effects including cancer and various cardiovascular and respiratory diseases [1, 2]. One important group of environmental

pollutants that are associated with PM and play an important role in the reported detrimental 544 health effects are the polycyclic aromatic hydrocarbons (PAHs) [3]. PAHs are ubiquitous 545 environmental pollutants that are naturally present as mixtures and are formed during 546 547 combustion of carbon-containing fuels. Both individual and mixtures of PAHs are classified as carcinogens or probable carcinogens by the International Agency for Research on Cancer 548 [4]. Recent data from us and others have suggested synergistic effects due to interactions 549 550 between PAHs in complex mixtures on the genotoxic and carcinogenic properties of PAHs [5-551 8], though conversely, strong antagonistic effects have also been observed in human cells, probably resulting from competitive inhibition of metabolizing enzymes [9-11]. However, the 552 553 role of interactions between PAHs in complex mixtures in relation to the adverse health effects of PAHs is poorly understood [12]. 554

The activator protein-1 (AP-1) transcription factor is a dimeric complex comprising 555 556 members of the ATF, FOS, JUN and MAF protein families that has functions in many areas of cellular homeostasis [13, 14]. In response to cellular stress stimuli AP-1 proteins are 557 558 activated by the mitogen-activated protein kinase (MAPK) family of proteins, including c-Jun N-terminal kinase (JNK), p38 and extracellular signal-regulated kinase (ERK) [15, 16]. The 559 protein MAPK kinase 4 (MEK4/MKK4) specifically activates JNK and p38 [17] and has been 560 561 identified as an important metastasis suppressor in several organs [18] and a possible target for small molecule inhibition in therapy for tumor necrosis factor alpha (TNF) mediated 562 diseases [19]. The present study focuses on activation of MAPK signaling in response to 563 environmental mixtures of PAHs compared to single benzo[a]pyrene (BP) exposure in 564 565 human-derived hepatoma (HepG2) cells. It has previously been shown that in vitro exposure to BP leads to activation of MAPK signaling associated with apoptotic cell death via p53 [20, 566 567 21]. However, the role of MAPK signaling in the stress response after exposure to nanomolar concentrations of PAHs in air PM remains unclear. 568

Using PAH-containing air PM extracts from Stockholm, Sweden and Limeira, Brazil 569 at nanomolar concentrations we studied the time-dependent activation of MAPK signaling 570 and downstream gene expression in HepG2 cells. Our results show that nanomolar 571 572 concentrations of PAH extracts more strongly activate MAPK signaling and proteins of the AP-1 transcription factor than BP alone suggesting effects due to interactions and that this 573 activation is mediated via MEK4 and JNK. Furthermore, the transactivation of cellular stress 574 mediators including interleukin 8 in response to PAH extract was shown to be mediated 575 576 through a MAPK. To the authors knowledge this is the first study to demonstrate activation of MEK4/JNK/AP-1 with downstream increased gene expression in the cellular stress response 577 578 after exposure to nanomolar levels of PAHs found in air PM.

579

580 2. Materials and Methods

581

582 2.1. Reagents and antibodies

Unless otherwise stated all chemicals, including BP, were of analytical grade and obtained 583 from Sigma Aldrich (Stockholm, Sweden). Detailed information on manufacturer and purity 584 of the standards and solvents used for PAH analysis have been published previously [22, 23]. 585 Gibco (Invitrogen, Paisley, UK) supplied all cell culture reagents. Cell Signaling Technology 586 (Beverly, MA) provided the following antibodies: phospho-ATF2 Thr71, phospho-cJun 587 Ser63, JNK, phospho-JNK Thr183/Tyr185, MEK4, phospho-MEK4 Thr261. Santa Cruz 588 Biotechnology (Santa Cruz, CA, USA) provided the Cdk2, phospho-Erk Tyr204 and 589 phospho-p38 Thr180/Tyr182 antibodies, secondary anti-rabbit, anti-mouse and siRNA 590 against MEK4 and control siRNA-A. Calbiochem (Gibbstown, NJ, USA) provided the JNK 591 592 inhibitor VIII.

594 2.2. Air sampling, sample preparation and PAH analysis

Air PM was collected at two sites: the campus of Stockholm University, Stockholm, Sweden 595 and the campus of the Faculty Technology at UNICAMP, Limeira, Brazil. At both collection 596 sites total PM was collected. The air PM sample from Stockholm was collected at roof-top 597 level on a Teflon-coated glass fiber filter (Ø149 mm, Pallflex Inc., Putnam, CT, USA) with an 598 average flow rate of 509 l min⁻¹ for 170 h. The total PM concentration for this sample was not 599 determined, but PM concentration from other similar urban sites in Stockholm during the 600 same season ranged from $10.4 - 19.4 \ \mu g/m^3$ (unpublished data). The air PM sample from 601 Limeira was collected at street level on a glass-fiber filter (254×233 mm, 0.33 mm pore size, 602 Energética Ind. Com. LTDA, Rio de Janeiro, RJ, Brazil) using a high-volume sampler 603 (Energética Ind. Com. LTDA, Rio de Janeiro, RJ, Brazil) operated at an average flow rate of 604 1130 l min⁻¹ for 24 h. The total PM concentration in the Limeira sample was 95.8 μ g/m³ [24]. 605 606 Extraction was performed using an ASE 200 accelerated solvent extraction system (Dionex 607 Corporation, Sunnyvale, CA, USA). Toluene was used as an extraction solvent at 200 °C and 608 3000 psi for five consecutive 30 min static extraction cycles as described previously [6]. PAH 609 content in the extracts was determined by HPLC-GC/MS as described previously [6, 22].

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611 **2.3. Cell culture and exposure**

Human-derived hepatocellular carcinoma cells (HepG2) were obtained from the American Type Culture Collection (Rockville, MD, USA). The motivation for the use of this cell line in this study is the metabolic competence for PAHs [25] and a previously demonstrated response to low levels of PAHs (in mixtures) extracted from environmental samples by ourselves and others [5-7]. HepG2 cells were cultured in minimal essential medium supplemented with 10 % fetal bovine serum, sodium pyruvate (1 mM), non-essential amino acids (0.1 mM), penicillin (100 units/ml) and streptomycin (0.1 mg/ml) and maintained at 37 °C in 5 % CO₂. Prior to exposure cells were seeded at 3×10^5 cells/ml in 6-well plates and cultured for 72 h unless otherwise stated. Cells were exposed to solvent control (0.1 % DMSO), BP, or PAH extracts for up to 24 h.

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623 2.4. RNA interference

Transfection of cells was performed using Lipofectamine 2000 reagent (Invitrogen, Paisley, UK). Briefly, cells were seeded into 35 mm culture dishes and after 24 h transfected with 50 nM siRNA. siRNA sequences are shown in Supplementary Table 1. After 48 h of incubation cells were exposed to PAHs or solvent control, and then harvested for Western blot analysis.

628

629 **2.5. Western blotting**

Western blotting was performed as described previously [6]. Briefly, whole cell lysates were 630 631 subjected to standard SDS-PAGE and separated proteins transferred to a PVDF membrane (Bio-Rad, Hercules, CA, USA) by wet electro-blotting. Non-specific antibody binding was 632 reduced by incubating membranes in 5 % non-fat dry milk. Signals were detected using 633 634 enhanced chemiluminescence (Amersham GE Healthcare Bio-Sciences AB, Uppsala, Sweden). Experiments were performed at least in triplicate and analyzed separately. 635 Densitometric analysis was performed using ImageJ software version 1.45s (National Institute 636 of Health, USA). 637

638

639 2.6. RNA purification and real-time RT-PCR

Total RNA was prepared using the RNeasy Mini Kit (Qiagen, Hilden, Germany) and 1 μg
used to generate cDNA with the High Capacity cDNA Reverse Transcription kit (Applied
Biosystems, Foster City, CA, USA) according to protocol. Subsequently, quantification of
gene expression was performed in duplicates using MaximaTM SYBR® Green qPCR Master

Mix (Fermentas, St. Leon-Rot, Germany) with detection on an Applied Biosystems 7500 Real-Time PCR System. The reaction cycles used were 95 °C for 2 min, and then 40 cycles at 95 °C for 15 s and 60 °C for 1 min followed by melt curve analysis using GAPDH as housekeeping gene. Primer sequences are shown in Supplementary Table 1. Relative gene expression quantification was analyzed with the mathematical model described in [26].

649

650 2.7. Statistical analysis

All data presented are means \pm SE. One-way ANOVA with Bonferroni's t-test correction was used to determine statistical significance (p < 0.05).

653

654 3. Results and discussion

655

656 **3.1. Analysis of PAH content in air PM extracts**

The PAH content in the two air PM extracts was determined using our recently developed 657 658 methodology that is capable of quantifying 42 unique PAHs of between 3 and 6 rings [6, 24] 659 (Supplementary Table 2). PAHs at the LIMEIRA sampling site mainly result from heavy traffic (including cars and trucks), industrial emissions and biomass burning, whereas those at 660 the STHLM site can mainly be attributed to heavy traffic emissions. The results showed that 661 the air PM extract from Limeira (LIMEIRA) had approximately 3-fold higher total PAH 662 content than the extract from Stockholm (STHLM) (10169.2 and 3392.6 pg/m³, respectively), 663 in agreement with recent data [24]. The level of BP was approximately 5-fold higher in the 664 LIMEIRA sample (807 pg/m^3) compared to the STHLM sample (160 pg/m^3). The level of the 665 highly potent dibenzo[a,l]pyrene was approximately 9-fold higher in the LIMEIRA sample 666 (9.07 pg/m^3) compared to the STHLM sample (1.05 pg/m^3) . 667

In order to compare the cellular response to the two PAH extracts and with BP alone, 668 the extracts were prepared in DMSO to contain a concentration equivalent of 1 μ M BP (BP_{eq}) 669 (actual 0.91 and 1.10 µM for STHLM and LIMEIRA respectively, Supplementary Table 2). 670 Cells were exposed to the PAH extracts with a final concentration of 1 nM BP_{eq}, and hence, 671 cells were also exposed to 1 nM BP alone for comparative purposes. The final total PAH 672 673 concentration the cells were exposed to was 21.6 and 14.4 nM for the STHLM and LIMEIRA 674 extracts respectively. When assessing human exposure to PAHs in ambient air BP is often used as a surrogate indicator [27, 28] and thus, normalizing the PAH extracts to a set 675 concentration of BP allows us to evaluate how well the BP content can predict the observed 676 effects. Neither the Stockholm [6] nor the Limeira extract (data not shown) demonstrated 677 cytotoxicity in the HepG2 cell line. 678

679

680 3.2. Nanomolar levels of PAH extracts activate JNK signaling

Activation of DNA damage signaling in cells after exposure to nanomolar concentrations of 681 the STHLM extract has been demonstrated previously [6]. To identify regulatory pathways 682 involved in different cellular responses including inflammation, apoptosis and cell cycle 683 control, we assessed activation of MAPK proteins that have previously been shown to be 684 activated in response to PAHs [29-32]. The results showed a significant increase in levels of 685 phosphorylated JNK (pJNK) whilst no significant effect was observed on total JNK protein or 686 on phosphorylation of Erk (pERK) or p38 (pp38) (Figure 1). Phosphorylation of JNK in 687 response to the two PAH extracts followed different kinetics with the STHLM extract 688 inducing a persistent increase in activation throughout the 12 hours whereas the LIMEIRA 689 extract induced the highest levels of pJNK after 3 h which decreased thereafter. It is probable 690 691 that this difference in trends is a result of different extract composition though further

investigation is required to confirm this. Both extracts induced a stronger activation of JNKthan exposure to 1 nM BP alone (Figure 1).

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Figure 1. Nanomolar concentrations of PAH extracts activate JNK signaling. Cells were exposed to the PAH extracts (1 nM BP_{eq}) or 1 nM BP alone. Total and phosphorylated levels of the indicated proteins were determined by Western blot at 3, 6 and 12 h. Cdk2 was used as a loading control. Densitometric analysis is shown to the right. *p<0.05 compared with DMSO control levels.

701

3.3. AP-1 transcription factors are activated in response to nanomolar levels of PAH extracts

704 ATF2 and cJun are important proteins that form part of AP-1 and that are activated downstream of JNK [33, 34]. In agreement with the increased levels of pJNK, we observed 705 increased phosphorylation of ATF2 and cJun (Figure 2A). Levels of phosphorylated ATF2 706 (pATF2) showed a significant increase in response to both BPeq extracts, with the STHLM 707 extract inducing higher and more sustained levels of pATF2 than the LIMEIRA extract, 708 displaying >8-fold higher levels than control up to 12 h post-exposure. Levels of 709 phosphorylated cJun (pcJun) displayed the same pattern as pATF2 with the highest levels in 710 response to the STHLM extract (Figure 2A). Similar to the effect on pJNK, both extracts 711

induced higher levels of phosphorylation of ATF2 and cJun compared to 1 nM BP alone 712 (Figure 2A). As shown in Figure 2B, significant increase in level of pATF2 could be detected 713 in response to the STHLM extract at BP_{eq} concentrations down to 0.1 nM (1.8-fold, p = 0.03, 714 715 total PAH concentration = 2.2 nM). These results suggest that pATF2 could be a sensitive biological marker for activation of MAPK signaling in response to PAHs. ATM-mediated 716 activation of ATF2 by phosphorylation at Ser490/498 is implicated in the DNA damage 717 response [35] and the possible role of ATF2 connecting MAPK and DNA damage signaling 718 719 in response to PAHs is interesting.

The results presented here show clear differences in the observed responses between 720 the PAH extracts. The signaling was also in general much stronger in response to the PAH 721 extracts compared to BP alone, similar to what we have reported earlier for DNA damage 722 signaling [6]. Since the total PAH content was quite similar for the 1 nM BP_{eq} STHLM and 723 724 LIMEIRA extracts this implies that the observed differences more likely are due to sample composition. An explanation for this observation could be that there are different PAHs 725 726 present in the STHLM extract that are more potent MAPK inducers than BP. Alternatively, 727 substituted PAHs such as nitro-PAHs, which are known to induce stress signaling [36], might also contribute to the effects of the extracts. In addition, non-PAH compounds could affect the 728 response of the extracts. The level of polychlorinated biphenyls were approximately 0.5 % of 729 the PAH level (pg/m³) in the STHLM extract (unpublished data) and thus are predicted to 730 have minimal effects. Other polychlorinated compounds such as dibenzo-dioxins and furans 731 may also contribute to the overall effect of the extracts [37, 38]. Metals are also known to be 732 present in environmental air PM, and although the levels of metals in our extracts is unknown, 733 we speculate that due to the sampling and processing methods the levels are likely to be low 734 [11]. 735



Figure 2. AP-1 transcription factors are activated in response to nanomolar levels of PAH extracts. Cells were exposed to the PAH extracts (1 nM BP_{eq}) or 1 nM BP alone. Total and phosphorylated levels of the indicated proteins were determined by Western blot at 3, 6 and 12 h (A). Cells were exposed to decreasing concentrations of the STHLM extract and level of pATF2 was assessed at 12 h (B). Cdk2 was used as a loading control. Densitometric analysis is shown below. *p<0.05 compared with DMSO control levels.

745 3.4. Activation of JNK/AP-1 signaling is mediated through MEK4

MEK4 has previously been shown to be involved in regulating pro-apoptotic signaling in human 293T and HeLa cells and rat F258 cells in response to BP treatment, albeit at higher concentrations than used here, leading to downstream caspase activation [39, 40]. However, it has not been established if MEK4 is activated in response to levels of PAHs found in urban air. The results showed significantly increased levels of phosphorylated MEK4 (pMEK4) after exposure to both extracts and 1 nM BP, though highest levels were observed after 12 h exposure to the STHLM extract (4.5-fold, p = 0.028, Figure 3A). No changes were observed on levels of total MEK4. These results clearly show that MEK4 is activated in response to nanomolar levels of PAHs in mixtures and that the levels are higher compared to BP alone.

To determine if JNK/AP-1 activation was dependent on activation of MEK4 HepG2 755 cells were exposed to the STHLM extract for 12 hours following pre-treatment with siRNA 756 against MEK4 (Figure 3B). Based on the effects in the time-response experiments shown in 757 758 Figure 3A, only exposure to the STHLM extract was investigated with siRNA. Transfecting the cells with siRNA against MEK4 significantly reduced the levels of total MEK4 protein 759 resulting in significantly reduced signaling through JNK, ATF2 and cJun (Figure 3B). No 760 effect was observed with control siRNA confirming that the observed response resulted from 761 interference of MEK4 and was not a by-product of the transfection procedure. Taken together, 762 763 these data show that activation of JNK/AP-1 signaling in response to environmental PAH extracts results from activation of the upstream MAPK kinase MEK4. To our knowledge this 764 765 is the first time MEK4 is identified as a mediator of stress signaling in response to 766 concentrations of PAHs found in urban air.



767

Figure 3. MEK4 mediates signaling through MAPK leading to activation of AP-1 768 transcription factors. Cells were exposed to the PAH extracts (1 nM BPeq) or 1 nM BP alone 769 770 and total and phosphorylated levels of MEk4 were determined by Western blot at 3, 6 and 12 771 h (A). Cells transfected with either mock siRNA or siRNA against MEK4 were exposed to the STHLM extract (1 nM BPea) for 12 h and effects on phosphorylation status of JNK, ATF2 772 773 and cJun were assessed by Western blot (B). Cdk2 was used as a loading control. 774 Densitometric analysis is shown to the right. *p<0.05 compared with DMSO control levels. [#]p<0.05 compared with STHLM treatment. 775

777 3.5. JNK mediates transactivation of cellular stress mediators through AP-1

To confirm the role of activation of JNK signaling in activation of AP-1 proteins in response to PAH extracts, HepG2 cells were pre-treated for 1 h with a JNK inhibitor (JNKi, 20 μ M) [41] followed by exposure to the STHLM extract for 12 h (Figure 4). Significantly reduced levels of both pATF2 and pcJun were observed confirming the involvement of JNK in activation of ATF2 and cJun in this study. JNK and cJun have previously been reported to be mediators of cellular stress responses to PAHs [42, 43]. However, this is the first time that activation of ATF2 can be linked to cellular stress signaling in response to PAHs.

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Figure 4. Activation of AP-1 transcription factors is mediated through JNK. Cells pretreated for 1 h with JNKi (20 μ M in DMSO) were exposed to the STHLM extract (1 nM BP_{eq}) for 12 h and effects on phosphorylation status of ATF2 and cJun was assessed by Western blot. Densitometric analysis is shown below. *p<0.05 compared with DMSO control levels. *p<0.05 compared with STHLM treatment.

To investigate if activation of MAPK signaling in response to nanomolar levels of 793 PAH extracts would result in induction of cellular stress mediators, effects on expression of 794 MAPK regulated genes were examined by qRT-PCR (Figure 5). The results showed 795 significant effects on the mRNA levels of tumor necrosis factor alpha (TNF), interleukin 8 796 (IL-8), tumor necrosis factor receptor superfamily member 6 (TNFR6 or FAS) and, epidermal 797 growth factor receptor (EGFR). Expression levels of TNF and IL-8 displayed the strongest 798 response with 13.3- and 5.7-fold up-regulation at 12 h, respectively. These genes are 799 800 transactivated via MAPK signaling and involved in stimulating inflammation, proliferation or apoptosis and have all been shown to be play important roles in regulation of human diseases 801 such as cancer (reviewed in [13, 14]. Moreover, in the presence of JNKi, mRNA levels of 802 TNF, IL-8 and FAS were significantly reduced 12 h post treatment to the level of the DMSO 803 control. Although the mRNA levels of EGFR were reduced in response to blocked JNK 804 805 signaling 24 h post treatment, no significant effects were observed. These results confirm the 806 involvement of MAPK signaling in transactivation of cellular stress mediators in response to 807 nanomolar levels of PAH mixtures.



Figure 5. Induction of gene expression of stress response mediators is mediated through a MEK4/JNK/AP-1 signaling pathway. Cells were exposed to the STHLM extract (1 nM BP_{eq}) for 12 h with or without JNKi pretreatment and effects on gene expression were determined by qRT-PCR. *p<0.05 compared with DMSO control levels. $^{\#}p$ <0.05 compared with STHLM 813 treatment.

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815 **3.6.** Comparison with toxic equivalency factors

In order to compare the extracts with BP they were prepared to have a final exposure concentration equivalent to 1 nM BP. An alternative approach is to derive BP equivalent concentrations using toxic equivalency factor (TEF) scales. Using previously published TEF values [44] we calculated BP_{TEQ} concentrations of 1.74 and 1.46 for the STHLM and LIMEIRA samples. Data for fold difference for pATF2, pcJun, pJNK and pMEK4 are given in Supplementary Table 3 and are presented as fold differences compared to BP. As can be

seen, the fold differences for pATF2 are higher than predicted based on BP_{TEO} concentrations 822 823 of the PAH extracts, emphasizing pATF2 as a sensitive biological marker for activation of MAPK signaling following PAH exposure. An explanation for this observation is that there 824 825 could be different PAHs present in the extracts that are more potent inducers of the stress response than BP. Fold differences were similar to what would be predicted for pcJun, pJNK 826 827 and pMEK4 based on BP_{TEO} concentrations. However, it should be noted that there are a 828 number of important considerations and requirements that make the TEF-based approach 829 insufficient for mixture assessment as discussed recently [12].

830

831 4. Conclusion

Here we report that nanomolar concentrations of environmental PAH mixtures, extracted 832 from urban air PM collected in Stockholm, Sweden and Limeira, Brazil, induce a time-833 834 dependent activation of MAPK signaling in HepG2 cells. We show that exposure to low levels of PAH extracts more strongly activates signaling pathways compared to BP alone 835 836 suggesting possible effects from interactions. Exposure to the PAH extracts induces activation 837 of MEK4 signaling with down-stream increased expression of several important stress response mediators. Abrogation of the MEK4-JNK pathway using siRNA and a specific 838 inhibitor against JNK significantly reduces the transactivation mediated through AP-1 839 transcription factors ATF2 and cJun. This is the first study showing activation of 840 MEK4/JNK/AP-1 pathway in in response to nanomolar levels of PAHs in environmental 841 842 mixtures.

843

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