


Interactions between polycyclic aromatic hydrocarbons and epoxide hydrolase 1 play roles in asthma

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Abstract Asthma, as one of the most common chronic diseases in children and adults, is a consequence of complex gene–environment interactions. Polycyclic aromatic hydrocarbons (PAHs), as a group of widespread environmental organic pollutants, are involved in the development, triggering and pathologic changes of asthma. Various previous studies reported the critical roles of PAHs in immune changes, oxidative stress and environment–gene interactions of asthma. *EPHX1* (the gene of epoxide hydrolase 1, an enzyme mediating human PAH metabolism) had a possible association with asthma by influencing PAH metabolism. This review summarized that (1) the roles of PAHs in asthma—work as risk factors; (2) the possible mechanisms involved in PAH-related

asthma—through immunologic and oxidative stress changes; (3) the interactions between PAHs and *EPHX1* involved in asthma—enzymatic activity of epoxide hydrolase 1, which affected by *EPHX1* genotypes/SNPs/diplotypes, could influence human PAH metabolism and people’s vulnerability to PAH exposure. This review provided a better understanding of the above interactions and underlying mechanisms for asthma which help to raise public’s concern on PAH control and develop strategies for individual asthma primary prevention.

Keywords Polycyclic aromatic hydrocarbons (PAHs) · Asthma · Epoxide hydrolase 1 (*EPHX1*) · Airway inflammation · Oxidative stress

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Introduction

Asthma is one of the most common chronic diseases (Global Initiative for Asthma 2018b). Approximately 334 million people suffer from asthma around the world with a prevalence ranging from 1 to 18% in different areas (Global Asthma Network 2014; Papi et al. 2018). In total, 14% of the children and 8.6% of young adults (18–45 years of age) around the world experience asthma symptoms, while 4.5% of young adults have been diagnosed with asthma and/or are taking treatment for asthma (Global Asthma Network

2014). The prevalence of asthma has increased during the past decades, particularly in westernized countries (World Allergy Organization 2013). Asthma is becoming increasingly common in developing countries because of increased industrialization and urbanization (World Allergy Organization 2013). From 2001 to 2010 in the USA alone, the overall prevalence of asthma has increased from 20.3 million (7.3%) to 25.7 million (8.4%), and asthma in children has increased from 8.7 to 9.3% (7.0 million) (Moorman et al. 2012). In Europe, asthma affects approximately 30 million children and adults under 45 years of age, with a prevalence ranging from 3 to 9% (European Respiratory Society 2013). The prevalence of asthma in China from 2000 to 2010, in urban settings has increased from 1.59 to 2.11% in children (0–14 years of age) and to 1.2% in adults (> 14 years of age) (Feng et al. 2014; Sha et al. 2015). As the 14th most important disorder in the world in terms of the extent and duration of disability, asthma places a heavy economic burden on families and countries globally (Global Asthma Network 2014).

Host-environment interactions in asthma have been studied over different spatial scales and timescales, such as CD14-endotoxin, HLA-allergens and ORMDL3-tobacco smoke, but they cannot fully explain the pathogenesis of asthma (Lee et al. 2015; Papi et al. 2018). Host factors include age, gender and genetic predisposition. Among them, SNPs and epigenetics have attracted a lot of attention in recent years (Lee et al. 2015). Polymorphisms for immune-related genes (*IL33*, *IL1RL1/IL18R1*, *HLA-DQ*, *SMAD3*, *IL2RB9*, *TSLP*) and airway function-related genes (*ZPBP2*, *GSDMB*, *ORMDL3*) have been studied in previous host-environment studies of asthma (Miller et al. 2018; Papi et al. 2018; Torgerson et al. 2011). Environment factors inducing to asthma include indoor and outdoor pollution, allergens, microorganism and cigarette smoke (Lee et al. 2015). Among them, varieties of air pollution (sulfur dioxide, nitrogen dioxide, carbon monoxide, ozone, particulate matter with aerodynamic diameters less than 10 and 5 μm) have attracted a lot of attentions in recent years, whereas the effects of individual compounds are needed to be examined (Hehua et al. 2017; Zhang et al. 2016). For the most complex future scenario in which both genes and environment are unknown, large sets of environmental exposures and specific asthma phenotypes need to be defined (Lee et al. 2015).

Polycyclic aromatic hydrocarbon (PAH) is an environmental risk factor for asthma proved by amounts of epidemiologic studies, but the specific and quantitative relationships between PAH exposure and asthma, as well as underlying mechanisms, are unclear. Many studies focus on the involvement of complex PAH mixtures in asthma, such as vehicle exhaust, PM 2.5, tobacco smoke, instead of individual PAHs. The reason may lie in the physical and chemical properties of PAHs. Consisting of two or more fused aromatic (benzene) rings, PAHs are naturally deposited in coal, crude oil, peat and lignite (World Health Organization 2010; International Programme On Chemical Safety 1998). PAHs are released as mixtures to atmosphere and soil by incomplete combustion during daily living (traffic-related emission, tobacco smoking, cooking and heating) and industrial activities (coal-fired power plants, electronic waste recycling, asphalt, foundries and blast furnaces) (Chen et al. 2017; Guo et al. 2011; International Programme On Chemical Safety 1998; Xu et al. 2015). People in various areas suffer from PAH exposure and related health risks (Chen et al. 2017; Gosai et al. 2017; Keshavarzifard et al. 2017; Qu et al. 2015). With high lipophilic nature, PAHs are easily absorbed into human body through ingestion, inhalation and dermal contact, and then distribute rapidly and widely in the body (World Health Organization 2010). Humans have a high biotransformation potential for PAH, and the half-life of PAH dietary exposure in human body was only 2.5–6.1 h (Li et al. 2012). Although PAHs do not accumulate in human body, their reactive metabolites bound covalently to proteins and nucleic acids which cannot be repaired, resulting in genotoxicity and further adverse effects in almost all systems, including respiratory system (Guo et al. 2011, 2012; International Programme on Chemical Safety 1998; World Health Organization 2010; Xu et al. 2015). There are complex relationships between PAH exposure and asthma development, and multiple potential mechanisms might involve in this web of causation, including inflammatory responses and oxidative stress pathways (Karimi et al. 2015). In order to develop effective asthma prevention, research is needed to clarify the exact associations between individual PAH and asthma.

EPHX1, the gene of epoxide hydrolase 1, is an uncertain risk factor for asthma (Lee et al. 2011; Wang

and Karmaus 2017). *EPHX1*'s genotype and diplotype are associated with enzymatic activity of epoxide hydrolase 1, a phase I metabolic enzyme involved in the in vivo metabolism of PAHs and other organics (Henkler et al. 2012; Tung et al. 2011). Interaction between *EPHX1* SNPs and Phthalate metabolite involved in asthma has been explored in the previous study (Wang and Karmaus 2017). Both Phthalate and PAHs are organic pollutants needing epoxide hydrolase 1 for phase I metabolism in vivo. It provides a possibility that the interaction between *EPHX1* SNPs and PAHs may be involved in asthma. Very few literature focused on the roles of interactions between PAHs and *EPHX1* in asthma, let alone the inconsistent conclusions deduced from them.

Pathogenesis of asthma has not been fully defined, which limit the opportunities to develop targeted primary prevention, so a better understanding of the environment-gene interaction between PAHs and *EPHX1* involved in asthma will provide a reference for asthma primary prevention measures (Beasley et al. 2015). In order to explore above questions, the authors worked on the research articles and reviews on patterns of PAH exposure and asthma from different countries. These articles were collected in PubMed and official websites of World Health Organization (<http://www.who.int/>), International Programme On Chemical Safety (<http://www.inchem.org/documents/ehc/ehc/ehc202.htm>), Global Initiative for Asthma 2018 (<http://ginasthma.org/>), Global Asthma Network (<http://www.globalasthmanetwork.org/>), European Respiratory Society (<https://www.erswhitebook.org/>), and NCBI (<http://www.ncbi.nlm.nih.gov>) and the searching criteria are below: combined the terms "asthma" and the subheadings "pathogenesis" "immunology" "airway inflammation" "oxidative stress" "SNPs," as well as "polycyclic aromatic hydrocarbons" and "epoxide hydrolase 1"; articles from the 5 years prior to 2018 were mostly used with some exceptions. According to these literature, this review is summarized into three parts: (1) the roles of PAH exposure in asthma; (2) the possible mechanisms involved in PAH-related asthma; and (3) the interactions between PAHs and *EPHX1* involved in asthma.

The roles of PAH exposure in asthma

In this part, we reviewed the complex relationships between PAH exposure and asthma.

PAHs and diagnosed asthma

Jung et al. reported in an inner-city cohort that indoor air exposure to high concentrations (prenatal $> 2.61 \text{ ng/m}^3$ or current $> 1.01 \text{ ng/m}^3$) of pyrene (a kind of semi-volatile PAHs) was positively associated with asthma in 5- to 6-year-old children (Jung et al. 2012). Liu et al. found positive associations between urinary 1-pyrene and risk of diagnosed asthma in 6- to 19-year-old children, between urinary 2-phenanthrene and risk of diagnosed asthma in 13- to 19-year-old boys (Liu et al. 2016). Compared to reference area, children in benzo[a]pyrene exposed area Ostrava have higher asthma prevalence up to the age of 3.5 years (Sram et al. 2013). Serum naphthalene and pyrene are higher in asthmatic subjects than non-asthmatic subjects (Al-Daghri 2008). Possible mechanisms were summarized by Burton et al. that prenatal exposure to PAHs may be setting the stage for childhood asthma through DNA methylation in fetal lung or immune system (Burton 2009).

PAHs and asthma clinical manifestations

Increased wheezing was found in asthmatic children exposed to air phenanthrene and 4- to 6-ring particle-bound PAHs (Gale et al. 2012). Positive association between 4-phenanthrene and risk of wheezing was found in 13- to 19-year-old girls (Liu et al. 2016). Prenatal exposure to PAHs from fossil fuel combustion is a risk factor for wheezing without cold and the duration of wheezing in the chest during the first year of life (Jedrychowski et al. 2005).

Exposure to PAHs has been reported to cause impaired lung function in asthmatics. Forced expiratory volume in 1s (FEV1) and forced vital capacity (FVC) of asthmatic children are negatively associated with benzo(a)pyrene, low molecular weight PAHs, high molecular weight PAHs and total PAHs (Smargiassi et al. 2014). Similar negative associations are found between 2- to 4-ring PAHs and FEV1, FVC in healthy Chinese (Zhou et al. 2016).

PAH exposure linked to asthma biomarkers, especially in allergic asthma. Specific immunoglobulin (Ig)E levels and eosinophil counts are the most consistent biomarkers for the identification of infants and preschool children at high risk of allergic asthma (Wandalsen et al. 2016). Naphthalene, 4H-cyclobenta[def]phenanthrene, pyrene and 1,2-benzanthracene were correlated with IgE in Arab children (Al-Daghri et al. 2013). Mice exposed to diesel exhaust particles contained 522 micrograms of PAHs that have significant increases in eosinophils (Stevens et al. 2009). In view of complex asthma phenotypes, the associations between PAHs and asthma biomarkers are extremely complex and need more studies to explore.

PAHs and asthma pathologic changes

PAH exposure contributes to airway hyperresponsiveness. Exposure to PAH mixture in common traffic-related air pollutants is associated with reduced β 2-adrenergic receptor gene expression and increased airway hyperreactivity in mice, suggesting that PAH exposure may induce airway hyperreactivity via suppressing β 2-adrenergic receptor (Chu et al. 2013). In addition, there is a possible immune mechanism involved in PAH-related airway hyperreactivity as well. PAH exposure has a positive association with total plasma IgE in both non-asthmatics and asthmatics (Hew et al. 2015). The higher the concentration of IgE, the easier it is for the bronchus to be provoked by methacholine (Sunyer and Munoz 1996). Increased IgE levels contribute to eosinophilic airway inflammation, which is associated with bronchial hyperresponsiveness both in symptomatic and asymptomatic persons (Jansen et al. 1999; Postma et al. 2015). It is confirmed in mice model studies on exposure to diesel exhaust particle PAHs or PAHs (Ren et al. 2014). In addition, PAHs contribute to significant increased eosinophils and further airway hyperresponsiveness via increasing Th2-mediated cytokines IL-5 and IL-13 (Ren et al. 2014; Stevens et al. 2009). IL-5 and IL-13 show strong correlations with airway hyperresponsiveness in adult asthma patients as well (Agache et al. 2016). It is deduced from above that PAH exposure can induce the releases of IL-5, IL-13 and IgE, which contribute to airway eosinophilia and further airway hyperresponsiveness.

PAHs contribute to the impaired reversion of airway obstruction in the asthmatic. After exposure to PAH mixture, the expression and function (receptor responsiveness) of β 2-adrenergic receptor of murine tracheal epithelial cells and human airway smooth muscle cells were reduced, indicating that PAHs can impede β 2-adrenergic receptor-mediated airway relaxation, possibly via agonist-induced receptor desensitization (Factor et al. 2011).

PAHs play roles in airway inflammation through T lymphocytes, eosinophils, basophils, mast cells, dendritic cells, neutrophils and macrophages (Eng and DeFelice 2016; Global Initiative for Asthma 2018a; Xu et al. 2017) (Fig. 1). ① Type-2 inflammation: PAH-mediated Th2 skewing stimulates B cells to produce allergen-specific IgE and further induces eosinophilic airway inflammation (Karimi et al. 2015; Postma et al. 2015). Similarly, serum PAH levels are positively associated with IgE, in line with the fact that asthmatic children have higher PAH and IgE levels than non-asthmatic children (Al-Daghri et al. 2013; Wandalsen et al. 2016). Asian sand dust-bound PAHs contribute to the aggravation of ovalbumin-induced lung eosinophilia in mice (Ren et al. 2014; Wandalsen et al. 2016). PAHs in vehicle-emitted particles are proved by studies on allergic human and mice to induce basophil activation and increase basophil percentages (Lubitz et al. 2010; Zakharenko et al. 2017). ② Other inflammations: PAHs influence regulatory T cell (Treg)/Th17/Th22 balance through aryl hydrocarbon receptor (AhR), a transcription factor involved in Th17-/Th22-type polarization, and further neutrophil recruitment in both healthy and asthmatic people (Ple et al. 2015). Similarly, exposure to 100 mg/kg vehicle exhaust-PAHs increases neutrophil percentage in mice (Zakharenko et al. 2017). Degranulation and cytokine release from above-activated immune cells contribute to airway smooth muscle contraction and proliferation, while lung epithelium-derived cytokines also activate above innate immune cells, creating a feedback loop perpetuating asthma (Galowitz and Chang 2015).

PAHs are involved in airway remodeling through eosinophils, mast cells and vascular endothelial growth factor (VEGF) (Bakakos et al. 2016; Grainge et al. 2016; Kudo et al. 2013). PAH-mediated Th2 skewing can lead to chronic eosinophilic inflammation, contributing to airway remodeling and the development of fixed airflow obstruction in the long

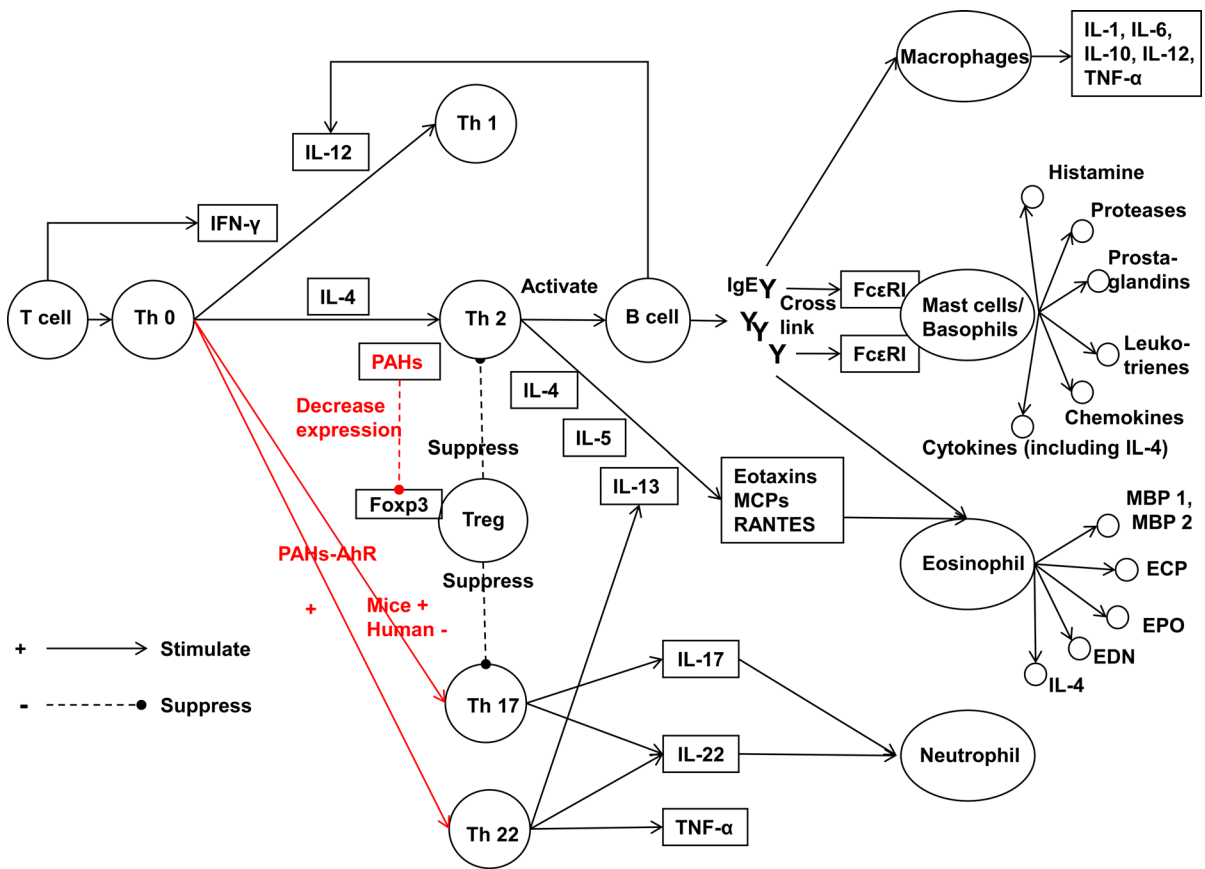


Fig. 1 Effects of PAHs on immune changes involved in asthma. Th2 and Th17 suppressions by Treg are decreased by PAHs. Th17 is downregulated, while Th22 is upregulated by PAHs bonding to AhR. (Eng and DeFelice 2016; Global Initiative for Asthma 2018a; Xu et al. 2017; Harper and Zeki

2015; Kudo et al. 2013; Toldi et al. 2011). MBP major basic proteins; ECP eosinophil cationic protein; EPO eosinophil peroxidase; EDN eosinophil-derived neurotoxin; MCP monocyte chemoattractant protein; RANTES (CCL5) Chemokine (C-C motif) ligand 5

term (Postma et al. 2015). Diesel exhaust particle PAH and benzo(a)pyrene exposure exacerbate IL-22 secretion but inhibit the production of IL-17A through AhR (Ple et al. 2015). IL22 plays roles in neutrophil recruitment, airway smooth muscle proliferation and tissue remodeling (Ple et al. 2015). Exposure to PAHs (AhR ligands) stimulates the degranulation of mast cell, releasing histamine, heparin and tryptase (Modena et al. 2016; Zhou et al. 2013). Increased tryptase can stimulate fibroblast mitogen and type-1 collagen synthesis, leading to airway smooth muscle proliferation (Modena et al. 2016; Zhou et al. 2013). In addition, PAHs induce VEGF through PI-3 K/AP-1-dependent and HIF-1a-independent pathways (Ding et al. 2006). VEGF plays a major role in enhanced vascular permeability and plasma exudation, which

enables inflammatory cells and other plasma components to reach extravascular inflammatory sites, a key process of inflammation (Bakakos et al. 2016). Furthermore, VEGF is also involved in enhanced allergic sensitization, and upregulates subsequent Th2-type inflammatory responses, monocyte chemotaxis, eosinophil chemotaxis and airway edema (Bakakos et al. 2016; Kim et al. 2010).

To explore the exact roles of PAH exposure in asthma risk, we listed the data of previous studies in Table 1. We summarized that prenatal and postnatal PAH exposure both can lead to asthma risk. Pyrene, phenanthrene and total airborne PAHs were risk factors for diagnosed asthma, and it seems that total airborne PAHs had bigger effect than individual PAHs. Total airborne PAH was a risk factor for

Table 1 PAHs and asthma

| Author | Population | Exposure duration | Detected substance | Pollutants | Outcomes | RR (95%CI) or OR (95%CI) |
|----------------------------|---------------------------------|---|--------------------------------------|---|---------------------------------|---|
| Jung et al. (2012) | Children at 5–6 years of age | Prenatal exposure (personal air monitoring during 48 h) Exposure at 5–6 years of age (2-week residential monitoring) | Residential air | High pyrene during pregnancy (> 2.61 ng/m ³) and 5–6 years of age (> 1.01 ng/m ³) | Diagnosed asthma | OR = 1.90 (1.13, 3.20) in whole children OR = 2.89 (1.77–5.69) in non-atopic children |
| Jung et al. (2014) | Children at 5–6 years of age | Monitor 2 weeks | Residential air | 3- to 6-ring PAHs | Diagnosed asthma at age 5 years | 1-methylphenanthrene: RR = 2.62 (1.17–5.88) 9-methylphenanthrene: RR = 2.17 (1.06–4.45) 3,6-dimethylphenanthrene: RR = 2.69 (1.21–5.94) All in children with obesity |
| Liu et al. (2016) | Participants aged 6–19 years | One spot individual exposure | Urine PAH metabolites | 2- to 4-ring PAHs | Diagnosed asthma | 1-pyrene quartile 4: OR = 1.444 (1.003–2.080) 2-phenanthrene in boys 13–19 years of age: OR = 2.35 (1.16–4.79) |
| Wang et al. (2017) | Children at 6 years of age | Individual exposure 3 years ago | Urine PAH metabolite | 1-hydroxypyrene | Diagnosed asthma | OR = 1.42 (1.18–1.70) |
| Jedrychowski et al. (2014) | 4 year-follow-up from pregnancy | Prenatal and postnatal exposure | Personal indoor airborne PAH monitor | Total airborne PAHs | Diagnosed asthma | OR = 7.80 (1.40, 43.47) |

Table 1 continued

| Author | Population | Exposure duration | Detected substance | Pollutants | Outcomes | RR (95%CI) or OR (95%CI) |
|----------------------------|---------------------------------|---|--------------------------------------|---------------------------|-------------------------------|---|
| Liu et al. (2016) | Participants aged 6–19 years | One spot individual exposure | Urine PAH metabolites | 2- to 4-ring PAHs | Ever wheeze | 4-phenanthrene in girls 13–19 years of age: OR = 4.086 (1.326–12.584) |
| Gale et al. (2012) | Children 6–11 years of age | Measured at 1-min intervals and aggregated into 24-h daily averages | Ambient particle-bound PAH | PAHs with 3 rings or more | Self-reported wheeze | 1 day: OR = 1.04 (1.01, 1.07) 14 days ago: OR = 1.06 (1.01, 1.13) 14-day moving average: OR = 1.01 (1.01, 1.02) OR = 1.61 (1.16, 2.24) |
| Jedrychowski et al. (2014) | 4 year-follow-up from pregnancy | Prenatal and postnatal exposure to PAHs | Personal indoor airborne PAH monitor | Total airborne PAHs | Recurrent wheezing | |
| Miller et al. (2010) | Children ≥ 5 year old | Current individual exposure | Urine PAH metabolites | 2- to 4-ring PAHs | Allergen (mouse)-specific IgE | 2-hydroxyfluorene: OR = 1.82 (1.01, 3.28) 3-hydroxyfluorene: OR = 2.21 (1.18, 4.19) 1-hydroxyphenanthrene: OR = 1.88 (1.03, 3.49) 3-hydroxyphenanthrene: OR = 2.08 (1.09, 4.00) $\beta = 0.27, p = 0.027$ |
| Wang et al. (2017) | Children at 6 years of age | individual exposure 3 years ago | Urine PAH metabolite | 1-hydroxypyrene | serum IgE | |

Table 1 continued

| Author | Population | Exposure duration | Detected substance | Pollutants | Outcomes | RR (95%CI) or OR (95%CI) |
|--------------------|----------------------------|---------------------|-------------------------|-------------------|----------|--|
| Zhou et al. (2016) | Residents aged 18–80 years | Individual exposure | Urinary PAH metabolites | 2- to 5-ring PAHs | FEV1 | Estimated Changes in ml (95% CI) 2-OHNap: - 23.79 (- 42.00, - 5.59) 9-OHFlu: - 19.36 (- 33.64, - 5.09) 2-OHFlu: - 41.76 (- 63.24, - 20.28) 1-OHPhe: - 39.53 (- 60.74, - 18.33) 2-OHPhe: - 34.35 (- 52.58, - 16.12) 3-OHPhe: - 27.37 (- 46.30, - 8.44) 4-OHPhe: - 36.87 (- 56.12, - 17.62) 9-OHPhe: - 33.47 (- 52.98, - 13.96) 1-OHPyr: 25.03 (- 41.99, - 8.07) ∑OH-PAHs: - 37.13 (- 58.59, - 15.68) 2-OHNap: - 24.39 (- 46.66, - 2.12) 2-OHFlu: - 33.90 (- 59.89, - 7.90) 1-OHPhe: - 28.56 (- 54.23, - 2.90) 2-OHPhe: - 27.46 (- 49.76, - 5.16) 4-OHPhe: - 27.15 (- 50.51, - 3.80) ∑OH-PAHs: - 27.99 (- 54.26, - 1.71) |
| | | | | | FVC | |

Table 1 continued

| Author | Population | Exposure duration | Detected substance | Pollutants | Outcomes | RR (95%CI) or OR (95%CI) |
|-------------------------------------|--|---|--|--|--|--|
| Smargiassi et al. (2014) | Children 7–12 years of age | Personal pesticide sampling. 10 consecutive days | Ambient PAHs | Benzene, Benzo(a)Pyrene, low molecular weight PAHs, high molecular weight PAHs | FEV1, FVC, FEF25–75% | No significant association |
| Immune Changes Lubitz et al. (2010) | 23–35 years of age | Human basophils | Diesel exhaust particles- PAH | B[a]P and Phe | IL-4 and IL-8 secretion from enriched basophils | Increase in birch pollen-allergic individuals who were exposed to B[a]P or Phe |
| Al-Daghri et al. (2014) | Rats | Treated with benzopyrene | – | Benzopyrene | IL-4 mRNA in whole blood | $\beta = 0.36, p < 0.001$ |
| Al-Daghri et al. (2013) | ≤ 15 years of age | Individual exposure | Serum PAHs | Various PAHs | IL-4 IL-5 IgE | Positive correlation |
| Al-Daghri et al. (2013) | ≤ 15 years of age | Individual exposure | Serum PAHs | Various PAHs | IL-8 IL-10 IFN- γ | Negative correlation |
| Ple et al. (2015) | Human peripheral blood mononuclear cells (PBMCs) | PBMCs were treated by PAH standard reference material and different purified PAHs | Diesel exhaust particle (DEP)-PAH and Benzo[a]Pyrene (B[a]P) | IL-22 IL-17A | Increased IL-22 but decreased IL-17A production in both healthy and asthmatic subjects | |

wheeze. Fluorene that has a bigger effect on lung function than other 2- to 5-ring PAHs. In view of that people in different areas and ages have different susceptibilities to PAH exposure, further meta-analyses are needed to explore the exact effects of individual PAHs. Furthermore, genetic susceptibilities should be taken into account.

Possible mechanisms involved in PAH-related asthma

According to previous studies, we summarized that several kinds of PAHs may increase the onset, symptoms, biomarkers and pathological changes of asthma. Although the responsible mechanisms in PAH-related asthma are not well understood, it was deduced that inappropriate changes in immune system and oxidative stress as well as PAH-*EPHX1* interaction may play roles (Ghosh et al. 2016; Tung et al. 2011; Wandalsen et al. 2016).

Immunologic mechanisms

Asthmatic patients have an imbalance of Treg/Th1/Th2/Th17/Th22 cells: decreased Th1/Th2 ratio, increased Th17/Treg ratio and increased Th22. PAHs are involved in above imbalance and further changes in immune molecules (immunoglobulins, cytokines, inflammatory mediators) and inflammatory cells (T cells, B cell, eosinophil, basophil, mastocyte, neutrophils, macrophages) (Harper and Zeki 2015; Kudo et al. 2013; Toldi et al. 2011) (Fig. 1).

Treg/Th1/Th2/Treg/Th17/Th22 imbalance

PAHs induce DNA methylation of CpG sites within the Forkhead Box P3 (FoxP3) promoter and thus reduce FoxP3 expression in Treg cells, resulting in Treg dysfunction: decreased Th2 suppression and increased Th2-mediated inflammation (Hew et al. 2015). PAHs play roles in Th17/Th22-type polarization through AhR, a transcription factor involved in the development of the Th17 and Th22 subsets (Ple et al. 2015). In mice, PAHs in standardized particulate matter sample, diesel exhaust and cigarette-smoke extract enhance Th17 differentiation (van Voorhis et al. 2013). In human, Th17 is downregulated, while Th22 is upregulated by PAH exposure (Ple et al. 2015).

Further variation of T helper cell-mediated cytokine

PAHs have been shown in previous studies to be associated with decreased Th1-mediated cytokine (IFN- γ) and increased Th2-mediated cytokines (IL-4, IL-5 and IL-13), which resulted from Th2 skewing, favoring an increase in sensitization of type-1 hypersensitivity involved in asthma (Al-Daghri et al. 2013; Hew et al. 2015). After PAH exposure, IL-17 (Th17-mediated cytokine) levels are increased in mice but decreased in human both through AhR, indicating possible species-specific effects of AhR agonists (Hong et al. 2016; Ple et al. 2015). PAHs (AhR agonists) increase IL-22 production but not IL-17 production in human through Th22 but not Th17 (Trifari et al. 2009). Furthermore, PAHs are negatively associated with IL-10, and low levels of IL10 play a role in the pathogenesis of asthma (Al-Daghri et al. 2013; Bohm et al. 2015; Hew et al. 2015). Epigenetics is one of the mechanisms of PAH-related cytokine changes. Maternal exposure to benzo[a]pyrene was associated with hypermethylation of IFN- γ but not IL-4 in cord blood DNA from cohort children (Tang et al. 2012). Increased IL-4 mRNA expression and polycyclic aromatic hydrocarbon concentrations were found in children with asthma (Al-Daghri et al. 2014). The expression of IL-4 mRNA in whole blood from rats treated with benzopyrene was higher than healthy control (Al-Daghri et al. 2014).

Further immunocyte activation and airway inflammation

PAHs enhance allergic inflammation and stimulate inflammatory responses through increasing IgE production mediated by productions of cytokines and chemokines, as well as the activation of macrophages and other mucosal cell types (Nel et al. 1998). Macrophage-derived cytokines induced by PAH exposure, namely IL-1, IL-6, IL-10, IL-12 and TNF- α , are important in allergic inflammation (Nel et al. 1998). When allergens cross-link with sensitized basophils and mast cells directly or through IgE, basophils and mast cells are activated and subsequently release anaphylactogenic mediators, such as histamine, proteases, prostaglandins, leukotrienes, chemokines and cytokines, responsible for the classical symptoms of the immediate phase (type-1 hypersensitivity) (Akdis and Akdis 2015; Chinthrajah et al.

2016). These basophil- and mast cell-released substances and their roles in airway pathological changes are showed in Table 2 (Modena et al. 2016). On the other hand, PAHs increase eosinophil quantity in mouse bronchoalveolar lavage fluid (Stevens et al. 2009). Eosinophils contribute to allergic airway inflammation, later development and severity of asthma in infants and preschool children by releasing granule components, secreting cytokines and regulating T cells (Ren et al. 2014; Wandalsen et al. 2016; Wilkerson et al. 2016). Pro-inflammatory and Th2 cytokine production induced by PAH exposure can stimulate the expression of eotaxin mRNA, a chemotactic factor that regulates eosinophils, and further induce eosinophils to secrete intracellular crystalloid granules (cell degranulation) (Ravin and Loy 2016). Cationic granular proteins released by activated eosinophil and their roles in airway pathological changes are showed in Table 2 (Chatzileontiadou et al. 2015; Morgan et al. 2005; Xia et al. 2016). This degranulation, in target airway tissues and respiratory secretions, is considered a key pathogenic mechanism in asthma because it induces tissue damage and dysfunction (Martinez-Giron and Martinez-Torre 2016).

Oxidative stress mechanisms

8-OHdG was used as a sensitive biological marker of oxidative DNA damage (Zhou et al. 2016). Increased reactive oxygen species (ROS) and reactive nitrogen species are found in asthmatic patients, and they induce asthmatic airway inflammation via pro-inflammation pathways (Andreadis et al. 2003; Guo et al. 2000; Zuo et al. 2013). H_2O_2 and O_2^- are produced during PAH metabolisms in human body (Fig. 2), and the ROS produced by PAHs probably contribute to asthma through immune response and direct airway damage as follows: ROS produced by PAH metabolism lead to transcriptional upregulation of genes involved in immune regulation and activate the promoters of cytokines and chemokines involved in allergic inflammation through activator protein-1 and NF- κ B signaling pathways, which may explain the exacerbation of allergic inflammation (Henkler et al. 2012; Karimi et al. 2015; Nel et al. 2001). Furthermore, oxidants produced by PAH metabolism can impair cilia function, reduce surfactant activity, injure fibroblasts, promote epithelial permeability, and make

other effects which could diminish lung mechanics and/or lung repair mechanisms (Repine et al. 1997). PAHs in diesel exhaust particles also induce apoptosis and necrosis in bronchial epithelial cells via a mitochondrial pathway (Nel et al. 2001).

PAH-EPHX1 interactions

EPHX1 expresses epoxide hydrolase 1, a protein-coding gene located at position 1q42.1. It is a critical biotransformation enzyme in the activation and detoxification of epoxides and in the metabolism of reactive oxidants. This gene has been shown to be involved in several human diseases including asthma (Ghosh et al. 2016; NCBI 2017; Salam et al. 2007; Vaclavikova et al. 2015).

EPHX1 polymorphisms, genotypes, diplotypes and enzymatic activities (Table 3) are associated with risks of lifetime, current, early-onset, early-persistent and late-onset asthma (Salam et al. 2007; Tung et al. 2011). Tung KY et al. found that Tyr/His and His/His at codon 113, Arg/Arg and Arg/His at codon 139, as well as 113His-139Arg and 113Tyr-139Arg diplotypes, were risk factors for lifetime asthma and early-onset asthma (risk: Tyr/His > His/His at codon 113, Arg/Arg > Arg/His at codon 139, 113His-139Arg > 113Tyr-139Arg) (Tung et al. 2011). Similarly, His/Arg at codon 139, 113His-139Arg, 113Tyr-139Arg, 113Tyr-139His and high *EPHX1* metabolic phenotype were risk factors for lifetime asthma, current asthma, early persistent asthma and late-onset asthma (Salam et al. 2007). Meanwhile, polymorphic *EPHX1* alleles in exon 3 and exon 4, as well as *EPHX1* diplotypes, are associated with altered *EPHX1* activity (Ghosh et al. 2013) (Table 3). These results suggest that *EPHX1* SNPs, genotypes and diplotypes related to higher *EPHX1* activities are associated with higher asthma risk. The underlying mechanism is probably related to PAHs: high-activity *EPHX1* produces excessive catechols as well as further hydrogen peroxide and superoxide anion during PAH metabolism in vivo (Fig. 2), leading to increased oxidative stress and ROS-mediated airway damage (Tung et al. 2011). In addition, *EPHX1* genotypes play roles in genetic susceptibility to DNA damage, chromosomal aberrations and epigenetic changes due to environmental exposure, which can explain the difference of asthma risk in people with different *EPHX1* SNPs, genotypes,

Table 2 Roles of mast cells (basophils) and eosinophils in asthma

| Activated cells | Stimulating factor | Activation mechanisms | Contents of cell degranulation | Functions of the cell degranulations |
|--|--------------------|--|--|---|
| Mast cells (or) basophils (Modena et al. 2016) | IgE (or) allergen | Cross-link with high-affinity IgE receptor (FcεRI) on basophils and mast cells | Histamine Heparin Proteases (tryptase) | Induce airway smooth muscle proliferation Cause immediate bronchoconstriction via histamine H1 receptors Correlates with bronchial hyperreactivity As mitogens for fibroblasts, stimulate the synthesis of type-I collagen, play roles in airway smooth muscle proliferation and histamine-induced contraction Degrade vasoactive intestinal peptide (vasodilator) Associated with airway remodeling |
| | | Convert arachidonic acid to eicosanoids | Prostaglandins Leukotrienes (Leukotriene C ₄ , D ₄ , E ₄) | Cause smooth muscle contraction Increase vascular permeability Stimulate mucus secretion Recruit effector cells |
| | | Influence gene transcription of cytokines by activating protein kinase B, protein kinase C, c-Jun N-terminal kinase, p38 and extracellular regulated protein kinases | IL-4 and IL-13 IL-3, IL-5 and GM-CSF Tumor necrosis factor-α (TNF-α) | Contributes to the development of Th2 cells and stimulates Th2 cell responses Promote eosinophil production and activation Promotes inflammation: stimulates cytokine production by many cell types activates endothelium |

Table 2 continued

| Activated cells | Stimulating factor | Activation mechanisms | Contents of cell degranulation | Functions of the cell degranulations |
|--|---|---|--|---|
| Eosinophils | IL-4 (Verma et al. 2017) | Exocytosis, piecemeal degranulation and cytolysis (granule release) | IL-4 | Contributes to the development of Th2 cells and stimulates Th2 cell responses |
| | IL-5 family cytokines (IL-5, IL-13, GM-CSF) (Ravin and Loy 2016) | | Major basic proteins (Morgan et al. 2005) | Induces nuclear factor-kappa B (NF- κ B) activation via extracellular regulated protein kinase 1 or 2 and protein kinase B, activating transcription of pro-inflammatory cytokines |
| | IL-5 family cytokine receptors | | Eosinophil cationic protein | Increases TNF- α production and triggers apoptosis by caspase-8 activation |
| | IL-5 regulates eosinophils differentiation and maturation by the mTOR pathway | | | |
| | G protein-coupled receptors | | | |
| Eotaxins, monocyte chemoattractant proteins and chemokine (C-C motif) ligand 5 | | | Eosinophil peroxidase | Oxidize substrates based on peroxide. Involved in oxidative stress |
| | | | Eosinophil-derived neurotoxin (Chatzileontiadou et al. 2015) | Displays limited cytotoxicity against respiratory epithelial cells |
| | | | | Enhances Th2 immune responses as a chemoattractant for human dendritic cells |

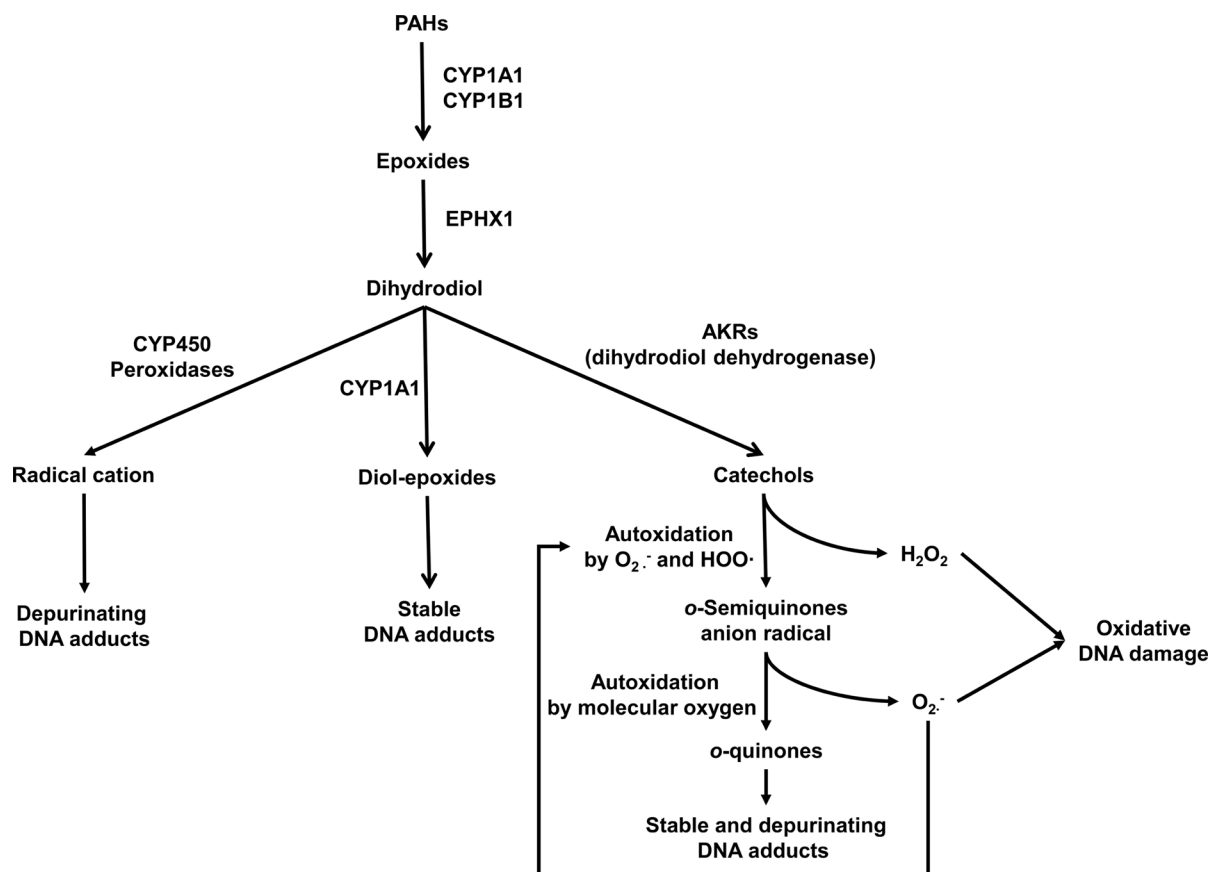


Fig. 2 Phase I metabolism of PAHs (Bolton et al. 2000; Henkler et al. 2012; McCoull et al. 1999). CYP1A1 cytochrome P4501A1; CYP1B1 cytochrome P4501B1; EPHX1 epoxide hydrolase 1; $O_2^{\cdot-}$ superoxide anion; AKR: aldo-keto reductase

diplotypes from another perspective (Iarmarcovai et al. 2008; Stiborova et al. 2014; Vaclavikova et al. 2015; Xiang et al. 2012). DNA damage levels, as detected by DNA adducts, are higher in smokers with *EPHX1* Arg/Arg than Arg/His and His/His genotypes at codon 139, suggesting that a human with higher *EPHX1* activity is more impressionable to environmental exposure (Peluso et al. 2013). Consistent with this, increased micronuclei frequency (chromosomal aberrations) related to PAH exposure is associated with *EPHX1* exon 3 Tyr/Tyr and *EPHX1* exon 3 His/Tyr in coke-oven workers (*EPHX1* activity: Tyr/Tyr > His/Tyr > His/His at exon 3) (Iarmarcovai et al. 2008). Butadiene-exposed workers with intermediate/high-activity *EPHX1* diplotypes have higher nucleoplasmic bridge frequency (chromosomal aberrations) than low-activity *EPHX1* diplotypes (Xiang et al. 2012). These studies proved that *EPHX1* genotypes and diplotypes related to higher *EPHX1*

activity are associated with DNA and chromosome damages due to PAH exposure, which contribute to genetic predisposition to asthma.

PAH exposure and *EPHX1* are both independent risk factors for asthma, the interactions between which are involved in asthma as well. *EPHX1* SNPs/genotypes/diplotypes and corresponding enzymatic activities influence PAH metabolism in vivo, as well as human vulnerability to PAH exposure (Ghosh et al. 2013; Tung et al. 2011). During metabolism in vivo, PAHs are oxidized to epoxide catalyzed by *CYP1A1* and *CYP1B1*, and then convert to dihydrodiol (diol) catalyzed by *EPHX1* (Henkler et al. 2012). The dihydrodiols further convert to diol-epoxides and produce DNA adducts or convert to catechols and further o-quinones, releasing hydrogen peroxide and superoxide anion (Bolton et al. 2000) (Fig. 2). As a result, *EPHX1* activity, which is influenced by *EPHX1* SNPs/genotypes/diplotypes, is supposed to be

Table 3 Genotypes, SNPs, diplotypes and activities of *EPHX1*

| Genotype (Ghosh et al. 2013) | | SNPs | | Allele frequencies (1000 genomes) (NCBI 2018a, b) | Enzyme activity (Hassett et al. 1994) |
|--|-----------------------|------------------------------|------------------------------|---|---|
| Wild | Variant | SNP name (Ghosh et al. 2013) | SNP name (Ghosh et al. 2013) | | |
| <i>EPHX1</i> in exon 3 | | | | | |
| Genotype | TT; Tyr113Tyr | TC; Tyr113His | CC; His113His | rs1051740 (Tyr > His at codon 113 exon 3) | Minor Allele Count Han Chinese in Beijing, China British in England and Scotland Esan in Nigeria |
| Prevalence | 46.5% | 37.8% | 15.6% | | C = 0.3133 C = 0.4320 C = 0.3571 C = 0.1162 |
| <i>EPHX1</i> in exon 4 | | | | | |
| Genotype | AA; His139His | AG; His139Arg | GG; Arg139Arg | rs2234922 (His > Arg at codon 139 exon 4) | Minor Allele Count Han Chinese in Beijing, China British in England and Scotland Esan in Nigeria |
| Prevalence | 68.1% | 27.7% | 4.2% | | G = 0.2155 G = 0.0971 G = 0.1593 G = 0.3485 |
| <i>EPHX1</i> diplotype (Ghosh et al. 2013) | | | | | |
| Genotype | 113Tyr/Tyr-139His/Arg | 113Tyr/Tyr-139Arg/Arg | 113Tyr/His-139Arg/Arg | 113Tyr/His-139Arg/Arg | High |
| Genotype | 113Tyr/Tyr-139His/His | 113Tyr/His-139His/Arg | 113His/His-139Arg/Arg | 113His/His-139Arg/Arg | Intermediate |
| Genotype | 113Tyr/His-139His/His | 113His/His-139His/His | 113His/His-139His/Arg | 113His/His-139His/Arg | Low |

positively associated with PAH-DNA adduct production and ROS production during PAH metabolism in vivo, contributing to PAH-related asthmatic airway damages. Correspondingly, DNA adducts produced during PAH metabolism can lead to point mutations such as G → T or A → T transversions, contributing to bigger possibility of general SNPs (Henkler et al. 2012). Although it is unclear whether PAH-related DNA adducts could cause specific SNPs in *EPHX1*, a possibility can be deduced. Above interaction between PAH and *EPHX1* provides a new idea of further research—a positive feedback loop of *EPHX1*-mediated asthma risk due to PAH exposure.

Conclusion

Despite various preventative activities aimed at reducing emissions over the decades, PAHs still are significant risk factors for asthma as well as other respiratory problems. The principal mechanisms by which PAHs contribute to asthma pathogenesis involve a complex interplay between genes, immune system and oxidative stress. Exact effects of each PAH on asthma risk need to be further explored. It is concluded from above that the risk of asthma due to PAH exposure is influenced by different activities of epoxide hydrolase 1, which are affected by *EPHX1* SNPs/genotypes/diplotypes. The reason is that activity of epoxide hydrolase 1 could alter human PAH metabolism and human vulnerability to PAHs. Mechanisms of the interaction between PAHs and *EPHX1* involved in asthma pathogenesis include ROS, immunological changes (including imbalance of Th1/Th2/Treg/Th17 and airway inflammation) and DNA damage.

Although PAHs have been reported as toxic chemicals and managed by Emergency Planning and Community Right-to-Know Act of 1986 (EPCRA) and other acts, they are still produced during daily life through vehicle exhaust emission, tobacco smoking, heating and cooking. PAHs play roles in various health risks, among which asthma is one of the top 5 respiratory diseases in the world, accounting for high mortality, morbidity and health-care costs worldwide (Chang 2013; Global Asthma Network 2014). As a result, more regulations and government policies should be made to control PAH pollution. On the other hand, this review probably provides new ideas of

asthma individual primary prevention: People with *EPHX1* SNPs/genotypes/diplotypes related to higher *EPHX1* activity should take more attention to PAH exposure and asthma risk. In the future, more GWAS, meta-analysis of gene-environment interaction studies can increase driving power further and provide robust estimates of gene-environment interactions.

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Compliance with ethical standards

Conflict of interest All authors declare that they have no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

Informed consent This article does not contain any studies with human participants or animals performed by any of the authors.

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