



# PM<sub>2.5</sub>, Fine Particulate Matter: A Novel Player in the Epithelial-Mesenchymal Transition?

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Epithelial-mesenchymal transition (EMT) refers to the conversion of epithelial cells to mesenchymal phenotype, which endows the epithelial cells with enhanced migration, invasion, and extracellular matrix production abilities. These characteristics link EMT with the pathogenesis of organ fibrosis and cancer progression. Recent studies have preliminarily established that fine particulate matter with an aerodynamic diameter of less than 2.5  $\mu$ m (PM<sub>2.5</sub>) is correlated with EMT initiation. In this pathological process, PM<sub>2.5</sub> particles, excessive reactive oxygen species (ROS) derived from PM<sub>2.5</sub>, and certain components in PM<sub>2.5</sub>, such as ions and polyaromatic hydrocarbons (PAHs), have been implicated as potential EMT mediators that are linked to the activation of transforming growth factor  $\beta$ (TGF-β)/SMADs, NF-κB, growth factor (GF)/extracellular signal-regulated protein kinase (ERK), GF/phosphatidylinositol 3-kinase (PI3K)/Akt, wingless/integrated (Wnt)/β-catenin, Notch, Hedgehog, high mobility group box B1 (HMGB1)-receptor for advanced glycation end-products (RAGE), and aryl hydrocarbon receptor (AHR) signaling cascades and to cytoskeleton rearrangement. These pathways directly and indirectly transduce pro-EMT signals that regulate EMT-related gene expression in epithelial cells, finally inducing the characteristic alterations in morphology and functions of epithelia. In addition, novel associations between autophagy, ATP citrate lyase (ACLY), and exosomes with PM<sub>2.5</sub>induced EMT have also been summarized. However, some debates and paradoxes remain to be consolidated. This review discusses the potential molecular mechanisms underlying PM<sub>2.5</sub>-induced EMT, which might account for the latent role of PM<sub>2.5</sub> in cancer progression and fibrogenesis.

Keywords: PM<sub>2.5</sub>, epithelial-mesenchymal transition, cancer, fibrosis, signaling pathway, molecular toxicology, air pollution, environment and human health

# INTRODUCTION

Air pollution, especially that of developing countries, has become increasingly severe with the process of industrialization. Even before atmospheric brown cloud (ABC) was first observed in Asia, ambient particulate matter (PM) has been widely regarded as one of the major airborne pollutants. PM is composed of solids and/or liquids suspended in the atmosphere with a large variation in size. PM can be classified into four different categories according to aerodynamic diameters: total suspended particulates (TSPs); inhalable particles with an aerodynamic diameter less than 10  $\mu$ m (PM<sub>10</sub>); fine PM with an aerodynamic diameter less

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than 2.5  $\mu$ m (PM<sub>2.5</sub>); and ultrafine particles (PM<sub>0.1</sub>). Owing to the relatively high dispersity and small diameter, PM25 can be inhaled and deposited in airways and alveoli and can even penetrate into the bloodstream, systemically spreading and inducing damage to multiple systems and organs (Wang et al., 2013; Falcon-Rodriguez et al., 2016; Liu et al., 2019). PM<sub>2.5</sub> is derived from industrial and vehicle emissions, mineral dust, biomass incineration, and other diverse sources; thus, the composition of PM<sub>2.5</sub> is extremely complex (Belis et al., 2013; Falcon-Rodriguez et al., 2016). Transitional metals, soluble salts, organic/elemental carbon, and microbes that adhere to PM2.5 particles contribute to the toxic effects of PM<sub>25</sub> including inflammation, DNA damage, mutations, reactive oxygen species (ROS) accumulation, and mitochondria dysfunction. All these abnormal intracellular events are highly correlated with the pathogenesis and progression of a series of human diseases (Ghio et al., 2012; Valavanidis et al., 2013; Feng et al., 2016; Qi et al., 2019). Outdoor PM<sub>2.5</sub> exposure has been listed as the fifth most influential risk factor for global death, which caused 4.2 million deaths in 2015 (Schraufnagel et al., 2018). Besides, epidemiological studies have shown that PM<sub>25</sub> exposure was highly correlated with the morbidity and mortality of respiratory and cardiovascular diseases. Maternal exposure to PM<sub>2.5</sub> is also linked to an increased risk of airway disease development in offspring (Saha et al., 2018; Sanyal et al., 2018).

Epithelial-mesenchymal transition (EMT) is a process through which epithelial cells lose their apical-basal polarity and acquire the mesenchymal phenotype (Katsuno et al., 2013; Chaffer et al., 2016). A series of underlying molecular events, especially the repression of E-cadherin expression, the upregulation of N-cadherin and vimentin, and the disruption of adherin junctions, have been uncovered (Kourtidis et al., 2017; Miyazono et al., 2018). Other significant molecular features underlying EMT include cytoskeleton remodeling, such as actin stress fiber formation, and induction of mesenchymal biomarkers, including  $\alpha$ -smooth muscle actin ( $\alpha$ -SMA) and fibronectin (Kalluri and Weinberg, 2009). As EMT endows the epithelia with the potential of myofibroblast differentiation, increased motility, migration and invasion ability, this cellular event, if abnormally activated, will inevitably mediate the progression of organ fibrosis and cancer metastasis by facilitating the secretion of the extracellular matrix components or the dissociation of neoplastic cells from primary tumors and the subsequent intravasation (Stone et al., 2016; Yan et al., 2018; Lu and Kang, 2019). Furthermore, the enhanced anti-apoptosis and drug detoxification characteristics of cancer cells that have undergone EMT also result in drug resistance in cancer chemotherapy (Santamaria et al., 2019).

To date, three EMT subtypes have been determined based on their biological functions in tissue development and pathogenesis. Type 1 EMT is associated with the formation and implantation of embryo together with organ development. Type 2 EMT functions in wound healing by contributing to fibroblast generation and extracellular matrix production. Type 3 EMT refers to the phenotypic transformation in neoplastic epithelial cells, which enhances anti-apoptosis and invasion abilities (Kalluri, 2009; Kalluri and Weinberg, 2009; Zou et al., 2017).

Although massive statistical analyses have established the causal link between environmental PM2.5 exposure and morbidity/ mortality of multiple cancers as well as fibrotic diseases, and "outdoor air pollution, particulate matter in" has been indexed as one of 120 primary carcinogens, the exact in-depth mechanisms at the cellular or microscopic level are still largely unknown (Kim et al., 2018; Sese et al., 2018; Cheng et al., 2019; International Agency for Research on Cancer, 2019). As these diseases are currently largely irreversible and lethal, targeted approaches to prevent their onset should be developed. Current research has demonstrated that acute or chronic PM<sub>25</sub> exposure elicited the expression of characteristic EMT markers and EMT-related transcription factors (TFs) in the epithelia (Wei et al., 2017; Chi et al., 2018; Xu et al., 2019a). Similar altered expression patterns have also been detected in the lungs after mice were exposed to PM<sub>2.5</sub> (Fu et al., 2019). Hence, it is possible that PM<sub>2.5</sub> might serve as an exogenous promoter of fibrosis and cancer by initiating abnormal EMT in corresponding target epithelial tissues and cells. Although the molecular toxicology of PM2.5-induced EMT has not been well studied, on the basis of existing publications, this review aims to describe validated or potential molecular processes, especially the signaling pathways, participating in the action of PM<sub>2.5</sub> on pro-fibrotic or neoplastic EMT.

Abbreviations: EMT, Epithelial mesenchymal transition; PM25, Fine particulate matter with an aerodynamic diameter less than 2.5 µm; ROS, Reactive oxygen species; PAHs, Polyaromatic hydrocarbons; ABC, Atmospheric brown cloud; TSP, Total suspended particulates; PM<sub>10</sub>, Inhalable particles with an aerodynamic diameter less than 10 µm; PM<sub>0.1</sub>, Ultrafine particles; α-SMA, α-Smooth muscle actin; TFs, Transcription factors; LEF-1, Lymphoid enhancer-binding factor-1; HMG, High-mobility group protein family; TGF-β, Transforming growth factor β; COL1, Type I collagen; TβRII, The type II TGF-β receptor; TβRI, The type I TGF-β receptor; R-SMADs, Receptor-activated SMAD proteins; BMPR, Bone morphogenetic protein receptor; I-SMADs, Inhibitory SMADs; Wnt, Wingless/ Integrated; LRP5/6, LDL receptor-related protein-5/6; Dsh, Disheveled; GSK-3β, Glycogen synthase kinase-3β; RTKs, Receptor tyrosine kinases; GFs, Growth factors; EGF, Epidermal growth factor; FGF, Fibroblast growth factor; PDGF, Platelet-derived growth factor; IGF, Insulin-like growth factor; MEK, MAPK/ ERK kinase; ERK, Extracellular signal-regulated protein kinases; PI3K, Phosphoinositide 3-kinase; PKB/Akt, Protein kinase B; JAK, The Janus kinase; STAT3, Signal transducers and activators of transcription-3; IL-6, Interleukin-6; IL-8, Interleukin-8; Shh, The sonic hedgehog; PTCH, Protein patch homolog; SMO, Smoothend; Gli1/2/3, Glima-associated oncogene-1/2/3; ADAM, A disintegrin and metalloproteinase; NICD, Notch intracellular domain; HES, Hairy and enhancer of split family; HEY, The HES related with YRPW motif family; FAK, Focal adhesion kinase; ROCK, Rho-associated protein kinase; NOX, NADPH oxidase; LAP, Latency-associated peptide; EndMT, Endothelial-mesenchymal transition; NAC, N-acetyl cysteine; MMP, Matrix metalloproteinase; CYP1A1/B1, Cytochrome P450, family 1, member A1/B1; LncRNA, Long non-coding RNA; CSE, Cigarette smoke extract; MiRNA, Micro-RNA; PTP1B, Protein tyrosine phosphatase-1B; DEP1, Density-enhanced phosphatase-1; MAPK, Mitogen-activated protein kinase; PCNA, Proliferating cell nuclear antigen; SOD, Superoxide dismutase; F-actin, Fibrous actin; G-actin, Globular actin; PINK1, PTEN-induced kinase 1; RAGE, Receptor for advanced glycation end-products; ACLY, ATP citrate lyase; AHR, Aryl hydrocarbon receptor; ARNT, Ah receptor nuclear translocator protein; DEPs, Diesel exhaust particles; CpGs, CpG islands; GO, Gene Ontology; TRPM7, Transient receptor potential cation channel 7; ABCC3, ATP-binding cassette subfamily C member 3.

# OVERVIEW OF THE MOLECULAR PLAYERS IN EPITHELIAL-MESENCHYMAL TRANSITION

## **Key Transcription Factors**

The loss of E-cadherin is a typical EMT hallmark. The TFs that control the expression of E-cadherin include the Zn-finger proteins Snail and Slug, the two-handed Zn-finger proteins ZEB1 and ZEB2, and the basic helix-loop-helix family protein TCF and Twist have also been identified (Guaita et al., 2002; Burger et al., 2017). These TFs directly bind to 5' E-boxes of the human E-cadherin promoter and further silence the transcription of CDH1 (Batlle et al., 2000; Guaita et al., 2002; Vesuna et al., 2008). Lymphoid enhancer-binding factor-1 (LEF-1), a member of TCF/LEF family, also regulates EMT by recruiting the coactivator  $\beta$ -catenin to enhancers (Gilles et al., 2003; Santiago et al., 2017). Interactions and crosstalk between TFs have also been extensively recognized. Snail can induce the expression of ZEB1/2, Twist, Slug, and LEF-1 (Guaita et al., 2002; Dave et al., 2011; Cevenini et al., 2018). Twist can serve as the transcriptional initiator of Slug and ZEB1, whereas TCF-4 functions indirectly via ZEB1 (Taube et al., 2010; Sanchez-Tillo et al., 2011). LEF-1 can also exert its pro-EMT ability indirectly by upregulating Slug expression (Lambertini et al., 2010). In addition, a member of the high-mobility group (HMG) protein family, the transforming growth factor  $\beta$  (TGF- $\beta$ )/SMAD2/3dependent TF HMGA2, induces the expression of Snail, Slug, and Twist and mediates EMT (Thuault et al., 2006, 2008). NF-κB, a versatile TF involved in the regulation of proliferation, adhesion, and inflammation, executes its pro-EMT ability via Snail, Slug, and ZEB1/2 (Min et al., 2008; Sarkar et al., 2008; Techasen et al., 2012). Key TFs related to EMT and their transcriptional interactions are roughly summarized in Table 1.

## **Pro-Epithelial-Mesenchymal Transition Signaling Cascades**

TGF- $\beta$  is considered as the most powerful initiator of EMT. TGF-β can directly and positively regulate mesenchymal markers such as  $\alpha$ -SMA and type I collagen (COL1) and is also a potent regulator of cytoskeleton remodeling (Zavadil and Bottinger, 2005; Fernandez and Eickelberg, 2012). The type II TGF-β receptor (TβRII) is initially recruited by activated TGF- $\beta$  and forms a hetero-tetrameric complex with the type I TGF- $\beta$  receptor (T $\beta$ RI) by phosphorylating the GS domain of TBRI (Miyazawa et al., 2002; Huang and Chen, 2012; Vander Ark et al., 2018). SMAD2 and SMAD3, receptor-activated SMAD proteins (R-SMADs), are cytoplasmic mediators of TGF-β signaling whose recruitment and phosphorylation by TBRI result in their translocation to the nucleus in assistance of SMAD4 (Fabregat and Caballero-Diaz, 2018). SMAD2/3/4 together with other coactivators activates HMGA2, Snail, Slug, and ZEB1/2 expression, which further initiates the phenotypic transformation of EMT (Thuault et al., 2006; Katsuno et al., 2013). Another set of SMAD signaling cascades consisting of bone morphogenetic protein receptors (BMPRs) and the SMAD 1/5/8 also enhances Slug and Twist expression

TABLE 1	Positive transcriptional regulation among pro-EMT transcription
factors.	

Transcriptional inducers	Effectors	Reference
Snail	Slug	Cevenini et al. (2018)
	Twist	Cevenini et al. (2018)
	ZEB1	Dave et al. (2011)
	ZEB2	Cevenini et al. (2018)
	LEF-1	Guaita et al. (2002)
LEF-1	Slug	Lambertini et al. (2010)
Twist	Slug	Taube et al. (2010)
	ZEB1	Taube et al. (2010)
TCF-4	ZEB1	Sanchez-Tillo et al. (2011
HMGA2	Snail	Thuault et al. (2008)
	Slug	Thuault et al. (2006)
	Twist	Thuault et al. (2006)
NF-ĸB	Snail	Sarkar et al. (2008)
	Slug	Storci et al. (2010)
	ZEB1	Min et al. (2008)
	ZEB2	Min et al. (2008)

EMT, epithelial-mesenchymal transition.

(McCormack et al., 2013; Li et al., 2014; Ahn et al., 2016; Wang et al., 2016). SMAD6 and SMAD7, two inhibitory SMADs (I-SMADs), participate in the inhibition of signal transduction *via* competitive binding with T $\beta$ RI and BMPRI (Itoh and ten Dijke, 2007; Gonzalez-Nunez et al., 2013; Koganti et al., 2018). There are also non-canonical TGF- $\beta$  cascades linked with EMT, in which T $\beta$ RII phosphorylates Par6 and further modulates activity of RhoA *via* ubiquitination mediated by Smurf1, resulting in the loss of tight junction and EMT (Choi et al., 2017; Simeone et al., 2018).

β-Catenin is the main effector of Wnt pathway. The cytoplasmic accumulation of β-catenin after activation of Wnt signaling, or the release of β-catenin due to the loss of E-cadherin, which allow the interactions between β-catenin and LEF-1, can induce the upregulation of Snail, Slug, Twist and mesenchymal markers such as fibronectin (Guo et al., 2012; Ghahhari and Babashah, 2015). When the Wnt ligands bind to Frizzle and LDL receptorrelated protein-5/6 (LRP5/6) receptors, extracellular signals are transduced by LRP to phosphorylated Disheveled (Dsh), which in turn block the activity of glycogen synthase kinase-3β (GSK-3β), a key EMT suppressor that mediates the ubiquitination of Snail and the degradative phosphorylation of β-catenin (Doble and Woodgett, 2007; Heuberger and Birchmeier, 2010; Lam and Gottardi, 2011; Gonzalez and Medici, 2014).

The receptor tyrosine kinases (RTKs) and their downstream effectors are also pivotal in EMT. There are numerous growth factors (GFs), including epidermal GF (EGF), fibroblast GF (FGF), platelet-derived GF (PDGF), and insulin-like GF (IGF), which serve as RTK ligands (Jechlinger et al., 2006; Cevenini et al., 2018; Shu et al., 2018; Yamaoka et al., 2018). Binding of GFs with RTKs and the ensuing tyrosine autophosphorylation of RTKs can result in binding of GTP to Ras and the recruitment of Raf, activating mitogen-activated protein kinase (MAPK)/extracellular signal-regulated protein kinase (ERK) kinase (MEK), which further phosphorylates ERKs. Ligand-bound RTKs also activate

phosphoinositide 3-kinase (PI3K), which activates Akt *via* PIP<sub>3</sub> converted from PIP<sub>2</sub>. Activation of Akt and ERK leads to the inactivating phosphorylation of GSK-3β, which promotes EMT (Oloumi et al., 2004; Zhou et al., 2004; Ding et al., 2005; Doble and Woodgett, 2007; Lemmon and Schlessinger, 2010; Tripathi and Garg, 2018). Akt activation also contributes to signal transduction through the NF-κB/Snail pathway (Julien et al., 2007).

The Janus kinase/signal transducers and activators of transcription-3 (JAK/STAT3) pathway, which were initially defined as the inflammation response-related pathway, also actively participate in EMT. Interleukin-6 (IL-6) activates JAK after binding to IL-6 receptor, which subsequently facilitates the phosphorylation and the following dimerization of STAT3. STAT3 homodimer then translocates into the nucleus and regulate the transcription (Yan et al., 2018). The IL-6/JAK/STAT3 pathway can effectively upregulate pro-EMT TFs, including Snail, Slug, and Twist and modify the expression of EMT-related genes (Colomiere et al., 2009; Sullivan et al., 2009; Yadav et al., 2011; Chen et al., 2015). In addition, interleukin-8 (IL-8) can also induce similar JAK/STAT3-dependent responses through interactions with IL-8 receptor (Fernando et al., 2011; Fu et al., 2015).

The sonic hedgehog (Shh) signaling pathway consisting of Shh, protein patch homolog (PTCH), smoothend (SMO), and glimaassociated oncogene-1/2/3 (Gli1/2/3) mediates embryonic development. Recently, the importance of this pathway in cancer and EMT has also been revealed (McCubrey et al., 2016; Zou et al., 2017). Upon binding to the transmembrane G proteincoupled receptor PTCH, secretive Shh releases the repressed SMO-bound PTCH, which further induces the transcriptional activity of Glis, promoting the transcription of Snail, Slug, and other EMT-related gene targets (Li et al., 2006; Pain et al., 2014; Flemban and Qualtrough, 2015; Zhang et al., 2016a).

Novel studies have described the participation of Notch signaling, an original paracrine pathway, in angiogenesis, tumor progression, cell proliferation, and EMT induction. The initiation of Notch relies on the trans-interactions between Notch ligands (Jag1, Jag2, Delta1, Delta3, and Delta4) at cell surface of signaling-sending cells and extracellular domains of noncovalent heterodimeric transmembrane Notch receptors (Notch1, Notch2, Notch3, and Notch4) on the surface of signaling-receiving cells. An initial cleavage at the extracellular site of the notch receptor mediated by a disintegrin and metalloproteinase (ADAM) follows the activation of Notch receptor (Meurette and Mehlen, 2018; Chatterjee and Sil, 2019). After the second intracellular cleavage mediated by y-secretase, Notch intracellular domain (NICD) with activated transcriptional activity is released and then translocates into the nucleus, mediating the transcriptional upregulation of hairy and enhancer of split (HES) family genes and the HES related with YRPW motif (HEY) family genes in cooperation with co-regulators. These effectors further induce the corresponding downstream transcriptional modification, such as the induction of Snail and Slug (Thiery et al., 2009; Vinson et al., 2016; Leonetti et al., 2019).

A specific consequence of the multiple signal transduction networks reviewed above is the increase of cell motility. To drive the process of migration and invasion, the subtle remodeling of cytoskeleton dynamics accompanied by the tuning of epithelial adhesion, which is directly regulated by focal adhesion kinase (FAK), Rho family GTPase, and Rho-associated protein kinase (ROCK) signaling, is highly activated, leading to actin polymerization, stress fiber assembly, lamellipodia and filopodia formation, and the creeping-like motions of the cells (Cavallaro and Christofori, 2001; Yilmaz and Christofori, 2009; Jiang et al., 2017; Jansen et al., 2018). A schematic overview of the pro-EMT pathways and key messengers is shown in **Figure 1**.



**FIGURE 1** Brief schema of the putative signaling transduction mechanisms underlying EMT. Activation of the Wnt/ $\beta$ -catenin, PI3K/Akt, Ras/ERK, TGF- $\beta$ / SMAD2/3, BMP/SMAD1/5/8, JAK/STAT3, Shh, and Notch pathways is highly correlated with EMT. After ligand-receptor binding, intracellular secondary messengers are activated and initiated downstream transduction, which generally induce the nuclear translocation of signaling-specific TFs and the transcriptional regulation of EMT-related genes, such as CDH1 and CDH2, EMT TFs, and mesenchymal markers, accompanied by a series of alterations on cellular physiological or pathological activities (e.g., disjunction of adherin junctions, cytoskeleton remodeling, and increase of cellular motility). Arrows represent the molecular interactions in which downstream messengers are activated; T shape arrows represent inhibitive molecular interactions. EMT, epithelial-mesenchymal transition; PI3K, phosphoinositide 3-kinase; ERK, extracellular signal-regulated protein kinase; TGF- $\beta$ , transforming growth factor  $\beta$ ; JAK, Janus kinase; Shh, sonic hedgehog; TFs, transcription factors.

# POTENTIAL MECHANISMS OF PM<sub>2.5</sub>-INDUCED EPITHELIAL-MESENCHYMAL TRANSITION

## Potential Reactive Oxygen Species-Dependent Mechanisms in PM<sub>2.5</sub>-Induced Epithelial-Mesenchymal Transition

ROS are physiologically produced as byproducts of biological reactions in the cytoplasm, mitochondria, and peroxisomes catalyzed by cytochrome P450 and NADPH oxidase (NOX). ROS have primary functions to actively defend against invading pathogens (Bardaweel et al., 2018; Lee et al., 2018). However, excessive cytoplasmic retention of ROS generally results in cellular oxidative stress, which can alter intracellular signaling, DNA damage, and apoptosis (Danielsen et al., 2009; Deng et al., 2014; Vattanasit et al., 2014; Cho et al., 2018). Intracellular ROS can be generated by cellular exposure to external contaminants, including the main components of PM2.5, such as black carbon, redox-active metals (e.g., Fe, Cu, Ni, Zn, Cr, As, and Mn), and PAHs (e.g., naphthalene, benzo-*a*-pyrene, and anthracene) (Shuster-Meiseles et al., 2016; Niranjan and Thakur, 2017; Sun et al., 2018). PM<sub>2.5</sub> particles have also been characterized as strong inducers of ROS, as they directly release ROS, catalyze redox reactions, or participate in redox cycles as substrates (Squadrito et al., 2001; Knaapen et al., 2004; Risom et al., 2005; Valavanidis et al., 2013; Cho et al., 2018; Jin et al., 2018).

As ROS has been well characterized as one of the fundamental intermediaries of the  $PM_{2.5}$ -induced response and injury, and evidence verifying  $PM_{2.5}$ -induced EMT *via* ROS *in vivo* and *in vitro* has been emerging, this section will be mainly focused on the potential pathogenic role of  $PM_{2.5}$ -derived ROS in EMT (Thevenot et al., 2013; Yan et al., 2016; Yi et al., 2017; Palleschi et al., 2018; Li et al., 2018b). Some essential information including the sources and the concentrations of  $PM_{2.5}$  utilized, as well as the antioxidant used for treatment and the effective concentrations, is summarized in **Table 2**.

#### PM<sub>2.5</sub>-Reactive Oxygen Species Participates in SMAD-Dependent Epithelial-Mesenchymal Transition

TGF-β has been shown to involve ROS formation *via* NOX4, whereas ROS also stimulate the epithelial excretion of TGF-β (Latella, 2018). ROS can also convert latent TGF-β to its active form by oxidizing the latency-associated peptide (LAP) (Liu and Gaston Pravia, 2010; Montorfano et al., 2014; Jaffer et al., 2015). Excessive ROS derived from protein oxidation can induce TβRI/II expression and further initiate TGF-β/SMAD signaling, which induces EMT in hepatocytes *in vivo* and *in vitro* (Sun et al., 2017). These studies indicate that ROS can activate TGF-β/SMAD signaling at different points along the pathway, including ligand-receptor interactions and intracellular signaling.

An *in vivo* study demonstrated that long-term  $PM_{2.5}$  exposure induced increased TGF- $\beta$ 1 expression, SMAD2/3 phosphorylation, and collagen accumulation in mice lungs, indicating potential links among  $PM_{2.5}$  exposure, the TGF- $\beta$ 1/SMAD2/3 pathway, and

pro-fibrotic EMT (Gu et al., 2017). Another study supported this pathogenesis in mice model: Maternal exposure to PM25 could also result in significant oxidative stress, activation of TGF-B/ SMAD3 signaling, and EMT in fetal mice lung, which contributed to postnatal pulmonary dysfunction (Tang et al., 2017). In addition, exposure of mice to PM25 for 4 weeks not only elicited SMAD3 phosphorylation and cardiac fibrosis but also induced excessive ROS accumulation and NOX4 expression in heart tissues, indicating that the potential occurrence of PM2.5-induced EMT or endothelialmesenchymal transition (EndMT) might be ROS dependent (Qin et al., 2018). Our previous in vitro study validated this mechanism: The release of TGF-\$1, the activation of the TGF-\$1/SMAD3 pathway, and the altered expression of hallmark EMT proteins in human bronchial epithelial cells were observed after 30-passage low-dose PM<sub>2.5</sub> exposure (Xu et al., 2019a). In another study, the exposure of alveolar epithelial cells to PM2,5 not only induced the activation of latent TGF- $\beta$  but also increased cell contractility and elongated cellular morphology in a dose-dependent manner. These effects could be reversed by NAC treatment, demonstrating the role of ROS in this pathogenic event (Dysart et al., 2014). In addition, increased TGF-B1 mRNA expression was observed in bronchial epithelial cells after 7 days' consecutive exposure to PM2.5, and treatment with the antioxidant NAC could also effectively offset the toxicity of PM25 exposure (Tripathi et al., 2018). However, the detailed EMT transcription patterns induced by PM25-induced ROS through the SMAD2/3-dependent pathway remain unknown.

In summary, these data demonstrate that  $PM_{2.5}$  might induce EMT *via* ROS in a TGF- $\beta$ /SMAD2/3 signaling-dependent manner. However, additional research is needed to further establish a firm causal link.

#### $PM_{2.5}$ -Reactive Oxygen Species Might Induce Epithelial-Mesenchymal Transition *via* NF- $\kappa$ B Cascades

The activation of NF-KB can be evoked by ROS. NF-KB is activated as the response of cellular oxidative stress, responsible for inflammation, apoptosis, and differentiation. Moreover, the activation of NF-KB by ROS is also correlated with Snail upregulation and EMT phenotype transformation in epithelial cells (Valavanidis et al., 2013; Cichon and Radisky, 2014). Different antioxidant treatments targeting ROS in human non-small cell lung carcinoma cells, pancreatic cancer cells, and hepatocellular carcinomatous cells all effectively inhibit NF-kB activation, which further represses matrix metalloproteinase (MMP) expression together with cellular migration and invasion (Lee and Lim, 2011; Chao et al., 2017; Huang and Xin, 2018). In addition, IL-6 and IL-8, which are transcriptionally upregulated by ROS-activated NF-kB, also exert pro-EMT abilities via downstream JAK/STAT3 signaling (Gupta et al., 2012). In gastric cancer cells, even the regulatory effects of IL-6/JAK/STAT3 on expression of pro-EMT TFs and EMT markers relied on NOX4, indicating the potential comprehensive role of ROS in the transduction of NF-KB/IL-6 signaling (Gao et al., 2017). NF-KB is also able to induce TNF- $\alpha$  expression in response to ROS stimulation, and activated TNF-α receptors in turn upregulate NF-κB transcription with further Snail expression, implying positive feedback loops underlying ROS-induced EMT via NF-kB (Dong et al., 2007).

TABLE 2 | Summary table about exposure assays of some studies reviewed in section "Potential Reactive Oxygen Species-Dependent Mechanisms in PM<sub>2.5</sub>-Induced Epithelial-Mesenchymal Transition."

Source of PM <sub>2.5</sub>	Dose of PM <sub>2.5</sub> exposure	Duration of exposure	Cell type	Antioxidant	Dose of antioxidant	Reference
Collected at Atlanta, USA, from March 1, 2004 to June 30, 2004 using Teflon filter	0.1, 1, 10 μg/cm²	5 days	Rat alveolar type II epithelial cell line (RLE-6TN cells)	N-Acetyl cysteine (NAC)	5 µmol/L	Dysart et al. (2014)
Collected at Beijing, China, from January 19, 2015 to January 21, 2015 using 90-mm Emfab filter	1, 5, 30 μg/cm²	Single exposure: 1 day Repeated exposure: 7 days	Human bronchial epithelial cell line (BEAS-2B cells)	NAC	100 μmol/L	Tripathi et al. (2018)
Collected at Changchun, China, from November 2015 to March 2016 using quartz filter	25 μg/cm²	1, 6, 12, 24 h	Human bronchial epithelial cell line (BEAS-2B cells)	NAC	5 μmol/L	Song et al. (2017)
Ni ions were bought from Sigma, USA	Ni <sup>2+</sup> : 0.4 µmol/L	24 h	Human lung cancer cell line (A549 cells) Human lung fibroblast cell	NAC	5 mmol/L	Yang et al. (2018)
Collected at Guangzhou, China, using quartz filter	20, 50, 100 μg/ml	24 h	line (MRC-5 cells) Human corneal epithelial cell line (HCEC cells)	NAC	1 mg/ml	Cui et al. (2018)
Bought from National Institute of Standards and Technology (NIST), USA (the product label: SRM 2786)	2.5, 5, 10 μg/ml	24 h	Human hepatic stellate cell line (LX-2 cells) Human primary hepatic stellate cells (HSCs)	NAC	1 mmol/L	Qiu et al. (2019)
Collected at Beijing, China, from January 2009 to June 2009 using nitrocellulose filter	8, 16, 32, 64 μg/cm <sup>2</sup>	12, 24, 48 h	Human lung cancer cell line (A549 cells)	NAC	5 mmol/L	Deng et al. (2017)

A novel publication confirmed the positive role of NF-KB in PM25-induced EMT. Organic extracts of PM25 enhanced the binding of NF-KB with the promoter of long non-coding RNA (IncRNA) MALAT1, and MALAT1 relieved the expression silencing of ZEB1 by sponging miR-204 targeting ZEB1 mRNA, resulting in the mesenchymal phenotype transition of pulmonary epithelial cells (Luo et al., 2019). Another novel study showed the correlation between PM2.5, ROS, NF-KB, and pro-fibrotic EMT in vivo. The oxidative stress within the rat lungs exacerbated during PM2.5 exposure but disappeared after the termination of exposure, and the upregulation of RelA/p65, deteriorated pulmonary fibrosis, and EMT in rat lungs were observed in the post-exposure phase, indicating that PM2.5 might lead to pulmonary fibrosis by oxidative stress-initiated NF-KB/inflammation/EMT pathway (Sun et al., 2019). Moreover, a previous study demonstrated that NF-κB activation following PM2.5 exposure can be ROS dependent: The inhibition of ROS effectively abrogated the sustained NF-KB activation in BEAS-2B bronchial epithelial cells induced by PM<sub>2.5</sub> exposure (Song et al., 2017). Mice exposed to ultrafine carbon black particles showed oxidant-dependent NF-KB activation and increased expression of NF-κB responsive genes including TNF-α and IL-6 in lung tissues (Shukla et al., 2000). Silica particles, a kind of well-described pro-fibrotic agent, were able to induce a similar pathological response in silicosis murine models, whereas non-fibrogenic particles failed to induce this effect. These results implied that ROS-derived NF-KB and its downstream inflammatory mediators actively participate in fibrogenesis, in which EMT might act as a major participant (Hubbard et al., 2002). Additionally, an in vitro study showed increased IL-6 level and downstream JAK2/STAT3 signaling activation concomitant with the emergence of oxidative stress in PM25-treated alveolar cancer cells, whereas a similar pattern was also observed in another in vitro study, in which ROS accumulation, IL-6/IL-8 release, and JAK2/STAT3 signaling pathway activation were observed to be mediated by cytochrome P450, family 1, member A1/B1 (CYP1A1/B1) after PM<sub>25</sub> exposure to human bronchial epithelial cells (Yuan et al., 2019). This evidence partly substantiated the hypothesis that PM<sub>2.5</sub> might induce EMT via ROS/NF-kB/IL-6/8/JAK/STAT3 axis (Xu et al., 2015). Although the NF-kB activation and following release of IL-6, IL-8, TNF-a, or mitochondrial dysfunction in epithelial tissues induced by PM25-derived ROS have been validated to be significant in lung inflammation and cell death, the in-depth regulatory role of this shared pathway in EMT is largely unknown (Bourgeois and Owens, 2014; Leclercq et al., 2018; Liu et al., 2018; Wang et al., 2018; Xin et al., 2018). Currently, the link between cigarette smoke extract (CSE) and pulmonary inflammation together with EMT in airway epithelia has been preliminarily verified. CSE-induced inflammatory responses in human bronchial cells include NF-KB activation and further increased IL-6 transcription, which promote phenotype transformation via downregulation of miR-200-c, a proven anti-EMT micro-RNA (miRNA) family member. Hence, ROS in conjunction with NF-кB might lie at the intersection of  $PM_{2.5}$ -derived inflammation and EMT, although the exact mechanisms remain to be elucidated (Zhao et al., 2013). Controversy on this issue also existed. Fe<sub>3</sub>O<sub>4</sub>, one of the major anthropogenic components in PM, could result in a delayed NF- $\kappa$ B response in A549 neoplastic pulmonary epithelial cells as a result of the decrease in I $\kappa$ B degradation induced by excessive ROS (Konczol et al., 2011).

In summary, whether  $PM_{2.5}$ -intracellular ROS induced NF- $\kappa B$  phosphorylation could initiate EMT is still obscure, as the small amount of peripheral proof is too weak to conclusively establish this stand.

# PM<sub>2.5</sub>, Reactive Oxygen Species, and Receptor Tyrosine Kinase Signaling

ROS are strong initiators of pro-EMT PI3K/Akt and Ras/ERK signaling. ROS have been shown to directly induce the phosphorylation of EGF and PDGF receptors in the absence of ligand and to enhance VEGF-induced receptor phosphorylation via oxidative repression of the intracellular inhibitors protein tyrosine phosphatase-1B (PTP1B) and density-enhanced phosphatase-1 (DEP1) (Lei and Kazlauskas, 2009; Oshikawa et al., 2010; Leon-Buitimea et al., 2012). The ROS-induced conversion of PIP<sub>2</sub> to PIP<sub>3</sub> also initiates Akt signaling events (Zhang et al., 2016b). Additionally, glutathione peroxidase inactivation-induced ROS accumulation resulted in the acquisition of mesenchymal characteristics of pancreatic cancer cells by the Akt/GSK-3β/Snail regulation (Meng et al., 2018). Likewise, the inhibition of GSK-3β, which increases Snail transcriptional activity and an EMT-like phenotype following ROS-stimulated ERK activation instead of Akt, was observed in Helicobacter pylori-treated gastric cancer cells (Ngo et al., 2016). Besides, the definitive role of ROS in activating ERK to promote the invasion of vascular smooth muscle cells and keratinocytes has also been unfolded. ROS-mediated ERK phosphorylation is also a significant alternative pathway for TGF-β-induced EMT in renal tubular epithelial cells (Rhyu et al., 2005; Wu, 2006).

 $PM_{2.5}$  has been extensively regarded to stimulate the ERK or Akt pathway.  $PM_{2.5}$  could induce MMP-13 expression, invasion, and migration of hepatocellular carcinoma cells *via* Akt (Zhang et al., 2017a). The increased secretion of EGF by human alveolar epithelial cells after  $PM_{2.5}$  exposure and the further initiation of intracellular EGFR/ERK/NF-κB have also been observed (Jeong et al., 2017). In addition, a microfluidic system-based study on  $PM_{2.5}$ -treated bronchial epithelial cells showed significant activation of PI3K/Akt pathway, FGF/FGFR/MAPK/VEGF signaling, and the JAK/STAT pathway, which led to cell proliferation and apoptosis evasion. And increased intracellular and mitochondrial ROS levels implicated that  $PM_{2.5}$ -derived ROS could be correlated with the activation of these signaling series (Zheng et al., 2017).

In addition to ERK, other members of the MAPK family have been shown to participate in  $PM_{2.5}$  responses. The coordination of p38 MAPK with proliferating cell nuclear antigen (PCNA) was responsible for  $PM_{2.5}$ -induced vascular smooth muscle cell proliferation, and the positive role of ROS was also implied by upregulation of superoxide dismutase (SOD), a cellular oxidative stress biomarker (Wan et al., 2018). Nevertheless, current research on the toxicology of  $PM_{2.5}$ -ROS also primarily focuses on the linkage between Akt or MAPK activation and inflammation or apoptosis, suggesting a double-edged role of  $PM_{2.5}$ -ROS that could either induce cell death or enhance cell viability (An et al., 2018; Li et al., 2018a). Abundant in  $PM_{2.5}$ , Ni<sup>2+</sup> was shown to be responsible for cellular oxidative stress and the phenotype transformation of alveolar epithelial cells, and ROS/Akt-dependent MMP-9 and COL1 induction. Similarly, Ni<sup>2+</sup>/ROS/Akt also led to the inflammation of pulmonary epithelia and mice lung tissues (Yang et al., 2018). Hence, there is also crosstalk between  $PM_{2.5}$ -ROS-induced inflammation and EMT *via* RTK-related cascades. However, further research is needed to clarify the interplay of  $PM_{2.5}$ , ROS, Akt, and ERK with EMT.

#### PM<sub>2.5</sub>-Derived Reactive Oxygen Species: The Double-Edged Sword on Cytoskeleton Remodeling

Increase of cell invasion/migration is the characteristic of EMT regulated by subtle cytoskeleton remodeling and shifting in adhesion. TGF-β-induced intracellular ROS via NOX4 accelerates the polymerization of globular actin (G-actin) to fibrous actin (F-actin) in human umbilical vein endothelial cells, which is essential for lamellipodia and filopodia formation (Hu et al., 2005; Lamouille et al., 2014). ROS generated by NOX1 was also able to induce the spindle-like cellular morphology, EMT, and differentiation of human gingival epithelial cells via the posttranscriptional accumulation of CK18, a kind of pro-EMT intermediate filament (Sattayakhom et al., 2014). And ROS/ErbB2 signaling was also reported to be responsible for the aggressiveness of breast epithelial cells by phosphorylating FAK and activating RhoC (Wang et al., 2017). In another study, although mere  $H_2O_2$ treatment was not sufficient to induce complete EMT in retinal pigment epithelial cells due to the transiency of the stimulation, ROS could also initiate Rho-GTP binding, resulting in stress fiber formation (Inumaru et al., 2009).

PM<sub>2.5</sub> has been verified as the modulator of cytoskeleton inducing incomplete contact between adjacent human bronchial epithelial cells, in which strong oxidative stress was also observed (Longhin et al., 2016). Besides, long-term chronic PM<sub>2.5</sub> exposure to human bronchial epithelial cells could enhance RhoA-GTP binding and stress fiber formation, although no increase of cellular proliferation was observed (Dornhof et al., 2017). In another research, however, PM<sub>2.5</sub> that stimulated ROS generation in corneal epithelial cells failed to promote EMT via cytoskeletal regulation. On the contrary, PM<sub>2.5</sub> inhibited FAK and paxillin phosphorylation, which further repressed RhoA activity and epithelial cell migration. Now that these inhibitory processes could be reversed with NAC treatment, the discrepant roles of PM<sub>2.5</sub>-derived ROS in cytoskeleton regulation have been identified (Cui et al., 2018). In summary, the lack of comprehensive data leaves the role of PM2.5 in cytoskeleton modulation shadowy.

#### Something New: PM<sub>2.5</sub>-Reactive Oxygen Species-Induced Autophagy Participates in Epithelial-Mesenchymal Transition

Autophagy is a cellular degradation process that is activated in response to environmental stressors such as GF depletion and hypoxia (Yang et al., 2015; Marcucci et al., 2017). Recent evidence has linked autophagy and EMT through shared signaling pathways and functional causality in cancer progression and metastasis (Lv et al., 2012; Li et al., 2013; Catalano et al., 2015; Gugnoni et al., 2016; Zhang et al., 2017b). A recent study verified that PM25 participated in liver fibrosis via ROS-mediated mitophagy. Hepatic stellate cells, a principal liver cell type with EMT plasticity, displayed enhanced α-SMA and COL1 expression after PM<sub>25</sub> treatment. These processes were mediated by ROS-induced PTEN-induced kinase 1 (PINK1) and Parkin, which signified mitophagy (Choi et al., 2009; Qiu et al., 2019). In lung cancer cells, PM<sub>2.5</sub>-induced cell migration and invasion depended on autophagy, which was initially induced by increased intracellular ROS and its downstream effector lncRNA, loc146880 (Deng et al., 2017). Another study revealed an alternative mechanism underlying PM25-autophagy-EMT in lung cancer cells, in which upregulated lncRNA LCPAT1 served as a messenger that mediated autophagy and cell migration by interacting with RCC2 after PM<sub>2.5</sub> exposure (Lin et al., 2018). This evidence not only validates the correlation between autophagy and PM25induced epithelia phenotype transformation but also provides new insight into the epigenetic toxicology of PM<sub>2.5</sub>.

## Other Molecular Events Underlying PM<sub>2.5</sub>-Induced Epithelial-Mesenchymal Transition

Information about exposure assays in this section is selectively summarized in Table 3.

# Participation of Novel Signaling and Molecules in PM<sub>2.5</sub>-Induced Epithelial-Mesenchymal Transition

PM<sub>2.5</sub> can also activate EMT via diverse signaling pathways, including HMGB1-receptor for advanced glycation end-products (RAGE), Shh, Wnt/β-catenin, and Notch pathway together with SMAD1 signaling, in which the role of ROS has not been elucidated. HMGB1 and its cognate receptor RAGE were both induced in human bronchial epithelial cells and in the murine airway in response to PM<sub>2.5</sub> exposure. HMGB1 binding further activated TGF-B1 and PDGF release, providing strong evidence that HMGB1 is a mediator of PM2.5-induced EMT (Zou et al., 2018). Increased Shh expression activated downstream Shh/Gli1 signal transduction and further enhanced Snail expression as well as cell migration after low dose PM<sub>2.5</sub> exposure to human bronchial smooth muscle cells (Ye et al., 2018). Moreover, the enhanced expression of Notch1 together with downstream TFs Hes1, Snail, Slug and biomarkers of EMT was detected in lungs of mice after intratracheal instillation of PM<sub>2.5</sub> with varied concentrations. The induction of cancer stem cells markers including OCT4 and SOX2 in A549 neoplastic pulmonary epithelial cells following the activation of PM2.5/Notch1 pathway further validated the pro-EMT property of PM2.5 (Wang et al., 2019). Furthermore, unlike the SMADs-dependent EMT mechanisms stated above, SMAD1 activity could also be indirectly induced by repressing expression of SMAD6/7 after PM2.5 treatment on neoplastic pulmonary epithelial cells, resulting in the inhibition of SMAD1 degradation and induction of the spindle-like cellular morphology with cadherin switch (Yang et al., 2017). Interestingly,

rather than directly responding to PM<sub>2.5</sub> exposure, Wnt/β-catenin signaling promoted the proliferation of human alveolar cancer cells and xenograft tumor growth via PM2.5-induced Wnt3aenriched exosomes (Xu et al., 2018). Our recent research was focused on exosomal miRNAs of EMT-like pulmonary epithelia after PM<sub>25</sub> exposure. It predicted the abnormal regulation of multiple cancer-related pathways by exosomal miRNAs in a systematic perspective, further emphasizing the significance of diverse interactions between exosomes and signaling pathways in the process of PM2,5-induced EMT (Xu et al., 2019b). ATP citrate lyase (ACLY) linking glycolytic and lipidic metabolism has been considered as a novel anticancer target, and recently, it has also been found responsible for PM25-induced EMT (Granchi, 2018). Increase of intracellular ACLY expression and citrate acid levels synchronized with EMT phenotype transformation of human bronchial epithelial cells after longterm PM<sub>2.5</sub> exposure, and the knock down of ACLY significantly abrogated the in vivo metastasis ability of the cells (Fu et al., 2019).

# Polyaromatic Hydrocarbons Might Function in PM<sub>2.5</sub>-Induced Epithelial-Mesenchymal Transition Through Aryl Hydrocarbon Receptor

Showing high affinity for a variety of PAHs, ligand-bound aryl hydrocarbon receptor (AHR) is able to interact with Ah receptor nuclear translocator protein (ARNT) and further mediate the toxicities of PAHs by stimulating the expression of target genes such as CYP1A1, which oxidizes PAHs and generally enhances their toxicities (Safe et al., 2013; Noakes, 2015). The AHR-ARNT complex can also promote cell proliferation by binding to the Slug promoter, activating ERK in the absence of external GFs, and enhancing FGF, PDGFA, and PCNA production (Shimba et al., 2002; Diry et al., 2006; Randi et al., 2008; Wang et al., 2009; Safe et al., 2013; John et al., 2014). Because PAHs account for a large portion of the organic constituents in PM2.5, their contribution to PM2.5-induced EMT might be nonnegligible. The significant *cyp1a1* upregulation following the exposure of HBE cells to diesel exhaust particles (DEPs) or the exposure of BEAS-2B and A549 cells to PM<sub>2.5</sub> proved the ability of PM to activate AHR signaling (Gualtieri et al., 2011, 2012; Rynning et al., 2018). Likewise, inhibiting AHR or CYP1A1 in BEAS-2B and A549 epithelial cells before PM<sub>2.5</sub> exposure could effectively rescue PM<sub>2.5</sub>-induced E-cadherin downregulation and N-cadherin upregulation. In this study, lncRNA MALAT1 showed synchronized expression tendency with N-cadherin, indicating that it functions as an effector regulating EMT at downstream of PM<sub>2.5</sub>/AHR signaling, in addition to its role in NF-κB pathway reviewed above (Huang et al., 2017). These studies indicated that PM2.5/PAHs/AHR/CYP1A1 signaling significantly participates in EMT initiation, although more exploration is urgently needed.

# PM<sub>2.5</sub> Induces Pro-Epithelial-Mesenchymal Transition Epigenetic Regulations

Epigenetic regulations through lncRNAs and miRNAs underlying  $PM_{2.5}$ -induced EMT have been partly reviewed above. Besides that, miR-16-1-3p directly targeting Twist mRNA could be inhibited by  $PM_{2.5}$  exposure, participating in  $PM_{2.5}$  exposure-induced EMT of hepatocellular carcinoma

TABLE 3 | Summary table about exposure assays of some studies reviewed in section "Other Molecular Events Underlying PM<sub>2.5</sub>-Induced Epithelial-Mesenchymal Transition."

Source of PM <sub>2.5</sub> for treatment	Dose of PM <sub>2.5</sub> exposure	Duration of exposure	Cell type	Reference
In vitro assays				
Collected at Beijing, China, from December 2016 to February 2017	25, 50, 100 μg/ml	Chronic exposure for 5 passages	Human lung cancer cell line (A549 cells)	Wang et al. (2019)
using glass fiber filter			Human bronchial epithelial cell line (BEAS-2B cells)	
Collected at Shenyang, China, in winter using nitrocellulose filter	5, 10, 20 μg/cm²	72 h	Human lung cancer cell line (A549 cells)	Yang et al. (2017)
			Human lung cancer cell line (H292 cells)	
Collected at Shanghai, China, from November 2017 to June 2018 using glass fiber filter	50 µg/mL	Chronic exposure for 30 passages	Human bronchial epithelial cell line (BEAS-2B cells)	Xu et al. (2019b)
Bought from NIST, USA (the product label: SRM 1648a)	100, 500 μg/ml	Chronic exposure for 30 passages	Human bronchial epithelial cell line (HBE cells)	Fu et al. (2019)
Collected at Nanjing and Shanghai, China, in Autumn 2014	Organic extract of PM <sub>2.5</sub> : 5 μg/ml	48 h	Human lung cancer cell line (A549 cells)	Huang et al. (2017)
using quartz filter			Human bronchial epithelial cell line (BEAS-2B cells)	
Obtained from a biomass power plant	100 μg/ml	5 weeks	Human bronchial epithelial cell line (BEAS-2B cells)	Hesselbach et al. (201
Collected at Shanghai, China in four seasons using glass fiber filter	20, 40, 60, 80, 100 μg/ml	24 h	Human bronchial epithelial cell line (BEAS-2B cells)	Zheng et al. (2017)
Source of PM <sub>2.5</sub> for treatment	Dose of PM <sub>2.5</sub> exposure	Method and duration of exposure	Animal	Reference
In vivo assays				
Collected at Beijing, China, from	2.5, 10, 20 mg/kg	Intratracheal instillation	8-week-old male BALB/c mice	(Wang et al., 2019)
December 2016 to February 2017 using glass fiber filter	Diluted in saline	Once/3 days, lasted for 90 days		
Bought from NIST, USA (the product label: SRM 1648a)	0.4 mg/m <sup>3</sup>	Dynamic inhalation exposure using the exposure chambers and aerosol generator	8-week-old C57BL/6 mice	(Fu et al., 2019)
		Lasted for 21 days		

cells (Zhang and Li, 2019). Moreover, PM<sub>2.5</sub> exposure also participates in initiation of EMT of bronchial epithelial cells by altering DNA methylation (Li et al., 2017). After 5 weeks of PM<sub>2.5</sub> exposure, hypomethylated CpG islands (CpGs) in the genome of bronchial epithelial cells were significantly enriched in genes associated with GTPase activity, extracellular matrix organization, and GF stimuli, whereas hypermethylated CpGs were clustered in genes responsible for cell adhesion and ion transportation (Hesselbach et al., 2017). Another set of DNA methylation analyses on bronchial epithelial cells after PM<sub>2.5</sub> exposure for 24 h showed comparable results, as Gene Ontology (GO) terms related with regulation on actin filament and adherin junction were significantly enriched in hypomethylated gene list (Shi et al., 2019). Because these annotated genes play dominant roles in EMT, these in silico analyses strongly indicated an association between PM2.5 exposure and EMT from a systematic perspective.

# Calcium Might Act as an Initiator of Epithelial-Mesenchymal Transition in PM<sub>2.5</sub>?

Calcium signaling is highly correlated with multiple malignant cancers. Alterations in the expression of  $Ca^{2+}$  channels or

transporters have been identified in tumor cells, indicating that ectopic Ca2+ signal transduction might play a role in EMT (Cui et al., 2017). For example, the activation of transient receptor potential cation channel 7 (TRPM7) and Ca2+ influx through TRPM7 indicates the initiation of EMT. Furthermore, EGF-induced TRPM7-Ca<sup>2+</sup>-dependent STAT3 activation significantly upregulated Twist, Snail, and EMT marker expression in breast cancer cells (Davis et al., 2014).  $Ca^{2+}$  is also able to elicit the expression of the ATP-binding cassette subfamily C member 3 (ABCC3), a promoter of Twist and EMT in breast cancer cells (Stewart et al., 2015). As Ca2+ has been well characterized as one of the most plentiful cations in PM2.5, and PM2.5 is able to penetrate into the bloodstream or be taken by cells, PM<sub>2.5</sub> exposure might result in increased Ca2+ concentration in microenvironment around the epithelia or cytoplasm, which could further regulate the activity of pro-EMT Ca<sup>2+</sup> signaling (Huang et al., 2018; Qin et al., 2018; Xie and Zhao, 2018). In our recent study, pulmonary epithelial cells showed EMT-like phenotype after long-term low dose PM2.5 exposure, and a subset of the intracellular differentially expressed genes was significantly related to the cellular response to calcium ion (Xu et al., 2019b). However, although limited in vitro studies have reported that

 $PM_{2.5}$  exposure could raise the intracellular Ca<sup>2+</sup> concentration of BEAS-2B cells and another non-epithelial cell line, the biological correlation of this event with EMT was yet to be clearly figured out (Zheng et al., 2017; Zhao et al., 2019).

# CONCLUSIONS

Accumulating evidence has shown that PM<sub>2.5</sub> can exert its toxic effect on somatic cells resulting in disorders including carcinogenesis and fibrosis. As EMT endows the epithelia with the characteristics of mesenchymal cells, it has been recognized as one of the major pathogenic mechanisms that promote malignant tumor metastasis and fibrogenesis. We and other researchers have originally identified PM<sub>2.5</sub> as an initiator of EMT. On the basis of studies investigating PM<sub>25</sub> toxicology, in this review, we describe that PM<sub>25</sub> might induce EMT by intermediary ROS, which induce the secretion of TGF- $\beta$ , IL-6, IL-8, and TNF- $\alpha$ , as well as the activation of the SMADs, NF-KB, JAK/STAT3, ERK, Akt, and Rho GTPasedependent cascades. However, only the role of PM2.5-derived ROS in EMT induction mediated by TGF-B/SMAD2/3 pathway has been relatively clearly uncovered, whereas other mechanisms are revealed by limited research. Because PM25-induced inflammation and apoptosis largely share collective key messengers with putative EMT molecular processes, the underlying subtle mechanisms that regulate these cellular events remain to be elucidated. In addition, preliminary evidence has shown a correlation between PM2.5-ROS-induced autophagy and EMT, although the interactions at the molecular level remain to be explored. Furthermore, PM25induced EMT is also dependent upon HMGB1-RAGE, Shh, Wnt/β-catenin, Notch, SMAD1 signaling, and ACLY enzyme, in which the involvement of ROS remains unclear. It is worth mentioning that epigenetic regulations involving miRNAs, lncRNAs, and DNA methylation might act as transcriptional or posttranscriptional regulators in PM2.5-induced EMT. PAHs and  $Ca^{2+}$ , the primary constituents of PM<sub>2.5</sub>, might specifically induce EMT by AHR and Ca<sup>2+</sup> signaling, respectively Figure 2.

However, our present understanding of the toxicology of PM<sub>2.5</sub> is still highly limited, as studies on PM<sub>2.5</sub> toxicology are confined to a series of factors that might result in ineluctable systematic errors. It is clear that different sampling sites inevitably bring about variance of PM2.5 composition, as climate characteristics and social, economic, and cultural features are extremely diverse around the world. This natural diversity might make the results of different studies incomparable. Nevertheless, detailed studies investigating the toxicology of the exact components of PM2.5 could be difficult to perform. Second, although sampling protocols have been preliminarily standardized, inconsistencies between the actual operations of researchers uncontrollably exist, which might lead to a reduction in internal authenticity. Besides, the methods of PM<sub>2.5</sub> treatment, including the selected vehicle solvent and the optimal concentrations to imitate the actual exposure state of humans, also significantly affect the physiology and pathological responses of cultured cells and murine models. According to existing studies, NAC is the widely used antioxidant against PM2.5



**FIGURE 2** | Potential regulatory routes of PM<sub>2.5</sub> in EMT. PM<sub>2.5</sub> might function as an EMT initiator by activating TGF-β/SMAD2/3, NF-κB, ERK, Akt, and mediating cytoskeleton rearrangement *via* ROS. In addition to epigenetic mechanisms such as InCRNAs, miRNAs, and DNA methylation regulation, HMGB1-RAGE, Shh, SMAD1, Wnt3a/β-catenin, and Notch pathways have also been originally validated as effector signaling of PM<sub>2.5</sub> in the process of EMT. ACLY might act as a key metabolic modulator in PM<sub>2.5</sub>-induced EMT. Autophagy following PM<sub>2.5</sub>-ROS can also promote EMT. Specific components within PM<sub>2.5</sub> might be EMT promoters, as PAHs can initiate EMT *via* AHR/ CYP1A1 signaling, and Ca<sup>2+</sup> ions might function by activating Ca<sup>2+</sup> signaling. EMT, epithelial-mesenchymal transition; TGF-β, transforming growth factor β; ERK, extracellular signal-regulated protein kinase; ROS, reactive oxygen species; RAGE, receptor for advanced glycation end-products; Shh, sonic hedgehog; ACLY, ATP citrate Iyase; PAHs, polyaromatic hydrocarbons; AHR, aryl hydrocarbon receptor.

exposure, which shows strong efficacy of ROS elimination in vitro. However, the opposite effect of NAC on lung cancer cells, that is, growth promotion effect by reducing ROS, has been observed (Sayin et al., 2014). Besides, the failure of PANTHER combined therapy consisting of prednisone, azathioprine, and NAC designed for idiopathic pulmonary fibrosis also indicates that precise drug prevention is still far from mature (Idiopathic Pulmonary Fibrosis Clinical Research Network et al., 2012). Therefore, additional in-depth research and consensus are urgently needed. Owing to the relatively limited understanding of the underlying mechanisms of PM<sub>2.5</sub>induced EMT, we comprehensively reviewed potential molecular events participating in PM2.5-induced EMT in various epithelial cell types that might be targeted by PM<sub>2.5</sub> exposure. As tissue/ cell type-specific responses to PM2.5 inevitably exist, the definitive role of PM<sub>2.5</sub> in EMT should be further explored and confirmed.

# AUTHOR CONTRIBUTIONS

ZX was responsible for literature searching, information aggregation, and manuscript preparation. WD participated in the review and language revision of this manuscript. XD contributed to the concept of this review and participated in the manuscript revision. XD and WD obtained the funding and financially supported the publication of this review. All authors have read and approved the final version of this manuscript.

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**Conflict of Interest:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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