



Article Dopant-Dependent Toxicity of CeO₂ Nanoparticles Is Associated with Dynamic Changes in H3K4me3 and H3K27me3 and Transcriptional Activation of NRF2 Gene in HaCaT Human Keratinocytes

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Abstract: Despite advances in the preparation of metal oxide (MO) nanoparticles (NPs) as catalysts for various applications, concerns about the biosafety of these particles remain. In this study, we prepared transition metal-doped cerium oxide (TM@CeO₂; TM = Cr, Mn, Fe, Co, or Ni) nanoparticles and investigated the mechanism underlying dopant-dependent toxicity in HaCaT human keratinocytes. We show that doping with Cr or Co but not Fe, Mn, or Ni increased the toxicity of CeO_2 NPs in doseand time-dependent manners and led to apoptotic cell death. Interestingly, while both undoped and transition metal-doped NPs increased intracellular reactive oxygen species (ROS), toxic Cr@CeO2 and Co@CeO2 NPs failed to induce the expression of NRF2 (nuclear factor erythroid 2-related factor 2) as well as its downstream target genes involved in the antioxidant defense system. Moreover, activation of NRF2 transcription was correlated with dynamic changes in H3K4me3 and H3K27me3 at the promoter of NRF2, which was not observed in cells exposed to Cr@CeO2 NPs. Furthermore, exposure to relatively non-toxic Fe@CeO2 NPs, but not the toxic Cr@CeO2 NPs, resulted in increased binding of MLL1 complex, a major histone lysine methylase mediating trimethylation of histone H3 lysine 4, at the NRF2 promoter. Taken together, our findings strongly suggest that failure of cells to respond to oxidative stress is critical for dopant-dependent toxicity of CeO₂ NPs and emphasize that careful evaluation of newly developed NPs should be preceded before industrial or biomedical applications.

Keywords: cerium oxide nanoparticles (CeO₂ NPs); transition metal doping; reactive oxygen species (ROS); NRF2-KEAP1 pathway; histone lysine methylation

1. Introduction

Metal oxide nanoparticles (MONPs) have been used for various chemical and biological applications, for example, as chemical sensors, biosensors, drug delivery agents, and for cancer therapy and in electrochemical reactions, due to their unique physicochemical properties [1–4]. MONPs are produced and consumed in large quantities, and the breadths of their applications are rapidly expanding. However, concerns have been expressed regarding their adverse effects on human health and the environment, as MONPs could enter the human body through ingestion, infection, inhalation, or skin contact [5–9]. The toxicities of MONPs depend on particle size and surface area, dosage, exposure time, pH, and extent of agglomeration [7,10–14]. In vitro and in vivo studies have suggested that induction of reactive oxygen species (ROS) by MONPs predominantly underlies their toxicities by causing oxidative stress and inflammation, leading to intracellular component damage and aberrant expressions of genes associated with cellular homeostasis [7,15]. In addition, changes in epigenetic modification, such as DNA methylation and histone modification, have recently been suggested as alternative mechanisms of MONPs-mediated



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Copyright: © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). toxicity [16]. However, the effects of MONPs on histone modification, especially at the ROS-related genes, and the effects of histone modifications on MONPs-mediated toxicity are not fully understood.

 CeO_2 is a lanthanide element metal oxide, and CeO_2 nanoparticles (NPs) have been used in wide-ranging applications, such as photo-catalysts, solid-oxide fuel cells, and dyesensitized solar cells [17–19]. CeO₂ NPs are also being considered for potential biological and biomedical applications because of their ability to mimic the actions of enzymes, such as superoxide dismutase (SOD) and catalase [20–22]. In addition, various strategies (e.g., synthetic protocol, metal (anion) doping, and physicochemical property modifications) have been developed to enhance the activities of CeO_2 NPs. In particular, transition metal doping has been proven to be effective in enhancing photocatalytic activity [23–29]. As has been performed for other MONPs, the toxicities of CeO₂ NPs have been evaluated in various cellular and organismal contexts, but published results are inconclusive due, at least in part, to differences between the physicochemical properties of the CeO2 NPs tested and cell-type dependent responsiveness [30–39]. Although most studies have reported at best modest toxic effects or even protective effects [33-35], some have suggested CeO₂ NPs may be toxic and cause cell death, presumably due to oxidative stress (e.g., reactive oxygen species (ROS) production), DNA damage, alterations in cell signaling, and deregulated gene expression [36–39].

NRF2 (nuclear factor erythroid 2-related factor 2) is a transcription factor that controls the cellular antioxidant defense system [40]. Its function is mainly regulated at the posttranscriptional level. Upon the oxidative stimuli, NRF2 is freed from KEAP1 (Kelch like ECH associated protein 1), a negative regulator of NRF2, and enters the nucleus, where it activates an array of antioxidative metabolizing/detoxifying genes by binding to ATE (antioxidant response element) [41,42]. NRF2 is also regulated at the transcriptional level. Studies have shown that transcription factors, such as AhR, NF-kB, and even NRF2 itself, regulate the expression of NRF2 [43–45]. In addition, epigenetic modifications, such as DNA methylation and histone methylation, have recently been reported to be key regulators of NRF2 [46].

The effects of CeO₂ NPs on NRF2-KEAP1 signaling have been reported in several studies, but results are not conclusive [38,47–50]. It has been shown that exposure to CeO₂ NPs induces oxidative stresses, increases nuclear NRF2 level, and eventually causes cell death [38]. However, it has also been reported CeO₂ NPs have protective effects due to the transcriptional and posttranscriptional activation of NRF2 signaling [47,48], and yet others have reported CeO₂ NPs exposure resulted in no significant change or even a reduction in NRF2 level [49,50]. Moreover, the effect of CeO₂ NPs on the epigenetic modification of the *NRF2* gene has not been studied in detail. In this study, we synthesized five different TM@CeO₂ NPs (where TM = Cr, Mn, Fe, Co, or Ni) and investigated their effects on HaCaT human keratinocytes and the mechanism responsible for dopant-dependent toxicity. Our comparative analysis provides evidence that transcriptional activation of the *NRF2* gene and dynamic changes in H3K4me3 and H3K27me3 histone modifications play a critical role in dopant-dependent toxicity of TM@CeO₂ NPs.

2. Results and Discussion

2.1. Effects of Transition Metal Doping on Cell Viability

To investigate the effects of transition metal doping on the toxicity of CeO₂ NPs, we first analyzed the crystal structure of TM@CeO₂ NPs by X-ray diffraction (XRD) and transmission electron microscopy (TEM). The XRD pattern of CeO₂ NPs was typical of fluorite structured CeO₂ without any obvious structural changes. All tested TM@CeO₂ NPs generated XRD spectra with peaks at $2\theta = 28.7^{\circ}$, 33.2° , 47.7° , 56.5° , 59.2° , 69.5° , 76.9° , and 79.3° (Figure 1a), which corresponded to the reflections from the (111), (200), (220), (311), (222), (400), (331), and (420) planes of undoped CeO₂ NPs (JCPDS card No. 41–1455). TEM images demonstrated undoped CeO₂ and TM@CeO₂ NPs had similar sizes (~20 nm) and shapes (Figure 1a, inset). In addition, the *c* axis lattice constants of TM@CeO₂ NPs were

almost the same as that of undoped CeO_2 NPs (Figure 1b). These observations suggest that transition metal doping is unlikely to cause significant changes in the surface structures of CeO_2 NPs.

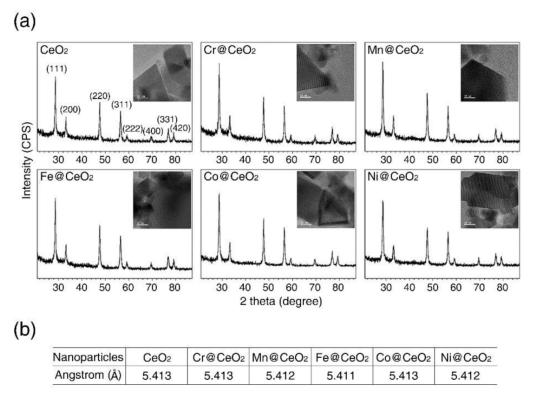
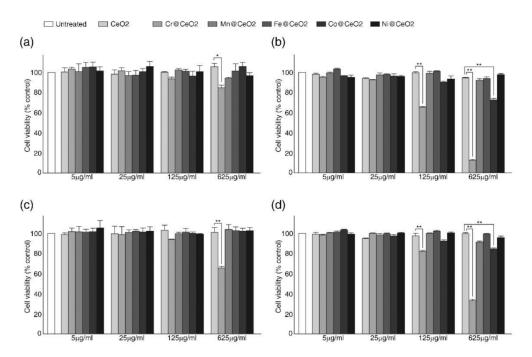


Figure 1. Effect of transition metal doping on the surface structure of CeO_2 NPs. (**a**) X-ray diffraction (XRD) analysis of undoped CeO₂ and TM@CeO₂ NPs. The insets present corresponding transmission electron microscopy (TEM) images. (scale bar is 10 nm) (**b**) Lattice constant of CeO₂ and TM@CeO₂ NPs.

We next conducted MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) and NRU (neutral red uptake) assays to assess the effects of transition metal doping on cell viabilities using three different cell lines, that is, HaCaT human keratinocytes, HEK293T cells (a human embryonic kidney cell line), and C3H10T1/2 mouse mesenchymal stem cells, respectively (Figure 2 and Figure S1). Consistent with previous studies, which showed CeO_2 NPs were relatively non-toxic [51,52], the viability of HaCaT cells fed with undoped CeO₂ NPs was comparable with that of untreated control cells even at a concentration of $625 \ \mu g/mL$ for up to 72 h (Figure 2). Furthermore, no significant decrease in viability was observed in cells treated with Mn-, Fe-, or Ni-doped CeO2 NPs for 24 and 72 h (Figure 2). In contrast, $Co@CeO_2$ and $Cr@CeO_2$ NPs exhibited significant toxicities (Figure 2). While exposure to Co@CeO₂ NPs for 24 h had no significant effect on cell viabilities even at the highest concentration used (625 μ g/mL) (Figure 2a,c), exposure to Co@CeO₂ NPs at 625 μ g/mL for 72 h reduced cell viability by ~30% (Figure 2b,d). Notably, exposure to Cr@CeO₂ NPs caused a dose- and time-dependent decrease in viability (Figure 2). In HaCaT cells, exposure for 24 h resulted in modest but meaningful reductions (\sim 7% at 125 µg/mL and \sim 15% at 625 µg/mL) and exposure for 72 h caused a further decreased the viability of HaCaT cells (\sim 30% at 125 µg/mL and by >80% at 625 μ g/mL) (Figure 2b,d). The viabilities of HEK293T cells were not significantly affected by exposure to relatively non-toxic NPs, but similar reductions were observed after exposure to Cr- or Co-doped NPs (Figure S1a-d). Interestingly, Co@CeO₂ NPs, which showed modest but significant toxicity in both HaCaT and HEK293T cells, had no significant effect on the viability of C3H10T1/2 mouse mesenchymal stem cells, and only cells exposed to



 $625 \ \mu g/mL$ of Cr@CeO₂ NPs for 72 h showed a reduction in viability of ~ 20%. These results indicated responsiveness to TM@CeO₂ NPs is cell-type dependent (Figure S1e–h).

Figure 2. Transition metal doping increased the toxicity of cerium oxide nanoparticles (CeO₂ NPs) in a dopant-dependent manner. HaCaT cells were incubated with undoped CeO₂ or indicated TM@CeO₂ NPs (5 to 625 μ g/mL) for 24 (**a**,**c**) and 72 h (**b**,**d**). Cell viabilities were assessed and quantified using (**a**,**b**) MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) and (**c**,**d**) NRU (neutral red uptake) assays, as described in Materials and Methods. Shown are representative data of at least three independent experiments. Mean \pm SD. * *p* < 0.05, ** *p* < 0.01.

We next investigated whether differences in intracellular localization and cellular uptake efficiency predominantly determined dopant-dependent toxicity (Figure S2). Both relatively non-toxic Fe@CeO₂ and toxic Cr@CeO₂ NPs were readily internalized and localized in the perinuclear region of HaCaT cells (Figure S2a). Moreover, fluorescence-based cellular uptake assays revealed that uptake efficiencies of toxic Cr@CeO₂ NPs were no higher than those of Fe@CeO₂ NPs at 5~625 μ g/mL after exposure up to 24 h (Figure S2b). Taken together, these data suggest that transition metal doping can affect the intrinsic toxicity of CeO₂ NPs, and that doping with Cr or Co, dose- and time-dependently increases CeO₂ nanoparticle toxicity.

2.2. Dopant-Dependent Toxicities of TM@CeO₂ NPs Were Associated with Apoptotic Cell Death in HaCaT Cells

We next investigated whether the observed decreases in cell viability were associated with apoptotic cell death (Figure 3). HaCaT cells were used for the in vitro analysis because they are derived from normal adult skin cells, and skin is one of the primary tissues affected by NPs. In addition, we used NPs at 125 μ g/mL as both toxic and non-toxic NPs resulted in comparable viabilities at this concentration after 24 h but differences in viability after incubation for 72 h (Figure 2 and Figure S1). Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assays revealed extensive and prolonged DNA fragmentation in cells treated with toxic Cr@CeO₂ NPs but lesser effects in cells exposed to Co@CeO₂ NPs, no significant fragmentation in cells fed with undoped CeO₂ or relatively non-toxic TM@CeO₂ NPs (TM = Mn, Fe, and Ni) (Figure 3a). RT-qPCR analysis confirmed increased expressions of pro-apoptotic sensor genes *BID* (BH3 interacting domain death agonist) and *BAD* (BCL2 associated agonist of cell death) and the pro-apoptotic effector gene

BAX (BCL2 associated X) in cells exposed to 125 μ g/mL of Cr@CeO₂ or Co@CeO₂ NPs after 72 h (Figure 3b). Conversely, mRNA levels of the anti-apoptotic genes *BCL-2* (B-cell CLL/lymphoma 2), *BCL-XL* (BCL2 like 1), and *MCL-1* (Myeloid cell leukemia sequence 1) were markedly decreased in cells treated with Cr- or Co-doped CeO₂ NPs (Figure 3b). Notably, while no significant changes in pro- and anti-apoptotic gene expressions were observed in HaCaT cells exposed to undoped CeO₂ or relatively non-toxic TM@CeO₂ NPs after 24 h, prolonged exposure (72 h) resulted in modest but meaningful increases in pro-apoptotic gene expressions in cells (Figure 3b). These data indicate that decreases in cell viability by toxic TM@CeO₂ NPs (TM = Cr or Co) are at least in part due to apoptotic cell death.

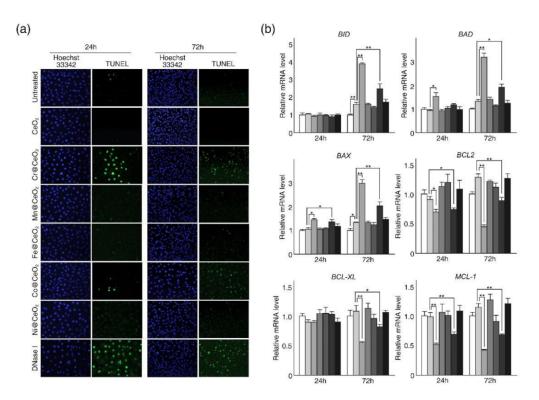


Figure 3. Exposure to toxic TM@CeO₂ NPs led to apoptotic cell death in HaCaT cells. (**a**) Cells were exposed to 125 µg/mL of NPs (undoped CeO₂ and TM@CeO₂) for the indicated times (24 and 72 h). Shown are representative photomicrographic images of Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) (green) and Hoechst 33342 (blue) double-stained cells ($20 \times$). Cells treated with DNase I were used as positive controls. (**b**) RT-qPCR analysis of genes involved in apoptotic cell death in untreated control and NPs treated cells. The total RNAs were isolated from untreated control, CeO₂ NPs treated, and indicated TM@CeO₂ NPs treated cells at the indicated times, and the relative mRNA levels of pro-apoptotic *BID* (BH3 interacting domain death agonist), *BAD* (BCL2 associated agonist of cell death), and *BAX* (BCL2 associated X) and anti-apoptotic *BCL2* (B-cell CLL/lymphoma 2), *BCL-XL* (BCL2 like 1), and *MCL-1* (Myeloid cell leukemia sequence 1) were measured by RT-qPCR. The mRNA levels of indicated genes were first normalized to the mRNA level of *GAPDH* (Glyceraldehyde-3-phosphate dehydrogenase), and data are presented as ratios of mRNA levels in NPs treated cells to mRNA levels in untreated cells at each time point (24 and 72 h). The qPCR data shown are representative of at least three independent experiments and are presented as mean \pm SD (n = 3~5). * *p* < 0.05, ** *p* < 0.01.

2.3. Effect of Transition Metal Doping on Intracellular ROS Generation

Since exposure to MONPs often causes oxidative stress, such as intracellular ROS generation, and these stresses are believed to be major factors of NP toxicity, we next examined the effect of transition metal doping on intracellular ROS generation (Figure 4). Surprisingly, we found that HaCaT cells exposed to NPs generated more ROS than un-

treated cells regardless of toxicity (Figure 4). However, levels of ROS measured in cells exposed to toxic TM@CeO₂ NPs (TM = Cr, Co) were significantly greater than levels in undoped CeO₂ NPs, whereas exposure to relative non-toxic TM@CeO₂ NPs (TM = Fe, Mn, Ni) resulted in the ROS level similar to those observed in undoped NPs (Figure 4a, b). Levels of intracellular ROS appeared to decrease after 72 h, but HaCaT cells treated with toxic TM@CeO₂ NPs (TM = Cr or Co) maintained higher ROS levels than those treated with relatively non-toxic NPs (Figure 4b). Considering that all tested NPs increased intracellular ROS generation but only Cr- and Cr-doped CeO₂ NPs showed discernible cytotoxicity, these results suggest that either ROS level or the ability of cells to respond to ROS more critically determine NPs-mediated toxicity than oxidative stress itself.

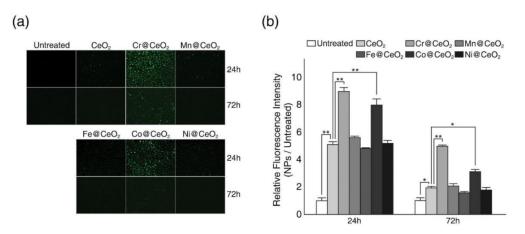


Figure 4. Effect of transition metal doping on intracellular reactive oxygen species (ROS) generation. Both undoped and TM@CeO₂ NPs cause increased intracellular ROS generation in HaCaT cells, but exposure to toxic TM@CeO₂ NPs (TM = Cr, Co) induced higher ROS levels. (**a**) Cells were treated with 125 µg/mL of NPs (undoped CeO₂ and TM@CeO₂) for the indicated times (24 and 72 h), and intracellular ROS levels were monitored using H2DCFDA, as described in Materials and Methods. Shown are representative photomicrographic images for intracellular ROS generation (20×). (**b**) ROS levels were quantified by measuring fluorescence intensity. Results are presented as the ratios of fluorescence intensities after NP treatment to fluorescence intensities of untreated cells. Shown are representative data of at least three independent experiments (n = 3~6). Mean ± SD. * *p* < 0.05, ** *p* < 0.01.

2.4. Dopant-Dependent Toxicity Was Associated with a Failure of Cells to Activate NRF2 Expression

Because oxidative stresses induced by reactive oxidants are mainly countered by the NRF2-KEAP1 signaling pathway (a major antioxidant defense system), we investigated whether ROS increases by CeO_2 or TM@CeO₂NPs led to the activation of this pathway (Figure 5). RT-qPCR analysis revealed increased expression of NRF2 and decreased expression of *KEAP1* (a negative regulator of NRF2) in HaCaT cells treated with undoped CeO_2 NPs and similar results in cells treated with relatively non-toxic TM@CeO₂ NPs (TM = Mn, Fe, or Ni) (Figure 5a). Surprisingly, no significant increase in NRF2 mRNA level and decrease in KEAP1 mRNA level was observed in cells exposed to toxic TM@CeO2 NPs (TM = Cr or Co) despite elevated intracellular ROS levels (Figures 4 and 5a). Immunoblot analysis confirmed increased NRF2 levels in nuclear and cytosolic fractions and decreased KEAP1 levels after exposing cells to relatively non-toxic CeO₂ or Fe@CeO₂ NPs, but not in cells exposed to toxic Cr@CeO₂ NPs (Figure 5b and Figure S3). Next, we examined the expression of downstream target genes of NRF2, which include CAT (catalase), SOD1 (superoxide dismutase 1, cytosol), SOD2 (superoxide dismutase 2, mitochondria), HO-1 (heme oxygenase 1), and NQO1 (NAD(P)H quinone dehydrogenase 1) (Figure 5c). As was expected, the expression of NRF2 target genes was markedly increased in HaCaT cells exposed to relatively non-toxic NPs but not in cells exposed to toxic TM@CeO2

NPs (Figure 5c). These observations suggest that intracellular ROS increases induced by relatively non-toxic NPs can be countered in cells, at least in part, by activation of the antioxidant defense system mediated by NRF2, and that the failure of cells to cope with elevated ROS levels underlies the dopant-dependent toxicity of CeO_2 NPs.

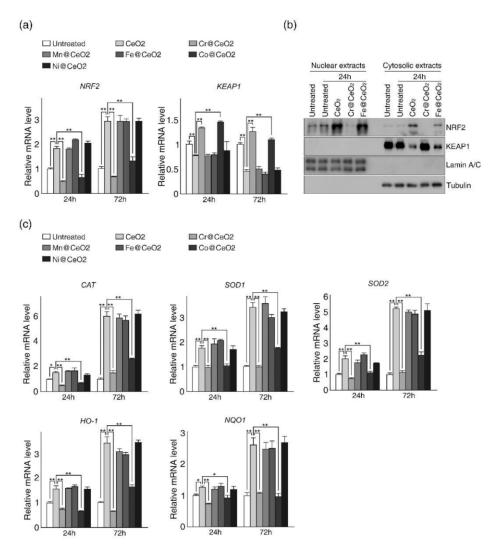


Figure 5. Toxic TM@CeO₂ NPs (TM = Cr, Co) failed to activate the NRF2 dependent antioxidant defense system. (a,b) HaCaT cells treated with Cr@CeO₂ or Co@CeO₂ NPs failed to activate NRF2 expression. (a) RT-qPCR analysis of NRF2(nuclear factor erythroid 2-related factor 2) and KEAP1 (kelch like ECH associated protein 1) genes in non-treated controls and NPs-treated cells. The total RNAs were isolated from untreated control, CeO2 NPs-treated, and TM@CeO2 NPs-treated cells after the indicated treatment time and relative mRNA levels were measured by RT-qPCR. (b) Immunoblot analysis of NRF2 and KEAP1 before and after NPs exposure. Nuclear and cytosolic extracts were prepared from cells treated or not with NPs for 24 h and subjected to immunoblot analysis to detect NRF2, KEAP1, Lamin A/C, and Tubulin. Lamin A/C and Tubulin were used as controls for nuclear and cytosolic fractions, respectively. (c) RT-qPCR analysis of target genes of NRF2 in control and NPs-treated cells. Relative mRNA levels of CAT (catalase), SOD1 (superoxide dismutase 1, cytosol), SOD2 (superoxide dismutase 2, mitochondria), HO-1 (heme oxygenase 1), and NQO1 (NAD(P)H quinone dehydrogenase 1) were measured using cDNA prepared from the same cells used in (a). The mRNA levels of indicated genes (a,c) were normalized to mRNA level of GAPDH, and data are presented as ratios of mRNA levels in NP-treated cells to those in untreated cells at each time point (24 and 72 h). The qPCR results are representative of at least three independent experiments and presented as mean \pm SD (n = 3~5). * p < 0.05, ** p < 0.01.

2.5. Dopant Dependent Toxicity Was Associated with H3K4me3 and H3K27me3 Modification at NRF2 Promoter

Since lysine methylation of core histories is known to be involved in both activation and repression of genes depending on the site and status of modification [53], we next investigated whether the failure of NRF2 expression following exposure to toxic TM@CeO₂ NPs was associated with changes in histone lysine methylation (Figure 6a, b). Chromatin immunoprecipitation (ChIP) assays revealed that the exposure of HaCaT cells to undoped CeO₂ or Fe@CeO₂ NPs resulted in significant increases in the trimethylation of histone H3 lysine 4 (H3K4me3) and a discernible decrease in the trimethylation of histone H3 lysine 27 (H3K27me3) at NRF2 promoter (Figure 6a, upper right and lower left panel). However, exposure to toxic Cr@CeO₂ NPs had little effect on H3K4me3 or H3K27me3 at the promoter (Figure 6a). Interestingly, trimethylation of histone H3 lysine9, which also marks repressed gene expression, was not affected by NPs exposure (Figure 6a, lower right panel). Because levels of histone methylation are determined by methylation and demethylation, we conducted a time course chromatin immunoprecipitation analysis to confirm that exposure to Cr@CeO₂ NPs did not promote H3K4me3 demethylation. As shown in Figure 6b, H3K4me3 level at the promoter of NRF2 gradually increased after exposure to undoped CeO₂ or Fe@CeO₂ NPs for up to 24 h, but no discernible change in H3K4me3 level was detected after treatment with Cr@CeO₂ NPs for the same time. Finally, we examined the binding of the MLL1 (mixed-lineage leukemia 1) complex (a major histone lysine methylase for H3K4 trimethylation) at NRF2 gene. As was expected, exposure to relatively non-toxic NPs but not to toxic Cr@CeO₂ NPs increased bindings of MLL1 and ASH2L (a key component of MLL1 complex) at NRF2 promoter (Figure 6c). Taken together, these data strongly suggest that oxidative stresses induced by CeO_2 and relatively non-toxic TM@CeO₂ NPs can be countered by transcriptional activation of NRF2 via dynamic changes in H3K4me3and H3K27me3, and that failure of NRF2 activation is an underlying cause of the dopant-dependent toxicity of TM@CeO₂ NPs.

In conclusion, our current study shows that TM@CeO2 NPs could exhibit dopantdependent toxicity. Cr was the most toxic dopant among the transition metal tested, and Fe, Mn, or Ni appeared to have no significant effect on the intrinsic toxicity of CeO₂ NPs. In particular, our data support the idea that activation of NRF2 signaling pathway rather than oxidative stress per se critically determines NPs-mediated toxicity, as all tested CeO₂ NPs elevated intracellular ROS levels but only the relatively non-toxic NPs induced intracellular antioxidant defense mechanism at least in part by activating NRF2 expression. In addition, our observations of dynamic changes in H3K4me3 and H3K27me3 histone modifications and increased binding of MLL1 complex at the NRF2 promoter following NPs exposure suggest MLL1 complex participates in the regulation of NRF2 expression, which we hope provides new insights into the molecular mechanism responsible for activating NRF2 dependent antioxidant defense system. Lastly, it should be noted that despite the observed relatively non-toxic natures of undoped CeO₂ and Fe-, Mn-, and Ni-doped CeO₂ NPs, the safety of these NPs with respect to long-term exposure remains undetermined, and thus, the study emphasizes the importance of carefully evaluating engineered NPs for biological safety before they are adopted for industrial and biomedical purposes.

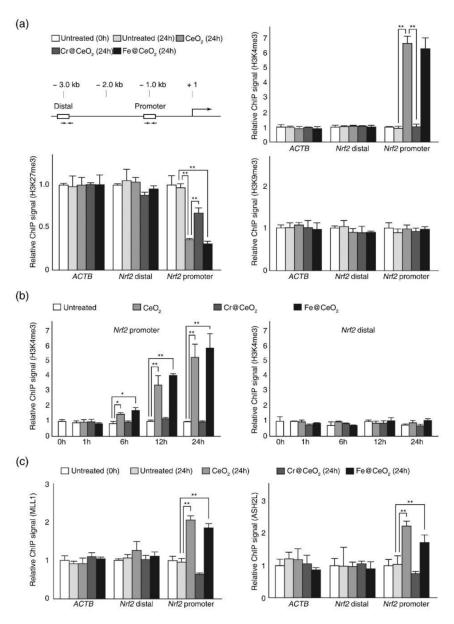


Figure 6. Dopant-dependent TM@CeO2 toxicity was associated with dynamic changes in histone lysine modifications. (a) CeO2 and Fe@CeO2 NPs, but not toxic Cr@CeO2 NPs, increased H3K4me3 but decreased H3K27me3 level at the promoter of NRF2 gene. (upper left) Schematic representation of the NRF2 gene with amplicons (promoter and distal regions) analyzed by chromatin immunoprecipitation (ChIP)-qPCR. Chromatins prepared from the cells before (0 h) and after (24 h) NPs exposure were precipitated with α -H3K4me3, α -H3K9me3, or α -H3K27me3 antibodies. qPCR analysis was performed to assess the enrichment of modified histones at the promoter and distal regions of the NRF2 gene. (b) Time course ChIP analysis for H3K4 trimethylation induced by NPs. Chromatins were prepared from HaCaT cells exposed to NPs for the indicated times and precipitated with α -H3K4me3 antibodies. (c) Binding of MLL (mixed-lineage leukemia) complex at NRF2 promoter increased after non-toxic NPs treatment but not after treatment with toxic Cr@CeO2 NPs. Chromatins were prepared as described in (a) and precipitated with α -MLL1 (left) or α -ASH2L (right) antibodies. For each chromatin, ChIP using IgG was performed to check chromatin quality. qPCR analyses shown in (b,c) were performed as in (a). For the relative ChIP signal, the % input (indicated antibody) was calculated for all samples, and data are presented as ratios of % input (indicated antibody) in NP-treated cells to those in untreated control cells. qPCR data are representative of at least three independent experiments and are presented as mean \pm SD (n = 3~5). * p < 0.05, ** p < 0.01.

3. Materials and Methods

3.1. Preparation of Transition Metal-Doped CeO₂ NPs

CeO₂ NPs were synthesized using a modified thermal method [25,26]. For transition metal doping, precursor solutions were prepared by one-pot synthesis. The desired amount (1 mol%) of each TM dopant (Cr, Mn, Fe, Co, and Ni) in the form of $TM(NO_3)_3 \cdot 9H_2O$ (99% purity) was added to each synthetic gel solution with stirring until the solution became homogeneous and transparent. The solution was then transferred to a Teflon-lined autoclave and heated at 220 °C for 10 h in a convection oven. The resulting CeO₂ and TM@CeO₂ NPs were filtered and washed with deuterium-depleted water (DDW) to remove residues. All substances used for doping were purchased from Sigma–Aldrich (Sigma, St Louis, MO, USA).

3.2. Characterization of TM@CeO₂ NPs

The structures of fabricated CeO₂ NPs and the five TM@CeO₂ NPs were analyzed by using a JEM-3010 high-resolution transmission electron microscopy (HR-TEM, JEOL, Tokyo, Japan) at 300 kV and X-ray diffraction (XRD) patterns were obtained using Ni-filtered Cu–K α radiation from a D8 Advance diffractometer (Bruker, Karlsruhe, Germany).

3.3. Cell Culture and NPs Exposure

HaCaT human keratinocytes were kindly provided by Dr. S. Kwon (Inha University, Korea). Cells were maintained in Dulbecco's modified Eagle's medium (DMEM, Wel-GENE, Gyeongsan, Korea) supplemented with 10% fetal bovine serum (FBS, WelGENE, Gyeongsan, Korea) and 1% penicillin–streptomycin (GE Healthcare, Madison, WI, USA) in a humidified atmosphere with 5% CO₂ at 37 °C. For NPs exposure, 10 mg/mL of TM@CeO₂ NPs in DMEM supplemented with 10% FBS were prepared using a vortex mixer to prevent aggregation and then added to culture plates at the final concentrations of 5, 25, 125, or 625 μ g/mL.

3.4. Cell Viability Assays

The effects of TM@CeO₂ NPs on cell viability were assessed by MTT and NRU assays, as previously described [54,55]. Briefly, HaCaT, HEK293T, and C3H10T1/2 cells were seeded at 2×10^4 cells per well in 96-well cell culture plates and cultured for 24 h. Cells were then exposed to undoped CeO₂ or TM@CeO₂ NPs for 24 or 72 h. For MTT assays, cells were washed twice with phosphate-buffered saline (PBS, GIBCO, Grand Island, NY, USA), and then MTT solution (Sigma, St Louis, MO, USA) was added to each well to a final concentration of 0.5 mg/mL. One hour later, formazan crystals that formed were dissolved in 50% dimethyl sulfoxide (DMSO, Sigma, St Louis, MO, USA)/50% methanol (Merck, Darmstadt, Germany). For NRU assays, cells were washed twice with PBS following exposure to NPs for 24 or 72 h and then incubated for 4 h in OPTI-MEMI (GIBCO, Grand Island, NY, USA) containing 40 ng/mL of neutral red reagent (Sigma, St Louis, MO, USA). After incubation, wells were eluted with 50% ethanol (Merck, Darmstadt, Germany)/1% glacial acetic acid (Merck, Darmstadt, Germany). Absorbances were measured using an XFluor4 microplate reader (Tecan, Männedorf, Switzerland) at 595 nm for MTT assays and 540 nm for NRU assays. Cell viabilities were expressed as percentages of control cells using $\{(O.D. sample - O.D. blank)/(O.D. control - O.D. blank) \times 100\}$.

3.5. TUNEL Assay

Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assays were performed using the In Situ Cell Death Detection Kit, Fluorescein (Roche, Mannheim, Germany). HaCaT cells were seeded at 2×10^4 cells per well in a 96-well cell culture plate and 24 h later, exposed to 125 µg/mL of undoped CeO₂ or TM@CeO₂ NPs for 24 or 72 h. Following fixation with 4% paraformaldehyde (EMS, Hatfield, PA, USA) for 30 min and permeabilization with 0.1% Triton X-100 (Merck, Darmstadt, Germany) in PBS for 10 min, cells were incubated with TUNEL reaction solution for 1 h at 37 °C in the dark and stained

with Hoechst 33342 (Invitrogen, Carlsbad, CA, USA) for 5 min. Images were taken at $20 \times$ magnification using an Olympus IX71 inverted microscope equipped with a U-RFL-T mercury lamp (Olympus, Tokyo, Japan). Cells treated with 1,000 units/mL of DNase I (Promega, Madison, WI, USA) for 10 min were used as positive controls.

3.6. Measurement of Intracellular Reactive Oxygen Species (ROS) Levels

Intracellular ROS levels were measured using dichlorofluorescein diacetate oxidation, as previously described [56]. Cells were seeded at 2×10^5 cells per well in 6-well plates, incubated for 24 h, and exposed to 125 µg/mL of undoped CeO₂ or TM@CeO₂ NPs for 24 or 72 h. Following exposure, cells were washed with PBS and incubated with 50 µM of 2',7'-dichlorofluorescin diacetate (DCFDA, Invitrogen, Carlsbad, CA, USA) for 30 min. Images were taken using an Olympus IX71 inverted microscope equipped with a U-RFL-T mercury lamp at excitation wavelengths of 488 nm and processed using Adobe Photoshop CC2018 software (Adobe Systems, San Jose, CA, USA). To quantify ROS levels, fluorescence intensities were measured using a Synergy HTX multi-mode microplate reader (Bio-Tek, Winooski, VT, USA) and Gen5 software (Bio-Tek, Winooski, VT, USA) at excitation and emission wavelengths of 485 nm and 528 nm, respectively. Relative fluorescence intensity was presented as a ratio of (O.D. sample – O.D. blank) to (O.D. untreated – O.D. blank).

3.7. Cell Fractionation and Immunoblot Analysis

HaCaT cells were washed with PBS and lysed with hypotonic buffer (10 mM HEPES pH 7.9, 10 mM KCl, 0.1 mM ethylenediaminetetraacetic acid (EDTA) pH 8.0, and 0.3% NP-40) in the presence of a protease inhibitor cocktail (Roche, Mannheim, Germany). Lysates obtained were passed through a 26G1/2 needle 10 times, incubated on ice for 10 min, and then centrifuged at $5,000 \times g$ for 10 min. Supernatants were used as a cytosolic fraction, and nuclear fractions were prepared by suspending pellets in radioimmunoprecipitation assay (RIPA) buffer (10 mM Tris-HCl, pH 7.5, 1 mM EDTA, pH 8.0, 150 mM NaCl, 1% Triton X-100, 1% sodium deoxycholate, and 0.1% sodium dodecyl sulfate (SDS)), sonicating at 40% amplitude for 5×30 s using a VCX130 sonicator (Sonics, Newtown, CT, USA), and then centrifugation at $13,000 \times g$ for 20 min. Immunoblot analysis was performed using a standard protocol. Detailed information regarding antibodies and working concentrations is provided in Supplementary Material (Table S1).

3.8. Quantitative RT-PCR Analysis (RT-qPCR)

For RT-qPCR analysis, total RNA was isolated using an RNeasy plus mini kit (QIA-GEN, Hilden, Germany), and cDNA was synthesized using a GoScript reverse transcription system (Promega, Madison, WI, USA), according to the manufacturer's instructions. Quantitative PCR was conducted using a QuantStudio 1 Real-Time PCR system (ThermoFisher Scientific, Waltham, MA, USA) using SYBR Green I (Invitrogen, Carlsbad, CA, USA) and i-StarTaq DNA polymerase (Intron, Sungnam, Korea). mRNA levels were normalized to *GAPDH* mRNA, and data are presented as indicated in Figures 3 and 5. Primer sets used are detailed in Supplementary Materials (Table S2).

3.9. Chromatin Immunoprecipitation (ChIP)-qPCR Analysis

ChIP assays were performed as previously described [57]. Briefly, 100~300 µg of sonicated chromatins were precleared for 2 h using protein A/G sepharose 4 Fast Flow (GE Healthcare, Madison, WI, USA) in the presence of 4 mg/mL salmon sperm DNA (Invitrogen, Carlsbad, CA, USA) and 0.5 mg/mL bovine serum albumin (Sigma, St Louis, MO, USA) and then subjected to immunoprecipitation using appropriate antibodies. Purified DNA obtained was analyzed by quantitative PCR (qPCR) using a QuantStudio 1 Real-Time PCR system. For quantification, the % input value per sample was calculated, and the data are presented as relative ChIP signals as indicated in Figure 6. The antibodies and primers used for ChIP-qPCR analysis are listed in Tables S1 and S3.

3.10. Statistical Analysis

Results of cell viability assays and all qPCR-based experiments are representative of at least three independent experiments (as indicated in the figure legends) and are presented as the means \pm SDs. Statistical significance and *p*-values were determined by two-tailed *t*-tests of the indicated paired groups using Microsoft Excel (version 2102, Microsoft, Redmond, WA, USA). Differences were considered significant when *p*-values were < 0.05.

Supplementary Materials: The following are available online at https://www.mdpi.com/1422-0 067/22/6/3087/s1, Figure S1: Effect of transition metal doping on the viabilities of HEK293T and C3H10T1/2 cells. Figure S2: Intracellular localization and cellular uptake efficiency of toxic Cr@CeO₂ NPs and relatively non-toxic Fe@CeO₂ NPs. Figure S3: Exposure to relatively non-toxic undoped or Fe-doped CeO₂ NPs led to increased NRF2 and decreased KEAP1 in HaCaT cells. Table S1: Information on the antibodies used in this study, Table S2: Information on the primers used for RT-qPCR, Table S3: Information on the primers used for ChIP-qPCR, References.

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