

NF- κ B, a pivotal transcription factor in silica-induced diseases

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Abstract

Inhalation of silica in a number of occupational settings can result in debilitating and costly lung disease. It is thought that the pathological replacement of functional lung tissue with fibrotic lesions in silica-induced lung disease is the result of chronic inflammation mediated by products of the silica-exposed alveolar macrophage. In particular, inflammatory cytokines, growth factors and reactive oxygen species have been implicated in many acute and chronic inflammatory lung diseases. Pharmacological intervention to modify the production of these mediators has been shown to ameliorate several of these disease processes. Recent studies have demonstrated that the production of these inflammatory mediators is altered as a result of the activation of nuclear factor- κ B (NF- κ B). NF- κ B is a pivotal transcription factor activated by silica in macrophages and other types of lung cells. The understanding of how silica induces NF- κ B activation and what signaling pathways are involved in this silica-induced NF- κ B activation is important and should provide valuable new information related to both the etiology and potential treatment of silica-related lung diseases. This review summarizes the molecular mechanisms involved in silica-induced NF- κ B activation and discusses the importance of NF- κ B as a critical transcription factor in mediating silica-induced lung diseases. (*Mol Cell Biochem* **234/235**: 169–176, 2002)

Key words: silica, NF- κ B, apoptosis, cancer

Introduction

It has been 6 years since the discovery that silica is a potent inducer for nuclear factor κ B (NF- κ B) [1, 2], a pivotal eukaryotic transcription factor governing the expression of early response genes involved in inflammation and cancer [3–5]. Recent studies indicate that NF- κ B is also an important transcription factor regulating processes of viral replication, embryonic development, control of cell proliferation and apoptosis, and tissue degeneration [6, 7]. Therefore, it is not surprising that silica has long been recognized as one of the most potent inducers for proliferative lung diseases, such as lung fibrosis and possibly cancer.

NF- κ B is an ubiquitous transcription factor that governs the expression of genes encoding cytokines, chemokines, growth factors, cell adhesion molecules and some acute phase proteins [3, 7]. This transcription factor was first identified as a B cell nuclear factor and named NF- κ B based on its ability to bind to an intronic enhancer of the immunoglobu-

lin κ -light chain gene [8]. Since then, NF- κ B has been identified in numerous cell types and found to be activated by a wide range of inducers including UV irradiation, cytokines, inhaled occupational particulates, and bacterial and viral products [3]. In resting cells, NF- κ B is sequestered in the cytoplasm in an inactive form by a group of inhibitory proteins known as I κ B of which I κ B α , I κ B β , and I κ B ϵ appear to be the key members [9, 10]. Upon cellular activation by extracellular stimuli, I κ B is phosphorylated and proteolytically degraded or processed by proteasomes and other proteases. Following these processes, NF- κ B is activated and translocated into the nucleus. In nuclei, NF- κ B can initiate or regulate early response gene transcription by binding to decameric motifs GGGRNNYYCC [κ B motif] found in the promoter or enhancer regions of specific genes.

The degradation of I κ B α is a key step required for the activation of NF- κ B. This occurs through signal-induced phosphorylation of two serines (Ser32 and Ser36) on I κ B α molecule [6]. Replacement of Ser32 and Ser36 by threonine or alanine

residues significantly decreases signal-induced phosphorylation and degradation of I κ B α protein [11]. Phosphorylation of these conserved S residues in response to inducers leads to the immediate polyubiquitination of I κ B proteins by SCF- β -TrCP complex [12, 13], a step which has been shown recently to be inhibited by the nonpathogenic *Salmonella* bacteria in gut epithelial cells [14]. This modification subsequently targets I κ B proteins for rapid degradation by the 26S proteasome [15]. A major breakthrough in the studies of NF- κ B signaling in the last few years has been the identification of a high-molecular-weight I κ B kinase (IKK) complex that phosphorylates I κ B α or I κ B β [16, 17]. This complex contains two catalytic subunits, IKK α and IKK β , and a structural component named NEMO/IKK γ /IKKAP [5]. An earlier report by Cohen *et al.* [18] suggested the presence of a scaffold protein named IKK complex-associated protein (IKAP) in the IKK complex, which could not be confirmed in other studies. A recent study by the group, who originally identified IKAP, indicated that the observed association of IKAP with IKK was due to a non-strict elution condition of chromatographic extracts during the purification of IKK [19]. Recently, two groups independently reported the identification of a novel protein, CIKS/Act1, associated with the IKK complex and suggested that CIKS/Act1 functions as an anchoring protein in the assembly of the IKK complex and in providing a possible connection between IKK and c-Jun-N-terminal kinase (JNK) signaling [20, 21]. IKK α and IKK β share 52% sequence homology in their kinase domain. Both proteins contain an amino terminal kinase domain, a carboxy terminal region with a leucine zipper, and a helix-loop-helix domain. *In vitro* or *in vivo* studies indicate that although both IKK α and IKK β are capable of phosphorylating I κ B α on ser32 and ser36, IKK β is more potent in I κ B α phosphorylation induced by proinflammatory stimuli [5]. Intriguingly, recent studies suggested a kinase- or NF- κ B-independent effect of IKK α on the differentiation of keratinocytes [22]. A distinct IKK complex, named IKKi/ ϵ that does not contain IKK α , β or γ , was also identified recently in T cells [23–25]. IKKi/ ϵ shares 27% homology with IKK α and IKK β and possibly mediates NF- κ B-activating kinase (NAK) signaling, PMA/PKC ϵ -induced S36 phosphorylation of I κ B α , and NF- κ B activation [26, 27].

Although silica has been recognized as a potent inducer for NF- κ B [1, 28, 29] and the signaling pathways leading to the activation of NF- κ B have been well defined [3, 5], there has been no information on how silica stimulates the signaling pathways leading to the activation of NF- κ B. Recent publications describing the mechanism of action of other NF- κ B inducers, such as cytokines [30], LPS [31], HTLV Tax protein [32, 33], and CD28 signal [34], have been focused on the role of the IKK, or other upstream kinases possibly participating in the activation of IKK. However, no evidence has been presented to demonstrate or indicate that silica, or re-

active oxygen species (ROS) generated by silica-mediated reactions, can affect the activation or activity of these kinases. While silica-induced lung diseases have been considered a world-wide health problem in terms of both the quality of life for the worker and the national expenditure for lost production, health care costs and disability compensation, only a relatively small number of researchers are investigating the mechanistic aspects of silica-induced lung diseases. In view of the fact that activation of NF- κ B plays a key role in the initiation and progression of silica-induced lung diseases, elucidation of molecular mechanisms determining silica-induced NF- κ B activation and its various functions may lead to the development of novel preventive and therapeutic strategies for diseases resulting from silica inhalation.

Silica activates NF- κ B

Silica exposure causes macrophages to release a number of inflammatory mediators including PGE2 [35], nitric oxide [36], TNF α [37], IL-1 [37] and IL-6 [38]. At the DNA level, a common structural characteristic of the genes responsible for the generation of these mediators is the presence of one or several NF- κ B binding sites in the promoter or 5'-flanking region [4]. This raises the possibility that silica-induced release of divergent inflammatory mediators may be dependent on a common mechanism, NF- κ B activation. Indeed, the earlier work conducted by Chen *et al.* [1] indicated that silica could induce the nuclear translocation of NF- κ B in murine macrophages. Analysis of the composition of the nuclear translocated NF- κ B subtypes induced by silica suggested that both the p50/p50 homodimer and the p50/p65 or p52/p65 heterodimer of NF- κ B are induced at either earlier or later time points. In contrast, only a heterodimer composed either p50/p65 or p52/p65 could be induced in the earlier time points by LPS. These results indicate that the mechanisms for silica-induced NF- κ B activation may differ from that for LPS-induced NF- κ B activation. Dose-response experiments *in vitro* suggested that NF- κ B activation by silica follows a bell-shaped dose-response curve with peak activity for silica at 50 to 100 μ g/ml. At relatively high doses of silica (200–400 μ g/ml), the activation of NF- κ B was decreased, which may explain why some reports have suggested that silica had no effect on the release of inflammatory mediators in certain experimental systems.

Previously, an oxidative stress model was proposed for the activation of NF- κ B by diverse agents [39]. It is reasonable to speculate that ROS derived either from the interaction of the surface of silica particles with aqueous medium or as a result of chronic respiratory burst activity in the lung is responsible for silica-induced NF- κ B activation [40, 41]. This hypothesis was based on several lines of evidence. First, ROS

have been shown to be increased in some cell types in response to silica exposure [41]. Second, direct incubation of certain cell lines with H_2O_2 activates NF- κ B [42]. Third, addition of compounds possessing antioxidant properties, such as N-acetyl-L-cysteine (NAC), catalase, deferoxamine, ascorbate, and formate, can inhibit signal-induced NF- κ B activation [43].

The question is whether ROS, resulting from silica exposure, activates NF- κ B through mechanisms similar to those of IL-1, TNF α , or LPS. Up to now, there is no evidence indicating that silica and its ROS derivatives stimulate the IKK kinase activity, suggesting a possible IKK-independent mechanism. There are a number of other pathways by which silica may activate NF- κ B. Both silica and ROS have been implicated in the activation of mitogen-activated protein kinases (MAPKs), such as Erk, p38 and JNK [44, 45]. It is possible that certain molecules in MAPK signaling pathway may have the potential to stimulate the IKK kinase. The oxidative damage or modification of a protein or DNA might be another measure for the effects of silica on NF- κ B. It has been proposed that oxidation and reduction could affect the assembly of both kinase complexes and NF- κ B-DNA binding complexes [46].

Silica induces different proteolytic system for the degradation of I κ B α

Two major proteolytic pathways have been studied with regard to their role in signal-induced NF- κ B activation: proteasomes and calpains [3]. Evidence suggests that the ubiquitin-proteasome pathway plays a major role in the degradation of I κ B α protein and consequently in the activation of NF- κ B transcription factor [4, 6]. Several recent studies have shown that the calpain system might also be involved under certain circumstances in basal or signal-induced degradation of I κ B α and the activation of NF- κ B [28, 29, 47–50].

Calpains are calcium-dependent cysteine proteinases present in a variety of cells [51]. Two major groups of calpains, termed ubiquitous calpains and tissue-specific calpains, have been identified. The ubiquitous calpains include calpain 1 (μ -calpain) and calpain 2 (m-calpain), which require micromolar and millimolar concentrations of calcium for their activation, respectively. The tissue specific calpains, mainly calpain 3 and calpain 4, are found in skeletal muscle and smooth muscle, respectively. Only nanomolar concentrations of calcium are required for the activation of calpain 3 and calpain 4. Experiments using synthetic inhibitors of calpains have shown that calpains are pivotal proteases participating in a limited proteolytic reaction of a number of cellular structural or regulatory proteins, such as cytoskeletal proteins [52], kinases [53],

cytokines [54] and the tumor suppressing protein, p53 [55–58]. However, the reliability of the use of synthetic pharmacological inhibitors to delineate the role of calpains has been compromised due to the low cellular permeability and poor specificity of these inhibitors. These inhibitors include calpain inhibitor I/II, the family of E64 compounds and leupeptin [51, 59].

The most direct evidence demonstrating that calpain system contributes to silica-induced I κ B α degradation and subsequent activation of NF- κ B is provided by the use of ectopic expression of an endogenous calpain inhibitor, calpastatin, in both a murine macrophage cell line and in human bronchial epithelial cells [29]. Whereas a potent proteasome inhibitor, MG132, failed to abrogate silica-induced I κ B α degradation in macrophages, transient overexpression of calpastatin, a specific endogenous inhibitor for calpain, resulted in an appreciable inhibition of I κ B α degradation induced by silica [29]. *In vitro* digestion of recombinant I κ B α by purified calpain or cytosolic extracts from silica-stimulated cells demonstrated further that calpain was capable of degrading I κ B α protein by the cleavage of several leucine rich domains. In an independent study, Han *et al.* showed that calpain provides a parallel proteolytic pathway to the ubiquitin-proteasome pathway for TNF- α -induced I κ B α degradation in human HepG2 cells [47]. In WEHI231 immature B cells, a rapid degradation of I κ B α was insensitive to proteasome inhibitors, but was substantially inhibited by calpain inhibitors [49]. More recently, Baghdiguian and associates [48] provided direct evidence demonstrating that patients with an autosomal muscular dystrophy caused by calpain 3 deficiency exhibited a substantial impairment of I κ B α degradation and NF- κ B activation in muscle cells.

The evidence for involvement of calpain in silica-induced I κ B α degradation and NF- κ B activation warrant future studies on the mechanisms of calpain activation, consequences of calpain deficiency or overfunction, cross-talk with proteasome and other proteolytic systems, and the feasibility of targeting calpains to interfere with silica-related disease processes.

Silica, NF- κ B and cancer

Whether silica is a carcinogen is still a debatable issue [60–64]. While epidemiological data indicate links between silica exposure and cancer [63], only limited laboratory or animal evidence exists for the carcinogenic effects of silica [62, 64]. The carcinogenic effect of many known carcinogens inducing transformation is believed to be exerted through a mutagenic effect of these agents on the genome. No substantial evidence, however, indicates that silica is genotoxic [62]. Thus, if silica is carcinogenic, it is most likely that it acts through epigenetic processes, such as an alteration of intracellular sig-

nal transduction mechanisms that affect the regulation of cell cycle progression, DNA repair, protein ubiquitination, transcription factor activation, or oncogenic gene expression. The ability of silica to activate NF- κ B indicates a potential link between silica and cancer, since increased activation of NF- κ B has been observed in a number of human cancers [65], including breast cancer, non-small cell lung carcinoma, thyroid cancer, T- or B-lymphocyte leukemia, melanoma, colon cancer, bladder cancer, and several virally-induced tumors.

One of the most important mechanisms linking NF- κ B to the processes of carcinogenesis is the anti-apoptotic role of NF- κ B [3, 4]. Fausto *et al.* found that NF- κ B is required for the liver regeneration and hepatocyte proliferation after partial hepatectomy [66]. A NF- κ B *relA* gene knockout mouse model exhibits massive liver cell apoptosis and embryonic lethal phenotype [67]. Treatment of *RelA* deficient [*RelA*^{-/-}] mouse embryonic fibroblasts and macrophages with TNF α resulted in a significant reduction in viability, while *RelA*^{+/+} cells from a wild type mouse were unaffected. Reintroduction of *RelA* into *relA*^{-/-} fibroblasts resulted in an enhanced survival [67]. It is believed that the protective role of NF- κ B against apoptosis may be through the induction of anti-apoptotic genes including cIAP1, cIAP2 [68], xIAP [69], IEX-1L [70], Bcl-xl [71], Bcl-2 homolog Bfl-1/A1 [72] and zinc finger protein A20 [73]. It has been demonstrated that the transcriptional regulation of NF- κ B on the genes encoding zinc finger protein A20 and a Bcl-2 family member, Bfl-1/A1 [72], is through one or two NF- κ B binding sites located in their promoter regions [73].

Increased expression of many antiapoptotic genes, especially bcl-xl and survivin, has been frequently observed in a number of human tumors [74]. Bcl-xl was first identified using a murine bcl-2 cDNA probe under low stringency conditions to identify bcl-2-related genes in chicken lymphoid cells. The product of bcl-xl gene, Bcl-xl, has been shown to protect cells from apoptosis induced by a wide range of agents that also activate NF- κ B transcription factor in a variety of cell lines [75]. Bcl-xl is transiently expressed in immature intermediate cells such as pro- and pre-B cells and double-positive T cells [76], and is known to be up-regulated as a consequence of antigen receptor cross-linking, an important extracellular signal leading to the activation of NF- κ B. In macrophages, Bcl-xl was up-regulated by IFN- γ and LPS, two well-known NF- κ B activators [77]. Bcl-xl was predominantly expressed in malignant cells in which NF- κ B was usually over-activated [78, 79].

It appears plausible to speculate that NF- κ B and its regulated expression of antiapoptotic genes, especially bcl-2 family of genes, may account for the potential carcinogenic effect of silica. Indeed, analysis of protein expression for Bcl-2 family proteins in macrophages indicated that the expression of Bcl-xl is increased in response to silica and the level of expression of Bcl-xl is correlated with the status of NF- κ B

activation [71]. The contribution of NF- κ B in this silica-induced bcl-xl expression was further confirmed by both promoter activity assay and NF- κ B DNA binding analysis, which showed that enhancement of NF- κ B activity increased the bcl-xl promoter reporter gene activity through at least three putative NF- κ B binding sites within the 5'-flanking region of bcl-xl gene [71].

Tumorigenesis or oncogenesis is a multistep process and the steps reflect defects in regulatory circuits that govern normal cell proliferation, differentiation, and death [80]. While abnormal activation or function of NF- κ B has been clearly demonstrated in the initiation or facilitation of oncogenesis, the central question that has to be answered is: how many and what steps are influenced by NF- κ B? NF- κ B has been shown to antagonize the function of p53 as demonstrated by several reports [81–83]. Obviously, this antagonism of p53 by NF- κ B will result in the escape of cells from stress-induced cell cycle arrest and/or programmed cell death and consequently sensitize the cells for genomic instability. Furthermore, NF- κ B could promote cell cycle transition by a direct transcriptional upregulation of the cyclin D1 gene [84, 85]. Although it remains to be confirmed, this increased expression of cyclin D1 may possibly provide cells with an uncontrolled or limitless replicative potential. Upregulation of anti-apoptotic genes, such as cIAP1, cIAP2, XIAP, and bcl-xl, by NF- κ B [3] is an additional mechanism for cells to escape from or resist to signal-induced apoptosis. Other NF- κ B-regulated genes include those encoding intercellular adhesion molecule-1 (ICAM-1), extracellular matrix protein tenascin-C, vascular endothelial growth factor (VEGF), chemokines, and cyclooxygenase-2 [4]. These gene products are directly associated with tumor cell metastasis and tumor tissue angiogenesis.

The key role that NF- κ B plays on multiple steps of oncogenesis makes this factor a central and favorable target for therapeutic intervention of cancer, especially, certain types of leukemia or lymphomas [86]. Indeed, experimental data suggest that inhibition of NF- κ B by antisense oligonucleotides to *relA*, degradation resistant I κ B α , and aspirin or non-steroidal anti-inflammatory drugs could enhance the efficacy of cancer chemotherapies and radiation [7, 87]. Studies by Wang *et al.* [88] showed that inhibition of NF- κ B by infecting the cells with an adenovirus carrying a modified form of I κ B α (super-repressor I κ B α) leads to dramatically enhanced apoptosis of HT1080 fibrosarcoma cells in response to ionizing radiation or daunorubicin treatment. Consistent with these reports, working with pancreatic cancer cell lines exposed to VP16 or doxorubicin, Arlt and colleagues [89] demonstrated recently that NF- κ B inhibition by pharmacological proteasome inhibitors or transfection of the cells with a N-terminal truncated I κ B α variant efficiently reduces chemoresistance of these cells. Using similar or different approaches to inhibit NF- κ B, this effect has also been noted in a variety

of other cell types including non-small cell lung cancers [90], head and neck squamous carcinomas [91], human myeloblastic leukemia cells [92], colorectal cancer [93], and bladder cancer cells [94]. In spite of these encouraging observations, however, care has to be taken when using different approaches to inhibit NF- κ B. Indeed, different approaches for the inhibition of NF- κ B do not necessarily lead to the same extent of inactivation of NF- κ B, since NF- κ B exists as functionally and stoichiometrically different complexes that respond to different activation signals [3, 4]. Also, the inhibitory effects of NF- κ B inhibitors can vary considerably among different cell types because of unique simultaneous or asynchronous events triggered by these inhibitors in any given cell type [65].

Summary

The detailed molecular mechanisms by which the NF- κ B transcription factor contributes to cell growth control, such as cell apoptosis, cell cycle transition and oncogenesis, remain to be determined. One of the major challenges in understanding mechanisms of cell growth regulation by NF- κ B in response to silica is the elucidation of how signal transduction pathways are activated and how signaling cross-talk and specificity are achieved when several signaling pathways that elicit different cellular responses are activated simultaneously by silica. For instance, why does activation of the NF- κ B, an anti-apoptotic transcription factor, coincide with obvious apoptotic features in cells undergoing silica-induced stress responses? Since many stress inducers and their mediators are highly reactive but nonspecific, activation of only one specific signaling pathway is hard to achieve in the cells in response to a particular inducer. Even in a single signaling pathway, because of their highly reactive and nonspecific characteristics, certain stress inducers and their mediators can in principle induce conflicting signals by affecting signaling molecules at different levels. A good example is the effects of oxidative stress on the NF- κ B signaling pathway. It has been frequently observed that in certain types of cells oxidative stress amplified or potentiated NF- κ B activation, whereas at the same time oxidation of IKK or NF- κ B proteins inhibited NF- κ B function. Translating the knowledge gained by studying the connections among NF- κ B activation, cell apoptosis, cell cycle regulation, and oncogenesis may aid in identifying novel preventive and therapeutic measures for silica-related diseases.

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