Human Polynucleotide Phosphorylase (hPNPase<sub>old-35</sub>): A Potential Link between Aging and Inflammation

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ABSTRACT

Chronic inflammation is a characteristic feature of aging, and the relationship between cellular senescence and inflammation, although extensively studied, is not well understood. An overlapping pathway screen identified human polynucleotide phosphorylase (hPNPase<sup>old-35</sup>), an evolutionarily conserved 3′,5′-exoribonuclease, as a gene up-regulated during both terminal differentiation and cellular senescence. Enhanced expression of hPNPase<sup>old-35</sup> via a replication-incompetent adenovirus (Ad.hPNPase<sup>old-35</sup>) in human melanoma cells and normal human melanocyte cells results in a characteristic senescence-like phenotype. Reactive oxygen species (ROS) play a key role in the induction of both in vitro and in vivo senescence. We now document that overexpression of hPNPase<sup>old-35</sup> results in increased production of ROS, leading to activation of the nuclear factor (NF)-κB pathway. Ad.hPNPase<sup>old-35</sup> infection promotes degradation of IκBα and nuclear translocation of NF-κB and markedly increases binding of the transcriptional activator p50/p65. The generation of ROS and activation of NF-κB by hPNPase<sup>old-35</sup> are prevented by treatment with a cell-permeable antioxidant, N-acetyl-L-cysteine. Infection with Ad.hPNPase<sup>old-35</sup> enhances the production of interleukin (IL)-6 and IL-8, two classical NF-κB-responsive cytokines, and this induction is inhibited by N-acetyl-L-cysteine. A cytokine array reveals that Ad.hPNPase<sup>old-35</sup> infection specifically induces the expression of proinflammatory cytokines, such as IL-6, IL-8, RANTES, and matrix metalloproteinase (MMP)-3. We hypothesize that hPNPase<sup>old-35</sup> might play a significant role in producing pathological changes associated with aging by generating proinflammatory cytokines via ROS and NF-κB. Understanding the relationship between hPNPase<sup>old-35</sup> and inflammation offers a unique opportunity to mechanistically comprehend and potentially intervene in these physiologically important processes.

INTRODUCTION

Human polynucleotide phosphorylase (hPNPase<sup>old-35</sup>) was identified as a previously unknown gene, old-35, due to its up-regulation during cellular differentiation and senescence (1). hPNPase<sup>old-35</sup>, a 3′,5′-exoribonuclease, is a predominantly type I interferon-inducible gene and is highly evolutionary conserved in plants, prokaryotes, and eukaryotes, with similar domain structures and functional properties in all species (1–3). Expression of hPNPase<sup>old-35</sup> is also augmented in senescent progeroid fibroblasts in comparison with young fibroblasts (1). Overexpression of hPNPase<sup>old-35</sup> via a replication-incompetent adenovirus (Ad.hPNPase<sup>old-35</sup>) in HO-1 human melanoma cells and normal human melanocytes (NHuMel) produced a senescent phenotype and is up-regulated by generating proinflammatory cytokines via ROS and NF-κB. Understanding the relationship between hPNPase<sup>old-35</sup> and inflammation offers a unique opportunity to mechanistically comprehend and potentially intervene in these physiologically important processes.

property, and defined senescence-associated gene expression changes (4). These profound alterations induced by hPNPase<sup>old-35</sup> suggest an essential role in controlling senescence and differentiation, and it is likely that important intracellular mechanisms are modulated by hPNPase<sup>old-35</sup> to elicit these remarkable changes in cellular physiology.

Oxidative stress is a potential mediator of both in vitro replicative and premature senescence and in vivo aging (5). The free radical theory of aging, as proposed by Harman (6), states that endogenous reactive oxygen species (ROS) are generated in cells, resulting in a pattern of cumulative damage. Oxidative damage can be measured by formation of 8-oxo-2′-deoxyguanosine in DNA or free 8-oxoguanine base release by cells (7). Replicative senescent cells contain approximately 30% more 8-oxo-2′-deoxyguanosine in their DNA and produce four times more free 8-oxoguanine bases (7). Tissues from aged individuals or aged experimental animals accumulate oxidative damage in their DNA, protein, and lipids (7). Moreover, repeated subcytotoxic oxidative damage can induce premature senescence in multiple cell types such as fibroblasts, keratinocytes, melanocytes, or umbilical vascular endothelial cells (8), and treatment with a cell-permeable antioxidant or culturing cells in a reduced ambient oxygen content can reverse growth arrest of fibroblasts induced by expression of activated Ras (9). ROS comprise a variety of diverse chemical species including superoxide anions, hydroxyl radicals, and hydrogen peroxide (5). Although cytosolic enzymes such as NADPH oxidases contribute to the generation of ROS, the majority of intracellular ROS production is generated from mitochondria (5). Additionally, aged animals contain defective mitochondria and produce higher levels of ROS than their young counterparts (10).

A prominent mechanism by which ROS modulates diverse intracellular molecular processes is by regulating the activity of transcription factors, most notably nuclear factor (NF)-κB (11). As a corollary to increased ROS generation during the aging process, increased NF-κB DNA binding activity has been documented in multiple tissues of aged animals compared with young animals (12–15). In resting cells, NF-κB resides in the cytoplasm in an inactive form bound to an inhibitory protein known as IκB (16). On receiving a stimulus, such as ROS, IκB kinase is activated, which in turn phosphorylates IκB proteins, making them susceptible to ubiquitin-proteosome–mediated degradation (16). The destruction of IκB unmasks the nuclear localization signal of NF-κB, leading to nuclear translocation and regulation of gene transcription by binding to the decameric motif GGGRNA/NYYCC in the promoters of target genes (16). Presently, five mammalian NF-κB family members, NF-κB1 (p50/p105), NF-κB2 (p52/p100), p65 (RelA), RelB, and c-Rel, have been identified and cloned (16). The most abundant activated form of NF-κB is a heterodimer composed of a p50 and a p65 subunit that functions predominantly as a transcriptional activator. The subcellular localization of hPNPase<sup>old-35</sup> is predominantly in the mitochondrial compartment (17). Based on these
findings, we have now assessed whether hPNPase\textsuperscript{old-35} modulates ROS status in cells and, subsequently, the NF-kB signaling pathway. These experiments document that overexpression of hPNPase\textsuperscript{old-35} generates ROS that is responsible for activating the NF-kB pathway and its downstream genes, especially proinflammatory cytokines such as interleukin (IL)-6 and IL-8. Aged individuals are chronically incapacitated by inflammation, supporting the hypothesis that up-regulation of hPNPase\textsuperscript{old-35}, which leads to the release of proinflammatory cytokines via ROS and NF-kB during senescence, might be an initiating factor mediating the pathogenesis associated with chronic inflammation.

**MATERIALS AND METHODS**

**Cell Lines, Reagents, and Virus Infection Protocol.** The human cervical carcinoma HeLa cell line was cultured as described previously (3). N-Acetyl-l-cystine (NAC) and Tiron were obtained from Sigma (St. Louis, MO). The recombinant replication-incompetent adenovirus expressing hPNPase (Ad. hPNPase) was created in two steps as described previously and plaque-purified by standard procedures (1). Cells were infected with a multiplicity of infection (m.o.i.) of 1 to 50 plaque-forming units (pfu)/cell of Ad. vec (control replication-incompetent adenovirus) or Ad.hPNPase as described previously (18).

**Transient Transfection and Luciferase Assay.** Cells (5 \times 10^4 cells per well in 12-well plates) were either uninfected or infected with either Ad. vec or Ad. hPNPase at a m.o.i. of 50 pfu/cell. Transient transfection was conducted 12 hours after infection using LipofectAMINE 2000 transfection reagent (Invitrogen, Carlsbad, CA) and 1.2 \mu g of plasmid DNA per well that included 1 \mu g of pGL3Basic, 3x-B-Luc, or 3x-Bmut-Luc plasmids (19) and 0.2 \mu g of \beta-galactosidase expression plasmid (pSV-\beta-gal; Promega, Madison, WI). For inhibition experiments, the cells were pretreated with different inhibitors for 2 hours before transfection. Luciferase assays were performed 48 hours after transfection using a Luciferase Reporter Gene Assay kit (Promega) according to the manufacturer’s protocol. The \beta-galactosidase activity was determined using the Galacto-Light Plus kit (Tropix, Bedford, MA). Luciferase activity was normalized by \beta-galactosidase activity, and the data from triplicate determinations were expressed as mean \pm SD.

**Generation of Anti-hPNPase old-35 Antibody.** A COOH-terminal His-tagged hPNPase\textsuperscript{old-35} protein was produced in a baculovirus expression system (PharMingen, San Diego, CA) according to the manufacturer’s instructions. The protein was purified by Ni-NTA-agarose column and subsequently by ion-exchange chromatography. The purified protein was used to immunize chickens to generate anti-hPNPase\textsuperscript{old-35} antibody (Genetel Laboratories, Madison, WI).

**Cell Fractionation and Electrophoretic Mobility Shift Assay.** Cells were harvested, and the cytoplasm and nucleus were fractionated by the modified Schreiber’s method as described previously (20). Electrophoretic mobility shift assay (EMSA) using the nuclear extracts was performed as described previously (20). The sequences of the consensus and mutated NF-kB probes are 5'-AGTTGAAGGAGGCTCTTCCCAGG-3' and 5'-AGTTGAAGGAGGCTCAGG-3', respectively (Santa Cruz Biotechnology, Santa Cruz, CA). The antibodies used for supershift analysis were anti-p50, anti-p65, anti-p52, and anti-cRel (rabbit polyclonal antibodies; Santa Cruz Biotechnology).

**Preparation of Whole Cell Lysates and Western Blot Analysis.** Whole cell lysates were prepared, and Western blotting was performed as described previously (20). The primary antibodies used were anti-p65, anti-p50, 1xBo (rabbit polyclonal antibody; 1:250; Santa Cruz Biotechnology), anti-EF1\alpha (mouse monoclonal antibody; 1:1000; Upstate Biotechnology, Lake Placid, NY), and anti-hPNPase\textsuperscript{old-35} (chicken; 1:10,000).

**RNA Extraction and Reverse Transcription-Polymerase Chain Reaction.** Total RNA was extracted from the cells using the RNeasy mini kit (Qiagen, Hilden, Germany) according to the manufacturer’s protocol. Two micrograms of total RNA were used for reverse transcription-polymerase chain reaction (RT-PCR) according to standard methods. The primers used were as follows: IL-6 sense, 5'-CCACACAGACGACACTCCAC-3'; IL-6 antisense, 5'-TGGCATTGGGGTGGTGAC-3'; IL-8 sense, 5'-GGTGCAAGGAGTGTTGGAGAA-3'; IL-8 antisense, 5'-GCAGACTAGGTTGGCAGATT-3'; glyceraldehyde-3-phosphate dehydrogenase sense, 5'-ATGGGAGGAGTGAAGTTGGAGTC-3'; and glyceraldehyde-3-phosphate dehydrogenase antisense, 5'-GCTGATGACTTGAGCCTGTC-3'.

**RESULTS**

**Ad.hPNPase\textsuperscript{old-35} Infection Generates hPNPase\textsuperscript{old-35} Protein.** The expression of hPNPase\textsuperscript{old-35} in HeLa cells after Ad.hPNPase\textsuperscript{old-35} infection was analyzed 2 days after infection by Western blot analysis. As shown in Fig. 1A, hPNPase\textsuperscript{old-35} expression was detected only in Ad.hPNPase\textsuperscript{old-35}-infected cells. Subcellular localization revealed that Ad.hPNPase\textsuperscript{old-35}-generated protein localizes in the mitochondria (data not shown), indicating that Ad.hPNPase\textsuperscript{old-35} infection generates functional protein.

**Infection with Ad.hPNPase\textsuperscript{old-35} Induces Reactive Oxygen Species.** The levels of intracellular ROS after Ad.hPNPase\textsuperscript{old-35} infection were determined using two dyes, DCFH-DA, which detects hydrogen peroxide, and HE, which detects superoxide or free hydroxyl radicals (21).

**Reactive Oxygen Species Mediates Activation of the Nuclear Factor-kB Pathway after Ad.hPNPase\textsuperscript{old-35} Infection.** To test whether Ad.hPNPase\textsuperscript{old-35} infection activates the NF-kB pathway, HeLa cells were either uninfected or infected with Ad. vec or Ad. hPNPase\textsuperscript{old-35} and then transfected with either empty vector (pGL3Basic), 3x-B-Luc containing three tandem NF-kB binding sites upstream of the luciferase gene, or 3x-Bmut-Luc containing mutated NF-kB binding sites (19), and luciferase activity was analyzed. Cells transfected with either pGL3Basic or 3x-Bmut-Luc showed only basal luciferase activity under any experimental condition (Fig. 2A). In control and Ad. vec-infected cells, transfection of 3x-B-Luc increased basal activity over transfection of either pGL3Basic or 3x-Bmut-Luc, which is most likely a consequence of constitutive NF-kB DNA binding activity in HeLa cells. However, infection with Ad.hPNPase\textsuperscript{old-35} resulted in a 10- to 12-fold induction in relative luciferase activity in comparison with control or Ad. vec-infected cells (Fig. 2A). This activation could be effectively inhibited by treatment with increasing doses of either NAC or Tiron, indicating the involvement of ROS in Ad.hPNPase\textsuperscript{old-35}-mediated NF-kB activation (Fig. 2B). NAC was much more potent than Tiron, and in additional studies, NAC was used.

The activation of NF-kB on Ad.hPNPase\textsuperscript{old-35} infection was further analyzed by EMSA using radiolabeled consensus NF-kB binding site as a probe and nuclear extracts from HeLa cells. As shown in Fig. 3A,
in independent experiments, each performed in triplicate. Carried out 48 hours after transfection. Cells were pretreated with NAC or Tiron 2 hours before transfection. Luciferase assay was normalized by luciferase activity was analyzed by Western blot analysis 2 days after infection. The generation of ROS was measured by flow cytometry. The panels represent flow cytometry histograms at 24 hours after infection. The data represent the mean ± SD of three independent experiments, each performed in triplicate.

The levels of p50 and p65 subunits of NF-κB and its inhibitor, IκBα, were analyzed in cytoplasmic and nuclear extracts after Ad.hPNPaseold-35 infection. As shown in Fig. 3E, the levels of both p65 and p50 proteins began decreasing in the cytoplasmic extract of cells 2 days after Ad.hPNPaseold-35 infection, whereas the level of p65 protein started increasing in the nuclear extract of Ad.hPNPaseold-35-infected cells 2 days after infection. These effects were not apparent in control or Ad.vec-infected cells (Fig. 3E and F), indicating that Ad.hPNPaseold-35 infection resulted in translocation of p65 from the cytoplasm to the nucleus. The basal p50 protein level in the nucleus was quite high, and this level was not modulated substantially after Ad.hPNPaseold-35 infection.
ROS plays a pivotal role in activating NF-κB with NAC (Fig. 3G) or Ad.

HeLa cells were infected with Ad.
hPNPase old-35 from 2 days onward after infection with Ad.
hPNPase old-35 or with Ad.
 vec. As a result, moderate elevation of IL-6 and tumor necrosis factor (TNF) receptor was observed. Ad.
hPNPase old-35 infection increases NF-κB DNA binding and nuclear translocation by generating ROS. A HeLa cells were infected as described in Fig. 1A with Ad.vec at 50 m.o.i. or with Ad.
hPNPase old-35 at 1, 5, 10, or 50 m.o.i., and NF-κB DNA binding was analyzed in the nuclear extracts of the cells by EMSA at the indicated time points. B HeLa cells were infected with Ad.vec or Ad.
hPNPase old-35 at 50 m.o.i., and NF-κB DNA binding was analyzed 2 days after infection. C Cold WT, unlabeled consensus NF-κB probe; cold MUT, unlabeled mutated NF-κB probe. Supershift analysis was carried out with the indicated antibodies. *, supershifted band by anti-p50 antibody; **, supershifted band by anti-p65 antibody. C HeLa cells were infected with the indicated adenoviruses at 50 m.o.i., and NF-κB DNA binding was analyzed 2 days after infection. D HeLa cells were infected with Ad.vec or Ad.
hPNPase old-35 at 50 m.o.i. and treated with 20 mmol/L NAC or not treated. NF-κB DNA binding was analyzed 2 days after infection. E and F HeLa cells were infected as described in Fig. 1A, and the expressions of the indicated proteins were analyzed in (E) cytoplasmic extract and (F) nuclear extract by Western blot analysis at the indicated time points. G HeLa cells were infected as described in Fig. 1A and treated with 20 mmol/L NAC. The expressions of the indicated proteins were analyzed by Western blot analysis 2 days after infection.

Interleukin-6 and -8 Are Induced by Ad.
hPNPase old-35 Infection. Expressions of mRNAs and secreted proteins of IL-6 and IL-8, two NF-κB target genes, were analyzed by RT-PCR and ELISA, respectively, after Ad.
hPNPase old-35 infection. A time-dependent increase in the expressions of both IL-6 and IL-8 mRNAs and secreted proteins occurred from 2 days onward after infection with Ad.
hPNPase old-35, but not after Ad.vec infection (Fig. 4, A−C). Treatment with NAC markedly inhibited Ad.
hPNPase old-35-induced secretion of both IL-6 and IL-8 (Fig. 4B and C).

Analysis of Cytokine Expression Profiles after Ad.
hPNPase old-35 Infection. Because Ad.
hPNPase old-35 infection induced two potently proinflammatory cytokines, IL-6 and IL-8, the induction of other cytokines in culture supernatants 2 days after infection was also tested using a human cytokine antibody array that analyzes the expression levels of 36 cytokines. Ad.
hPNPase old-35 infection had a very specific cytokine induction profile resulting in marked up-regulation of IL-8, moderate elevation of IL-6 and tumor necrosis factor (TNF) receptor 1, and up-regulation of RANTES and MMP-3 to a lesser extent (Fig. 4, D−F).

DISCUSSION

We presently demonstrate that hPNPase old-35 activates the NF-κB pathway via the generation of ROS in HeLa cells. ROS is involved in the induction of a senescent phenotype characterized by irreversible growth arrest (8). Overexpression of hPNPase old-35 induces a senescence-like growth arrest and also generates ROS. Moreover, inhibition of ROS impedes the induction of NF-κB−responsive genes. The question naturally arises whether the inhibition of ROS can rescue HeLa cells from hPNPase old-35-mediated growth inhibition. Our initial findings revealed that a noncytotoxic dose of NAC could prevent Ad.
hPNPase old-35−mediated growth inhibition. It is possible that gene expression changes, such as down-regulation of c-myc and up-regulation of p27kip1 (4), resulting from Ad.
hPNPase old-35−infected might be primarily responsible for initiating growth arrest, whereas the generation of ROS might be involved in specifically regulating other cell signaling pathways such as NF-κB. Additional studies using normal human melanocytes or human diploid fibroblasts might provide additional insights to clarify these issues and help to define the function of hPNPase old-35.
Contrasting results have been obtained regarding NF-κB binding activity during aging. No difference in NF-κB binding was observed between senescent and presenescent human fibroblasts as a function of in vitro replicative senescence (22). A reduced NF-κB activation in T cells from aged humans and mice has been reported previously (23). On the other hand, an increase in constitutive NF-κB DNA binding in older animals over young animals has been demonstrated in multiple studies (12–15). A gradual rise in ROS was evident in kidneys from Fischer rats from 6 to 24 months of age, and this increase correlated with an age-dependent augmentation in binding of p50/p65 NF-κB, an age-dependent elevation in NF-κB subunits, such as p50, p52, and p65, could be observed. However, no change in the level of IkBα was detected. From these studies, it might be inferred that tissue-specific regulatory mechanisms may be involved in NF-κB activation during senescence. Although NF-κB activation requires degradation of IkBα, IkBα itself is a NF-κB–responsive gene (16, 24). During acute activation of NF-κB by TNF-α or related stimuli, there is an initial decrease in the cytoplasmic IkBα level followed by gradual restoration because of NF-κB–mediated transcription (24). Infection with Ad.hPNPaseold-35 resulted in a persistent decrease in the cytoplasmic IkBα level, indicating that even though NF-κB is activated by hPNPaseold-35, there might be an additional regulatory mechanism of IkBα transcription during senescence as compared with acute stimuli. A recent study has shown the lack of involvement of ROS in NF-κB activation by acute stimuli such as TNF-α (25). It is possible that in a state of chronic oxidative stress, such as senescence, ROS plays a role in activating NF-κB. Another intriguing observation is the selective induction of NF-κB–responsive genes by hPNPaseold-35 (Fig. 4), indicating that in addition to the primary transcriptional activation of NF-κB by hPNPaseold-35, there might be a secondary level of regulation that targets the transactivation of specific NF-κB target genes.

What is the significance of induction of NF-κB–responsive genes by hPNPaseold-35 in the context of senescence? Ad.hPNPaseold-35 infection results in the up-regulation of proinflammatory cytokines via activation of NF-κB. By turning on proinflammatory cytokines, NF-κB functions as a central transcription factor for the development of chronic inflammatory diseases (26). Gene expression analysis by microarray in human hepatic stellate cells confirms that replicative senescence in these cells is associated with a pronounced inflammatory phenotype characterized by up-regulation of proinflammatory cytokines, including IL-6 and IL-8 (27). An aging-induced proinflammatory shift in cytokine expression profile has been observed in rat coronary arteries (28). Several studies have documented an increased...
blood level of proinflammatory cytokines such as IL-1, IL-6, TNF-α, and IL-8 in aged individuals as compared with young individuals (29). The onset and course of a spectrum of age-associated diseases, such as cardiovascular disease, osteoporosis, arthritis, type 2 diabetes, Alzheimer’s disease, certain cancers, periodontal disease, frailty, and functional decline, might be associated with the production of proinflammatory cytokines (30, 31). Multiple studies have established an association between elevated levels of IL-6 and diseases of old age. IL-6 induces the production of C-reactive protein (CRP), an important risk factor for myocardial infarction (31). High concentrations of CRP predict the risk of future cardiovascular disease in apparently healthy men (31). IL-8 plays a crucial role in initiating atherosclerosis by recruiting monocytes/macrophages to the vessel wall, which promotes atherosclerotic lesions and plaque vulnerability (32). Elevated levels of IL-6 and CRP predict the development of type 2 diabetes in healthy women (33). In another study, elevated serum IL-6 levels predicted future disability in older adults especially by inducing muscle atrophy (34). IL-6 and CRP also play a pathogenic role in several diseases such as osteoporosis, arthritis, and congestive heart failure, all of which have increasing incidence with age (34). Moreover, increased serum levels of IL-6 and IL-8 have been detected in patients with chronic obstructive pulmonary diseases, and chemokines such as IL-8 and RANTES play important roles in the pathogenesis of these diseases (35, 36). Various inflammatory mediators, such as IL-1, TNF-α, IL-6, IL-8, RANTES, and MMP-3, are responsible for chronic inflammatory rheumatoid diseases such as osteoarthritis and rheumatoid arthritis, both of which occur during aging (37). The observation that the senescence-associated molecule hPNPase old-35 induces proinflammatory cytokines that are intimately involved in the development of aging-associated diseases suggests a potential involvement of hPNPase old-35 in these pathological processes.

In summary, we now document that hPNPase old-35 induces the expression of proinflammatory cytokines by generating ROS and activating NF-κB and hypothesize that these fundamental physiologic changes promoted by this gene might be essential contributors to aging-associated diseases. Additional studies are necessary to directly evaluate the role of hPNPase old-35 in chronic inflammatory diseases. These investigations will use cell culture and animal models and targeted inhibition experiments using dominant negative mutants and small interfering RNA to hPNPase old-35. Should a cause and effect relationship be observed between modulating hPNPase old-35 activity and delimiting inflammatory disease, such strategies might be amenable as therapeutic modalities for these debilitating and inevitable diseases of aging.

REFERENCES

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