

AP-1 as a potential therapeutic target in allergic airways inflammation

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Abstract

Asthma is characterized by a complex inflammatory response of airways eosinophilia, edema, mucus hypersecretion and hyperactivity that is accompanied by structural changes of the airways, termed airways remodeling. Airways remodeling in asthma results in alterations in the airways epithelium, lamina propria and submucosa, leading to thickening of the airways wall. Bronchoalveolar lavage (BAL), biopsy and autopsy data indicate that the severity of the disease is correlated with increased T-helper cell type 2 (Th2) cytokines (IL-4, IL-5 and IL-13). These changes may predispose asthma patients to exacerbations and even death due to airways obstruction. Over the last decade there has been a growing appreciation that chronic airways inflammation is integral to the development of severe asthma and underlies the development of airways hyperactivity. Consequently, increasing emphasis has been placed on the treatment of the underlying inflammatory component of asthma rather than physiological antagonism of the airways smooth muscle response. Most existing asthma treatments treat either the acute bronchoconstriction (β -agonists) or a portion of the acute inflammatory response (leukotriene antagonists), or they have severe dose-limiting side effects (corticosteroids). In this review, we describe the feasibility of inhibiting a novel drug target, the AP-1 transcription factor, as a therapy for asthma. AP-1 elements and AP-1 activation are associated with the transcription of a variety of Th2 cytokines, as well as other inflammatory mediators.

Introduction

Asthma is a chronic disease that has reached epidemic proportions, with about 200 million individuals affected worldwide (1). This disorder can be life-threatening if not properly managed. Current medications used to control asthma fall into one of the following five groups: 1) inhaled bronchodilator medications; 2) antiinflammatory medications; 3) systemic bronchodilators; 5) systemic corticosteroid drugs; and 5) leukotriene modifiers. These medications do not cure the disease, and debilitating symptoms associated with asthma return soon after treatment is stopped, even after long-term therapy (2, 3). To compound the problem, there has been a lack of new therapeutic agents since the introduction of the leukotriene modifiers in the mid-1990s, with the exception of Xolair (omalizumab), a monoclonal anti-IgE antibody (4). Thus, there is a clear need to identify and validate new molecular targets to reduce and/or prevent airways inflammation and remodeling in asthma.

Asthma

Asthma is characterized by a complex inflammatory response comprised of airways eosinophilia, edema, mucus hypersecretion and hyperactivity that is accompanied by structural changes of the airways, termed airways remodeling (5, 6). As with many diseases, the genetics of asthma are multigenic and complex. Inhaled allergen challenge in allergic patients with asthma provokes an immediate airways hypersensitivity reaction, the early-phase airways response (EAR), which is frequently followed several hours later by a delayed airways reaction, the late-phase airways response (LAR). After recovery from the LAR, there is an increase in acquired airways hyperreactivity (AHR) to agents such as methacholine that may persist for several days. Following allergen challenge, the immediate phase of bronchoconstriction in the EAR appears to be in large part dependent upon IgE-mediated mast cell degranulation, with release of leukotriene C₄ (LTC₄), prostaglandin D₂ (PGD₂) and histamine. The LAR comprises a complex sequence of

events that includes mucus hypersecretion, inflammatory cell recruitment, cytokine secretion, enhanced microvascular permeability and acquisition of AHR (7, 8). Separate genetic components may be involved in the early-phase atopy and in the development of AHR, which appears to be acquired through airways remodeling. *Post mortem* studies and investigations using fiber optic bronchoscopy with airways sampling by lavage and biopsy have revealed mucosal inflammatory changes similar to those in the LAR, even in the absence of provoking allergen (8). Hence, over the last decade there has been a growing appreciation that chronic airways inflammation is integral to the development of severe asthma and underlies the development of AHR (7, 8). Consequently, increasing emphasis is being placed on the treatment of the underlying inflammatory component of asthma rather than physiological antagonism of the airways smooth muscle response (9).

Airways inflammation in asthma

Bronchoalveolar lavage (BAL), biopsy and autopsy data indicate that asthmatics have eosinophilia, epithelial cell disruption, subepithelial collagen deposition, smooth muscle and mucus gland hyperplasia, increased numbers of CD4⁺ T-helper (Th) cells and a corresponding increase in T-helper cell type 2 (Th2) cytokines (IL-4, IL-5 and IL-13), but not Th1 cytokines, such as interferon gamma or IL-2 (10).

Th2 cytokines in asthma

The CD4⁺ T-cell is essential for the chronic inflammation of asthma. CD4⁺ T-cells infiltrate the airways of asthmatic subjects, and antigen challenge recruits additional CD4⁺ T-cells into the airways. CD4⁺ T-cells in asthmatic patients exhibit a Th2 phenotype, with secretion of IL-4, IL-5 and IL-13. In animal models, depletion of CD4⁺ T-cells by pretreatment with a specific monoclonal antibody prior to allergen challenge – but after allergen sensitization – prevents AHR and eosinophil recruitment. Allergic airways responses including AHR and eosinophilia can be adoptively transferred with antigen-primed CD4⁺, but not CD8⁺ T-cells in Brown Norway rats, and with sensitized T-cells in mice. Potential immunopathological roles for Th2 cells in asthma have been hypothesized based in part on the roles that IL-4, IL-5 and IL-13 play in the stimulation of IgE production, mucosal mastocytosis and eosinophilia (11). Activating protein-1 (AP-1) elements and AP-1 activation are associated with the transcription of a variety of Th1 and Th2 cytokines (12).

Airways remodeling and fibrosis in asthma

Airways remodeling is defined as irreversible structural changes in the asthmatic airways and is considered to

be a major determinant of morbidity and mortality in asthma. The pathogenesis of airways remodeling in patients with chronic asthma is unclear. Bronchial biopsies demonstrate thickening of the subepithelial lamina reticularis in the airways in patients with asthma compared to normal controls (13). Morphometric analyses of autopsied lungs from asthmatics demonstrate a marked increase in airways smooth muscle and goblet cells compared to nonasthmatic controls (14). Remodeling involves extracellular matrix (ECM) accumulation and fibrosis in the airways. Particularly characteristic of airways remodeling is the excess deposition of collagen, fibronectin, laminin and tenascin found in the interstitium beneath the basement membrane in patients with asthma (15).

Oxidant/antioxidant imbalance in asthma

Another hallmark of asthma is the oxidant/antioxidant imbalance. Reactive oxygen species (ROS) released by eosinophils and other leukocytes infiltrating the airways play an important role in the airways tissue injury and remodeling process observed in asthma. These ROS include superoxide, hydrogen peroxide (H₂O₂), hydroxyl radicals and nitric oxide (NO) (16). The major eosinophil granule protein by mass is eosinophil peroxidase (EPO). During the respiratory burst, eosinophils and other leukocytes release superoxide and its dismutation product, H₂O₂. The oxidative action of H₂O₂ on target cells is markedly amplified by its EPO-mediated conversion to highly reactive hypophalous acids. In contrast to neutrophil myeloperoxidase (MPO), which uses chloride as a substrate, EPO preferentially utilizes bromide as a substrate to form brominated oxidants. There is an increase in 3-bromotyrosine, an indicator of protein modification by reactive brominating oxidants, at baseline in bronchoalveolar lavage fluid (BALF) of asthmatics compared to nonasthmatics, with a further increase in BALF of asthmatics after segmental allergen challenge (17, 18). Eosinophils also convert NO to a more potent reactive nitrogen species, such as peroxynitrite (ONOO), formed by the interaction of NO and oxygen and 3-nitrotyrosine, which is detected in airways tissue (19, 20) and BALF (17) of asthmatics. Co-localization of EPO with 3-nitrotyrosine is found in lung tissue from patients with fatal asthma (17). These data suggest that eosinophils are a major source of reactive oxygen and nitrogen species released in the airways in asthma.

Asthmatic patients additionally exhibit decreased vitamin C and vitamin E levels in lung lining fluid, even though blood levels are normal or increased (21). The normal epithelial lining fluid in the lungs has approximately 10 times the concentration of the antioxidant glutathione (GSH) than plasma, with reduced levels found in asthmatic lungs (22–24). Increased amounts of oxidized glutathione are found in the airways of asthmatics, indicating increased oxidative stress (25). However, the mechanism by which increased oxidative stress leads to the molecular hallmarks of acute asthma (*i.e.*, Th2

cytokine release) or chronic asthma and the development of fibrosis has not been elucidated. The development of an oxidant/antioxidant imbalance in the lung may lead to activation of redox-sensitive transcription factors, such as NF- κ B and AP-1. For the purpose of this review, we will focus only on AP-1.

Activating protein-1 (AP-1)

AP-1 was one of the first mammalian transcription factors to be identified (26) and belongs to the family of basic domain leucine zipper transcription factors. AP-1 is not a single protein, but consists of a dimer of Jun and Fos family members. Jun family members (c-Jun, Jun B and Jun D) form homo- and heterodimers that recognize a TGAGTCA consensus DNA sequence. Fos family members (c-Fos, Fos B, Fra 1 and Fra 2), which are unable to dimerize with each other, augment transcriptional activation by association with Jun family members (23). AP-1 activity is inducible by a variety of stimuli, including cytokines, growth factors and T-cell activators (27).

AP-1 transcription in asthma

The transcriptional activity of AP-1 is redox-sensitive. Hydrogen peroxide and other ROS increase the expression of AP-1 (28-31). The DNA binding of AP-1 increases with a reduction in critical cysteine residues (Cys²⁵² in Jun), or mutation from a cysteine to a serine in v-Jun. The DNA binding to AP-1 is decreased when these residues are oxidized (32).

AP-1 is a proinflammatory element that is believed to be an important contributor to the expression of the Th2 cytokines IL-4, IL-5 and IL-13 (33). AP-1 binding sites are found in the promoter regions of many proinflammatory genes besides Th2 cytokines, including adhesion molecules and cell proliferation growth factors (34-36). The gene for Muc5B, responsible for airways mucus production, contains a putative AP-1 consensus site in its promoter (37). The IL-5 proximal promoter element contains an overlapping binding site for the constitutive binding factor Oct-1 and inducible AP-1 (38). Transcriptional induction has been ascribed to the inducible binding element, since a mutant binding element (which lost constitutive Oct-1 binding but maintained inducible AP-1 binding) exerted 3 times greater transcriptional activity than the wild-type element. The IL-4 promoter exists in multiple allelic forms, and a particular allele has high transcriptional activity. A single nucleotide polymorphism located just upstream of the NFAT (nuclear factor of activated T-cells) site appears responsible for the increased promoter strength and markedly enhances the binding affinity of AP-1 complexes (39).

AP-1 as a potential therapeutic target

Glucocorticoids are the most effective therapy for the long-term control of asthma. Their efficacy appears to be

largely due to inhibition of abnormal transcriptional regulation of gene expression (40). Inhibition of the proinflammatory transcription factors via transrepression decreases AP-1, as well as NF- κ B, STAT (signal transducer and activator of transcription) and NFAT transcriptional activity (41). Glucocorticoids inhibit the transcription of several cytokines and chemokines that are relevant to asthma, including GM-CSF (granulocyte-macrophage colony-stimulating factor), IL-4, IL-5 and eotaxin (42-45). The reduction of GM-CSF and IL-5, key cytokines for eosinophil survival, leads to apoptotic death of eosinophils (46).

A small percentage of asthmatic patients, however, fail to respond to even high doses of glucocorticoids due to resistance (47). Monocytes and lymphocytes from these patients exhibit a marked reduction in the number of activated glucocorticoid receptors in the nucleus after exposure to glucocorticoids compared to normal individuals (48). These same patients also exhibit a reduced inhibitory response on AP-1 activation and elevated JNK activity (49-52). However, glucocorticoid-resistant asthma patients are not resistant to the endocrine and metabolic effects of glucocorticoids, which are major side effects associated with glucocorticoid therapy (53). Corticosteroid-resistant (CR) asthma is associated with increased activity of the proinflammatory transcriptional element AP-1 in peripheral blood mononuclear cells (PBMCs). Significantly increased expression of c-fos, phosphorylated c-jun and phosphorylated Jun N-terminal kinase (JNK) was found in CR patients compared to corticosteroid-sensitive (CS) patients (52).

Taken together, these data offer compelling evidence for the clinical validation of inhibition of AP-1 transcription as a therapeutic target in asthma.

Redox regulation of AP-1 transcription and asthma

Redox regulation of transcription is important in a variety of inflammatory disease states, including asthma (54, 55). General antioxidants, such as *N*-acetylcysteine (NAC), have been evaluated in animal models and in human subjects (56, 57). However, controversy exists regarding the beneficial effects of antioxidants on asthma (58). Our knowledge concerning the specific factors involved and the scope of this regulatory process remains in its infancy (32, 59).

Thioredoxin (TRX) was originally isolated in *Escherichia coli* as a hydrogen donor for ribonucleotide reductase (60). It is a small multifunctional protein that has a redox-active disulfide/dithiol with a conserved Cys-Gly-Pro-Cys sequence. The human analogue was identified by Yodoi *et al.* (61) as adult T-cell leukemia-derived factor (ADF), which enhanced the production of IL-2R α -chain in HTLV-1-infected lymphocytes. Thioredoxin is known to translocate from the cytosol to the nucleus under a variety of stress-inducing stimuli and is believed to directly regulate the expression of the AP-1 family of genes through the redox factor Ref-1 (62, 63) and the

Table 1: Conserved cysteine residues in the AP-1 family of transcription factors.

Fos/Jun family	
c-fos	RRERNKMAAAKCRNRRREL
c-jun	KRMNRNRIASKCRRLKLERI

NF- κ B family (64). Thioredoxin has been implicated in the reduction of an oxidized form of Cys⁶² (likely the S-nitroso species) which is required for full transcriptional activation. Based upon the X-ray structure of a p50 NF- κ B homodimer complexed with its oligonucleotide binding site (65, 66), Cys⁶² makes contact with the 3'-phosphate of the oligonucleotide backbone.

Ref-1 is a protein which has both endonuclease and redox activity and is involved in the reduction of conserved cysteine residues in fos and jun (Table 1). Gronenborn *et al.* have shown by NMR analysis that peptides derived from NF- κ B (67) and Ref-1 (64) can bind to the active site of TRX in an extended-strand conformation. More recently, it has become evident that TRX is part of a superfamily of oxidoreductases that are involved in regulating inflammatory and other processes.

AP-1 and TGF- β in airways fibrosis in asthma

Transforming growth factor- β (TGF- β) is a pleiotropic cytokine involved in cell proliferation and differentiation, apoptosis, deposition of ECM, as well as cell adhesion (68). A role for TGF- β as a key mediator in the development of fibrosis in the airways of patients with chronic asthma may be due to its ability to act as a chemoattractant for fibroblasts, stimulate fibroblast procollagen gene expression and protein synthesis, and inhibit collagen breakdown. TGF- β also stabilizes the ECM by inhibiting the expression of ECM proteases and stimulating the expression of ECM protease inhibitors (69-71). Th2 cytokines, in particular IL-13, induce TGF- β (72). TGF- β , together with other factors, such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF) and insulin-like growth factor (IGF), stimulates the release of ECM proteins from myofibroblasts (73, 74). The fibrinolysis system is essential in ECM accumulation and fibrosis. Inhibition of fibrinolysis results in the accumulation of fibrin and ECM.

Plasminogen activator inhibitor-1 (PAI-1) is a key inhibitor of fibrinolysis. Activated mast cells produce abundant PAI-1. These cells may further increase the PAI-1 level in the airways by activating adjacent fibroblasts with TNF- α and TGF- β . Transcriptional regulation by TGF- β is a complex process that involves crosstalk between different DNA-responsive elements and transcription factors to achieve maximal promoter activation and specificity (75). Of particular note, a subset of TGF- β immediate-response target promoters, including TGF- β ₁ and most of the TGF- β ECM genes, mediate their

response through synergistic SMAD/AP-1 complexes (76-78). The SMADs are a relatively recently identified family of proteins that effect transcription downstream of various members of the TGF- β superfamily (79). Interestingly, the PAI-1 promoter contains several transcription factor binding sites, including AP-1- (80) and SMAD-binding elements (81), that promote PAI-1 induction by TGF- β (82).

Validation of AP-1 as a target for asthma therapeutics

Mouse model of asthma

Important insights into the mechanisms of allergic airways inflammation and AHR in asthma have come from investigations using animal models. Sensitization to a variety of allergens and subsequent airways challenge with the allergen produce typical features of the asthmatic inflammatory response in mice, rats, guinea pigs and nonhuman primates. From these studies, T-cells and eosinophils have clearly emerged as critical cells in mediating the chronic inflammation of asthma. We and others have utilized mouse models which reproduce key morphological and physiological features of human asthma. Henderson *et al.* developed a protocol for the administration of ovalbumin (OVA) as a model allergen to induce allergen-specific pulmonary disease in normal BALB/c and C57BL/6 mice (83-89). This asthma protocol includes immunization of mice with intraperitoneal (i.p.) OVA in alum adjuvant on days 0 and 14 followed by intranasal (i.n.) challenge with OVA in normal saline on days 14, 25, 26 and 27. Control mice receive alum alone for i.p. injection and normal saline alone for i.n. administrations. On day 28 of this protocol, OVA-treated mice display a disease strikingly similar to allergen-induced human asthma, including increased circulating levels of total and OVA-specific IgE, increased release of LTB₄ and LTC₄ in BALF; marked eosinophil influx into BALF and the pulmonary parenchyma; airways goblet cell hyperplasia with mucus occlusion of small airways; increased expression of Th2 cytokines (IL-4, IL-5 and IL-13) and decreased expression of Th1 cytokines (IL-2 and interferon gamma) in bronchial lymph node tissue; and pulmonary hyperreactivity, as assessed by a significantly more rapid decline in airways conductance and dynamic compliance with increasing doses of methacholine compared to control mice.

Small-molecule regulators of redox-regulated AP-1 transcription

To validate AP-1 as a molecular target for asthma, we investigated the development of novel, specific redox regulators of AP-1 transcription. Based on structural information, an extended-strand templated system that can act as a reversible inhibitor (pseudosubstrate) of redox proteins (89-91) was designed (Fig. 1). It was anticipated

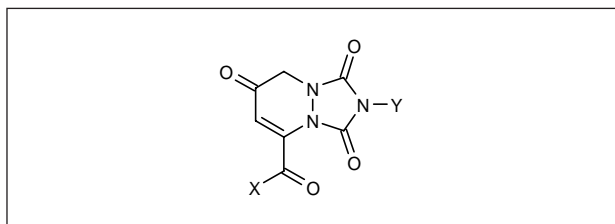


Fig. 1. Pseudosubstrate oxidoreductase template.

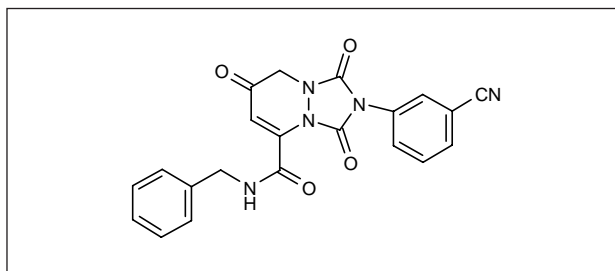


Fig. 2. Molecular structure of the Ref-1/AP-1 inhibitor PNRI-299.

that, through variations in X and Y functionality, specificity for individual redox factors could be achieved. This was based upon the amino acid variations surrounding the conserved cysteine residues of DNA-binding domains within families of transcription factors (92-94).

A limited library of compounds (2×6), where X was either NHCH_3 or NHCH_2Ph and Y was methyl, phenyl, *m*- NO_2 -phenyl, *m*-acetylene, *m*-cyanophenyl or *m*-methylbenzoate, were initially prepared. These analogues were evaluated for their ability to inhibit transcription in transiently transfected human lung epithelial A549 cells by either an NF- κB or an AP-1 reporter. The compound designated PNRI-299 (Fig. 2) selectively inhibited AP-1 transcription with an IC_{50} of 25 μM , without affecting NF- κB transcription at up to 200 μM ; this analogue was also non-reactive with TRX at up to 200 μM .

Identification of Ref-1 as the molecular target of PNRI-299

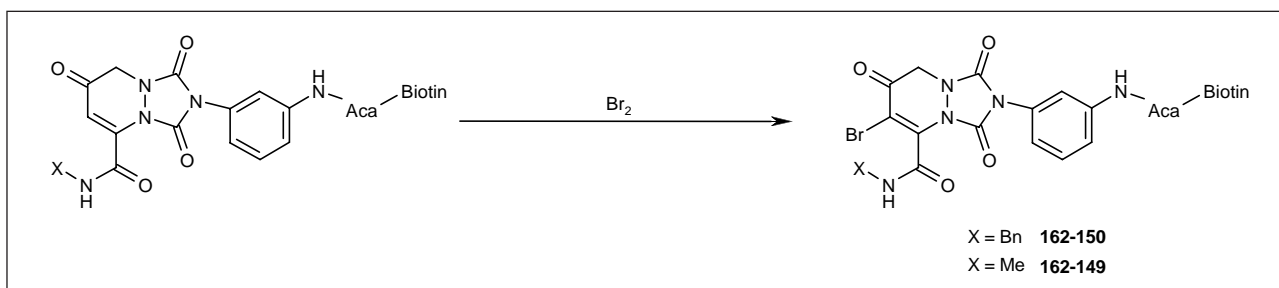
To determine the molecular target(s) of the AP-1 inhibitor PNRI-299, we utilized an affinity chromatography

approach. The initial screen indicated that an acylaniline analogue had only slightly decreased activity (~2-fold). To increase the likelihood of affinity-purifying the molecular target(s), we modified the enedione portion by addition of a bromine atom to provide analogue **162-150** (Fig. 3) (95). The affinity reagent **162-150** incorporated an aminocaproic acid (Aca) linker to provide a sufficient distance between the affinity probe and the biotin moiety that was used to bind to the agarose-streptavidin beads. As a negative control, we prepared analogue **162-149**, the design of which was based upon an inactive analogue (Fig. 3). Using affinity chromatography, the molecular target of PNRI-299 was identified as the redox protein Ref-1. Overexpression of Ref-1 could override the effect of PNRI-299 (Fig. 4).

Effect of PNRI-299 on allergic airways inflammation

We next examined the effect of PNRI-299 on airways inflammation in the acute mouse asthma model. Treatment with PNRI-299 significantly decreased the influx of eosinophils into the BALF (Fig. 5a) and airways edema (Fig. 5b) in OVA-treated mice. The OVA-sensitized/challenged mice developed a striking infiltration of the airways by eosinophils and other inflammatory cells and mucus hypersecretion (Fig. 6a) that was not observed in saline-treated controls (Fig. 6c). Treatment with PNRI-299 significantly decreased the influx of eosinophils, monocytes and macrophages (no significant reduction of lymphocytes was observed) into the lung interstitium (Fig. 6b), BALF and airways mucus (Fig. 6b), as well as the edema observed in OVA-treated mice. As assessed by RT-PCR, the gene expression of IL-4 and IL-5 was markedly increased, that of eotaxin was minimally increased and that of CCR3 was unchanged in whole lung tissue of the OVA-sensitized/challenged mice compared to saline-treated controls (96). The increased IL-4 gene expression in the OVA-treated mice was attenuated in a dose-dependent manner by PNRI-299 (0.75-2 mg/kg). However, the increased IL-5 and eotaxin gene expression in the OVA-treated mice was unaffected by either dose of PNRI-299.

Another potential benefit achievable through AP-1 inhibition is a decrease in the cysteinyl leukotriene LTC_4 . Cysteinyl leukotrienes modulate contraction in airways

Fig. 3. Affinity probe synthesis: Generation of the affinity reagents **162-150** and **162-149**.

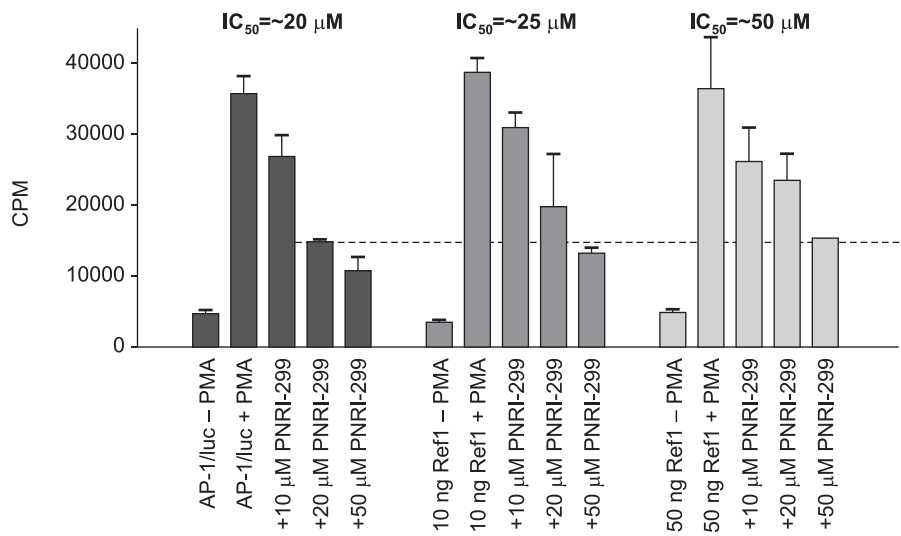


Fig. 4. Identification of Ref-1 as the molecular target of the AP-1 inhibitor PNRI-299. Cotransfection of Ref-1 expression vector in A549 cells transfected with an AP-1-luciferase reporter gene construct.

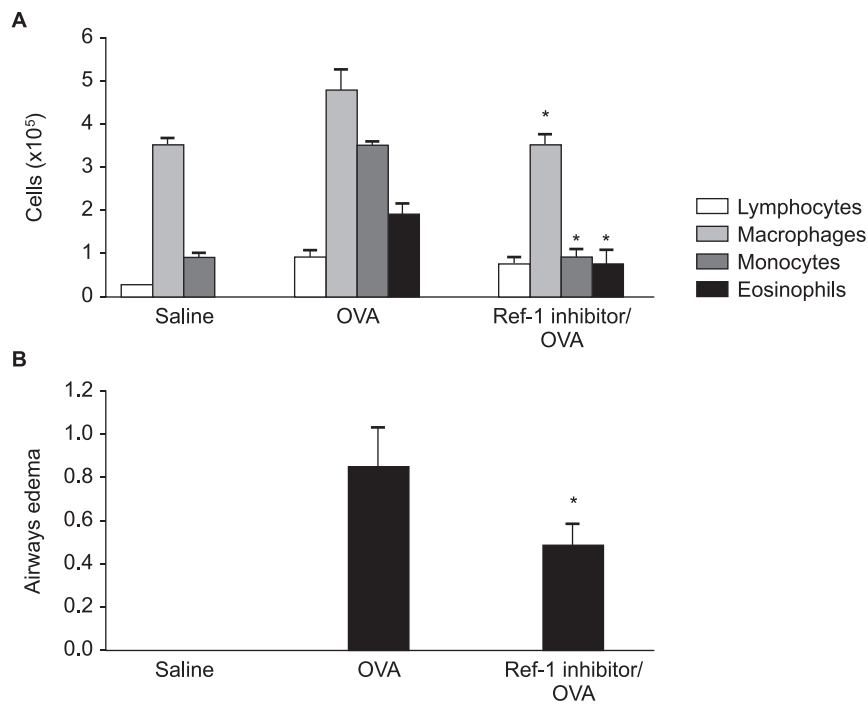


Fig. 5. Reduction of asthmatic response. Bronchoalveolar lavage fluid eosinophils, monocytes, macrophages and lymphocytes (A) and airways edema (B) were determined in controls (saline) and ovalbumin (OVA)-treated mice in the absence (OVA) or presence (Ref-1 inhibitor/OVA) of PNRI-299. **p* < 0.05 vs. OVA by Student's two-tailed *t*-test.

smooth muscle, promote smooth muscle proliferation, inflammatory cell influx, increase vascular permeability and induce mucus secretion (96-99). LTC₄ synthase is a specific glutathione-S-transferase located in the nuclear envelope that converts LTA₄ to LTC₄ in the final step of LTC₄ biosynthesis (100). A recent report described a puta-

tive AP-1 element in the LTC₄ synthase proximal promoter (101). Reporter gene assays in THP-1 cells demonstrated a modest reduction in LTC₄ synthase expression induced by PNRI-299. Furthermore, PNRI-299 demonstrated a dose-dependent reduction in LTC₄ synthase expression in the lungs of OVA-sensitized mice (102).

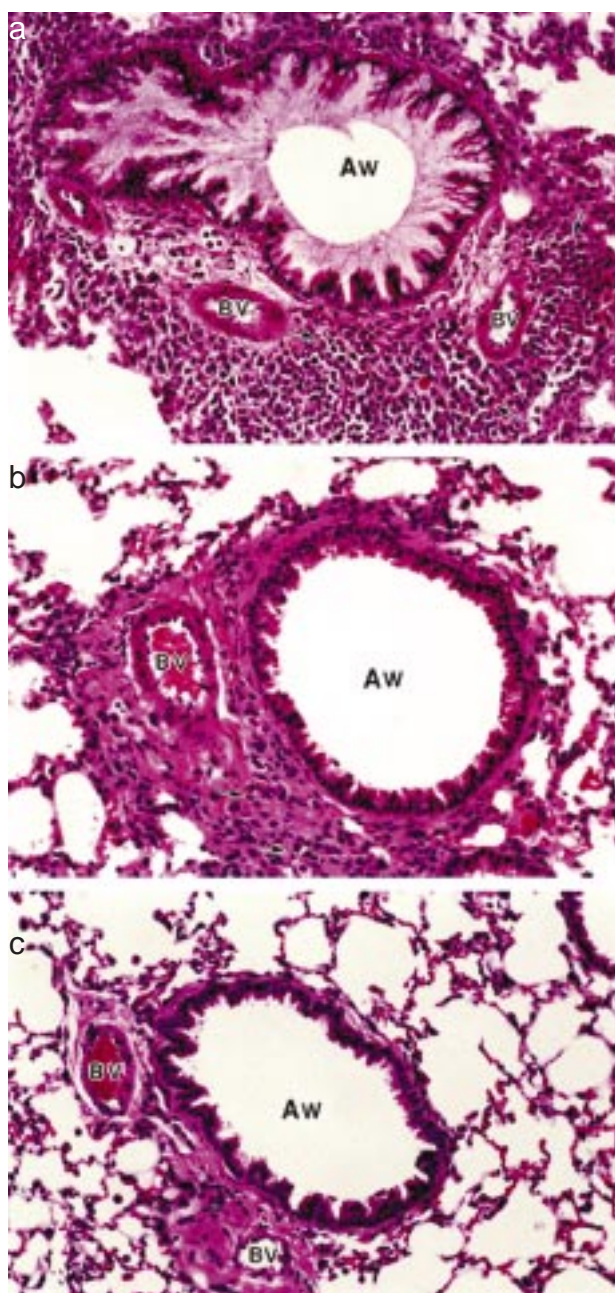


Fig. 6. Ref-1 inhibitor PNRI-299 reduces allergic airways inflammation. (a) Ovalbumin (OVA)-treated mice have a dense inflammatory cell infiltrate (arrows) surrounding the airways (Aw) and blood vessels (BV) and mucus hypersecretion not seen in saline controls (c). (b) PNRI-299 (0.75 mg/kg) reduced the airways inflammatory cell infiltration (arrows) and mucus release in OVA-treated mice.

Conclusions

AP-1 was one of the first mammalian transcription factors identified (26). Its activity is induced by a wide array of stimuli, and in turn, it regulates a wide range of cellular processes, including cell proliferation, differentiation,

survival and death (103). AP-1 elements are found in the promoter regions of a plethora of inflammatory mediators, cytokines and chemokines. AP-1 transcription is increased during oxidative stress, which accompanies chronic asthma and pulmonary fibrosis (104, 105). Most existing antiasthmatic agents treat the acute bronchoconstriction (β -agonists) or a portion of the acute inflammatory response (leukotriene antagonists), or they have severe dose-limiting side effects (corticosteroids). Increased activation and expression of AP-1 have been demonstrated in the airways of asthmatic patients (106). Inhibition of AP-1 transcription offers the benefit of treating the underlying inflammatory process and reducing the production of inflammatory cytokines and chemokines that are important in chronic asthma, which can eventually lead to pulmonary fibrosis.

Our work (96) demonstrated the efficacy of a novel inhibitor of redox-regulated AP-1 transcription in a murine model of allergic asthma. Furthermore, recently, a small-molecule inhibitor of JNK (SP-600125) demonstrated the ability to reduce eosinophil and lymphocyte infiltration in a rat model of chronic asthma (107). These studies set the stage for further efforts to develop novel, selective, small-molecule inhibitors of AP-1 transcription and for the clinical evaluation of these inhibitors in chronic asthma and pulmonary fibrotic diseases. One caveat is worth noting – as AP-1 transcription is involved in such a broad range of cellular processes, concerns arise as to potential liabilities associated with the systemic use of AP-1 transcriptional regulators. Although clearly a concern, we have demonstrated (96) that specific inhibitors of AP-1 transcription have a selective rather than a global effect on the expression of inflammatory genes. Furthermore, glucocorticoids, which more broadly inhibit gene transcription through both AP-1 and NF- κ B, and also activate glucocorticoid-responsive genes and therefore possess potent systemic toxicities, remain a mainstay of antiasthmatic therapy. The questions and concerns raised regarding the prospects for this novel approach to the treatment of asthma and pulmonary fibrosis will hopefully be answered by the further development of selective AP-1 transcriptional regulators and their entry into the clinic.

Acknowledgements

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