Table 2. Differential Counts of Brushed Cells Collected by Bronchoscopy

	Never smoked	Current smokers
At trachea		
Total number, \times 10 ⁶	2.3 ± 0.5	1.2 ± 0.4
Epithelial cells, %	97.3 ± 0.6	98.1 ± 0.7
Neutrophils, %	0.3 ± 0.2	0.3 ± 0.2
Lymphocytes, %	1.1 ± 0.4	0.5 ± 0.3
Macrophages, %	1.3 ± 0.3	1.1 ± 0.5
Eosinophils, %	0.0 ± 0.0	0.0 ± 0.0
At subsegmental bronchus		
Total number, \times 10 ⁶	4.0 ± 1.3	4.0 ± 0.5
Epithelial cells, %	97.1 ± 0.8	97.0 ± 0.7
Neutrophils, %	1.3 ± 0.8	0.8 ± 0.3
Lymphocytes, %	0.6 ± 0.1	0.8 ± 0.5
Macrophages, %	1.0 ± 0.4	1.3 ± 0.4
Eosinophils, %	0.1 ± 0.1	0.1 ± 0.1

Data are presented as mean ± SE.

compared to the individuals who have never smoked, both at the trachea (median, range: 4.6, 2.5–5.4 vs. 7.2, 4.3–9.8, p=0.0285) (Fig. 2a) and at the subsegmental bronchus (5.7, 3.1–6.3 vs. 10.0, 5.7–19.7, p=0.0285) (Fig. 2b). In contrast, Duox2 was significantly upregulated in current smokers, as compared to the individuals who have never smoked, both at the trachea (12.1, 7.1–31.5 vs. 3.7, 2.8–6.1, p=0.0062) (Fig. 3a) and at the subsegmental bronchus (8.6, 4.7–25.6 vs. 4.0, 3.5–6.6, p=0.0446) (Fig. 3b). These results imply that chronic smoking diversely affects the epithelial expression of Duox1 and Duox2 at large airways.

Upregulation of epithelial Duox2 mRNA is not accompanied by increased IFN-γ in epithelial lining fluid in large airways

Since a Th1-specific cytokine, IFN- γ , is the only molecule known to dramatically induce Duox2 transcription *in vitro* (18), we hypothesized that IFN- γ might be increased in the lining

fluid which overlays airway epithelial cells, leading to Duox2-specific upregulation in those cells in current smokers. However, there was no significant difference in the levels of IFN- γ in the epithelial lining fluid from individuals who have never smoked and current smokers either at the trachea (471 pg/ml trachea lining fluid; range: 0–2088 vs. 0; 0–1243, NS) (Fig. 4a) or at subsegmental bronchus (512 pg/ml bronchial lining fluid; range: 0–1118 vs. 0; 0–778, NS) (Fig. 4b). Furthermore, there was no positive correlation between epithelial Duox2 expression and IFN- γ levels in epithelial lining fluid at either site (data not shown), suggesting no direct link between airway Duox2 expression and IFN- γ in airways.

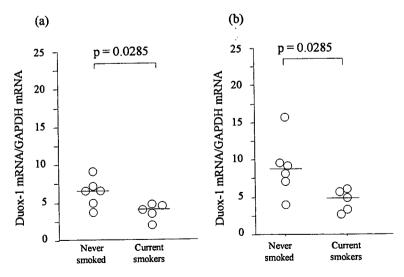
Expression of Duox1 and Duox2 mRNA is downregulated in bronchiolar epithelium in COPD

To determine if altered expression of Duox in bronchiolar epithelium might be linked to smoking histories and/or COPD, we compared the expression of Duox1 and Duox2 among the three groups: 10 individuals who have never smoked, 10 former smokers without COPD, and 10 former smokers with mild or moderate COPD. Duox1 mRNA levels in the bronchiolar epithelium were significantly decreased in former smokers with mild or moderate COPD as compared to individuals who have never smoked and former smokers without COPD (2.0, 1.0–3.2 vs. 4.0, 2.0–7.8 and 2.9, 1.6–6.3, p=0.0015, p=0.0034, respectively) (Fig. 5). Surprisingly, levels of Duox2 expression were also significantly decreased in the groups of former smokers, both with and without COPD, compared to individuals who have never smoked (2.5, 0.9–3.6 and 2.8, 1.3–6.0, vs. 5.4, 2.6–10.3, p=0.0019, p=0.0126, respectively) (Fig. 6).

No change in mRNA expression of alveolar Duox1 and Duox2

Duox was also present in the alveolar septa, although to a lesser extent than in the bronchiolar epithelium. Using a microscope-assisted manual dissection technique, we harvested not only alveolar epithelial cells, but also the cells that com-

FIG. 2. Duox1 mRNA expression in tracheal and subsegmental bronchial epithelial cells. (a) Tracheal Duox1 mRNA; (b) Bronchial Duox1 mRNA. Duox1 expression at trachea and at subsegmental bronchus was significantly downregulated in current smokers as compared to individuals who have never smoked. Medians are indicated by horizontal lines.



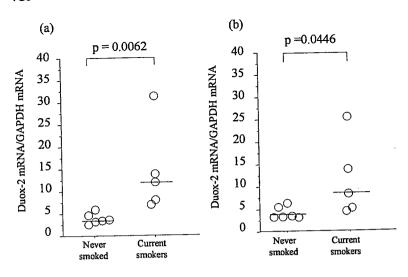


FIG. 3. Duox 2 mRNA expression in tracheal and subsegmental bronchial epithelial cells. (a) Tracheal Duox2 mRNA; (b) Bronchial Duox2 mRNA. Duox2 expression at the trachea and subsegmental bronchus was significantly upregulated in current smokers as compared to individuals who have never smoked. Medians are indicated by horizontal lines.

pose the alveolar septa, including capillary endothelial cells and inflammatory cells. It remains to be elucidated which cell types are the source of alveolar Duox. However, Duox1 and Duox2 mRNA expression levels in the alveolar septa did not significantly differ among the three groups (Figs. 7 and 8).

DISCUSSION

We report that Duox1 is decreased while Duox2 is increased in large airways of current smokers. On the other hand, both Duox1 and Duox2 are downregulated in bronchiolar epithelium, but not in alveolar septa, of the former smokers as compared to individuals who have never smoked, although Duox1 did not reach statistical significance. In subjects with mild or moderate COPD, their expressions appear to be further decreased compared with the smoking controls, although only Duox1 reaches a statistical difference. These preliminary data indicate that airway epithelial expressions of Duox1 and Duox2 might be diversely affected by chronic smoking and/or its cessation, and the development of early stage COPD.

The effects of cigarette smoking on airway epithelial cells over time may result from several processes that have different time frames. Duox1 mRNA levels in normal, human bronchial epithelial cells in culture are unchanged by 2 h exposure to cigarette-smoke condensates, indicating that acute exposure to cigarette smoke has no effect on the transcriptional levels of Duox l in vitro (22); however, no study has been conducted to assess a possible link between Duox2 and cigarette smoke exposure. Affymetrix arrays were recently used for global gene expression analysis in bronchial brushings, revealing the downregulation of Duox1 and upregulation of Duox2 in current smokers compared to nonsmokers (29); this finding is consistent with our current findings on large airways. However, it remains unclear whether these altered Duox1 and Duox2 mRNA expressions in large airways of healthy current smokers are related to the development of COPD because large airways might not directly contribute to airflow obstruction. We have, therefore, extended our studies to analysis of these gene expressions in bronchiolar epithelium.

In former smokers with mild or moderate COPD, the bronchiolar expression of both Duox1 and Duox2 was significantly downregulated. Perhaps, a decrease in Duox1 is detected in re-

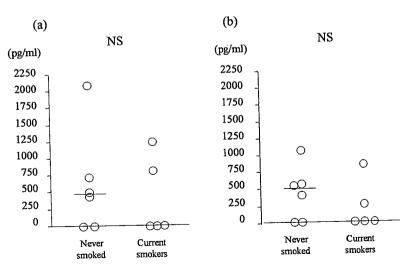


FIG. 4. Levels of IFN- γ in epithelial lining fluid. (a) IFN- γ in epithelial lining fluid at the trachea; (b) IFN- γ in epithelial lining fluid at bronchus. There was no significant difference in the levels of IFN- γ in epithelial lining fluid at the trachea or subsegmental bronchus of individuals who have never smoked and current smokers. Medians are indicated by *horizontal lines*.

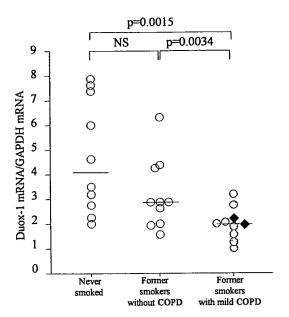


FIG. 5. Duox1 mRNA expression in bronchiolar epithelial cells. Duox1 mRNA levels in the bronchiolar epithelium were significantly decreased in former smokers with COPD as compared to individuals who have never smoked and former smokers without COPD. COPD patients were classified by GOLD (Stage I: closed circles, Stage II: closed diamonds). Medians are indicated by horizontal lines.

sponse to repeated smoke exposure; but, after smoking cessation, the levels go back to normal in subjects who are not susceptible to COPD. However, the Duox1 levels in subjects who stopped smoking but had already developed COPD, even an early stage of COPD, could not rebound properly and the decrease was amplified, suggesting that there is a link between COPD and decreased Duox1.

On the other hand, bronchiolar Duox2 mRNA was significantly decreased, even in former smokers without COPD, which is in sharp contrast to the increase of tracheal and bronchial Duox2 mRNA observed in current smokers. We cannot address the question in this study whether this discrepancy in the regulation of Duox2 might be due to regional differences along the airways, large airways versus small airways, or differences in the smoking status on examination, current smokers versus former smokers.

To get further insight into the mechanism of epithelial Duox2 mRNA upregulation in current smokers, we quantified the levels of IFN- γ in epithelial lining fluid. Although IFN- γ transgenic mice develop inflammation and emphysema (23, 41), cigarette smoke exposure reportedly suppresses IFN- γ (3, 28). In the present study, the levels of IFN- γ in tracheal and bronchial lining fluid did not differ between individual who have never smoked and current smokers. Also, the IFN- γ levels and epithelial Duox2 mRNA expression at given sites were uncorrelated. Therefore, a direct link between epithelial Duox2 and IFN- γ in epithelial lining fluid in large airways was not established in the present study.

Bacterial colonization in airway epithelium is a prominent feature of cystic fibrosis. When Wright et al. performed microarray analysis of nasal respiratory epithelium to investigate

the molecular basis of variability in cystic fibrosis phenotype, they found that Duox2 is one of the genes most reduced in cystic fibrosis patients (44). Long-term cigarette smoking also appears to disrupt these innate immune mechanisms, and as a consequence, microbial pathogens are able to persist in the lower airways (38). Some of these mechanisms might be further amplified, but not in a linear fashion, in individuals who develop COPD (19, 24, 29, 34, 35). Sethi et al. demonstrated the relationship between bacterial colonization and increased levels of IL-8 in bronchoalveolar lavage fluid in COPD patients (35). We also reported that increased levels of IL-8 in bronchoalveolar lavage fluid were found in smokers with subclinical emphysema, but not in smokers without emphysema (39). Also, the expression of IL-8, macrophage inflammatory protein-2 and monocyte chemoattractant protein-1 was upregulated in LCMretrieved bronchiolar epithelium (14), in which both Duox 1 and Duox2 were reversely downregulated in patients with early COPD. Wesley et al. recently demonstrated that Duox1-targeted small interfering RNA suppressed wound closure and epithelial cell migration, suggesting another role for Duox1 as an important component of airway epithelial repair in response to injury (42). Taken together, these studies indicate that decreased Duox expression and upregulation of inflammatory chemokines in bronchiolar epithelium may contribute to persistent inflammation, impaired wound repair, and progressive airway obstruction in COPD patients, and these problems persists even after cessation of smoking.

Although Duox1 and Duox2 likely serve specific functions (e.g., host defenses and signaling for cell migration), they also might damage or adversely affect airway epithelial cells by overproducing ROS as an endogenous oxidant. Shao et al.

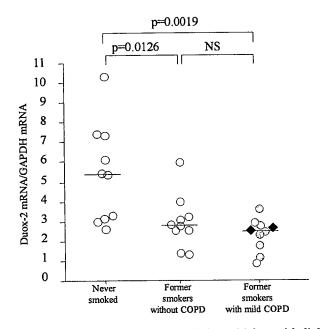


FIG. 6. Duox2 mRNA expression in bronchiolar epithelial cells. Levels of Duox2 expression were significantly decreased in smokers with and without COPD as compared to individuals who have never smoked. COPD patients were classified by GOLD (Stage I: closed circles, Stage II: closed diamonds). Medians are indicated by horizontal lines.

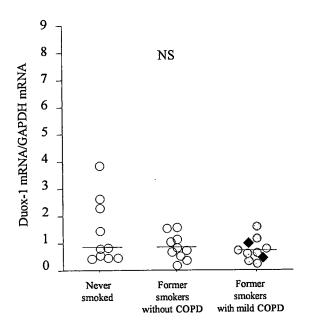


FIG. 7. Duox1 mRNA expression in alveolar septa. Duox 2 mRNA expression levels in the alveolar septa did not significantly differ among the three groups. COPD patients were classified by GOLD (Stage I: closed circles, Stage II: closed diamonds). Medians are indicated by horizontal lines.

showed that ROS produced by Duox1 in airway epithelial cells are involved in mucus hypersecretion (36). Knockdown of Duox1 by small interfering RNA reduced lipopolysaccharide-induced $\rm H_2O_2$ generation and IL-8 production through a neutrophil elastase/tumor necrosis factor- α -converting enzyme/epidermal growth factor pathway (27). Duox is possibly involved in chronic airway inflammation with mucus hypersecretion, providing novel mediators of these disease processes. It should be noted, however, that individuals with productive coughs were not included in the present study. Moreover, very few PAS-positive cells were found in epithelial cells obtained by brushing, nor was goblet cell hyperplasia observed in surgical tissue specimens (data not shown). It is unlikely that upregulated Duox2 contributes to airway hypersecretion in healthy current smokers.

Recently, it has been reported that emphysema is developed either by overexpression or deficiency of NADPH in mice (21, 46), although the precise mechanism remains to be elucidated. Accordingly, alteration of Duox expression in airway epithelium might have some causative relationship with COPD.

Although we collected epithelial cells with >95% purity by bronchoscopic brushing, and the LCM specifically targeted bronchiolar epithelium (14), it should be noted that the cells harvested were likely a mixture of various epithelial cell types that were present at a given level. Epithelial heterogeneity in the airways could be important under certain circumstances, such as in long-term smokers. In the same context, the analyses of gene expression in alveolar septa also have limitations.

There are also some limitations with respect to the study population. The study of the effects of current smoking on Duox1 and Duox2 is limited only in large airways. We could not examine the effects of current smoking on the bronchiolar and

alveolar expressions of Duox1 and Duox2 because surgical tissues were only available from former smokers, and there was a considerable variation in the length of smoking cessation among the former smokers. In the group of smokers without COPD, four subjects had stopped smoking for <1 month, two subjects had stopped smoking for many years. In the surgical tissue specimens, the bronchiolar gene expression might be influenced by the small turnor located within the same lobe. However, it could be negligible because the six or more tissue specimens were randomly sampled from tumor-free peripheral lung and no metastasis was found in the lungs of those patients. Another study limitation is that most of the COPD patients in the surgical tissue study had only mild or moderate COPD. To obtain a better understanding of the involvement of Duox in the progression of COPD, a larger sample of patients with more advanced disease should be assessed.

The present study demonstrates that current smoking diversely regulates the epithelial Duox1 and Duox2 expression only at the transcriptional levels. An attempt to correlate Duox1 and Duox2 gene expression with protein translation should be made, and the relative importance of these isoforms should be further investigated at their protein levels. However, to the best of our knowledge, Duox1- or Duox2-specific antibodies do not currently exist, as the Duox antibodies that are currently available recognize motifs on both Duox proteins (5). According to the previous reports using that antibody recognizing both Duox1 and Duox2 (11, 15), the diverse regulation of Duox1 and Duox2 should exclusively occur within epithelial cells.

Very few studies have examined the regulation of other oxidases by smoking. Higher traces of xanthine oxidase (XO) substrates were detected in BAL fluid from COPD patients compared to the controls, suggesting the increased activity of XO in COPD patients (30). On the other hand, the two subtypes of monoamine oxidase (MAO) A and MAO B were both downregulated by cigarette smoking (12, 13). Impaired induction of

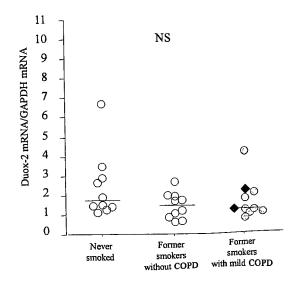


FIG. 8. Duox2 mRNA expression in alveolar septa. Duox 2 mRNA expression levels in the alveolar septa did not significantly differ among the three groups. COPD patients were classified by GOLD (Stage I: closed circles, Stage II: closed diamonds). Medians are indicated by horizontal lines.

Duox may cause an unwanted host defense imbalance that may contribute to smoking-induced lung disorders, including COPD. Our findings suggest bronchiolar epithelium as a possible cellular target for the development of new host defense approaches (40) that may help protect cells from the accumulation of smoking-related damage.

ACKNOWLEDGMENTS

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ABBREVIATIONS

COPD chronic obstructive pulmonary disease; Duox, dual oxidase; FEV₁, forced expiratory volume in one second; GOLD, Global Initiative for Obstructive Lung Disease; GAPDH, lyceraldehyde-3-phosphatase-dehydrogenase; H_2O_2 , hydrogen peroxide; IFN- γ , interferon- γ ; IL, interleukin, MAO, monoamine oxidase; NADPH, nicotinamide adenine dinucleotide phosphate; PAS, periodic acid-Schiff; ROS, reactive oxygen species; SE, standard error; XO, xanthine oxidadase.

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Address reprint requests to:
Tomoko Betsuyaku, M.D., Ph.D.
First Department of Medicine
Hokkaido University School of Medicine
N-15, W-7, Kita-ku
Sapporo 060-8638, Japan

E-mail: bytomoko@med.hokudai.ac.jp

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High Incidence of Extracellular Matrix Metalloproteinase Inducer Expression in Non-Small Cell Lung Cancers

Association with Clinicopathological Parameters

Nobuyuki Hakuma^a Tomoko Betsuyaku^a Ichiro Kinoshita^b Tomoo Itoh^d Kichizo Kaga^c Satoshi Kondo^c Masaharu Nishimura^a Hirotoshi Dosaka-Akita^b

^aFirst Department of Medicine, and Departments of ^bMedical Oncology and ^cSurgical Oncology, Hokkaido University School of Medicine, and ^dDepartment of Surgical Pathology, Hokkaido University Hospital, Sapporo, Japan

Key Words

Basigin · CD147 · EMMPRIN · Immunohistochemistry · Lung cancer · Matrix metalloproteinases

Abstract

Objective: Extracellular matrix metalloproteinase inducer (EMMPRIN) is a highly glycosylated transmembrane protein that is widely present on the surface of various tumor cells, assisting in tumor progression by stimulating the production of several matrix metalloproteinases in adjacent stromal cells. However, its clinical relevance remains to be evaluated in lung cancers. Therefore, we aimed to investigate the relationship between EMMPRIN expression in non-small cell lung cancer (NSCLC) and clinicopathological characteristics and prognosis. Methods: EMMPRIN expression was semiquantified by immunohistochemistry with anti-human EMMPRIN monoclonal antibody in 208 surgically resected NSCLCs and was analyzed statistically in relation to various characteristics. Results: EMMPRIN expression was seen in most NSCLC samples (92%). High levels of EMMPRIN expression were significantly associated with differentiation and pT₁ stage in adenocarcinomas. There were no significant differences in overall survival between patients with tumors having high and low levels of EMMPRIN expression in pathological stage I NSCLCs (5-year survival rates, 69 vs. 60%). **Conclusions:** EMMPRIN was preferentially expressed in most NSCLCs. High levels of expression were associated with early T stage and well-differentiated adenocarcinoma, and were not a prognostic factor in NSCLC.

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Introduction

Lung cancer is one of the leading causes of cancer death throughout the world. Although the management and treatment of non-small cell lung cancers (NSCLCs) have improved, there is no evidence to suggest that therapeutic advances have resulted in a marked increase in survival rates, and the overall 5-year survival rate remains <15% [1]. The clinical observations that patients with NSCLCs in comparable stages may have different clinical courses and may respond differently to similar treatments have yet to be elucidated. A more sophisticated understanding of the pathogenesis and biology of these tumors could therefore provide useful information for identifying molecular targets for treatment [2, 3].

Extracellular matrix metalloproteinase inducer (EMMPRIN), which is also known as CD147, basigin, tu-

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mor collagenase stimulatory factor and M6 antigen, was initially characterized as a transmembrane glycoprotein, and has been identified as a member of the immunoglobulin superfamily [4]. EMMPRIN is strongly expressed on the cell surface of malignant human tumor cells [5, 6], where it interacts with fibroblasts and induces various matrix metalloproteinases (MMPs), such as interstitial collagenase (MMP-1), gelatinase A (MMP-2) and stromelysin-1 (MMP-3). EMMPRIN is known to induce MMP production in both primary fibroblasts and tumor cells themselves, thereby facilitating tumor invasion, and probably acting in an autocrine and/or paracrine manner [7–9].

Human breast cancer cell clones transfected with EMMPRIN cDNA were considerably more tumorigenic and invasive than control plasmid-transfected cancer cell clones [10]. EMMPRIN is also implicated in several aspects of tumor progression, including angiogenesis via expression of vascular endothelial growth factor [11, 12], and anchorage-independent growth and multidrug resistance in a hyaluronan-dependent fashion [13, 14]. Tumors expressing high levels of EMMPRIN include carcinomas of the urinary bladder [15], kidney [16], breast [17, 18], lung [17, 18], oral cavity [19], stomach [20], esophagus [21, 22], liver [23] and skin [24, 25], as well as malignant lymphomas [26, 27] and malignant peripheral nerve sheath tumors [28]. Elevated EMMPRIN is therefore correlated with progression and/or metastasis in various tumors [29, 30]; to our knowledge, however, there have been no studies to elucidate the clinicopathological or prognostic roles of EMMPRIN expression in NSCLCs.

In this study, we investigated the expression and localization of EMMPRIN by immunohistochemistry, and examined the relationship between EMMPRIN expression and the clinical and clinicopathological characteristics of 208 NSCLCs obtained by surgical resection.

Patients and Methods

Patients and Tumor Specimens

Primary tumor specimens from 208 NSCLC patients were consecutively obtained by surgical resection at the Hokkaido University Hospital between 1976 and 1994. The histological classification and criteria of differentiation of the tumor specimens were based on WHO criteria [31]. NSCLC samples comprised 104 adenocarcinomas, 87 squamous cell carcinomas, 9 large cell carcinomas and 8 adenosquamous cell carcinomas. Clinical information was obtained from surgical and clinical charts. The 208 NSCLC samples were pathologically staged as follows: 112 in stage I, 17 in stage II, 70 in stage IIIA, 1 in stage IIIB and 7 in stage IV (1 unknown). The postsurgical pathological tumor-node-metas-

tasis stage (pTNM) was determined according to the guidelines of the American Joint Committee on Cancer [32]. The prognostic value of EMMPRIN/basigin expression was evaluated in the 95 stage I patients who (1) survived >3 months after surgery; (2) did not die of causes other than lung carcinoma within 5 years of surgery, and (3) were observed >2 years after surgery (for patients who remained alive). Thirteen patients who did not meet the above criteria (4 died within 3 months of surgery and 9 died of causes other than lung carcinoma within 5 years) were excluded from survival analysis. Eleven patients for whom no postoperative survival records were obtained were also excluded from survival analysis. While 110 patients received chemotherapy as postsurgical treatment, radiation therapy was not performed before or after surgery in any patients. Because all patients enrolled in the current study were coded, they could not be individually identified.

Immunohistochemistry for EMMPRIN

Lung tumor specimens were obtained from 208 subjects at lobectomy or pneumonectomy for treatment of primary lung cancer, fixed in 10% phosphate-buffered formalin and embedded in paraffin. Five-micrometer sections were deparaffinized in xylene and dehydrated with a graded alcohol series. Antigenic activity was retrieved by incubation in 10 mm citrate buffer (pH 6.0) in a microwave oven for 5 min. After washing in phosphate-buffered saline (PBS), slides were processed for immunohistochemistry using a CSA kit (DAKO Japan, Kyoto, Japan), as described previously [33]. Primary antibody was anti-human EMMPRIN monoclonal antibody (Chemicon, Temecula, Calif., USA) diluted 1:500 with PBS. For negative controls, we used sections where PBS or non-immune mouse serum was used instead of primary antibody. In order to avoid run-to-run variations in immunoreaction, we stained an EMMPRIN-positive lung adenocarcinoma tissue sample as a positive control for each staining batch. We assessed one peripheral lung tissue section from 1 block per patient, in which at least one representative cancer region could be identified. Because the amount and distribution of cancer cells within the tissues was heterogeneous, immunostained tissue sections were thoroughly investigated to evaluate the percentage of positively stained area in the whole cancer cells in the given specimens. Distribution of EMMPRIN-positive tumor cells was scored as 1 (0-25%), 2 (26-50%), 3 (51-75%) or 4 (76-100%) according to the percentage of positively stained area in the given NSCLC specimens. Two observers (N.H. and T.B.) evaluated the staining levels of EMMPRIN on each section independently and were blinded to patient clinicohistological information. Discordant evaluations were adjusted using multihead microscopes and discussion with other observers (I.K. and H.D.-A.).

Statistical Analysis

Associations between EMMPRIN expression and categorical variables were analyzed by χ^2 test or Fisher's exact test, as appropriate. Associations between EMMPRIN expression and age were analyzed by Student's t test. Survival curves were estimated using the Kaplan-Meier method, and differences in survival distributions were evaluated by the generalized Wilcoxon test. Cox's proportional hazards model of factors potentially related to survival was performed in order to identify factors having a significant influence on survival. The significance level chosen was p < 0.05, and all tests were two sided.

Table 1. Relationship between EMMPRIN expression and clinical and clinicopathological characteristics in the 208 surgically resected NSCLCs

Characteristics	EMMPRIN	p value		
	low	high		
Age, years	61.6 ± 8.9	64.0 ± 9.3	0.07	
Sex				
Male	49	90	0.3	
Female	19	50		
Smoking history				
Nonsmoker	14	45	0.07	
Smoker	52	84		
0-20 pack-years	19	46	0.4	
≥20 pack-years	46	82		
Histology				
SCC '	33	54	0.1	
Adenocarcinoma	27	77		
Other	8	8		
Differentiation				
Well	8	39	0.04	
Moderate/poor	41	79		
pT classification				
T_1	13	45	0.07	
T_2-T_4	55	94		
pN classification				
N ₀	42	82	0.7	
N_1-N_3	26	57		
pM classification				
M ₀	63	137	0.04	
M_1	5	2		
Pathological stage	•	_		
I	37	75	0.058	
ĪĪ	2	15		
IIIA	23	47		
IIIB	0	1		
IV	5	2		

SCC = Squamous cell carcinoma; Other = large cell carcinoma and adenosquamous cell carcinoma. Numbers of patients are shown except for age.

Results

Immunohistochemistry for EMMPRIN

We observed EMMPRIN expression (scores of 2-4) in 192 (92%) of the 208 NSCLC tumors specimens, including 99 (95%) of the 104 adenocarcinomas, and 78 (90%) of the 87 squamous cell carcinomas. As shown in figure 1, 16 samples were scored as 1 and considered negative for EMMPRIN, 14 were scored as 2, 38 were scored as 3, and 140 were scored as 4. High levels of EMMPRIN expression, scored as 4, were observed in 140 (67%) of the

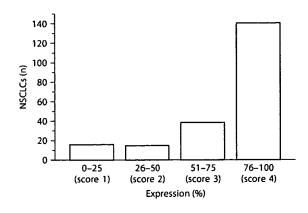


Fig. 1. In resected NSCLC specimens, low-level EMMPRIN expression (score 0-3) was observed in 68 (33%) of the 208 NSCLC samples and high-level EMMPRIN expression (score 4) in 140 (67%) samples.

208 NSCLC samples, including 77 (74%) of the 104 adeno-carcinomas and 54 (62%) of the 87 squamous cell carcinomas. Low levels of EMMPRIN expression, scored as 0–3, were observed in 68 (33%) of the 208 NSCLC samples, including 27 (26%) of the 104 adenocarcinomas and 33 (38%) of the 87 squamous cell carcinomas. A range of immunohistochemical staining patterns was observed for EMMPRIN expression. In contrast to the weak labeling of EMMPRIN at the apical pole in normal bronchiolar epithelial cells in smokers (fig. 2a), some tumors showed predominant staining toward the basolateral aspect of the cells, consistent with basement membrane localization (fig. 2b). Others were diffusely stained in tumor nests (fig. 2c) and lined carcinoma cells (fig. 2d), whereas the surrounding stroma was exclusively negative.

EMMPRIN Expression and Clinical and Clinicopathological Variables

The relationship between low- or high-EMMPRIN expression and clinical and clinicopathological characteristics was analyzed in the 208 NSCLCs (table 1). Tumors having high-level EMMPRIN expression were well differentiated compared to those having low-level EMMPRIN expression (p = 0.04). However, EMMPRIN expression patterns were not associated with any of the following variables: age, gender, histology, pT or pN classification, and pathological stage. The relationship between EMMPRIN expression and clinical and pathological characteristics was then analyzed in 104 adenocarci-

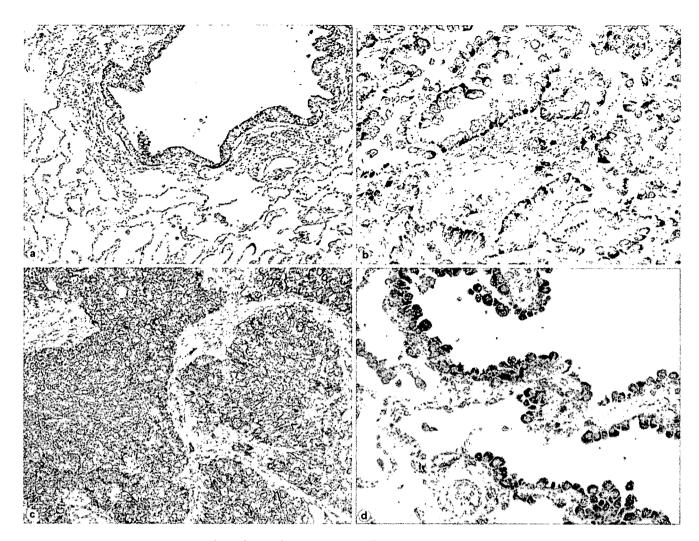


Fig. 2. Immunohistochemical staining patterns for EMMPRIN in NSCLCs showed weak labeling of EMMPRIN at the apical pole in normal bronchiolar epithelial cells in non-cancerous lesions from a smoker (\mathbf{a} , $\times 80$) and predominant staining toward the basolateral aspect of the cells, consistent with basement membrane localization in adenocarcinoma (\mathbf{b} , $\times 400$). \mathbf{c} , \mathbf{d} EMMPRIN diffusely stained in tumor nests of adenocarcinoma (\mathbf{c} , $\times 400$) and in cytoplasm of lined bronchoalveolar-type adenocarcinoma (\mathbf{d} , $\times 400$).

nomas (table 2) and in 68 squamous cell carcinomas (table 3). High levels of EMMPRIN expression were significantly associated with differentiation (p = 0.01) and pT_1 classification (p = 0.008) in adenocarcinomas, but not in squamous cell carcinomas. With regard to the relationship with smoking history, high levels of EMMPRIN expression were more frequently observed in smokers than nonsmokers among squamous cell carcinoma patients (p = 0.03), but were more frequently seen in nonsmokers than in smokers among adenocarcinoma patients (p = 0.02). Furthermore, heavy smokers with more than 20 pack-years of smoking demonstrated significant-

ly higher EMMPRIN expression when compared with light smokers having less than 20 pack-years of smoking among squamous cell carcinoma patients. In addition, we analyzed EMMPRIN expression in relation to the cell growth fraction determined by Ki-67 labeling index (LI), which we previously studied in the same cohort of NSCLCs [34]. Tumors with high- and low-level EMMPRIN expression showed similar Ki-67 LIs (high versus low; 36.1 ± 24.1 vs. $37.5 \pm 24.1\%$, means \pm SD, nonsignificant). It should be noted that 16 of the 208 NSCLCs demonstrated predominant staining toward the basolateral aspect of the cells, consistent with basement membrane

Table 2. Relationship between EMMPRIN expression and clinical and clinicopathological characteristics in 104 surgically resected adenocarcinomas (numbers of patients are shown except for age)

Table 3. Relationship between EMMPRIN expression and clinical and clinicopathological characteristics in 68 surgically resected squamous cell carcinomas (numbers of patients are shown except for age)

Characteristics	EMMPRIN expression		p value	Characteristics	EMMPRIN expression		p value
	low	high			low	high	
Age, years Sex	58.7 ± 8.6	62.9 ± 9.4	0.04	Age, years Sex	64.0 ± 8.5	65.4 ± 9.2	0.4
Male	13	33	0.8	Male	29	51	0.4
Female	14	44		Female	4	3	
Smoking history				Smoking history			
Nonsmoker	8	42	0.02	Nonsmoker	5	1	0.03
Smoker	18	28		Smoker	28	50	
0-20 pack-years	11	43	0.1	0-20 pack-years	7	1	0.005
≥20 pack-years Differentiation	15	27		≥20 pack-years Differentiation	25	49	
Well	5	36	0.01	Well	3	3	0.6
Moderate/poor pT classification	19	36		Moderate/poor pT classification	21	41	
T_1	3	32	0.008	T ₁	9	11	0.6
T ₂ -T ₄ pN classification	24	45		T_2 - T_4 pN classification	24	42	
N_0	14	45	0.7	N ₀	24	32	0.3
N ₁ -N ₃ pM classification	13	32		N ₁ -N ₃ pM classification	9	21	
M_0	25	75	0.2	M_0	32	53	0.3
M_1	2	2		M_1	l	0	
Pathological stage				Pathological stage			
I	12	43	_	I	21	29	0.4
II	1	9		II	1	5	
IIIA	1	0		IIIA	10	19	
IIIB	0	0		IIIB	0	1	
IV	2	2		IV	1	0	

localization (fig. 2b), including 9 adenocarcinomas, 2 large cell carcinomas and 5 squamous cell carcinomas. No statistical differences were found in clinical and pathological parameters, such as gender, smoking histories, clinical staging, and survival, to distinguish the patients with this particular staining pattern from the others.

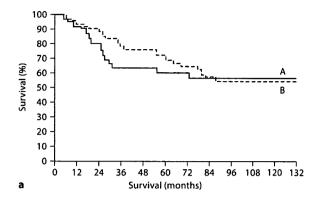
EMMPRIN Expression and Survival

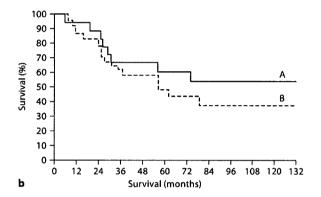
We analyzed the prognostic value of EMMPRIN expression in 95 pathological stage I NSCLCs patients. There was no significant difference in survival between patients with tumors having high- and low-level EMMPRIN expression in pathological stage I NSCLC samples (5-year survival rates, 69 vs. 60%, p = 0.3; fig. 3a). The EMMPRIN expression pattern was not a prognostic factor (p = 0.7) in Cox's proportional hazards model (data

not shown). Significant differences were not observed between these two groups in 42 squamous cell carcinomas (5-year survival rates, 48 vs. 60%, p = 0.4; fig. 3b). Although of the 47 adenocarcinoma patients analyzed, patients with high levels of EMMPRIN expression tended to survive for longer periods than those with low-level EMMPRIN expression (5-year survival rates, 91 vs. 62%, p = 0.09; fig. 3c), the difference was not statistically significant.

Discussion

In order to elucidate the biological significance of EMMPRIN in NSCLC, we conducted an immunohistochemical investigation of EMMPRIN in the 208 NSCLC





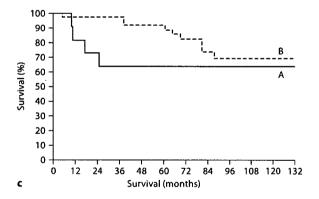


Fig. 3. Kaplan-Meier survival analysis revealed no significant differences in overall survival between patients with tumors having high- or low-level EMMPRIN expression in 95 NSCLC samples from pathological stage I patients (5-year survival rates; 69 vs. 60%, p = 0.4; **a**), in 5-year survival rates for squamous cell carcinoma (48 vs. 60%, p = 0.4; **b**) or in 5-year survival rates for adenocarcinoma (91 vs. 62%, p = 0.09; **c**). A = Low-level EMMPRIN (**a**: n = 33; **b**: n = 18; **c**: n = 11); B = high-level EMMPRIN (**a**: n = 62; **b**: n = 24; **c**: n = 36).

specimens. We demonstrated that most NSCLC specimens express EMMPRIN. Contrary to the results in other studies [7, 30], our study is the first to show that high levels of EMMPRIN staining are observed more frequently in early T stage and well-differentiated adenocarcinomas, and are not a prognostic factor in NSCLC.

The correlation with differentiation in NSCLCs, particularly in adenocarcinomas, is consistent with previous findings by Caudroy et al. [18] that EMMPRIN is strongly expressed in tumor clusters with intense staining in cells located on the periphery of well-differentiated adenocarcinomas in 6 lung specimens and 20 breast specimens, but is expressed at low levels in poorly differentiated adenocarcinomas. The unexpected negative correlation with T stage in adenocarcinomas and the absence of a link with metastasis and prognosis may reflect the relationship between EMMPRIN and differentiation.

Epithelial proliferation and alteration are frequent findings in diverse lung diseases, including NSCLCs, and may affect EMMPRIN expression. Bronchiolar desquamation and cuboidal cell metaplasia are often associated with 'bronchiolization' of the alveolar area in lung cancer [35] and in fibrotic lung diseases [36, 37]. We have recently reported increased EMMPRIN expression in alveolar bronchiolization in murine bleomycin-induced fibrosis [38] and in human interstitial pneumonia [39], suggesting that EMMPRIN may play a critical role in remodeling of pulmonary epithelium and stimulating production of MMPs following various injuries. In addition, EMMPRIN is strongly expressed in epithelial tissue during lung development [40], but only at low levels in normal adult lung in mice [38] and humans [33, 39]. Taken together, these results suggest that upregulation of EMMPRIN is related to growth of proliferating epithelial cells in well-differentiated NSCLC, which retain the characteristics of the original epithelial cells.

Interestingly, the NSCLC samples demonstrated distinctive patterns of immunostaining for EMMPRIN. In most NSCLC cells, basolateral or diffuse cytosolic accumulation of EMMPRIN was not observed in normal bronchiolar epithelial cells. The abnormal subcellular localization of EMMPRIN may play a significant role in the development of NSCLCs, although there was no significant relationship of NSCLCs with basement membrane localization of EMMPRIN with any clinicopathological parameters in this study.

Smoking itself upregulates EMMPRIN in various lung cells, and we have previously reported that alveolar macrophages and bronchiolar epithelium are major sources of EMMPRIN in the lungs of smokers [33]. The concen-

tration of EMMPRIN in bronchoalveolar lavage fluid is significantly higher in former and current smokers when compared to life-long nonsmokers without NSCLC [33]. In this study, high levels of EMMPRIN expression were frequently found in smokers, particularly heavy smokers, with squamous cell carcinoma, in contrast to nonsmoking adenocarcinoma patients. These findings suggest that smoking may stimulate EMMPRIN production in bronchiolar epithelium, from which squamous cell carcinoma may originate. In contrast, EMMPRIN was more frequently seen in nonsmokers than in smokers among adenocarcinoma patients (p = 0.02). This suggests that mechanisms other than smoking may also play some role in the regulation of EMMPRIN expression in adenocarcinomas. Recently, it has been reported that some growth factors upregulate EMMPRIN expression in corneal epithelial cells [41] and in human breast epithelial cells [42]. However, the regulatory mechanism of EMMPRIN expression in lung cells remains to be elucidated.

Molecular mechanisms may determine why NSCLC is different from other types of carcinoma, in which high EMMPRIN expression is linked to tumor metastasis, progression or prognosis. EMMPRIN may only be involved in early-phase NSCLC development or in the malignant transformation of bronchopulmonary epithelial

cells. It has recently been reported that EMMPRIN also serves as a chaperone protein to target monocarboxylate transporters (MCTs), and is required for the proper localization of MCT1 in a wide range of cells [43, 44], but not lung cells [44], thus suggesting that the biological relevance of EMMPRIN differs according to cell type.

In conclusion, we immunohistochemically investigated EMMPRIN expression in 208 NSCLC specimens, and examined its relationship with clinicopathological parameters and patient prognosis. Expression of EMMPRIN was observed in most NSCLC samples. Highlevel expression of EMMPRIN was significantly associated with early T stage and well-differentiated adenocarcinomas, thus suggesting that it might be involved in tumorigenesis, particularly in early stages. Although there are other factors affecting survival after surgery, expression of EMMPRIN was not a prognostic factor in NSCLCs.

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LIPOPOLYSACCARIDE-INDUCED NEUTROPHILIC INFLAMMATION IN THE LUNGS DIFFERS WITH AGE

Yoko Ito, Tomoko Betsuyaku, Yasuyuki Nasuhara, and Masaharu Nishimura			
u n p u p	In aged humans and animals, lung injuries are generally more serious and prolonged. From netic perspective, the authors thus assessed whether lung expression of proinflammatory cytokine altered with age following intratracheal lipopolysaccharide (LPS) challenge in mice. Tumo crosis factor α, interleukin-1β, macrophage inflammatory protein-1α, macrophage inflammator otein-2, and keratinocyte-derived chemokine were significantly higher in 65-week-old mice alon th sustained neutrophilia when compared to 11-week-old mice at 72 hours, but not at earlier tim ints. The authors concluded that the degree of LPS-induced neutrophilic inflammation and the pression of these cytokines differ with age at later phases of acute lung injury.		

In humans and animals, acute lung injury is generally more serious and is associated with higher mortality at advanced age [1–3]. Although a number of studies have suggested pivotal roles for proinflammatory cytokines in the pathogenesis of sepsis and acute lung injury/acute respiratory distress syndrome, no studies have been devoted to the age-related kinetic changes in these factors during the course of lung injury. We previously reported age-dependent differences in resolution of neutrophilic inflammation and rate of survival in a lipopolysaccharide (LPS)-induced lung injury model in mice, although the underlying mechanisms remain to be elucidated [4].

Tumor necrosis factor- α (TNF- α) and interleukin-1 β (IL-1 β) are proinflammatory cytokines with pleiotropic and overlapping biological properties [5, 6]. Although these factors are usually tightly regulated, exaggerated expression and/or release can result in severe injury to the lungs and other

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Address correspondence to Tomoko Betsuyaku, MD, PhD, First Department of Medicine, Hokkaido University School of Medicine, N-15, W-7, Kita-ku, Sapporo, Japan, 060-8638. E-mail: bytomoko@med.hokudai.ac.jp

organs [7]. Direct administration of intratracheal TNF- α and IL-1 β recapitulates LPS-induced acute and chronic inflammation [8]. We wondered whether the kinetics of TNF- α and IL-1 β expressions and the neutrophilic chemokines, such as macrophage inflammatory protein-1 α (MIP-1 α), macrophage inflammatory protein-2 (MIP-2), and keratinocyte-derived chemokine (KC), changes with age, and is related to prolonged neutrophilic inflammation in LPS-induced lung injury in 65-week-old mice. In this study, we subjected 11- and 65-week-old mice to LPS to induce lung injury, as described previously (4), and evaluated whole-lung expression of TNF- α , IL-1 β , MIP-1 α , MIP-2, and KC, at multiple time points following intratracheal LPS instillation.

METHODS

Animals and Lipopolysaccharide-Induced Acute Lung Injury Model

Male ICR mice (11- and 65-week-old mice) were obtained from Japan Clea (Tokyo, Japan). None of the mice were found to have gross pathological lesions. Animals were anesthetized with a mixture of ketamin (1.74 mg/body) (Sigma Chemical St. Louis, MO) and xylazine (260 µg/body) (Sigma Chemical). Fifty microliters of saline containing LPS (200 µg/body) (Sigma Chemical) was intratracheally administered as described previously [9]. Nonmanipulated mice at 11 and 65 weeks of age served as controls. All mice were kept in plastic chambers with free access to food and water. Experimental protocols and procedures were approved by the Ethics Committee on Animal Research of the Hokkaido University School of Medicine.

Bronchoalveolar Lavage and Tissue Homogenates

Mice were sacrificed before or at specified time points after LPS instillation. Bronchoalveolar lavage (BAL) was performed after drawing out circulating blood from the lungs through the inferior vena cava, and lung tissue was immediately frozen on dry ice as described elsewhere (n = 5-13) at each time point) [4, 9, 10].

Total Protein Assay

Total protein concentration in BAL fluid (BALF) was quantified using the bicinchoninic acid microassay method (Pierce Chemical, Rockford, IL).

Quantitative Reverse Transcriptase-Polymerase Chain Reaction for Cytokines

Total RNA extraction from lung homogenate's, cDNA synthesis using reverse transcriptase (RT) (Applied Biosystems, Foster City, CA) and polymerase chain reaction (PCR) with an ABI Prism 7700 Sequence Detector (Applied Biosystems) were performed as described previously (10), using Taqman PCR Universal master mix (Applied Biosystems) according to the manufacturer's instructions. The relative amount of target mRNA in the samples was assessed by interpolation of threshold cycles from a standard curve. Each mRNA was then normalized against β 2-microglobulin (β 2-MG) mRNA and fold increase relative to levels in untreated 11-week-old mice was determined. In some experiments, β -glucuronidase (BGUS) and hypoxanthine ribosyltransferase (HPRT) mRNA were used for normalization.

Assays-on-Demand Gene Expression probes for TNF-α, IL-1β, MIP-1α, MIP-2, and KC were derived from the boundaries between exons 1 and 2 of the murine TNF-α gene sequence (GenBank accession number NM013693), between exons 3 and 4 of the murine IL-1β gene sequence (GenBank accession number NM008361), between exons 1 and 2 of the murine MIP-1α gene sequence (GenBank accession number NM011337), between exons 3 and 4 of the murine MIP-2 gene sequence (GenBank accession number NM009140), and between exons 3 and 4 of the murine KC gene sequence (GenBank accession number NM008176) (Applied Biosystems).

Quantification of TNF-α and IL-1β Proteins

TNF- α and IL-1 β protein levels in BALF were quantified by sandwich enzyme-linked immunosorbent assay (ELISA) according to the manufacturer's instructions (TNF- α : Biosource, Camarillo, CA; IL-1 β : R&D systems, Minneapolis, MN).

Statistical Analysis

All results were expressed as means \pm standard error (SE) of the mean. Unpaired t-test was used for comparison between 11- and 65-week-old mice at each time point. All tests were performed using StatView J 5.0 (SAS Institute, Cary, NC). Differences were considered significant at P < .05.

RESULTS

Different Degrees of Inflammation after Intratracheal LPS Administration between 11- and 65-Week-Old Mice

Following administration of LPS, 65-week-old mice exhibited significantly higher total cell number at 2 hours (Figure 1a), neutrophil levels

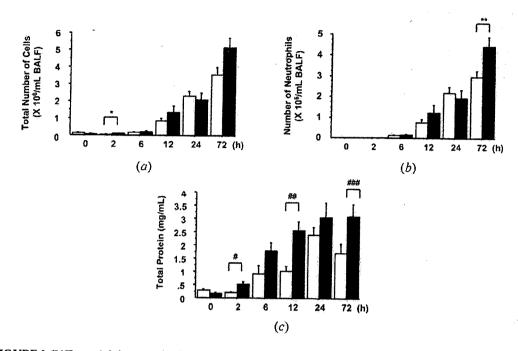


FIGURE 1 Differential degree of inflammation following a intratracheal LPS administration in 11-week-old vs. 65-week-old mice. (a) 65-week-old mice exhibited higher total number of cells when compared to 11-week-old mice at 2 hours $(0.09\pm0.01 \text{ vs.} 0.04\pm0.01\times106/\text{mL}$, *P=0.0115). (b) 65-week-old mice exhibited higher number of neutrophils when compared to 11-week-old mice at 72 hours $(4.43\pm0.47 \text{ vs.} 2.96\pm0.29\times106/\text{mL}$, **P=0.0434). (c) 65-week-old mice exhibited higher total protein levels when compared to 65-week-old mice at 2, 12 and 24 hours $(0.52\pm0.09 \text{ vs.} 0.20\pm0.03 \text{ mg/mL}$, *P=0.0095, $2.56\pm0.34 \text{ vs.} 1.02\pm0.20 \text{ mg/mL}$, **P=0.0028, $3.11\pm0.45 \text{ vs.} 1.70\pm0.36 \text{ mg/mL}$, **P=0.0291, respectively). (open bar; 11-week-old mice, closed bar; 65-week-old mice). The number of animals; 11-week-old mouse 0,2,6,12,24,72 h after LPS administration: n=5,6,6,6,12,5 respectively. 65-week-old mouse 0,2,6,12,24,72 h after LPS administration: n=5,6,5,6,12,8, respectively.

at 72 hours (Figure 1b), and total protein levels at 2, 12, and 72 hours (Figure 1c) in BALF when compared with 11-week-old mice, respectively, which was consistent to the results previously demonstrated [4]. None of the mice died throughout 72 hours after LPS administration regardless of age.

Whole-Lung Levels of TNF- α mRNA Expression and TNF- α Protein Levels in LPS-Induced Lung Injury

In mice treated with intratracheal LPS, no significant differences were seen in whole-lung TNF- α mRNA within 6 hours between the two age groups. However, it was significantly higher in 11-week-old mice than in 65-week-old mice at 24 hours (P=.0167), and was conversely higher in 65-week-old mice than in 11-week-old mice at 12 (P=.0179) and 72 (P=.0003) hours (Figure 2a). The significance in TNF- α mRNA expression between the 2 groups remained when normalized by either BGUS or HPRT (BGUS: P=.0066; HPRT: P=.0424), suggesting that the age-related difference

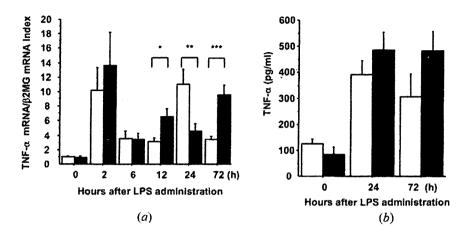


FIGURE 2 (a) Whole lung mRNA expression of TNF-α in mice treated with intratracheal LPS. 11-week-old mice exhibited higher expression of TNF-α when compared to 65-week-old mice at 24 hours $(11.0 \pm 2.1 \text{ vs. } 4.6 \pm 1.0, *^*P = 0.0167)$, while TNF-α expression was conversely higher in 65-week-old mice than in 11-week-old mice at 12 hours $(6.6 \pm 1.1 \text{ vs. } 3.1 \pm 0.5, *^*P = 0.0179)$ and 72 hours $(9.6 \pm 1.3 \text{ vs. } 3.4 \pm 0.5, *^*P = 0.00103)$. (b) TNF-α protein levels in BALF in mice treated with intratracheal LPS. There was no significant difference between the two groups of age. (open bar; 11-week-old mice, closed bar; 65-week-old mice). The number of animals; 11-week-old mouse 0,2,6,12,24,72 h after LPS administration: n = 6,6,6,6,13,8 respectively; 65-week-old mouse 0,2,6,12,24,72 h after LPS administration: n = 5,6,5,6,11,6, respectively.

was not dependent on the kinds of housekeeping genes used (data not shown). There were no significant differences in protein levels of TNF- α in BALF between the two age groups at any time points (Figure 2b).

Whole-Lung Levels of IL-1β mRNA Expression and IL-1β Protein Levels in LPS-Induced Lung Injury

Whole-lung IL-1 β mRNA expression was significantly higher in untreated 65-week-old mice than in 11-week-old mice at 0 hour (P=.0250). In mice treated with LPS, no significant differences were seen in whole-lung IL-1 β mRNA within 12 hours between the two age groups. However, it was significantly higher in 11-week-old mice than in 65-week-old mice at 24 hours (P=.0285), and was conversely higher in 65-week-old mice than in 11-week-old mice at 72 hours (P=.0008) (Figure 3a). At 72 hours, not only 11-week-old mice, but also 65-week-old mice, showed statistically elevated expression of IL-1 β when compared to their levels at 0 hour (11-week-old mice: P=.0027; 65-week-old mice: P=.0420), indicating that IL-1 β is still sustained at 72 hours even though the original IL-1 β is also high in 65-week-old mice.

No significant differences were seen for IL-1 β protein levels in BALF between the two age groups (Figure 3b).

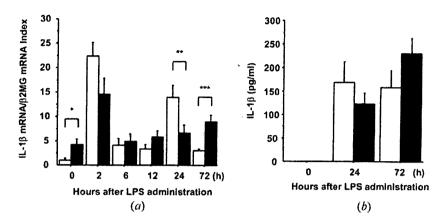


FIGURE 3 (a) Whole lung mRNA expression of 1L-1 β in mice treated with intratracheal LPS. IL-1 β expression was higher in 65-week-old mice than in 11-week-old mice at baseline (4.1 \pm 1.2 vs. 1.0 \pm 0.4, "P=0.0250). It was significantly higher in 11-week-old mice than in 65-week-old mice at 24 hours (13.9 \pm 2.5 vs. 6.6 \pm 1.7, "P=0.0285), however, conversely higher in 65-week-old mice than in 11-week-old mice at 72 hours (8.8 \pm 1.5 vs. 2.9 \pm 0.3, ""P=0.0008). (b) IL-1 β protein levels in BALF in mice treated with intratracheal LPS. There was no significant difference between the two groups of age. (open bar; 11-week-old mice, closed bar; 65-week-old mice). The number of animals is same as that of Fig. 2.

Whole-Lung Levels of MIP-1α, MIP-2, and KC mRNA Expression in LPS-Induced Lung Injury

In order to assess whether the prolonged neutrophilic inflammation after LPS instillation is related to altered chemokine expression in 65-week-old mice, mRNA for MIP-1 α , MIP-2, and KC were quantified by RT-PCR. The MIP-1 α expression was higher in 11-week-old mice than in 65-week-old mice at 24 hours (P=.0146); however, it was conversely higher in 65-week-old mice than in 11-week-old mice at 72 hours (P=.0176) (Figure 4a). The MIP-2 and KC expressions in 65-week-old mice were significantly higher when compared to 11-week-old mice at 72 hours (MIP-2: P=.0155; KC: P=.0015) (Figure 4b,c). Interestingly, there were no significant differences in the expressions of these chemokines between two age groups at earlier time points.

DISCUSSION

In this study, we demonstrated that TNF- α and IL-1 β expression in the lungs differs markedly with age, particularly in the later phases of injury (24 and 72 hours after LPS administration), but not in the early phases (within 12 hours of LPS administration), during the course of LPS-induced lung injury. We also found that three neutrophilic chemokines, MIP-1 α , MIP-2, and KC, were significantly elevated in the lungs of 65-week-old mice when