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**A New Model of Acute *Streptococcus Pneumoniae*
Infection in Human Lung Tissue: Cellular and Molecular
Mechanisms of the Pulmonary Inflammatory Response**

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Abbreviations

AEC: Alveolar epithelial cell

AM: Alveolar macrophage

AP: Activator protein

APS: Ammonium persulfate

ARDS: Acute respiratory distress syndrome

ASIM: A model of acute *S. pneumoniae* infection

ATCC: American Type Culture Collection

ATP: Adenosine triphosphate

BALF: Bronchoalveolar lavage fluid

BEC: Bronchial epithelial cell

bp: Base pair

BSA: Bovine serum albumin

CAP: Community-acquired pneumonia

CBP: Choline binding protein

cDNA: complementary Deoxyriboneucleic acid

CFU: Colony forming unit

Cox: Cyclooxygenase

cp: Crossing point

DEPC: Diethylpyrocarbonate

DNA: Deoxyriboneucleic acid

ECL: Enhanced chemiluminescence

EDTA: Ethylenediamine tetraacetic acid

ELISA: Enzyme-linked immunosorbent assay

ERK: Extracellular signal-regulated kinase

FCS: Fetal calf serum

Fig.: Figure

GM-CSF: Granulocyte-macrophage colony-stimulating factor

h: Hour

HCl: Hydrochloric acid

H₂O₂: Hydrogen peroxide

HOPE: Hepes-Glutamic acid buffer mediated Organic solvent Protection Effect

HRP: Horseradish peroxidase

H₂SO₄: Sulphuric acid

IFN: Interferon

Ig: Immunoglobulin

IKK: IκB kinase

IL: Interleukin

iNOS: inducible Nitric oxide synthase

IRAK: IL-1 receptor-associated kinase

IRF: Interferon regulatory factor

ISH: *In situ* hybridization

JNK: c-Jun N-terminal kinase

KCl: Potassium chloride

KH₂PO₄: Potassium dihydrogen phosphate

L: Liter

LDH: Lactate dehydrogenase

LPS: Lipopolysaccharide

LTA: Lipoteichoic acid

M: Molar

Mal: MyD88-adaptor-like

MAPK: Mitogen-activated protein kinase

MgCl₂: Magnesium Chloride

MHC: Major histocompatibility complex

min: Minute

MKK: MAPK kinase

MKKK: MAPK kinase kinase

mL: Milliliter

mRNA: messenger Riboneucleic acid

MyD88: Myeloid differentiation marker 88

NaCl: Sodium chlorid

NaHCO₃: Sodium bicarbonate

Na₂HPO₄: Sodium hydrogen phosphate

NaOH: Sodium hydroxide

ND: Non-determined

NEAA: Nonessential amino acid

NF-κB: Nuclear factor-κB

ng: Nanogram

PAF: Platelet activating factor

PAMP: Pathogen-associated molecular pattern

PBP: Penicillin binding protein

PBS: Phosphate-buffered saline

pg: Picogram

PGE₂: Prostaglandin E₂

PGN: Peptidoglycan

PMN: Polymorphonuclear leukocyte

PRR: Pattern recognition receptor

PspA: Pneumococcal surface protein A

PVA: Polyvinyl alcohol

rpm: Revolutions per minute

RT-PCR: Reverse transcription polymerase chain reaction

s: Second

SDS: Sodium dodecyl sulfate

SDS-PAGE: SDS-polyacrylamide gel electrophoresis

SEM: Standard error of mean

SSC: Standard saline citrate

TA: Teichoic acid

Tab.: Table

TAK: Transforming growth factor β -activated kinase

TBS: Tris buffered saline

TEMED: Tetramethylethylenediamined

TICAM: TIR domain-containing adaptor molecular

TIR: Toll/IL-1 receptor

TIRAP: TIR domain-containing adaptor protein

TLR: Toll-like receptor

TNF- α : Tumor necrosis factor- α

TRAF: Tumor necrosis factor receptor-associated factor

TRIF: TIR domain-containing adaptor-inducing IFN- β

Tris-Cl: Tris-chlorine

T-TBS: Tween-tris buffered saline

μg : Microgram

μM : Micromolar

V: Volt

VCAM: Vascular cell adhesion molecule

v/v: Volume per volume

w/v: Weight per volume

y: Year

1. Introduction

Despite the development of potent antimicrobial therapy, pneumonia is the sixth leading cause of death in the world and the main cause of infectious deaths (Wenger, 2001). As an encapsulated Gram-positive diplococcus, *Streptococcus pneumoniae* (the pneumococcus) is the most frequently isolated pathogen in community-acquired pneumonia (CAP) and one of the most common causes of death by infectious diseases such as septic shock, bacterial meningitis and acute respiratory distress syndrome (ARDS) (Schuchat et al., 1997; Fedson and Scott, 1999). Pneumococci cause 500,000 cases of pneumococcal pneumonia, 50,000 cases of bacteremia, 7,000,000 cases of otitis media and 3,000 cases of meningitis annually in United States (Austrian, 1999). Worldwide over 1 million children per year succumb to pneumococcal lung infection (Kadioglu and Andrew, 2004). The rise in antibiotic resistance of this pathogen and the limited efficacy of the widely used 23-valent polysaccharide vaccine urge further efforts to understand the host response mechanisms involved in pneumococcal pneumonia (Catterall 1999).

1.1 Bacterial factors in the pathogenesis of *S. pneumoniae* infection

The pathogenesis of *S. pneumoniae* is complex and the outcome of this infection depends on bacterial virulence factors and the effectiveness of the host response. The main factors of *S. pneumoniae* involved in the pathogenesis of pneumonia are the following:

1.1.1 The polysaccharide capsule

Since Avery found that the soluble substance surrounding the pneumococcus is composed of polysaccharide in 1925 (Avery and Heidelberger, 1925; Avery and Morgan, 1925), more than 90 serologically distinct polysaccharides have been found until now, each structurally and chemically different. Using genetically engineered pneumococci which differ only in capsular type, Kelly and colleagues proved that the virulence of the mutants compared to the parental strains is determined mainly, though not entirely, by the capsular type (Kelly et al., 1994). The capsule increases virulence by its antiphagocytic properties,

but does not play a role in inducing host inflammation (Tuomanen et al., 1987). The level of virulence is determined more by the chemical composition of the capsule than its size (Knecht et al., 1970).

1.1.2 The cell wall

The pneumococcal cell wall is a potent inflammation inducer, probably via the activation of complement and the induction of cytokines such as tumor necrosis factor (TNF)- α and Interleukin (IL)-8 (Winkelstein and Tomasz, 1978; Heumann et al., 1994). The active component of cell wall is polysaccharide, a complex teichoic acid (TA) or lipoteichoic acid (LTA), composed of extended repeat carbohydrates differing only in their attachment to the cell surface. TA links directly to the peptidoglycan (PGN) while LTA is hydrophobically anchored through its fatty acids to the plasma membrane (McCullers and Tuomanen, 2001). An unusual and important active component of cell wall among bacteria is phosphorylcholine which activates endothelial cells by attaching to platelet activating factor (PAF) receptor (Geelen et al., 1993). Cell wall components released during bacterial lysis induced by antibiotics are more potent inflammatory and chemotactic factors than are intact cell walls (Tomasz and Saukkonen, 1989).

1.1.3 Pneumolysin

As a cytoplasmic toxin, pneumolysin is released only when the cell wall undergoes lysis. This toxin can form large oligomeric pores and create transmembrane pores in cholesterol-containing membranes of eukaryotic cells (Rossjohn et al., 1998). Pneumolysin has been shown to cause respiratory ciliary slowing and epithelial damage, and impair the tight junctions of alveolar epithelial cells, facilitating bacterial proliferation and spread (Steinfort et al., 1989; Rayner et al., 1995). The laboratory pneumococcal strains deficient in pneumolysin reduce virulence compared to wild type strains (Benton, et al., 1995; Berry et al., 1995; Berry et al., 1999; Berry and Paton, 2000). Pneumolysin is also a main inducer of inflammation through both its cytotoxic activity and its characteristics to directly activate the classical pathway of complement (Paton et al., 1984; Cockeran et al., 2001). The molecular basis of pneumolysin induced complement activation may be related to the

structural similarity of domain 4 of pneumolysin to IgG Fc fragment, rather than the presumed homology of the toxin to C-reactive protein (Rossjohn et al., 1998).

1.1.4 Choline binding proteins (CBPs)

CBPs are a family of surface proteins bound to the choline component of cell wall TA or LTA via a conserved ligand binding domain. Autolysin, the enzyme which is responsible for cell wall lysis during stationary phase or in response to antibiotics, consists of at least three kinds of hydrolases or lytic enzymes: LytA, LytB, LytC. Autolysin degrades cell wall and allows the release of intracellular such as pneumolysin into external environment. Reduced virulence was shown when the normal virulent pneumococci were transformed with inactivated LytA (Berry et al., 1989). Pneumococcal surface protein A (PspA) is a surface protein involved in inhibition of complement activation by a pathway independent of complement regulatory protein factor H whereas PspC is essential for pneumococcal carriage by acting as a bridge between pneumococcal phosphorylation and the activation of human cell glycoconjugates (Gillespie and Balakrishnan, 2000).

1.1.5 Other proteins

Other proteins that may contribute to the pathogenicity and virulence of pneumococci include neuraminidase, hyaluronidase, a neutrophil elastase inhibitor, IgA₁ protease, protein adhesins, and etc., but their precise roles have not been well determined (Catterall, 1999; McCullers and Tuomanen, 2001). In addition, penicillin binding proteins (PBPs) are the transcarboxypeptidases located in the cell wall which also bind penicillin. With alterations of PBPs to different extent, the level of resistance to penicillin can vary considerably (Appelbaum, 1996). This gradual nature of penicillin resistance has direct relevance to clinical practice. Interest in pneumococcal proteins lies not only in their pathogenicity but also in the fact that they are T cell-dependent antigens and have the potential to be used in producing new pneumococcal vaccines (Catterall, 1999).

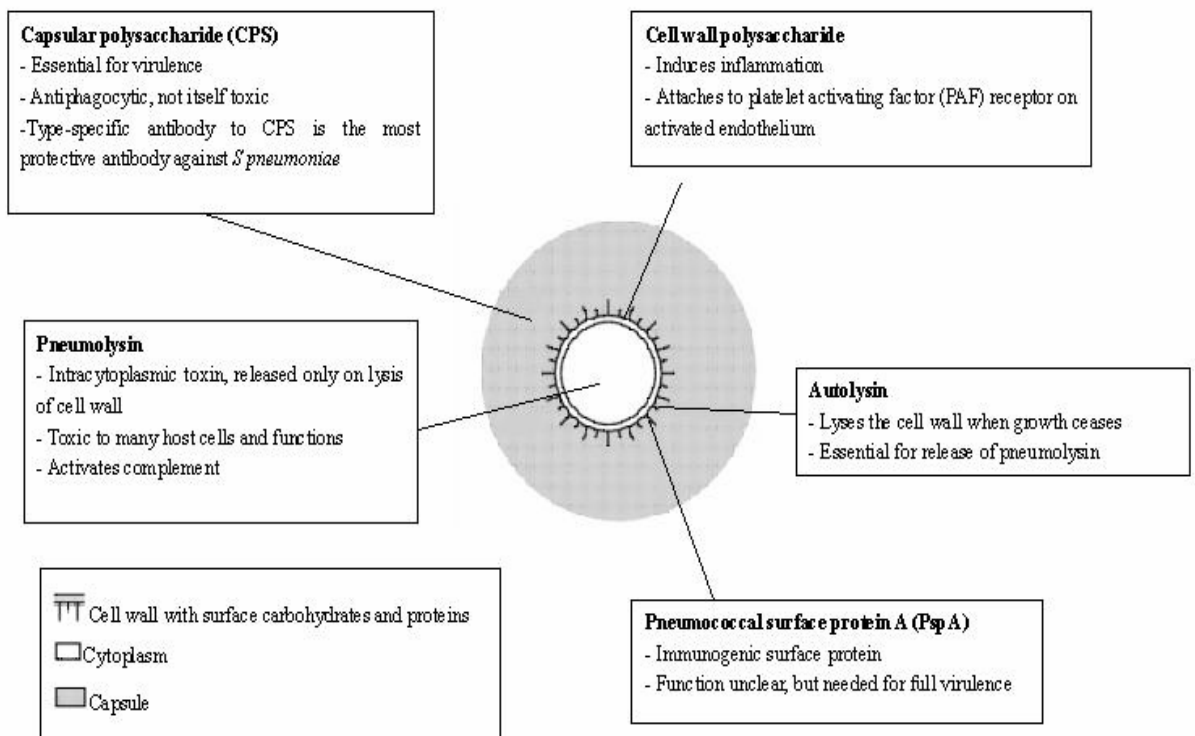


Fig. 1: Schematic figure of the known virulence factors of *Streptococcus pneumoniae* including their main functions and cellular location (Catterall 1999).

1.2 Host defense against *S. pneumoniae* infection

In recent years, it became clear that the interrelated and coordinated effort of multiple cell types, including respiratory epithelial cells lining the airways and alveoli, and both resident and recruited immune cells like macrophages, neutrophils, and lymphocytes, is implicated in the clearance of *S. pneumoniae* from the airways. Other than innate immunity, adaptive immune responses are also required for effective host defense, especially in cases of chronic bacterial infections (Sadikot et al., 2005). We illustrate the roles of different host cell types involved in *S. pneumoniae* infection and discuss individual host cell receptors and signaling cascades that have been shown to be important in host defense against this pathogen.

1.2.1 Respiratory epithelial cells

The respiratory epithelium is an important interface to environmental microorganisms. In

addition to provide a physical barrier against microbial invasion and contribute to mucociliary clearance, respiratory epithelial cells are actively involved in inflammation and host defense of the lung in multiple ways: activation of a host of pro- and anti-inflammatory mediators; and secretion of a variety of antimicrobial substances including acute phase proteins, bacteriolytic lysozyme and antimicrobial peptides (Kagnoff et al, 1997; Knowles et al, 2002; Hiemstra and Bals , 2004).

In particular, type II alveolar epithelial cells (AECs) as a defender of the alveolus are strategically located in alveoli where they contribute to the innate immune response against invading pathogens. Human Type II AECs express functional Toll-like receptor (TLR) 2 and TLR4 which can be modulated by lipopolysaccharide (LPS) and TNF- α . This suggests that AECs recognize microorganisms by pathogen-associated molecular patterns (PAMPs) and play an important role in local host defense (Droemann et al., 2003; Armstrong et al, 2004). Interestingly, TLR4 expression was unresponsive to LPS in the bronchial cell line BEAS-2B (Guillot et al., 2004). This may be explained by the fact that bronchial epithelia usually are exposed to larger amounts of airborne pathogens and contaminants than alveolar epithelia. The recognition of the key mechanisms of inflammatory signaling in epithelial cells may provide novel targets for modulation of pulmonary inflammation.

1.2.2 Macrophages

Pulmonary resident alveolar macrophages (AMs) are the first line of host defense against microorganisms by phagocytosing bacteria, generating antimicrobial peptides, secreting inflammatory cytokines and presenting antigens to T cells that links innate to adaptive immunity (Underhill and Ozinsky, 2002). However, the exact role of macrophages in inflammatory response and host defense has not been well elucidated. Using a low-dose pneumococcal infection model that is characterized by the clearance of bacteria without polymorphonuclear leukocytes (PMNs) recruitment, the absence of bacteremia, and the survival of mice without development of pneumonia, Dockrell and colleagues showed that alveolar macrophages have a key role in bacterial clearance from lung and apoptosis of macrophages contributes to host defense against pneumococci (Dockrell et al., 2003).

Similar results about the role of macrophages in bacterial clearance were observed in a low-dose *Klebsiella pneumoniae* infection (Broug-Holub et al., 1997). Knapp et al found that AM⁻ mice displayed a higher mortality in line with a significantly increased pulmonary proinflammatory cytokine production and elevated and prolonged PMNs accumulation in the lung as compared with AM⁺ control mice. These data suggest that AMs have a protective anti-inflammatory role by eliminating apoptotic PMNs. However, surprisingly, AM depletion did not alter bacterial clearance in AM⁻ mice (Knapp et al, 2003). The difference of bacterial clearance in two mouse models in the studies by Kanpp and Dockrell may be due to different models (fulminant vs resolving infection), differences in instillation methods (intranasal vs intratracheal) and mice with different genetic background (BALB/c vs C57BL/6 mice).

1.2.3 Polymorphonuclear leukocytes (PMNs)

PMNs play a critical role in host defense against microbial infection. The recruitment of PMNs as the key phagocytic cells involved in bacterial clearance into affected lung parenchyma is a major component of host response and appears to enhance other immune cells in the acute setting. Activated PMNs themselves are able to secrete IL-8 in an autocrine/paracrine manner to keep up local inflammatory response. Droemann et al reported that pulmonary neutrophils from patients with CAP showed a decreased rate of apoptosis and increased activation compared to peripheral neutrophils (Droemann et al., 2000). Enhanced neutrophil survival and activation in the pulmonary compartment can increase the antimicrobial phagocytic function in these patients. Subsequently, PMNs undergoing apoptosis are removed from the site of inflammation by macrophage engulfment, which is strongly associated with the resolution of pulmonary inflammation (Cox et al, 1995; Zysk et al., 2000).

1.2.4 T lymphocytes

Although the mechanisms of antigen-specific T lymphocyte response to bacterial pathogens are well illustrated in adaptive immune response, less is known about its role in innate immunity. There is increasing evidence that T lymphocytes have also an important

contribution to the early host response to pneumococci. Using major histocompatibility complex (MHC) class II-deficient mice which show CD4 T-cell-negative characteristics, Kadioglu et al have proved that knockout mice were more susceptible to pneumococcal infection at significantly earlier stage than wild-type strains. This suggests that CD4 T lymphocytes have a crucial protective role in the host response against *S. pneumoniae* (Kadioglu et al., 2004).

1.2.5 Toll-like receptors (TLRs)

The first line of defense against invading bacteria is provided by the innate immune system, which recognizes PAMPs, conserved microbial patterns shared by large groups of pathogens, but not found in higher eukaryotes (Zhang et al., 2000; Medzhitov, 2001). One of the central features of this system of microbial recognition is TLR-related signaling pathways that are critical in early host defense against the microbial invasion (Barton and Medzhitov, 2003; Iwasaki and Medzhitov, 2004). The Toll receptor was originally characterized in *Drosophila*, where it induces rapid induction of the antifungal peptide drosomycin in response to fungal infection (Lemaitre et al., 1996). At least 10 members of the TLR family (the homologues of the *Drosophila* Toll receptor) have been identified in humans until now. Different TLRs play crucial roles in the immune response by recognizing their distinct PAMPs. TLR1 recognizes triacyl lipopeptides from bacteria and mycobacteria (Takeuchi et al., 2002); TLR2 recognizes PGN, LTA and lipoproteins of Gram-positive bacteria whereas TLR4 recognizes LPS from Gram-negative bacteria. (Poltorak et al., 1998; Aliprantis et al., 1999; Schwandner et al, 1999); TLR3 has been identified as the receptor for virus double-stranded RNA (Kulka et al., 2004); TLR5 recognizes bacterial flagellin (Hayashi et al., 2001); TLR6 is shown to binds diacyl lipopeptides from mycoplasma, LTA from Gram-positive bacteria, zymosan from fungi (Schwadner et al, 1999; Ozinsky et al., 2000; Takeuchi et al., 2001); Imidazoquinolines and single-stranded RNA activate TLR7 and TLR8 (Jurk et al., 2002; Hemmi et al., 2002; Heil; 2004); CpG-containing DNA from bacteria and viruses is the ligand of TLR9 (Hemmi et al., 2000; Lund et al., 2003). However, the ligand of TLR10 has not yet been identified (Akira and Takeda, 2004). Recently, a *Toxoplasma gondii* profiling-like protein

has been defined as the first ligand for TLR11 in mice whereas there may be no functional TLR11 protein in humans (Zhang et al., 2004; Yarovinsky et al., 2005). The chromosomal locations and the ligands of the known TLR family members in humans are shown in Tab.1.

TLRs are mainly expressed on myeloid cells, such as macrophages, neutrophils, and dendritic cells. However, it has become clear that other cell types such as epithelial cells, endothelial cells express TLRs upon stimulation. This indicates that these cells are implicated in innate immunity and play a role in host defense against microorganisms to different extents. Among TLR family, TLR2 and TLR4 are best documented. These two receptors are implicated in *S. pneumoniae*-associated host immune responses which are elucidated as below.

1.2.6 TLR2 and S. pneumoniae

TLR2 was reported to form a heterophilic dimer with TLR1 or TLR6. Functional TLR2 is expressed in monocytes/macrophages, alveolar epithelial cells and lymphoid tissue (Droemann et al., 2003; Armstrong et al., 2004; Blasi et al., 2005). Some authors have pointed out that TLR2 is the key pattern recognition receptor (PRR) in the immune response to Gram-positive bacteria and mycobacteria (Takeuchi et al., 1999; Schwandner et al., 1999; Takeuchi et al., 2000a). Moreover, TLR2 appears to induce cellular activation by atypical LPS from *Leptospira interrogans* and *Porphyromonas gingivalis* whose structures are different from LPS from enterobacteria such as *Escherichia coli* (Tabeta et al., 2000; Werts et al., 2001).

Some studies have attributed an important role to TLR2 in activating inflammatory response in immune cells upon stimulation with components of Gram-positive bacteria including *S. pneumoniae*. Schwandner et al. reported that nuclear factor- κ B (NF- κ B) in human embryonic kidney 293 cells expressing TLR2, but not in cells expressing TLR1 or TLR4, was activated by whole Gram-positive bacteria, PGN, and LTA (Schwandner et al., 1999). Similarly, the association of TLR2 gene expression in human HL60 cells and mouse

Tab. 1: Human TLR family ligands (Modification from Qureshi and Medzhitov, 2003; Akira and Takeda, 2004. ND: Non-determined)

Chromosomal location		Ligands	Origin
TLR1	4p14	Triacyl lipopeptides	Bacteria, mycobacteria
		Soluble factors	<i>Neisseria meningitides</i>
TLR2	4q32	Lipoprotein/lipopeptides	A variety of pathogens
		Peptidoglycan	Gram-positive bacteria
		Lipoteichoic acid	Gram-positive bacteria
		Lipoarabinomannan	Mycobacteria
		A phenol-soluble modulin	<i>Staphylococcus epidermidis</i>
		Glycoinositolphospholipids	<i>Trypanosoma Cruzi</i>
		Glycolipids	<i>Treponema maltophilum</i>
		Porins	Neisseria
		Zymosan	Fungi
		Atypical lipopolysaccharide	<i>Leptospira interrogans</i>
		Atypical lipopolysaccharide	<i>Porphyromonas gingivalis</i>
		Atypical lipopolysaccharide	<i>Helicobacter pylori</i>
		Heat shock protein 70	Host
TLR3	4q35	Double-stranded RNA	Viruses
TLR4	9q32-33	Lipopolysaccharide	Gram-negative bacteria
		Taxol	Plant
		Fusion proteins	Respiratory syncytical virus
		Envelope proteins	Mouse mammary tumor virus
		Envelope proteins	Moloney murine leukemia virus
		Heat shock protein 60	<i>Chlamydia pneumoniae</i>
		Heat shock protein 60	Host
		Heat shock protein 70	Host
		Extra domain A of fibronectin	Host
		Oligosaccharides of hyaluronic acid	Host
		Polysaccharide fragments of heparan sulfate	Host
		Fibrinogen	Host
		Collectin surfactant protein-A	Host
TLR5	1q41-42	Flagellin	Bacteria
TLR6	4p14	Diacyl lipopeptides	Mycoplasma
TLR7	Xp22.3	Imidazoquinoline	Synthetic compounds
		Loxoribine	Synthetic compounds
		Bropirimine	Synthetic compounds
		Single-stranded RNA	Viruses
TLR8	Xp22	Imidazoquinoline	Synthetic compounds
		Single-stranded RNA	Viruses
TLR9	3p21.3	CpG-containing DNA	Bacteria
TLR10	ND	ND	May interact with TLR2

RAW264.7 cells with NF- κ B activation in response to PGN was observed (Liu et al., 2001). In addition, the activation of Chinese hamster ovary fibroblast cells expressing human TLR2 but not TLR4 was induced by heat-killed *S. pneumoniae* (Yoshimura et al., 1999). A recent report described that isolated AMs from TLR2^{-/-} mice failed to release TNF- α and keratinocyte chemoattractant (murine analogues of IL-8) upon stimulation with heat-killed *S. pneumoniae* compared to wild-type AMs. Therefore, TLR2 seems indispensable for alveolar macrophage responsiveness towards pneumococci and plays an important role in the induction of lung inflammatory response. These observations are in line with studies of Koedel and Schroder who also found a prominent role of TLR2 for pneumococci-related cell activation (Koedel et al., 2003; Schroder et al., 2003).

In addition, activation of TLR appears to be directly involved in induction of antimicrobial activity *in vitro*. The evidence demonstrates that TLR2 is directly involved in bacterial killing by monocytes/macrophages (Thoma-Uszynski et al., 2001). But some conflicting results about bacterial clearance still have been reported. Data from a murine *S. pneumoniae* meningitis model demonstrated that TLR2^{-/-} mice had higher bacterial loads in brain and a reduced survival period than wild-type mice, suggesting TLR2 have a role in pneumococcal clearance at least in brain (Echchannaoui et al., 2002). However, TLR2^{-/-} mice intranasally inoculated with *S. pneumoniae* at doses varying from non-lethal to lethal displayed an unaltered antibacterial defense, indicating TLR2 seems not to contribute to bacterial clearance and other PRRs likely are involved in the innate immune response to pneumococcal infection in this model (Knapp et al., 2004). Given the other factors involved in the innate immune response against *S. pneumoniae*, such as natural antibodies and complement, these mediators are likely candidates to compensate for the lack of TLR2 (Mold et al., 2002).

The activation of TLR2 which links innate immunity and adaptive immunity leads not only to the induction of inflammatory responses but also to the development of antigen-specific adaptive immune response. Activation of TLR2 by its synthetic ligand Pam3Cys was

reported to induce the expression of Th2-associated effector molecules (Redecke et al., 2004). Khan et al suggested that TLR2 has a role in shaping a type 1 IgG humoral immune response to pneumococci, although the exact underlying mechanisms need to be further investigated (Khan et al., 2005).

1.2.7 TLR4 and S. pneumoniae

TLR4 is required for the recognition of LPS from Gram-negative bacteria and the mutations of TLR4 gene generate two mouse strains (C3H/HeJ and C57BL10/ScCr) which are hyporesponsive to LPS (Poltorak et al., 1998; Qureshi et al., 1999). TLR4^{-/-} mice are also insensitive to LPS, confirming that TLR4 is an essential receptor for the recognition of LPS (Hoshino et al., 1999). The response to LPS is initiated upon its interaction with TLR4 in conjunction with the accessory proteins MD-2 and soluble or membrane-bound CD14.

Some investigations have shown that TLR4 still has a limited role in the innate immune response to *S. pneumoniae*. An *in vitro* study showed that TLR4-deficient macrophages lacked the response to Gram-positive bacterial cell wall components (Takeuchi et al., 1999), although this result was suspected by some authors because the LTA preparations used in earlier studies were easily contaminated with endotoxin (Gao et al., 2001; Morath et al., 2002). Indeed, an important role for TLR4 recognizing pneumolysin in the innate immune response to *S. pneumoniae* in the nasopharynx was reported by Malley and colleagues. They found that pneumolysin induced the inflammatory response of macrophages via TLR4. Furthermore, mutant mice lacking functional TLR4 were significantly more susceptible to lethal pneumococcal infection and displayed decreased survival after the challenge with wild-type pneumococci (Malley et al., 2003). Another investigation demonstrated that TLR4 mutant mice showed a reduced survival only after infection with low-level pneumococcal doses, which was associated with a higher bacterial burden in the lungs 48 h postinfection. But TLR4 mutant mice showed an unaltered inflammatory response in a model of pneumococcal pneumonia (Branger et al., 2004). Taken together, these findings suggest that the innate immune response to pneumococci is partly mediated by TLR4 (Kadioglu and Andrew, 2004).

1.2.8 TLR signaling pathways

The molecular mechanisms by which TLRs induce gene expression are being elucidated by using gene knockout mice. Increasing evidence indicates that there are myeloid differentiation marker 88 (MyD88)-dependent and MyD88-independent signaling pathways involved in TLR signal cascades.

MyD88, consisting of a N-terminal death domain and a C-terminal (Toll/IL-1 receptor) TIR domain, is a common adaptor to TLR family given the fact that most TLR ligands cannot induce inflammatory cytokine production in MyD88-deficient mice (Kawai et al., 1999; Hacker et al., 2000; Schnare et al., 2000; Takeuchi et al., 2000b; Hayashi et al., 2001; Hemmi et al., 2002). The MyD88-dependent pathway is analogous to IL-1 receptor signaling. Upon stimulation, MyD88 recruits IL-1 receptor-associated kinase (IRAK)-4 to the TLRs and initiates IRAK-4-mediated phosphorylation of IRAK-1. Then activated IRAK-1 associates with tumor necrosis factor receptor-associated factor (TRAF) 6 which leads to the activation of a mitogen-activated protein kinase kinase kinase (MKKK) named transforming growth factor β -activated kinase (TAK)-1. TAK-1 activates two distinct signaling pathways. One pathway activates the I κ B kinase (IKK) complex consisting of IKK α , IKK β , and IKK γ . The IKK complex phosphorylates and degrades I κ B, inducing nuclear translocation of NF- κ B which subsequently leads to the expression of inflammatory cytokines (Takeda and Akira, 2005). The other results in the activation of activator protein (AP)-1 transcription factors through the signaling of mitogen-activated protein kinase kinases (MKKs) and mitogen-activated protein kinases (MAPKs) including p38, p44/42 (extracellular signal-regulated kinase, ERK), and c-Jun N-terminal kinase (JNK). In addition, TIR domain-containing adaptor protein (TIRAP)/MyD88-adaptor-like (Mal) functions downstream of TLR2 and TLR4, but is not involved in other TLR signalings (Yamamoto et al., 2002a; Horng et al., 2002).

The investigation from MyD88-deficient mice showed that the MyD88-independent pathway is required for TLR3 and TLR4 to induce interferon (IFN)- β . Recent studies demonstrated that TIR domain-containing adaptor-inducing IFN- β (TRIF), also known as

TIR domain-containing adaptor molecule (TICAM)-1, appears to be responsible for inducing IFN- α/β genes by the activation of interferon regulatory factor (IRF) 3 (Kawai et al., 2001; Yamamoto et al., 2002b; Oshiumi et al., 2003), whereas two noncanonical IKKs: TBK1 and IKK ϵ /IKK ι have been revealed to function downstream of TRIF and upstream of IRF3 and NF- κ B (Sharma et al., 2003; Sankar et al., 2005). The divergences among individual TLR signaling pathways cannot be well explained by the known signaling components. Additional signaling mechanisms have yet to be unraveled (Barton and Medzhitov, 2003).

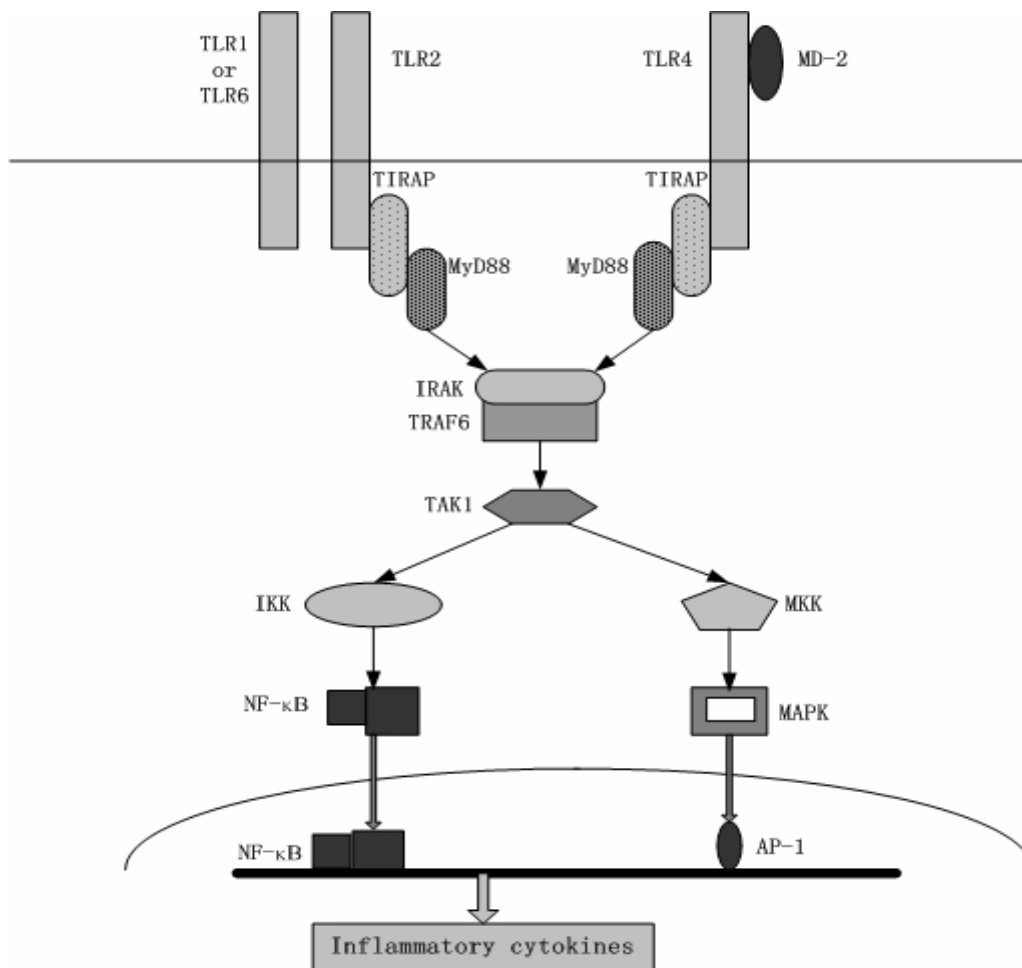


Fig. 2: The shared signaling pathways via TLR2 and TLR4 are shown. The main TLR2 and TLR4 signalings are transduced via IL-1 receptor signaling complex, which includes two essential adaptor proteins, MyD88 and TRAF6, then culminates in the activation of NF- κ B transcription factors, as well as MAPKs. This signal transduction pathway further coordinates the induction of multiple genes encoding inflammatory mediators.

1.2.9 P38 MAPK and inflammation

The MAPKs are proline-directed serine and threonine protein kinases that are usually activated by phosphorylation of threonine and tyrosine residues by MKKs (Davis 1993; Cobb and Goldsmith, 1995; Ono and Han, 2000). The differences among three types of MAPKs are their intervening amino acids: glycine in p38, glutamic acid in p44/42, and proline in JNK (Saklatvala, 2004). As central signal pathways in many host cells, MAPKs are involved in inflammatory cytokine expression, cytoskeletal reorganization, and stress reaction in addition to the mitogenic response to growth factors (Robison and Cobb, 1997). Previous studies have demonstrated the essential role of MAPK activation in proinflammatory cytokine responses to a number of microbial stimuli and their cell components such as group B streptococcus, mycoplasma membrane lipoproteins, staphylococcal peptidoglycan and LPS from Gram-negative bacteria (Dziarski et al., 1996; Sweet and Hune, 1996; Garcia et al., 1998; Rawadi et al., 1998; Mancuso et al., 2002).

To date, four p38 MAPKs have been published. P38 α was first isolated as 38-kDa protein which mediates the immune response to LPS stimulation (Han et al., 1993; Han et al., 1994). Three other members, p38 β , p38 γ , and p38 δ , were subsequently found in mammals. Sequence analysis showed that each p38 isoform has more than 60 % homology, but only 40 %-50 % identity to the other MAPK members (Ono and Han, 2000). The p38 α , p38 β and p38 δ are ubiquitously expressed whereas p38 γ is predominantly expressed in skeletal muscle and involved in muscle differentiation. An important function of p38 α (and probably p38 β) is to regulate the expression of inflammatory response genes, but the exact role of p38 γ and p38 δ in regulation of inflammation is unclear (Saklatvala, 2004). There is much evidence to support an essential role of p38 α (or simply p38) in inflammation. P38 signal pathway regulates the production of proinflammatory cytokines such as TNF- α , IL-6, and IL-1 β (Perregaux et al., 1995) and chemokines like IL-8, mediates the expression of intracellular enzymes such as cyclooxygenase (Cox)-2 and inducible nitric oxide synthase (iNOS) (Guan et al., 1998; Rupp et al., 2004; N'Guessan et al., 2006), and modulates the induction of adherent proteins including vascular cell adhesion molecule (VCAM)-1 and other inflammatory-related molecules (Pietersma et al., 1997). As p38 MAPK is implicated

in the production of key inflammatory mediators, p38 and the major components of p38 pathway can become obvious therapeutic targets for inflammatory diseases. The widely used p38 inhibitor, SB203580, only blocks p38 α and p38 β and competes for the adenosine triphosphate (ATP)-binding pocket (Saklatvala, 2004). *In vivo* animal studies demonstrated that inhibition of p38 by SB203580 can decrease mortality in a murine model of endotoxin-induced shock and has an anti-inflammatory effect in mouse and rat models of rheumatoid arthritis (Badger et al., 1996).

It should be noted that the activation of p38 MAPK and its regulation of inflammatory response depend on cell type and stimulus. Emphasis in further study should be placed on how p38 functions in a specific cell type upon a specific stimulus. Little is known of the role of p38 pathways in *S. pneumoniae*-induced cell and tissue responses. Recently, Schmeck et al reported that pneumococci induced IL-8 and granulocyte-macrophage colony-stimulating factor (GM-CSF) gene expression in human bronchial epithelial cells (BEAS-2B) via p38 MAPK signaling pathway and activated NF- κ B-dependent gene transcription in a p38 MAPK-dependent manner in HEK293 cells. Further experiments showed that blockade of p38 MAPK did not affect inducible nuclear translocation and recruitment of NF- κ B/RelA to the IL-8 promoter but did reduce the level of phosphorylated p65/RelA (serine 536) at IL-8 promoter and inhibited pneumococci-mediated recruitment of RNA polymerase II to IL-8 promoter. These data suggested that p38 MAPK plays an important role in pneumococci-induced inflammatory cytokine transcription by modulating p65 NF- κ B-mediated transactivation (Schmeck et al, 2004a). The components of signaling pathways and cross-talk between different signal molecules in the host immune response to *S. pneumoniae* are only partly understood. The critical signal molecules in the inflammatory response should be further investigated in order to modulate pneumococcal inflammation via small molecular approaches.

1.3 Aims of the current study

This study was undertaken to evaluate cellular and molecular mechanisms of host defense against *S. pneumoniae* in the human lung tissue. The specific aims of the present study were as follows:

- The establishment of cell culture models and a novel lung tissue model of acute *S. pneumoniae* infection for investigating interactions between pathogens and pulmonary host cells on the cell and tissue levels.

- Which pulmonary cell types are implicated as important host cells for acute *S. pneumoniae* infection?

- The role of alveolar macrophages in the inflammatory response was evaluated in human lung tissue depleted of macrophages by Clodronate/liposomes.

- The roles of TLR2, 4 and MAPK signalings in the inflammatory response of immune cells and human lung tissue stimulated with *S. pneumoniae* were investigated.

2. Materials and Methods

2.1 Materials

2.1.1 Chemicals and Kits

All chemicals and reagents were used in analytic degree of purity.

Acetic acid	Merck, Darmstadt, Germany
Acetone.....	Merck, Darmstadt, Germany
Acrylamide (30 %)/Bisacrylamid (0.8 %).....	Bio-Rad, Munich, Germany
Agarose.....	Invitrogen, Karlsruhe, Germany
Ammonium persulfate (APS).....	Sigma, Steinheim, Germany
Amphotericin-B.....	PAA, Pasching, Austria
Bovine serum albumin (BSA).....	Roth, Karlsruhe, Germany
Bromophenol blue.....	Bio-Rad, Muenichen, Germany
Calcium chloride.. ..	Sigma, Steinheim, Germany
Diethylpyrocarbonate (DEPC)	Sigma, Steinheim, Germany
Dithiothreitol	Sigma, Steinheim, Germany
EDTA	Merck, Darmstadt, Germany
Ethanol.....	Merck, Darmstadt, Germany
Ethidium bromide.....	Sigma, Steinheim, Germany
Faramount mounting medium.....	Dako, Hamburg, Germany
Formalin.....	Sigma, Steinheim, Germany
Formamide.....	Carl Roth, Karlsruhe, Germany
Fetal calf serum (FCS).....	Biochrom, Berlin, Germany
Gentamicin.....	Sigma, Steinheim, Germany
Giemsa.....	Merck, Darmstadt, Germany
Glycerol	Sigma, Steinheim, Germany
Glycine.....	Sigma, Steinheim, Germany
Hematoxylin.....	Chroma, Munich, Germany

HOPE-solution.....	DCS, Hamburg, Germany
Hydrochloric acid (HCl).....	Merck, Darmstadt, Germany
Hydrogen peroxide (H ₂ O ₂).....	R&D, Minneapolis, USA
Isopropanol.....	Merck, Darmstadt, Germany
L-Glutamin	PAA, Pasching, Austria
Lymphocyte separation medium.....	PAA, Pasching, Austria
Magnesium Chloride (MgCl ₂).....	Merck, Darmstadt, Germany
May-Grünwald.....	Merck, Darmstadt, Germany
Methanol.....	Merck, Darmstadt, Germany
Milk powder (non-fat).....	Frema, Lueneburg, Germany
New-fuchsin.....	Sigma, Steinheim, Germany
Nonessential amino acid (NEAA)	PAA, Pasching, Austria
Paraformaldehyd.....	Merck, Darmstadt, Germany
Polyvinyl Alcohol (PVA).....	Merck, Darmstadt, Germany
Potassium chloride (KCl)	Merck, Darmstadt, Germany
Potassium dihydrogen phosphate (KH ₂ PO ₄).....	Merck, Darmstadt, Germany
RPMI 1640	Biochrom, Berlin, Germany
Sodium bicarbonate (NaHCO ₃).....	Merck, Darmstadt, Germany
Sodium chlorid (NaCl).....	Merck, Darmstadt, Germany
Sodium citrate.....	Merck, Darmstadt, Germany
Sodium dodecyl sulphate (SDS).....	Boi-Rad, Munich, Germany
Sodium hydrogen phosphate (Na ₂ HPO ₄).....	Merck, Darmstadt, Germany
Sodium hydroxide (NaOH)	Merck, Darmstadt, Germany
Sucrose.....	Merck, Darmstadt, Germany
Sulphuric acid (H ₂ SO ₄).....	Merck, Darmstadt, Germany
Tetramethylbenzidine.....	R&D, Minneapolis, USA
Tetramethylethylenediamined (TEMED).....	Sigma, Steinheim, Germany
Tris-aminomethan.....	Bio-Rad, Munich, Germany
Tris-chlorine (Tris-Cl).....	Sigma, Steinheim, Germany
Trypan blue.....	Sigma, Steinheim, Germany

Trypsin/EDTA.....	PAA, Pasching, Austria
Tween-20	Merck, Darmstadt, Germany
Yeast tRNA.....	Roche, Mannheim, Germany
Clinical Chemistry LDH kit.....	Abbott, Wiesbaden, Germany
ECL Chemiluminescent Substrate System.....	Amersham, Freiburg, Germany
ELISA Kit.....	R&D, Minneapolis, USA
First-Strand PCR kit	Roche, Mannheim, Germany
LightCycler Detection System	Roche, Mannheim, Germany
NucleoSpin RNA II kit.....	Macherey-Nagel, Dueren, Germany
TMB Liquid Substrate System.....	Sigma, Steinheim, Germany

2.1.2 Solutions and buffers

Running gel buffer: 1.5M Tris-Cl (PH 8.8)

Stacking gel buffer: 0.5M Tris-Cl (PH 6.8)

10 % APS: 0.1g APS in 1mL dH₂O

10 % SDS: 0.1g SDS in 1mL dH₂O

5 x SDS-PAGE running buffer: 0.125 M Tris-HCl, 0.96 M glycine, 0.5 % SDS

Protein lysis buffer: 4 % w/v SDS, 10 mM dithiothreitol, 20 % v/v glycerol, 0.125 M Tris-Cl (pH 7.8), 0.4 % bromophenol blue

Blotting buffer: 25 mM Tris-aminomethan, 193 mM glycine, 20 % methanol

10 x TBS: 80 g NaCl, 24.2 g Tris-aminomethan in 1 L dH₂O (pH 7.4)

1 x T-TBS: 100 ml 10 x TBS, 1 mL Tween-20 in 1L dH₂O

Blocking buffer for immunoblot: 5 g non-fat dried milk in 100 mL T-TBS

1 x PBS for ELISA: 137 mM NaCl, 2.7 mM KCl, 8.1 mM Na₂HPO₄, 1.5 mM KH₂PO₄, pH 7.2-7.4

Wash buffer: 0.05% Tween 20 in 1 x PBS, pH 7.2-7.4

Block buffer for ELISA: 1% BSA in 1 x PBS, 0.2 µm filtered

Diluent reagent: 0.1% BSA, 0.05% Tween 20 in 1 x TBS (20 mM Trizma-aminomethan, 150 mM NaCl), pH 7.2-7.4, 0.2 µm filtered (for IL-8); 1% BSA in 1 x PBS, 0.2 µm filtered

(for IL-6 and TNF- α)

Substrate solution: 1:1 mixture of Color Reagent A (H₂O₂) and Color Reagent B (Tetramethylbenzidine)

Stop solution: 1M H₂SO₄

0.2 % DEPC: 0.2 mL DEPC in 100 mL dH₂O

20 x Standard saline citrate (SSC): 0.3 M Sodium citrate; 3 M NaCl

2.1.3 Bacterial strain and cell line

An encapsulated *S. pneumoniae* strain serotype 3 is obtained from American Type Culture Collection (ATCC 6303, Rockville, MD, USA).

Alveolar epithelial cell line A549 is obtained from European Collection of Cell Cultures.

2.1.4 Antibodies, inhibitors and their characteristics

Anti-phospho-p38 MAPK (rabbit monoclonal antibody) is from Cell Signaling Technology, Beverly, USA and used at 1:1000 dilution.

Anti-phospho-p44/42 MAPK (rabbit monoclonal antibody) is from Cell Signaling Technology, Beverly, USA and used at 1:1000 dilution.

Anti- β -actin (rabbit monoclonal antibody) is from Cell Signaling Technology, Beverly, USA and used at 1:2000 dilution.

Horseradish peroxidase (HRP)-conjugated goat anti-rabbit IgG antibody is from Cell Signaling Technology, Beverly, USA and used at 1:4000 dilution.

Anti-TLR2 monoclonal antibody (functional grade) is from eBioscience, San Diego, USA and used at 5 μ g/mL.

Anti-TLR4 monoclonal antibody (functional grade) is from eBioscience, San Diego, USA and used at 5 μ g/mL.

Alkaline phosphatase-conjugated anti-digoxigenin antibody is from Roche, Mannheim, Germany.

SB203580 (p38 MAPK inhibitor) is from Calbiochem, CA, USA and used at 20 μ M.

UO126 (p44/42 MAPK inhibitor) is from Calbiochem, CA, USA and used at 10 μ M.

2.1.5 Markers for nucleic acids and proteins

DNA marker:

1 Kb ladder.....Gibco, Karlsruhe, Germany

Protein marker:

MultiMark Standard.....Biolabs, Ipswich, USA

2.1.6 Instruments and equipments

Aeroset chemistry analyzer.....Abbott, Wiesbaden, Germany

Cell house 200.....Heto, Allerod, Danmark

Cell counter AC-8.....Assistant, Frankfurt, Germany

Centrifuge Rotina 35.....Hettich, Tuttlingen, Germany

Cytocentrifuge Cytospin II.....Shandon, Frankfurt, Germany

Eppendorf pipette.....Eppendorf, Hamburg, Germany

LightCycler.....Roche, Mannheim, Germany

Light microscope.....Carl Zeiss, Frankfurt, Germany

Mini-Protean II Electrophoresis Cell.....Bio-Rad, Munich, Germany

Photometer-340.....SLT, Salzburg, Austria

Plate shaker.....Heidolph, Schwabach, Germany

TissueLyser.....Qiagen, Hilden, Germany

Weighter AE 200.....Mettler-Toledo, Giessen, Germany

Cell culture flask.....Greiner, Frickenhausen, Germany

Cell scraper.....Greiner, Frickenhausen, Germany

Combitip Plus.....Eppendorf, Hamburg, Germany

ELISA plate.....Nalge-Nunc, Hereford, UK

Microlance.....Becton Dickson, Heidelberg, Germany

Nitrocellulose membrane.....Sartorius, Goettingen, Germany

Nylon membranes.....Roche, Mannheim, Germany

Sheep blood agar plate.....Biomerieux, Nuertingen, Germany

Superfrost⁺ microscope slide.....Menzel-Gläser, Braunschweig, Germany

Syringe filter.....	Nalge, Rochester, USA
Syringe.....	Becton Dickson, Heidelberg, Germany
24-well tissue culture plate.....	Biochrom, Berlin, Germany
48-well cell culture plate.....	Greiner, Frickenhausen, Germany

2.2 Subjects and Methods

2.2.1 Patients

The study population consisted of 26 patients. Bronchopulmonary infection was excluded by clinical examination, systemic inflammatory markers and chest x-ray. The demographic data of the study population are summarized in Tab. 2. The protocol was approved by the Ethical Committee of University of Luebeck, Germany.

Tab. 2: Demographic data of the study population

Patients	n = 26
Age (y)	64.0 ± 1.9
Gender	Male: 12 (46 %) Female: 14 (54 %)
FEV ₁ /IVC (%)	71.1±3.0
FEV ₁ % predicted	77.5±3.8
Underlying diseases	Lung cancer: 20 Metastases from extrapulmonary tumor: 5 Parasite (Cystic echinococcosis): 1

2.2.2 Culture of *S. pneumoniae*

The encapsulated *S. pneumoniae* strain serotype 3 was obtained from American Type Culture Collection (ATCC 6303; Rockville, MD, USA). Pneumococci were grown on sheep blood agar plates at 37 °C and 5% CO₂. Bacteria at midlogarithmic phase were used for stimulation.

2.2.3 Establishment of a new model of acute *S. pneumoniae* infection (ASIM)

Vital lung specimens were obtained from pulmonary resections of the patients mentioned above without clinical signs of acute respiratory infection. The normal lung specimens at least 5 cm away from pulmonary suspected nodules were used in the experiments. Lung tissue (1 cm³ size; 0.4-0.5g) was cultured in 800 µL of endotoxin-free RPMI1640 medium (Biochrom, Berlin, Germany) in 24-well flat-bottom, tissue culture plates (Biochrom). 50 µL of pneumococci were added into culture medium to a final concentration of 10⁷ CFU/mL. Preliminary experiments using increasing pneumococcal concentrations demonstrated a dose-dependent increase in inflammatory response (IL-8 release from ASIM 24 h postinfection: 179 ng/mL [10⁶ CFU/mL] vs 292 ng/mL [10⁷ CFU/mL] vs 353 ng/mL [10⁸ CFU/mL]); representative data from three independent experiments). After 4 h and 24 h stimulation, supernatants were harvested and stored at -70 °C, and lung specimens were fixed at 4 °C in the newly developed HEPES-Glutamic acid buffer mediated Organic solvent Protection Effect (HOPE)-solution (Goldmann et al., 2002). Schematic illustration of this *in vitro* lung tissue model infected with pneumococci is shown as Fig. 3.

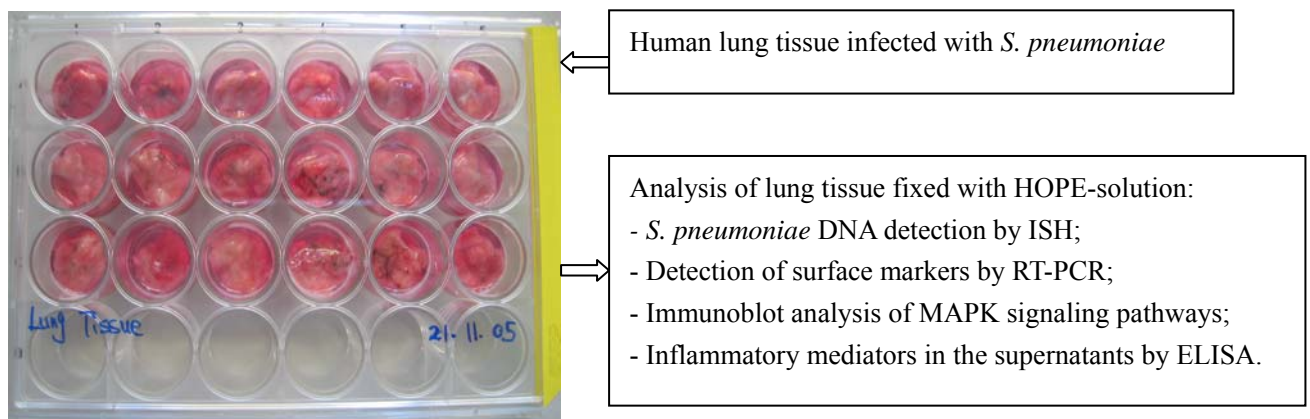


Fig. 3: A novel model of acute *S. pneumoniae* infection in human lung tissue

The viability of lung cells in the ASIM was evaluated by the release of lactate

dehydrogenase (LDH), an indicator of nonspecific necrotic cell death, into supernatants using AEROSSET System (Abbott, Wiesbaden, Germany). The LDH level in RPMI 1640 was used as blank control whereas maximum LDH release from a piece of lung tissue (1cm³) was performed by lung homogenization. The level of specific LDH was calculated by using the following formula: percentage of specific LDH release = ([experimental release - blank control] / [maximum release - blank control]). The relative LDH levels (expressed as the percentage of LDH release) demonstrated that the lung cells showed time-dependent necrosis in tissue culture whereas *S. pneumoniae* (10⁷CFU/mL) stimulation aggravated cell necrosis and LDH release in the time frame tested (Fig. 4). These results suggest that vital lung specimens could be infected with *S. pneumoniae* for 48 h in our ASIM.

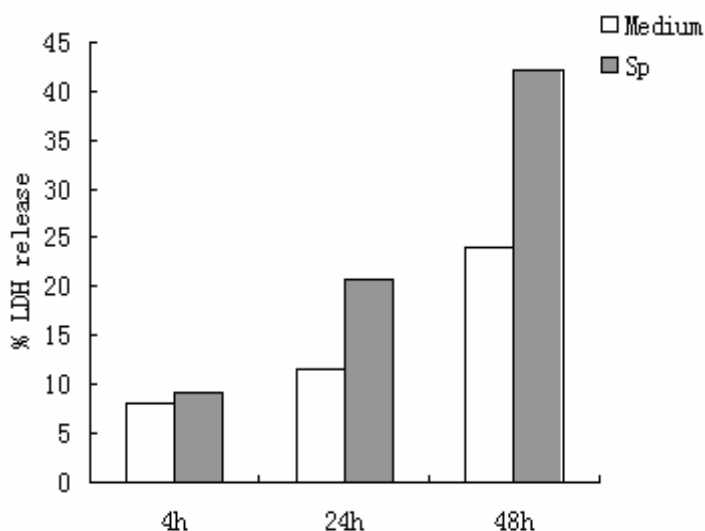


Fig. 4: Time-dependent necrosis of lung cells in the ASIM. LDH release (expressed as the percentage of LDH release) demonstrated that *S. pneumoniae* (10⁷CFU/mL) infection aggravated cell necrosis and LDH release compared to non-infected lung tissue within 48 h. Representative data from three independent experiments are shown. Sp: *S. pneumoniae*.

2.2.4 Cell culture and stimulation

2.2.4.1 An epithelial cell line: A549 cell

A549 cells were grown in 175 cm² polystyrene flasks (Greiner, Frickenhausen, Germany) with RPMI 1640 supplemented with 10 % heat-inactivated fetal calf serum (FCS), 2 mM

L-glutamine, 1 x nonessential amino acid (NEAA), 10 mg/L gentamicin and 2 mg/L amphotericin-B. Cells were maintained under an atmosphere of 5 % CO₂ at 37 °C by routine passage every 3 days. Before stimulation, A549 cells were passaged by exposure to 0.05 % trypsin plus 0.02 % EDTA into 48-well flat-bottom, cell culture plates (Greiner). Cells were seeded at 1 x 10⁵ cells per well. This produced an 80-90 % confluent monolayer after overnight incubation at 37 °C in a 5 % CO₂ humidified atmosphere.

2.2.4.2 Macrophages

Macrophages were got from bronchoalveolar lavage fluid (BALF) of 8 persons with no clinical signs of acute respiratory infections. Cells were differentiated counting a minimum of 600 cells on a cytocentrifuge smear (Cytospin II, Shandon, Frankfurt) stained with May-Grünwald/Giemsa solution, showing over 92 % of macrophages and less than 3 % of neutrophils. Gram stain was performed, and culture for bacteria and yeast was routinely done which did not show significant growth of pathogenic microorganisms. Macrophages were harvested after 2 h incubation at 37 °C and 5 % CO₂ for exclusion of nonadherent cells.

2.2.4.3 Blood leukocytes

Blood monocytes and PMNs were isolated from blood buffy coats of healthy donators as described before (Macey et al., 1995). 30 mL of blood, diluted 1:6 pyrogen-free PBS, was layered over 15 mL of lymphocyte separation medium (PAA, Pasching, Austria) and centrifuged at 1600 rpm for 20 min at room temperature. Mononuclear cells at the upper interface were collected and incubated at 37 °C and 5 % CO₂ for 2 h for exclusion of lymphocytes. The pellets containing PMNs were collected into a cylinder filled up with polyvinyl alcohol (PVA) to a total volume of 50 mL, and mixed well with a pipette. The supernatant was harvested from the cylinder after 20 min and centrifuged at 1600 rpm for 5 min at room temperature. The pellets were collected and suspended gently with 5ml of dH₂O for 45 s, then mixed with 5mL of pre-warmed 2 x PBS. PMNs were obtained after centrifuging at 1600 rpm for 5 min at room temperature. Determined by May-Grünwald/Giemsa stain, the purity of monocytes and PMNs obtained above is more than 90% and 92%, respectively.

2.2.4.4 Cell stimulation

A549 cells (5×10^5 cells/mL), PMNs (2.5×10^6 cells/mL) and monocytes/macrophages (1×10^6 cells/mL) were infected with *S. pneumoniae* (10 and/or 100 CFU/cell) and growth medium was replaced by an antibiotic-free medium (RPMI 1640 plus 10 % FCS). Inhibition experiments were carried out by 1 h pretreatment with the p38 MAPK inhibitor SB 203580 (20 μ M; Calbiochem, CA, USA) and p44/42 MAPK inhibitor UO126 (10 μ M, Calbiochem) before stimulation.

2.2.5 In situ hybridization (ISH)

After overnight fixation at 4 °C in the HOPE-solution, sections of 4 μ m were cut, mounted on Superfrost⁺ slides and deparaffinized with isopropanol and 70 % acetone for 1 h at 4 °C. Then lung specimens were dehydrated with acetone for 30 min for 6 times at 4 °C, followed by two incubations in isopropanol (10 min at 60 °C, 2 min at 60 °C) and air dried. Rehydration was achieved by incubation in 70 % (v/v) acetone for 10 min at 4 °C, diethylpyrocarbonate (DEPC)-treated water for 10 min at 4 °C, and slides were air dried. An ISH probe targeting *S. pneumoniae* was kindly provided by Dr. Goldmann (Research Center Borstel, Germany), and hybridization was performed overnight at 46°C in moist chambers. Hybridization solution was composed of 2 ng/mL fresh denatured probe, 250 g/mL yeast tRNA, 0.1% SDS, and 50 % formamide in PBS. Slides were washed by the following steps: 2-SSC twice for 10 min at ambient temperature, then 0.2-SSC twice for 30 min at 50 °C. The specimens were then incubated with an alkaline phosphatase-conjugated anti-digoxigenin antibody (Roche, Mannheim, Germany) using new fuchsin as a chromogen. Lung specimens were then counterstained with hematoxylin. Enumeration of the infection rates of lung cells (infected cells/ total cells x 100 %) was done by two independent investigators.

2.2.6 Reverse transcription polymerase chain reaction (RT-PCR)

Total RNA was extracted from homogenised lung tissues using the NucleoSpin RNA II kit (Macherey-Nagel, Dueren, Germany) and reverse transcribed into cDNA using

First-Strand cDNA Synthesis Kit (Roche) for RT-PCR. PCR amplification was performed using the LightCycler® Detection System (Roche Molecular Biochemicals). Semi-quantification of TLR2 mRNA (forward: CCA TTC CCC AGC GCT TT; reverse: CCG CTG AGC CTC GTC CAT) and TLR4 mRNA (forward: AAG AAA TTA GGC TTC ATA AGC T; reverse: ACC CTT TCA ATA GTC ACA CTC A) expression was performed against the endogenous control 18S rRNA gene (forward: TCA AGA ACG AAA GTC GGA GG; reverse: GGA CAT CTA AGG GCA TCA CA). PCR was run using the following protocol: 95 °C for 10 min, 40 cycles of 95 °C for 10 s, 60 °C for 5 s, and 72 °C for 10 s, yielding the product sizes of 200 bp (TLR2), 200 bp (TLR4), and 300 bp (18S rRNA) respectively. In a dissociation protocol single peaks were confirmed in each of the amplified sequences to exclude non-specific amplification. For the relative quantification crossing point (cp) values of targets were expressed as $2^{-\Delta\Delta cp}$ (fold) as described previously (Winer et al. 1999). The PCR products were analyzed on 1.5 % agarose gels, stained with ethidium bromide, and subsequently visualized. To assure the identity of the PCR-amplified fragments, the size of each amplified mRNA fragment was compared with the standard 1Kb ladder.

2.2.7 Western blot assay

Lung tissues were stimulated with *S. pneumoniae* (10^7 CFU/mL) and cells including A549 cells, alveolar macrophages, and peripheral blood leukocytes were infected with *S. pneumoniae* at a bacterium-to-cell ratio of 10:1 and/or 100:1. The lung tissues were homogenized in a tissue lyser and cells were harvested by scrapers after stimulation. Lung homogenates and cell pellets were lysed in lysis buffer (125mM Tris, pH 6.8, 4 % SDS, 20 % glycerol, 100mM dithiothreitol, and 0.05 % bromophenol blue) and heated for 5 min at 95 °C. Electrophoresis was performed at 200 V for 1 h with 12 % SDS-PAGE at room temperature. Proteins were transferred to nitrocellulose membrane at 75 V for 1.5 h by wet blot at 4 °C in Mini-Protean II (Bio-Rad, Munich, Germany). The membrane was then blocked with 5 % non-fat dried milk in T-TBS for 1 h, washed three times with T-TBS and incubated with the primary antibody (p-p38, p-p44/42; Cell Signaling Technology, Beverly,

USA) at 4 °C overnight. The blots were washed three times with T-TBS and incubated for 1 h with HRP-conjugated goat-anti-rabbit IgG antibody (Cell Signaling Technology) at room temperature. Immunoreactive bands were developed using an ECL chemiluminescent substrate (Amersham, Freiburg, Germany). Autoradiography was performed with exposure times of 30 s-15 min, whichever were adequate for visualization. In all experiments, β -actin (Cell Signaling) was detected simultaneously to confirm equal protein load.

2.2.8 Macrophage depletion experiments

Clodronate/liposomes, obtained from Dr. N. van Rooijen (Vrije University, Amsterdam, Netherlands), have been reported to be successfully used in animal models for the depletion of macrophages. Preliminary experiments showed that 24 h Clodronate/liposomes coincubation resulted in over 85 % reduction of alveolar macrophages *in vitro* whereas they exhibited no significant effect on an epithelial cell line (A549 cells), proving their specificity of phagocytic cells. In addition, there is no significant difference in cytokine release from pneumococci infected tissues between medium and PBS/liposomes pretreatment (Tab. 3). Therefore, tissue pretreated with PBS/liposomes was selected as a negative control in further macrophage depletion experiments. Lung tissue (1 cm³) was incubated with 1 mL of Clodronate/liposomes-RPMI 1640 mixture (1:1; containing 2.5 mg Clodronate), PBS/liposomes-RPMI 1640 mixture (1:1) for 24 h and 48 h respectively. To enhance the interaction between alveolar macrophages and Clodronate/liposomes, part of reagents was injected into lung tissue by a microlance. After washing with RPMI 1640, lung specimens were put into the wells of 24-well culture plates (Biochrom) and incubated with pneumococcal suspensions (10⁷ CFU/mL) for further 24 h. The supernatants were collected and stored at -70° C until detected. Lung specimens were harvested and fixed at 4 °C in HOPE-solution until pathological examination.

Tab. 3 Inflammatory cytokine release from infected lung tissues pretreated with medium, PBS/liposomes and Clodronate/liposomes for 24 h (A) and 48 h (B) respectively (n=3). Pre/Sti: Pretreatment/Stimulation; PBS-lipo: PBS/liposomes; Clo-lipo: Clodronate/liposomes; Sp: *S. pneumoniae*. **p* <0.05 vs medium/Sp treated tissue.

A. 24 h pretreatment

Pre/Sti	IL-8 (ng/mL)	TNF- α (pg/mL)	IL-6 (ng/mL)
Medium/Sp	416 \pm 43	526 \pm 152	1470 \pm 766
PBS-lipo/Sp	443 \pm 259	722 \pm 115	1282 \pm 817
Clo-lipo/Sp	541 \pm 63	167 \pm 110*	517 \pm 48

B. 48 h pretreatment

Pre/Sti	IL-8 (ng/mL)	TNF- α (pg/mL)	IL-6 (ng/mL)
Medium/Sp	325 \pm 81	597 \pm 278	1919 \pm 1099
PBS-lipo/Sp	507 \pm 174	615 \pm 184	2362 \pm 1413
Clo-lipo/Sp	190 \pm 24	<16*	285 \pm 96

2.2.9 Inhibition experiments in the ASIM

Lung specimens (1 cm³ size) were pretreated for 1 h with the functional TLR antibodies (anti-TLR2: 5 μ g/mL, anti-TLR4: 5 μ g/mL; eBioscience, San Diego, USA) and MAPK inhibitors (SB203580: 20 μ M, UO126: 10 μ M; Calbiochem), then stimulated with *S. pneumoniae* (10⁷ CFU/mL). The working concentrations of functional TLR2, 4 antibodies and MAPK inhibitors adopted in this experiment have been proved to efficiently block TLRs or MAPK signalings respectively in our previous work and other studies (Lien et al., 1999; Rupp et al., 2004; Droemann et al., unpublished). The supernatants were harvested 4 h and 24 h after pneumococcal stimulation, and stored at -70 ° C until ELISA.

2.2.10 Enzyme-linked immunosorbent assay (ELISA)

For the quantitative determination of IL-8, IL-6 and TNF-a, we performed ELISA assays as described by the manufacturer (R&D Systems, Minneapolis, USA). The detection limits

were 1.2 pg/mL for IL-8, 9.4 pg/mL for IL-6, 15.6 pg/mL for TNF- α . Assay procedure was briefly as follows: Dilute the capture antibody to the working concentration in PBS without carrier protein. Immediately coat a 96-well microplate with 100 μ L of the diluted capture antibody per well. Seal the plate and incubate overnight at room temperature. Aspirate each well and wash with wash buffer (300 μ L) for three times. After the last wash, remove any remaining wash buffer by inverting the plate and blotting it against clean paper towels. Block plates by adding 300 μ L of block buffer to each well. Incubate at room temperature for a minimum of 1 h, followed by the aspiration/washing step. Add 100 μ L of sample or standards in diluent reagent per well, and incubate 2 h at room temperature, followed by the aspiration/washing step. Add 100 μ L of the detection antibody, diluted in diluent reagent, to each well and incubate 2 h at room temperature, followed by the aspiration/washing step. Add 100 μ L of the working dilution of Streptavidin-HRP to each well and incubate for 20 min in dark at room temperature, followed by the aspiration/washing step. Add 100 μ L of substrate solution to each well and incubate for 20 min in dark at room temperature. Add 50 μ l of stop solution (1 M H₂SO₄) to each well, followed by tapping gently the plate to ensure thorough mixing. Determine the optical density of each well immediately, using a microplate reader set to 450 nm (Photometer-340, SLT, Salzburg, Austria).

2.2.11 Statistical analysis

Data are presented as the mean \pm SEM. For independent samples, One-way ANOVA with Posthoc tests by LSD was used for statistical analysis of the differences between groups. A *p* value <0.05 was considered statistically significant. Calculations were carried out with SPSS for Windows software program 11.5.

3. Results

3.1 Detection of *S. pneumoniae* in the ASIM

ISH analysis showed that *S. pneumoniae* DNA was detected in 80-90% of AMs and 15-30% of AECs showing the morphologic characteristics of type II cells 24 h after stimulation. However, bronchial epithelial cells (BECs) were only sporadically infected (<1%) (Fig. 5).

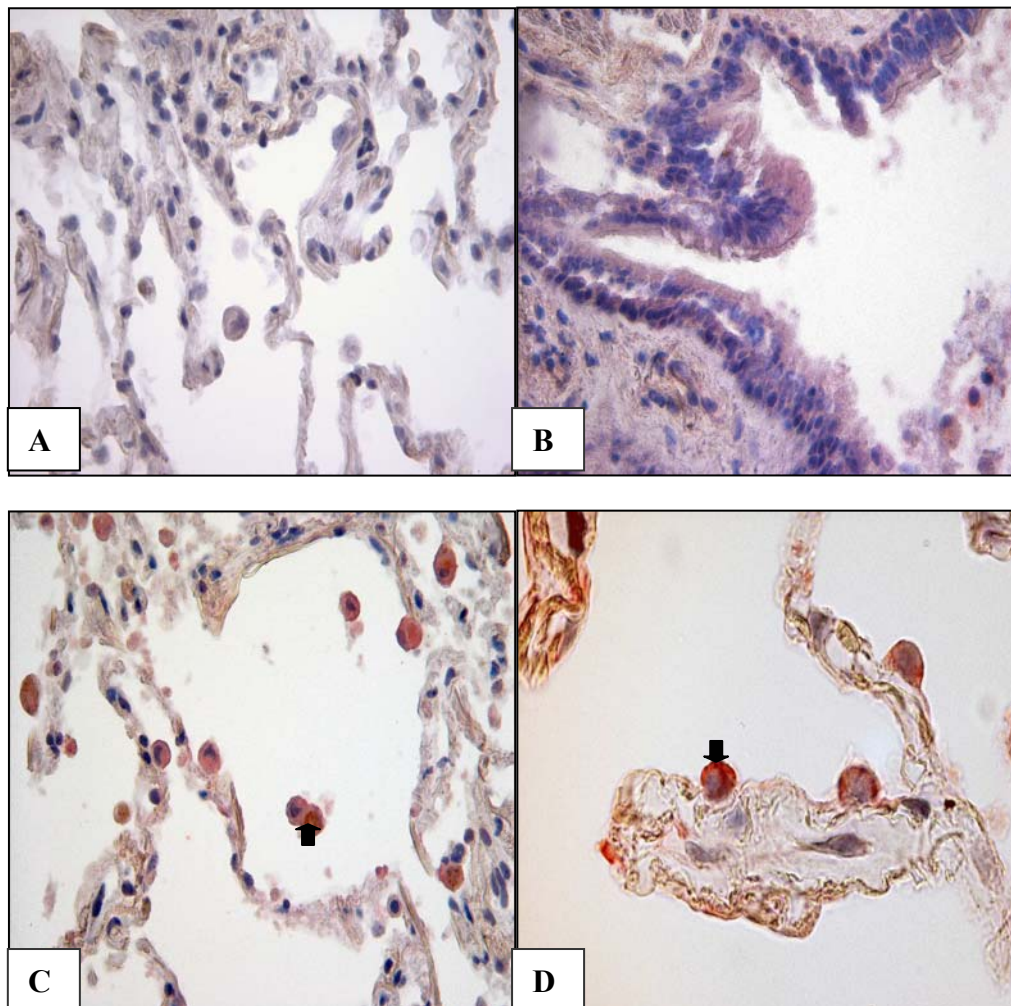


Fig. 5: ISH analysis of *S. pneumoniae* DNA in ASIM 24 h after stimulation. The human lung tissue without stimulation was used as a negative control (A: 400 x). Pneumococcal infection was sporadically found in BECs (B: 400 x). The presence of *S. pneumoniae* DNA was observed to be mainly located in AMs (C; 400 x, arrow) and AECs type II (D; 1000 x, arrow) in infected lung tissue 24 h after stimulation (n=26)

3.2 Macrophage depletion resulted in decreased inflammation in the ASIM

As shown in Methods 2.2.8, Clodronate/liposomes have the ability to deplete alveolar macrophages *in vitro*. In addition, neutrophils and epithelial cells cultured in the presence of Clodronate/liposomes were not affected (Van Rooijen and Sanders, 1994; our unpublished results). The macrophage-depleted lung tissue model was created using Clodronate/liposomes method. In the present study, Clodronate/liposomes inhibited the release of inflammatory mediators (TNF- α , IL-8 and IL-6) from infected lung tissue in a time-dependent manner. 48 h Clodronate/liposomes pretreatment fully ablated TNF- α production in infected lung tissue (Fig. 6). These data indicate that Clodronate/liposomes treatment results in decreased inflammation by suppressing macrophages in the ASIM, given the fact that pulmonary macrophages, not epithelial cell and neutrophil granulocytes, are the main cellular source of TNF- α (Knapp et al., 2004).

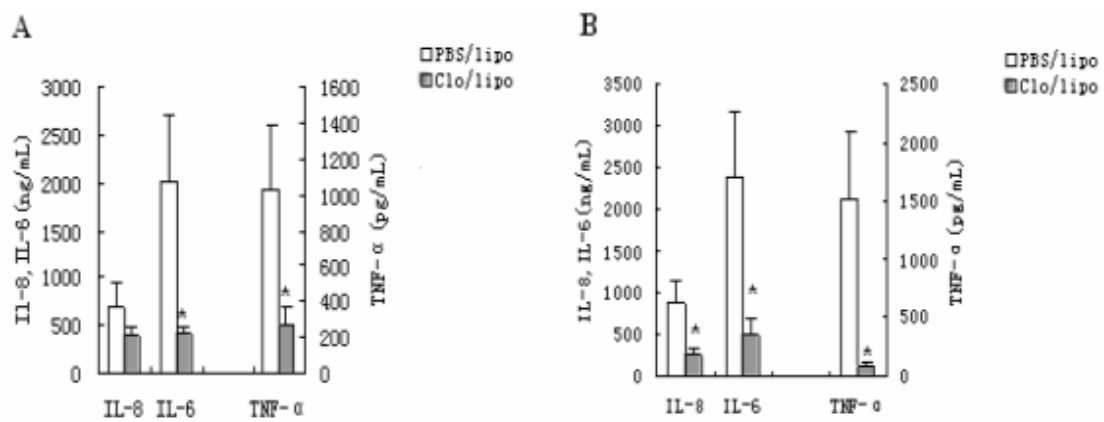


Fig. 6: Lung specimens were pretreated with PBS/liposomes or Clodronate/liposomes for 24 h (A, n=6) and 48h (B, n=5) respectively before 24 h *S. pneumoniae* infection. Clodronate/liposomes significantly inhibited the production of TNF- α , IL-8 and IL-6 in the ASIM in a time-dependent manner, suggesting macrophages hold an important role in the pulmonary inflammatory response. Especially, 48 h Clodronate/liposomes pretreatment fully ablated TNF- α production in infected lung tissue, indicating macrophage specificity of Clodronate/liposomes. PBS/lipo: PBS/liposomes; Clo/lipo: Clodronate/liposomes; Sp: *S. pneumoniae*. * $p < 0.05$ vs PBS/lipo-pretreated, Sp infected tissue.

3.3 RT-PCR analysis of TLR2 and TLR4 mRNA in the ASIM

Compared to non-infected lung specimens, *S. pneumoniae* stimulation resulted in a 2.9-fold increase in TLR2 mRNA expression 24 h postinfection. Similarly, there was a 2.7-fold increase in the expression of TLR4 mRNA in response to pneumococcal stimulation (Fig.7). These data indicate that TLR2 and TLR4 are both involved in the activation of lung cells in the ASIM upon pneumococcal infection.

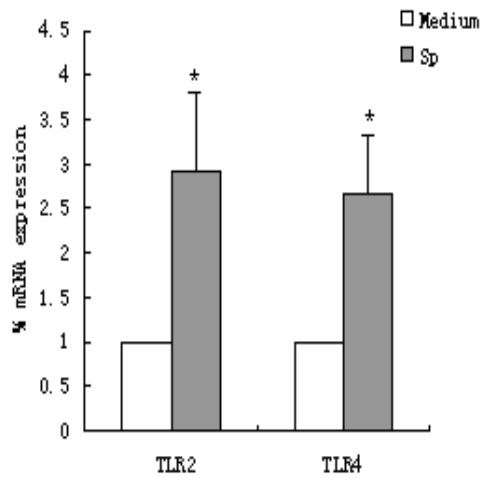


Fig. 7: Significantly enhanced TLR2 and TLR4 mRNA expression was detected by RT-PCR in lung tissue 24 h after pneumococcal infection (n=11). Sp: *S. pneumoniae*. * $p < 0.05$ vs medium-treated tissue.

3.4 Immunoblot assay of phosphorylation of p38 and p44/42 MAPKs in the ASIM and host cells

Activation of p38 MAPK is considered to participate in the regulation of pro-inflammatory cytokine expression. The significantly enhanced phosphorylation of p38 MAPK in lung tissue 4–24 h postinfection with pneumococci was observed in contrast to unchanged phospho-p44/42 expression. However, for all cell culture experiments, phosphorylation of the p38 and p44/42 MAPK was rapidly induced within 15-30 min after pneumococcal stimulation (Fig.8), suggesting that both p38 and p44/42 MAPK signalings are involved in the host cell activation upon pneumococcal infection.

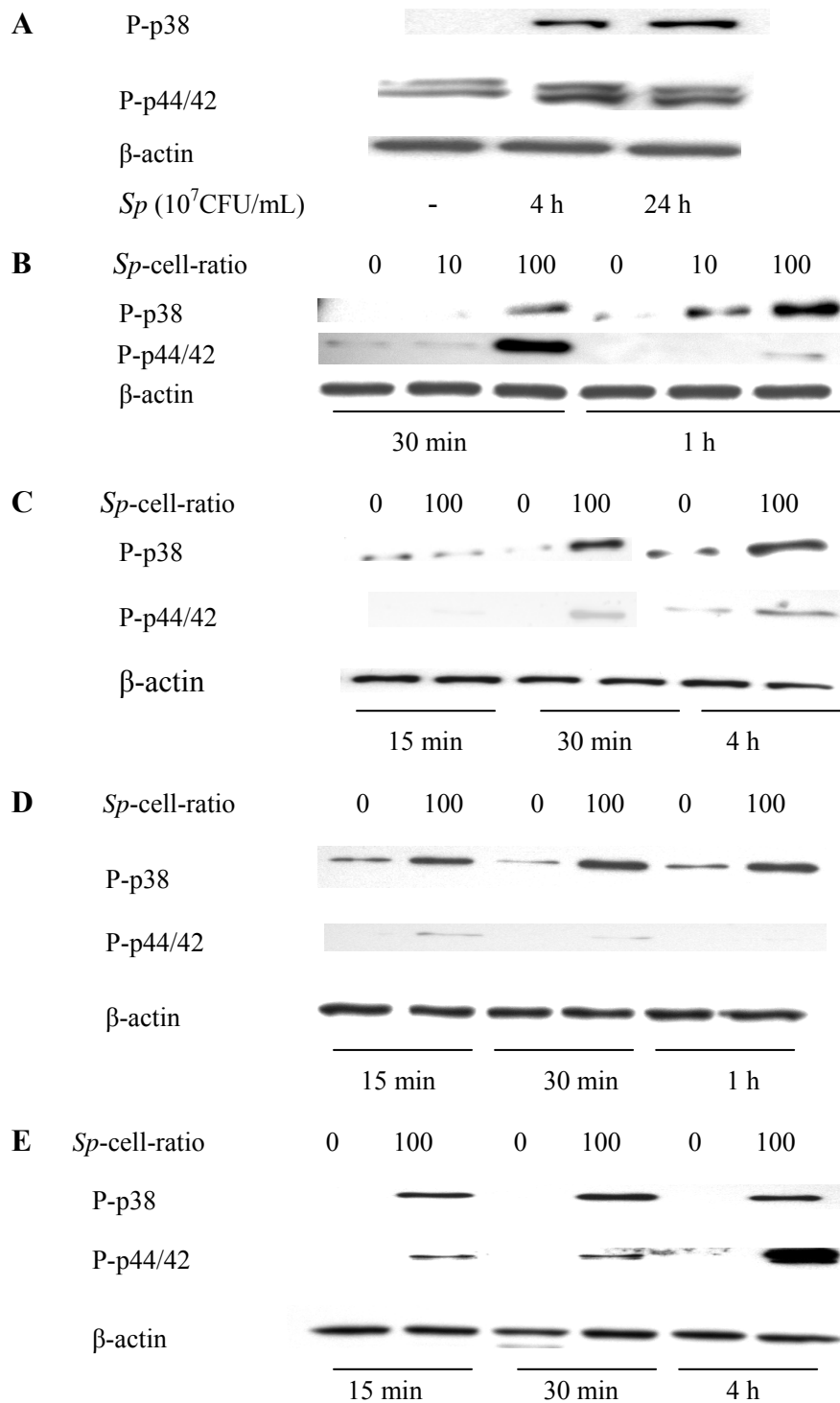


Fig.8: Immunoblot analysis of p38 and p44/42 MAPKs in the lung tissue and cells. The enhanced phosphorylation of p38 MAPK 4-24 h postinfection with pneumococci was observed in the ASIM (A). The expression of phospho-p38 and phospho-p44/42 was rapidly induced by *S. pneumoniae* 15-30 min postinfection in A549 cells (B), alveolar macrophages (C), blood monocytes (D) and PMNs (E), indicating that both p38 and p44/42 MAPKs are involved in host cell activation upon pneumococcal stimulation. Representative gels from each three independent experiments are shown as above. *Sp*: *S. pneumoniae*.

3.5 *S. pneumoniae* induced a time-dependent inflammatory response and the modulation of inflammation in the ASIM and host cells

S. pneumoniae (10^7 CFU/mL) induced a time-dependent inflammatory response within 24 h stimulation in the ASIM (Fig. 9). In order to further investigate the roles of TLR2, TLR4 and the p38, p44/42 MAPK pathways in the pulmonary inflammation, functional TLR2, 4 monoclonal antibodies, SB203580 (the p38 inhibitor) and UO126 (the p44/42 inhibitor), were adopted to block inflammatory cytokine production in the ASIM. ELISA data showed that infection of lung specimens with *S. pneumoniae* markedly enhanced the release of inflammatory cytokines after 24 h stimulation. TLR2 blockade reduced IL-8, TNF- α , and IL-6 production by 12.5 %, 29.8 %, and 23.0 % respectively without reaching statistical significance while blocking of TLR4 appeared to have no effect on pulmonary inflammatory response (Fig. 10A). Inhibition of p38 MAPK signaling by SB203580 significantly reduced inflammatory cytokine (IL-8, TNF- α , and IL-6) release from human lung tissues whereas blockade of p44/42 only inhibited the production of TNF- α , but not IL-8 and IL-6, in the ASIM (Fig. 10B).

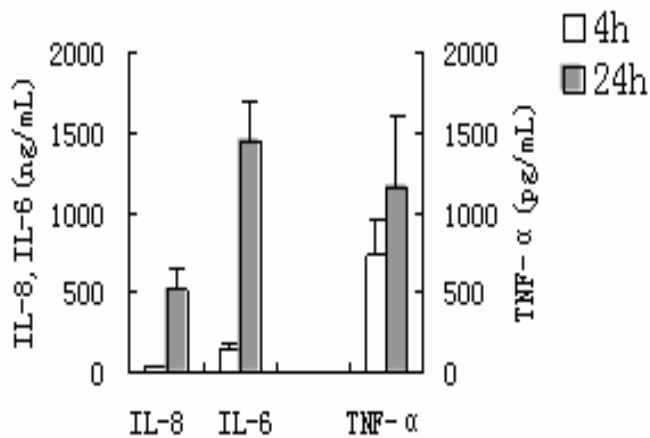


Fig. 9: *S. pneumoniae* (10^7 CFU/mL) induced a time-dependent inflammatory response within 24 h stimulation in the ASIM (n=8).

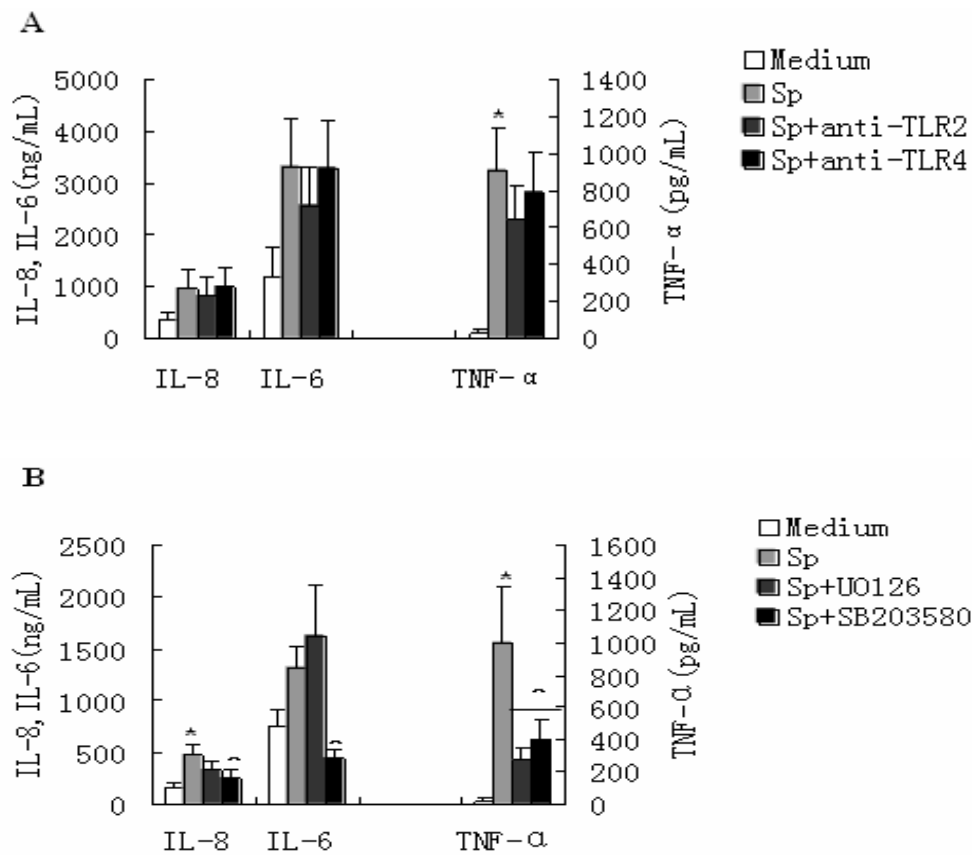


Fig. 10: The effect of anti-TLR2, 4 and MAPK inhibitors on inflammatory response in the ASIM. *S. pneumoniae* infection enhanced the release of inflammatory mediators such as IL-8, TNF- α and IL-6 from lung tissue after 24 h stimulation. Blockade of TLR2 generated a partially inhibitory effect on the production of IL-8, TNF- α , and IL-6 without reaching statistical significance whereas TLR4 blockade had no influence on pulmonary inflammation (A, n=5). The p38 MAPK inhibitor SB203580 markedly reduced the production of IL-8, TNF- α , IL-6 whereas blockade of p44/42 only inhibited the production of TNF- α , but not IL-8 and IL-6, in the ASIM (B, n=11). Sp: *S. pneumoniae*. * $p < 0.05$ vs medium-treated tissue, ^ $p < 0.05$ vs Sp-treated tissue.

In order to confirm our finding from the ASIM that p38 MAPK holds a predominant role in the regulation of pneumococci-related pulmonary inflammation, we further analyzed an alveolar epithelial cell line (A549 cells), alveolar macrophages and blood leukocytes as potential sources of inflammatory cytokines, given the fact that different lung cell types contributed differentially to the overall results obtained from lung tissue. The same downregulation in inflammation by p38 inhibitor SB203580 was observed in these cell culture models whereas the p44/42 inhibitor UO126 had no significant effect on the inflammatory response (Fig. 11). Taken together, these results demonstrate that SB203580 has a potential to downregulate pulmonary inflammation upon pneumococcal infection.

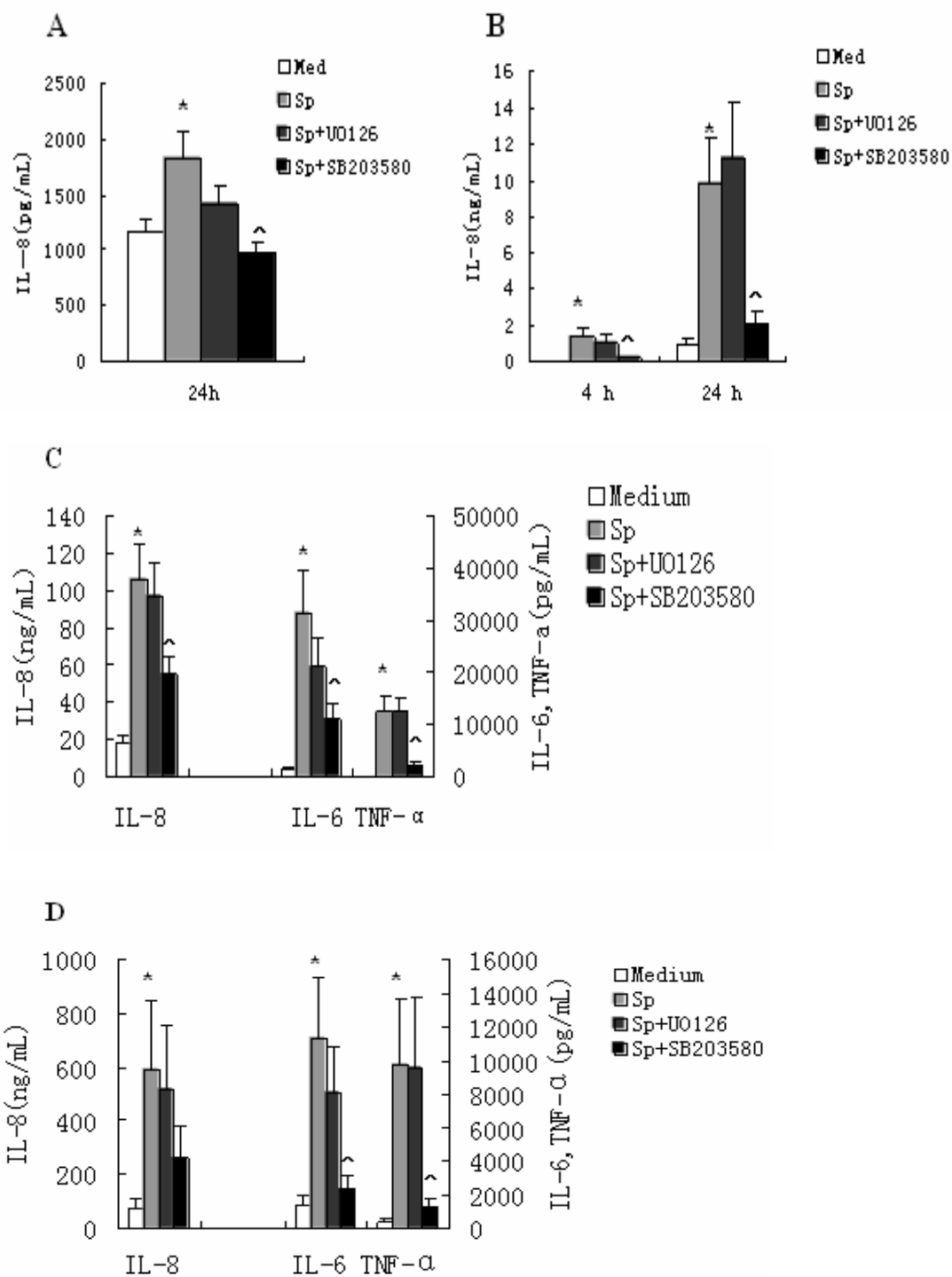


Fig. 11: The effect of p38 MAPK inhibitor on inflammatory response in different cell types. SB203580 significantly inhibits IL-8 release from A549 cells infected with *S. pneumoniae* (10 CFU/cell) (A, n=7) and PMNs stimulated with *S. pneumoniae* (100 CFU/cell) (B, n=6). The concentration of TNF- α in the supernatants of these two kinds of cells is undetectable. The proinflammatory cytokine expression was markedly suppressed by SB203580 in monocytes (C, n=7) and macrophages (D, n=8) infected with bacteria (100 CFU/cell) in contrast to UO126. Sp: *S. pneumoniae*. * $p < 0.05$ vs medium-treated cells, $\hat{p} < 0.05$ vs Sp-treated cells.

4. Discussion

S. pneumoniae is the most prevalent bacterial pathogen causing otitis media in children and community-acquired pneumonia in adults. Much of our knowledge about the pathogenesis of *S. pneumoniae* infection and pulmonary host defense is derived from animal studies on experimental pneumonia (Canvin et al., 1995; Rubins et al., 1995; Idanpaan-Heikkila et al., 1997; Kadioglu et al., 2000; Rijneveld et al., 2000; Wang et al., 2000; Dallaire et al., 2001; Gingles, et al., 2001; Kerr et al., 2002; Knapp et al., 2003; Dockwell et al., 2003; Knapp et al., 2004; Lysenko et al., 2005), whereas little is known about pathogen-cell interactions within the human pulmonary compartment. As lung tissue samples from patients with acute pneumococcal pneumonia are obviously not available we developed a novel model of acute *S. pneumoniae* infection to analyze the infection pattern and host cell response during acute infection, using vital lung specimens from patients undergoing lobectomy due to pulmonary nodules. This model was established according to a previously described model of short period stimulation of soft tissues (Olert et al., 2001; Goldmann et al., 2002). The tissue could be infected with pneumococci at least 48 h based on the results of LDH release. Recently, we had successfully used the same protocol to establish *in vitro* infection models with *Chlamydia pneumoniae* and nontypeable *Haemophilus influenzae* in human lung tissue (Rupp et al., 2004; Xu et al. 2005). Lung specimens after infection were treated with the recently developed HOPE-fixative, which provides an excellent preservation of proteins and antigenic structures for differential analysis by immunohistochemistry and Western blot (Goldmann et al., 2002). In addition, the most remarkable feature of HOPE is the extremely low degradation of nucleic acids leading to good results obtained by *in situ* hybridization (Olert et al., 2001; Uhlig et al., 2004).

The target cells within the lung in acute pneumococcal infection have not been well documented although they are crucial to the implicated pathology. Using various cell culture models, human pharyngeal epithelial cells, BECs, AECs type II and vascular endothelial cells have been proved as target cells for *S. pneumoniae* (Andersson et al.,

1983; Cundell and Tuomanen; 1994; Cundell et al., 1995; Cundell et al., 1996; Adamou et al., 1998; N'Guessan et al., 2005). Hament et al demonstrated that pneumococci are able to adhere to human erythrocytes by which way the bacteria are transported to the reticulo-endothelial system in the spleen (Hament et al., 2003). In the present study, ISH analysis showed that *S. pneumoniae* was found to be mainly located in AMs (80-90%) and AECs II (15-30%) 24 h after infection. This indicates that AMs and AECs might be the most important host cells in primary pneumococcal infection. Surprisingly, only few BECs were infected in the ASIM. In contrast to a tumor-derived alveolar cell line (A549) and a simian virus 40-transformed bronchial epithelial cell line (BEAS-2B) (Lieber et al., 1976; Reddel et al., 1988), the infection pattern of primary lung cells more directly reflects the complex interactions between pneumococci and airway epithelia in our tissue model. An investigation from Schulz et al demonstrated that there are some differences in the activation and cytokine release of BECs and AECs type II stimulated with LPS (Schulz et al., 2002). We hypothesize that the differences of infection rates between AECs and BECs may be due to their distinct characteristics with respect to pneumococcal adherence and invasion. Indeed, unlike other respiratory pathogens such as *Haemophilus influenzae* which initiate infection in the nasopharynx and often descend into the bronchi causing bronchitis, pneumococci do not typically cause bronchial infections although they have been reported to be associated with a few cases of exacerbated chronic bronchitis (Cole 1987; Adamou et al., 1998). The primary site of colonization for pneumococci is the nasopharynx and bronchial cells may serve as transient sites for pneumococcal attachment when the pathogens pass from the nasopharynx to the lower respiratory tract (Adamou et al., 1998). Even a few investigators thought that pneumococci cannot adhere to the ciliated epithelia of the tracheo-bronchial tree (McCullers and Tuomanen, 2001).

There are increasing data showing that airway epithelia prevent colonization and invasion of *S. pneumoniae* by releasing innate antimicrobial molecules such as proinflammatory cytokines, antimicrobial peptides, neutrophil elastase, and reactive oxygen intermediates. Once an organism evades host mucociliary clearance, it must adapt to the milieu, compete for iron, and avoid professional phagocytic cells and complement (Sadikot et al., 2005).

Talbot et al demonstrated the capacity of *S. pneumoniae* to invade A549 cells. The bacteria in AECs could be protected from professional phagocytes and shielded themselves from antibiotics (Talbot et al, 1996). The uptake by epithelial cells may be helpful for *in vivo* survival of pneumococci at least in the short period. The clinical importance of this phenomenon deserves further investigations.

S. pneumoniae has been shown to induce the apoptosis of human monocytes/macrophages and neutrophil granulocytes (Zysk et al., 2000; Ali et al., 2003; Dockrell et al., 2003). Recent studies demonstrated that pneumococci caused apoptosis in lung epithelial cells in a caspase 6-dependent manner and endothelial cells in a p38 MAPK and JNK-mediated caspase-dependent way (Schmeck et al., 2004b, N'Guessan et al., 2005). These results are in line with a marked upregulation of caspase 3, a key effector protease, in A549 cells, monocytes and PMNs after 20 h of pneumococcal stimulation found in our experiments (data not shown). In addition, LDH data in the present study demonstrated that *S. pneumoniae* (encapsulated strain ATCC 6303) stimulation resulted in time-dependent necrosis of lung cells within at least 48 h in the tissue model. Similarly, Schmeck et al reported that an encapsulated pneumococcal strain caused a massive LDH release in AECs and BECs whereas unencapsulated pneumococci only induced apoptosis (Schmeck et al., 2004b). A study by Zysk et al. showed that viable wild-type pneumococci induced PMN necrosis whereas heat-inactivated bacteria caused apoptosis (Zysk et al., 2000). These results indicate that the switch from apoptosis to necrosis depends on the intensity of the stimulus. Among pneumococcal products, the cytotoxin pneumolysin and H₂O₂ have been well illustrated to contribute to apoptosis and/or necrosis in lung epithelial cells, monocytes and brain neuronal cells (Zysk et al., 2000; Braun et al., 2002; Schmeck et al., 2004b). Pneumococcus-related apoptosis and necrosis of lung cells seem to hold important roles in pneumococcal pneumonia, which needs further elucidation.

Taken together, a new ASIM was established to investigate pathogen-cell-interaction in the early stage of acute respiratory infections. Advantages of this model are listed as follows:
(1) As human beings, but not mice, are natural hosts for *S. pneumoniae*, our *in vitro* ASIM

provides a novel tool to investigate interactions between *S. pneumoniae* and lung host cells in the phase of acute infection, and allows us to modify environmental factors within the pulmonary compartment. (2) HOPE-fixative has been adopted in the preservation and treatment of lung specimens. It facilitates the analysis of genomic and proteomic structures of bacteria and human host cells, and provides a novel tool in the detection of respiratory pathogens in human lung tissue. (3) The protocol for establishing the ASIM is applicable to investigate respiratory pathogens other than *S. pneumoniae*. Indeed, *in vitro*-infection models with *Chlamydia pneumoniae* and nontypeable *Haemophilus influenzae* in human lung tissue were developed to investigate infection pattern (acute versus chronic infections in human lungs), surface marker expression of target cells, and inflammation modulation in our research group. (Rupp et al., 2004; Xu et al. 2005).

At the same time, some limitations in our ASIM deserve consideration. Firstly, as the *ex vivo* infected lung tissues do not remain vital for a prolonged period, we are not able to analyze the interaction between host cells and respiratory microorganisms in a subacute phase of infection using this model. In addition, the host immune response to pneumococcal pneumonia has usually been characterized as an intense inflammatory reaction, initially implicating resident AMs followed by a massive neutrophil influx into the pulmonary compartment (Kadioglu and Andrew, 2004). Unfortunately, the contribution of neutrophils to the immune response in primary *S. pneumoniae* infection cannot be investigated properly in this ASIM.

Macrophages play an essential role in pulmonary host defense. They generate antimicrobial molecules, secrete cytokines, present antigens and phagocytize foreign materials, hence contributing to specific and nonspecific immune response to combat invading microorganisms (Underhill and Ozinsky, 2002). However, the exact role of AMs in host defense against pneumococci is unclear (Dockrell et al., 2003). The infection pattern in the ASIM showed a high infection rate of AMs, indicating that AMs are the most important early immune cells and target cells upon *S. pneumoniae* infection. Clodronate is

a bisphosphonate used for treatment of osteolytic bone diseases. However, phagocytic cells are killed by Clodronate through apoptosis, once the drug is delivered into phagocytic cells using liposomes as vehicles. Until now, Clodronate/liposomes have been proved to efficiently deplete AMs if they are adequately administered in a group of animal models of lung infections. (Van Rooijen and Sanders, 1994; Broug-Holub et al., 1997; Kooguchi et al., 1998; Cheung et al., 2000; Leemans et al., 2001; Dockrell et al., 2003; Knapp et al., 2003). Much of our knowledge about the role of alveolar macrophages in the pathogenesis of pneumonia is originated from animal studies of experimental pneumonia. Pulmonary macrophages, but not epithelial cells and granulocytes, have been shown to be the main cellular source of TNF- α in a mouse model (Knapp et al., 2004). The data from our cell stimulation experiments also demonstrated that TNF- α release from PMNs and A549 cells stimulated with *S. pneumoniae* was undetectable compared to higher expression of TNF- α in monocytes/macrophages. In the present study, Clodronate/liposomes were proved to have the ability to deplete human alveolar macrophages *in vitro*. Furthermore, the release of inflammatory cytokines including TNF- α from lung tissue upon pneumococcal stimulation was significantly suppressed in the ASIM pretreated with Clodronate/liposomes for over 24 h. Especially, 48 h Clodronate/liposomes treatment fully abolished TNF- α production in the ASIM. Overproduction of TNF- α has been shown to contribute to the pathogenesis of acute inflammatory states. The selective inactivation of AMs by Clodronate/liposomes resulted in a significantly decreased release of TNF- α from the lung tissue model, proving that AMs are the main source of proinflammatory cytokine production in the human lungs and hold an indispensable role in the host innate immune response against respiratory pathogens. Interestingly, an investigation from Knapp et al showed that AMs have a protective anti-inflammatory role by eliminating apoptotic PMNs in a mouse model of pneumococcal infection. The disparate findings between Knapp et al and our study might be due to the different experimental systems (mouse model *in vivo* and human lung tissue *in vitro*); the involvement of PMNs; and the complex dual function of AMs which initiate inflammatory response and recruit PMNs to alveolar space on the onset of pulmonary inflammation, and contribute to the resolution of inflammation in the final stage of inflammation.

The acute inflammatory response is a cornerstone in the innate immune response to infection. The identification of TLR family and illustration of their signal pathways provide insight as to how the airways respond to bacterial pathogens (Qureshi and Medzhitov, 2003; Koehler et al., 2004). However, knowledge of the role of TLR2 and TLR4 in host defense against respiratory tract pathogens is limited. Although some evidence from animal models showed that TLR2 is the predominant receptor involved in host immune response to *S. pneumoniae* and its cell wall components such as LTA and PGN (Yoshimura et al., 1999; Schwandner et al., 1999; Opitz et al., 2001; Schroder et al., 2003), to our knowledge, there are no definitive data confirming these observations in human lungs. TLR2 and TLR4 are constitutively expressed and are functional on alveolar macrophages and airway epithelia, indicating that they hold important roles in lung innate immune response against microorganisms. In the present study, we determined the role of TLR2, 4 and their downstream p38 and p44/42 MAPK signaling pathways in the innate immune response to *S. pneumoniae* in the novel ASIM. We found an upregulated expression of TLR2 and TLR4 mRNA in the lung tissue, followed by upregulated release of inflammatory mediators such as IL-8, IL-6 and TNF- α after pneumococcal infection. In addition, enhanced TLR2 expression on the surface of monocytes and neutrophils was observed compared to unaltered TLR4 expression after *S. pneumoniae* infection (Data not shown). In the study by Yoshimura et al, the activation of Chinese hamster ovary fibroblast cells expressing human TLR2 but not TLR4 was observed to be induced by heat-killed *S. pneumoniae* (Yoshimura et al., 1999). A recent report demonstrated that the isolated AMs from TLR2^{-/-} mice failed to release TNF- α and keratinocyte chemoattractant upon stimulation with heat-killed *S. pneumoniae* compared to wild-type AMs, suggesting that TLR2 is indispensable for alveolar macrophage responsiveness toward pneumococci and plays an important role in the induction of lung inflammatory response (Koedel et al., 2003). To delineate the roles of TLR2 and TLR4 in pathogen induced inflammation in human pulmonary compartment, we further performed blocking experiments using their monoclonal antibodies. TLR2 blockade showed a moderately decreased inflammation without reaching statistical difference compared to pathogen-infected lung tissue whereas TLR4 functional antibody had no effect on inflammatory response in our ASIM. This

phenomenon suggests that the inflammatory cytokine response in this model is only partly mediated via TLR2 and other PRRs beyond TLR2 signaling through MyD88 are involved in host defense against Gram-positive bacteria. Indeed, MyD88^{-/-}, but not TLR2^{-/-}, mice were markedly defective in their induction of multiple splenic proinflammatory cytokine- and chemokine-specific mRNAs after intraperitoneal challenge with heat-killed *S. pneumoniae* (Khan et al., 2005). Similar results were reported by Takeuchi et al who found that the production of TNF- α and IL-6 by peritoneal macrophages in response to heat-killed *S. aureus* was completely absent in MyD88^{-/-} mice and only reduced in TLR2^{-/-} macrophages, indicating a more definitive proinflammatory signaling defect conferred by MyD88 deficiency (Takeuchi, et al., 2000a).

p38 MAPK is a key element in inflammatory response by regulating the production of proinflammatory cytokines, and modulating inflammation-related intracellular enzymes and adhesion molecules (Perregaux et al., 1995; Pietersma et al., 1997; Guan et al., 1998; Rupp et al., 2004; N'Guessan et al., 2006). But little is known of the role of p38 pathways in *S. pneumoniae*-induced human cell and tissue responses. A study by Monier et al. illustrated that p38 MAPK is a key signaling pathway in the upregulation of iNOS and TNF expression in murine macrophages stimulated with antibiotic-killed pneumococci and pneumococcal cell wall preparations (Monier et al., 2002). Schmeck et al reported that p38 MAPK was rapidly activated and phosphorylated in the lung of mice and human bronchial epithelial cell line BEAS-2B when exposed to *S. pneumoniae*. Pneumococci activated NF- κ B-dependent gene transcription in HEK293 cells and induced IL-8 and GM-CSF expression in BEAS-2B cells via p38 MAPK signaling pathway (Schmeck et al., 2004a). A recent investigation showed that pneumococci induced Cox-2 expression and subsequent prostaglandin E₂ (PGE₂) synthesis via p38 MAPK and NF- κ B in lung epithelial cells. Furthermore, the recruitment of NF- κ B subunit p65 to the Cox-2 promoter depended on p38 activation (N'Guessan et al., 2006). Our data showed that phosphorylation and upregulation of p38 MAPK in the ASIM was detectable after 4 h infection and increased up to 24 h in contrast to unstimulated normal lung tissue. We also found that phospho-p38 and phospho-p44/42 MAPKs were rapidly increased in *in vitro* cell models such as blood

leucocytes, resident macrophages and A549 cells within 15-30 min upon stimulation and persisted to 1 h or 4 h respectively, suggesting that both p38 and p44/42 signaling pathways are implicated in pneumococci-related lung cell activation. The blockade of p38 MAPK using SB203580 markedly inhibited the release of proinflammatory cytokines such as IL-8, TNF- α , and IL-6 from lung tissue. The same downregulation of inflammation by the p38 inhibitor was proved in *in vitro* cell models. These results are in line with the finding from Schmeck et al that p38 MAPK plays an important role in pneumococci-induced inflammatory cytokines transcription by modulating p65 NF- κ B-mediated transactivation (Schmeck et al., 2004a). *In vivo* experiments deserve to be performed to verify the efficacy of p38 inhibitors which may aid in the identification of novel therapeutic intervention strategies to attenuate the pathology induced by pneumococcal infection. In addition, UO126, the p44/42 MAPK inhibitor, suppressed TNF- α production in the tissue model whereas it had no influence on the release of IL-8 and IL-6. But data from *ex vivo* cell models showed UO126 exerted no inhibitory effect on pneumococci-induced release of TNF- α , IL-8 and IL-6 from monocytes /macrophages. The reasons for the differential effects of UO126 on TNF- α production between the tissue and cell model are not clear. GM-CSF produced by tissue cells is increased in inflammation and participates in the inflammatory response by direct activation of leukocytes and resident macrophages at the local site of infection (Chung and Barnes, 1999). As p44/42 MAPK is rapidly phosphorylated and activated in response to stimulation with GM-CSF (Welham et al., 1992), we extrapolate that some cytokines such as GM-CSF released from airway epithelium upon *S. pneumoniae* are able to stimulate and strengthen p44/42 MAPK signaling in AMs within pulmonary compartment while there is no ample stimulation of these cytokines in the environment of *in vitro* AM culture.

TLRs and their downstream MAPK signalings have considerable implications with regard to innate immune responses and disease pathogenesis as central mediators. Identification of all relevant TLR ligands, combined with a comprehensive understanding of the pathways involved in pneumococcal induction of inflammation and their cross-talk could deepen our understanding of host-pathogen-interaction and lead to more specific agents to be used in

pneumococcal pneumonia. Inflammation is an important hallmark of pneumonia. Although appropriate inflammatory response is beneficial to bacterial clearance, inflammation itself can damage host cells that in turn stimulate inflammation if not properly mounted (Nathan, 2002). Uncontrolled host defenses and inflammatory responses have been shown to contribute to pulmonary disorders such as ARDS and systemic sepsis. For efficient control of airway inflammation, a fine balance between the need for clearance of the inflammatory stimulus and the risk of lung injury is important (Droemann et al., 2000). Modulating inflammation using drugs targeting multiple molecules or key inflammatory pathways could be effective, but this concept will need to be weighted against the risk of impairing the innate immune response (Koehler et al., 2004). Therefore, the combination of adjuvant immunotherapy that downregulates or upregulates inflammation as appropriate and conventional treatment with powerful antibiotics may provide an innovative way to treat severe bacterial pneumonia (Cazzola et al., 2005). In fact, the success from the use of dexamethasone to inhibit inflammatory response in the treatment of infants and children with bacterial meningitis has set a good example that intentionally downmodulating the host response during the early phase of antibiotic therapy has a beneficial effect on the outcome of infectious diseases (Lebel et al., 1988). Further studies on the mechanisms and pathways of lung inflammation will increase the understanding of respiratory physiology and pathology and potentially develop novel diagnostic markers and therapeutic strategies.

Summary

Streptococcus pneumoniae is the leading cause of community-acquired pneumonia. The lung plays an important role in initiating innate immune responses and clearing microbes. However, little is known concerning *S. pneumoniae*-host cell interactions within the human pulmonary compartment. Toll-like receptor (TLR) 2 is a key pattern recognition receptor for pneumococci-related cell activation. Mitogen-activated protein kinases (MAPKs) are involved in TLR-mediated signal transduction and contribute to nuclear factor- κ B transactivation and inflammatory cytokine expression. In the present study, we established a novel model of acute *S. pneumoniae* infection (ASIM) in vital lung specimens from pulmonary lobectomy. *In situ* hybridization analysis showed that *S. pneumoniae* DNA was detected in 80-90% alveolar macrophages and 15-30% of alveolar epithelial cells type II 24h after stimulation (n=26). The lung tissue depleted with Clodronate/liposomes exhibited a decreased TNF- α release upon pneumococcal infection. In addition, enhanced phosphorylation of p38 MAPK and increased TLR2 and 4 mRNA expression were observed in infected lung tissues using Western blot and RT-PCR. Inhibition of p38 MAPK significantly reduced inflammatory cytokine release from lung tissue in contrast to TLR2 and TLR4 blockade. To confirm findings from the ASIM, we further analyzed lung epithelial cells, alveolar macrophages and blood leukocytes as potential sources of inflammatory cytokines and demonstrated that p38 MAPK is a key element in the inflammatory response to intact pneumococci.

Altogether, alveolar macrophages are the important host cells in the human ASIM and are the main source of proinflammatory cytokine release. TLR2 appears to be implicated in cell activation although blockade of TLR2 only elicits a slight decrease of inflammatory response. P38 MAPK holds a major role in the pneumococci-induced pulmonary inflammation and could become a potential molecular target to modulate lung inflammation.

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